Supplemental Table 6. Gene ontology terms for contrasts of all sample groups.

category	over_represented_pvalue	under_represented_pvalue	numDEInCat	numInCat	term	ontology	p.adjust	EnsemblID	vessel
GO:0051276	4.52E-18	1	88	398	chromosome organization	BP	1.46E-14	HMGB1,MCM6,SREBF1,MCM4,POLE3,MCM7,RPA1,NCAPD2,ATAD2,HMGA1,HNRNPD,SMC1A,ZW10,ENSCAFG00000016482,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,CENPN,TOP3A,TRIP13,SGO1,GINS4,FBXO5,RAN,BIRC5,PRMT1,CDK1,RAD51,AURKB,DSN1,EZH2,CENPO,NCAPD3,NEK2,FBL,FEN1,SMARCC1,HMGB3,KIF22,UHRF1,CDCA8,CENPH,NCAPH,BRCA1,CENPI,NOC2L,SMC2,ESPL1,CDC6,NDC80,OIP5,IPO4,HIST1H1A,NUP62,SUV39H1,HASPIN,HMGB2,DMAP1,HIST1H2BB,SMC3,SMARCB1,CCNA2,ENSCAFG00000005299,SMC6,BUB1,RBM14,CENPW,CDC20,TTK,BAP1,SGO2,CENPP,GRWD1,SUPT16H,TADA2A,HAT1,HIST2H2AC,TINF2,H2AFX,UBE2C,MIS18A,HMGN1,CCT4,H3F3B,ZWINT,GEN1	down_ACOR_VSMC
GO:1903047	2.3E-17	1	66	257	mitotic cell cycle process	BP	3.71E-14	NCAPD2,ANLN,SMC1A,HINFP,UBE2S,ZW10,SMC4,CENPA,ENSCAFG00000017264,TRIP13,SGO1,POLE,FBXO5,RAN,BIRC5,CDK1,RAD51,CASP2,FANCI,AURKB,CDKN2C,TOPBP1,DSN1,EZH2,STMN1,NCAPD3,MAP3K20,NEK2,CDK4,RNASEH2B,PLK3,RCC1,KIF22,CKS2,CDCA8,NCAPH,POC1A,WDR62,SMC2,ESPL1,SPC25,CDC6,NDC80,NUP62,DTL,PDXP,HASPIN,REEP4,SMC3,CDK2,CCNA2,RAB35,STAG1,ENSCAFG00000005299,RBBP8,CLSPN,BUB1,CDC20,TTK,KIF11,CCNB3,UBE2C,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0022402	4.81E-17	1	87	407	cell cycle process	BP	7.06E-14	NCAPD2,ANLN,SMC1A,HINFP,UBE2S,ZW10,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,PPM1G,TRIP13,SGO1,POLE,FBXO5,RAN,PSMD13,BIRC5,CDK1,RAD51,CASP2,FANCI,TIMELESS,AURKB,CDKN2C,TOPBP1,DSN1,EZH2,STMN1,HAUS8,NCAPD3,MAP3K20,NEK2,FEN1,CDK4,MND1,RNASEH2B,PLK3,RCC1,KIF22,CKS2,GMNN,CDCA8,NCAPH,POC1A,BRCA1,WDR62,E2F8,SMC2,ESPL1,SPC25,CDC6,NDC80,NUP62,DTL,PDXP,PRR11,PLK4,HASPIN,REEP4,SMC3,CDK2,CCNA2,RAB35,STAG1,ENSCAFG00000005299,RBBP8,EZR,CLSPN,SASS6,BUB1,RBM14,CDC20,TTK,ASPM,SGO2,KNL1,CDC25A,KIF11,GLI1,CCNB3,UBE2C,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0007059	2.55E-16	1	43	127	chromosome segregation	BP	3.43E-13	NCAPD2,SMC1A,ZW10,SMC4,ENSCAFG00000017264,NDC1,CENPN,TRIP13,SGO1,FBXO5,RAN,BIRC5,AURKB,DSN1,NCAPD3,NEK2,FEN1,RCC1,KIF22,CDCA8,NCAPH,SMC2,ESPL1,SPC25,CDC6,NDC80,OIP5,NUP62,HASPIN,SMC3,ENSCAFG00000005299,SMC6,BUB1,CENPW,CDC20,TTK,SGO2,KNL1,KIF11,UBE2C,MIS18A,ZWINT,GEN1	down_ACOR_VSMC
GO:0007049	3.57E-16	1	105	560	cell cycle	BP	4.44E-13	MCM7,NCAPD2,ANLN,SMC1A,HINFP,UBE2S,WDR76,ZW10,INTS7,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,PPM1G,TRIP13,SGO1,POLE,FBXO5,RAN,PSMD13,BIRC5,CDK1,RAD51,CASP2,FANCI,TIMELESS,NF2,AURKB,CDKN2C,TOPBP1,DSN1,EZH2,STMN1,HAUS8,NCAPD3,MAP3K20,NEK2,CLIC1,CDCA3,FEN1,CDK4,TRIM35,MND1,RNASEH2B,PLK3,RCC1,KIF22,CKS2,GMNN,CDCA8,NCAPH,POC1A,BRCA1,WDR62,E2F8,SMC2,ESPL1,SPC25,CDC6,NDC80,NUP62,DTL,PDXP,PRR11,PLK4,IQGAP1,HASPIN,REEP4,SMC3,CDK2,DDX39B,ENSCAFG00000030087,CCNA2,RAB35,STAG1,ENSCAFG00000005299,RBBP8,EZR,CLSPN,SASS6,BUB1,RBM14,RAD23A,CENPW,PHACTR4,CDC20,TTK,BAP1,ASPM,SGO2,ARHGEF2,KNL1,CDC25A,KIF11,TADA2A,GLI1,H2AFX,ATRIP,CCNB3,UBE2C,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC

GO:0000280	1.19E-14	1	44	145	nuclear division	BP	1.07E-11	NCAPD2,SMC1A,UBE2S,ZW10,SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,RAN,PSMD13,BIRC5,RAD51,AURKB,DSN1,NCAPD3,NEK2,MND1,RCC1,KIF22,CKS2,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,PDXP,HASPIN,SMC3,STAG1,ENSCAFG00000005299,BUB1,CDC20,TTK,ASPM,SGO2,KIF11,UBE2C,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0000819	2.34E-14	1	33	87	sister chromatid segregation	BP	1.99E-11	NCAPD2,SMC1A,ZW10,SMC4,ENSCAFG00000017264,TRIP13,SGO1,FBXO5,RAN,BIRC5,AURKB,DSN1,NCAPD3,NEK2,FEN1,KIF22,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,HASPIN,SMC3,ENSCAFG00000005299,BUB1,CDC20,TTK,SGO2,UBE2C,ZWINT,GEN1	down_ACOR_VSMC
GO:0006259	2.53E-14	1	75	354	DNA metabolic process	BP	2.04E-11	HMGB1,MCM6,MCM4,USP1,MCM7,RPA1,HMGA1,HNRNPD,MCM3,SMC1A,HINFP,RRM1,POLA1,SLC29A1,TOP3A,TRIP13,PARPBP,POLA2,GINS4,RAD54L,POLE,UBE2T,RFC2,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,TIMELESS,FAM129B,AURKB,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,MND1,PCNA,TONSL,MCM10,UHRF1,GMNN,BRCA1,E2F8,TFRC,CDC6,POLH,NEIL3,DTL,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,RBBP8,SMC6,RBM17,RAD23A,CDC45,SMARCAL1,GRWD1,AIFM1,GLI1,TINF2,H2AFX,NUDT1,EXOSC5,MIS18A,HMGN1,APEX1,CCT4,GEN1	down_ACOR_VSMC
GO:0000278	3.82E-14	1	71	331	mitotic cell cycle	BP	2.93E-11	NCAPD2,ANLN,SMC1A,HINFP,UBE2S,ZW10,SMC4,CENPA,ENSCAFG00000017264,TRIP13,SGO1,POLE,FBXO5,RAN,BIRC5,CDK1,RAD51,CASP2,FANCI,AURKB,CDKN2C,TOPBP1,DSN1,EZH2,STMN1,NCAPD3,MAP3K20,NEK2,CDK4,TRIM35,RNASEH2B,PLK3,RCC1,KIF22,CKS2,CDCA8,NCAPH,POC1A,WDR62,E2F8,SMC2,ESPL1,SPC25,CDC6,NDC80,NUP62,DTL,PDXP,IQGAP1,HASPIN,REEP4,SMC3,CDK2,CCNA2,RAB35,STAG1,ENSCAFG00000005299,RBBP8,CLSPN,BUB1,CENPW,CDC20,TTK,KIF11,TADA2A,CCNB3,UBE2C,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0140014	4.26E-14	1	37	110	mitotic nuclear division	BP	3.12E-11	NCAPD2,SMC1A,UBE2S,ZW10,SMC4,ENSCAFG00000017264,TRIP13,SGO1,FBXO5,RAN,BIRC5,AURKB,DSN1,NCAPD3,NEK2,RCC1,KIF22,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,PDXP,HASPIN,SMC3,STAG1,ENSCAFG00000005299,BUB1,CDC20,TTK,KIF11,UBE2C,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0000070	5.22E-14	1	30	75	mitotic sister chromatid segregation	BP	3.66E-11	NCAPD2,SMC1A,ZW10,SMC4,ENSCAFG00000017264,TRIP13,SGO1,FBXO5,RAN,BIRC5,AURKB,DSN1,NCAPD3,NEK2,KIF22,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,HASPIN,ENSCAFG00000005299,BUB1,CDC20,TTK,UBE2C,ZWINT,GEN1	down_ACOR_VSMC
GO:0098813	1.27E-13	1	35	102	nuclear chromosome segregation	BP	8.52E-11	NCAPD2,SMC1A,ZW10,SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,RAN,BIRC5,AURKB,DSN1,NCAPD3,NEK2,FEN1,KIF22,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,HASPIN,SMC3,ENSCAFG00000005299,BUB1,CDC20,TTK,SGO2,KNL1,UBE2C,ZWINT,GEN1	down_ACOR_VSMC
GO:0048285	1.95E-12	1	44	166	organelle fission	BP	1.12E-09	NCAPD2,SMC1A,UBE2S,ZW10,SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,RAN,PSMD13,BIRC5,RAD51,AURKB,DSN1,NCAPD3,NEK2,MND1,RCC1,KIF22,CKS2,CDCA8,NCAPH,SMC2,ESPL1,CDC6,NDC80,NUP62,PDXP,HASPIN,SMC3,STAG1,ENSCAFG00000005299,BUB1,CDC20,TTK,ASPM,SGO2,KIF11,UBE2C,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0006261	2.59E-12	1	27	68	DNA-dependent DNA replication	BP	1.4E-09	MCM6,MCM4,MCM7,MCM3,SMC1A,POLA1,POLA2,GINS4,POLE,RFC2,RFC5,RFC3,RAD51,TOPBP1,RFC4,FEN1,PCNA,TONSL,MCM10,GMNN,E2F8,CDC6,SMC3,CDK2,CDC45,SMARCAL1,GEN1	down_ACOR_VSMC
GO:0006260	6.05E-11	1	31	98	DNA replication	BP	3.15E-08	MCM6,MCM4,MCM7,RPA1,MCM3,SMC1A,RRM1,POLA1,POLA2,GINS4,POLE,RFC2,RFC5,RFC3,RAD51,TOPBP1,RFC4,FEN1,PCNA,TONSL,MCM10,GMNN,E2F8,CDC6,SMC3,CDK2,CDC45,SMARCAL1,GRWD1,GLI1,GEN1	down_ACOR_VSMC

GO:0051321	3.41E-10	1	23	61	meiotic cell cycle	BP	1.57E-07	NCAPD2,SMC1A,SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,PSMD13,CDK1,RAD51,DSN1,MND1,CKS2,NCAPH,SMC2,ESPL1,SMC3,CDC20,TTK,ASPM,SGO2,CCNB3	down_ACOR_VSMC
GO:0071103	6.32E-10	1	26	80	DNA conformation change	BP	2.83E-07	HMGB1,MCM6,MCM4,MCM7,NCAPD2,HMGA1,SMC4,CENPA,TOP3A,GINS4,RAD51,NCAPD3,HMGB3,NCAPH,NOC2L,SMC2,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,CENPP,GRWD1,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:2000145	1.92E-09	1	54	279	regulation of cell motility	BP	0.0000105	PLK2,TEK,SELP,PRCP,CXCL8,DOCK4,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,MEF2C,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,HMGB1,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0051270	1.96E-09	1	56	296	regulation of cellular component movement	BP	0.0000105	PLK2,TEK,SELP,PRCP,CXCL8,DOCK4,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,PDE4D,MEF2C,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,STMN1,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,HMGB1,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0071459	2.19E-09	1	9	10	protein localization to chromosome,	BP	8.83E-07	ZW10,CENPA,CDK1,AURKB,NDC80,HASPIN,TTK,KNL1,MTBP	down_ACOR_VSMC
GO:0006974	2.86E-09	1	61	333	cellular response to DNA damage stimulus	BP	0.00000112	HMGB1,USP1,MCM7,RPA1,DDX39A,CBX5,HMGA1,SMC1A,HINFP,NEDD4,WDR76,INTS7,MNDA,POLA1,TRIP13,PARPBP,GINS4,RAD54L,POLE,UBE2T,RFC2,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,FANCD2,TIMELESS,TOPBP1,MAP3K20,RFC4,FEN1,MND1,RNASEH2B,PLK3,PCNA,TONSL,MCM10,BRCA1,POLH,NEIL3,DTL,SUV39H1,DMAP1,SMARCB1,DDX39B,ENSCAFG00000030087,RBBP8,CLSPN,SMC6,RBM17,RAD23A,SMARCAL1,H2AFX,CDC5L,ATRIP,NUDT1,HMGN1,APEX1,GEN1	down_ACOR_VSMC
GO:0023052	2.92E-09	1	191	1602	signaling	BP	0.0000106	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,TEK,RASGRP3,HCLS1,PCDH12,IL7R,NPR1,ADGRF5,SELP,RGS16,KIT,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,TNFAIP3,ADGRL2,MAP3K11,TNIP1,LRRC8D,AMOT,PDGFB,STK10,SH2D3C,BAIAP2L1,TSPAN8,RELN,FGD6,KDR,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,TSPAN15,EIF2B2,GATA3,EDN1,RALB,APLNR,ARAP3,SMAD1,NTN4,SNCAIP,HOMER3,IGSF3,ARHGAP28,PIK3C2A,EGFL7,FIGNL1,PELI1,PPP3CA,RAPGEF3,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,SNAP23,LRRC8C,PDE7B,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,HHEX,SPNS3,CHN2,CAV2,PREX2,SLC12A7,SLK,BMP2K,SH3BP5,RALBP1,PDZD8,GNG11,ARHGAP29,DOCK6,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNGR1,RIOK3,ANGPT2,ARHGEF12,IQGAP2,ENSCAFG00000010224,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,TSPAN12,RAP1A,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,TSPAN9,NCK1,KCNJ2,OTUD4,WSB1,NET1,FES,JAG1,PITPNM2,GUCY1B1,GRM8,PTGS2,RAPGEF2,PLCG2,CTDSPL2,CREB1,BCL10	up_VCAV_EC
GO:0030334	3.28E-09	1	52	267	regulation of cell migration	BP	0.0000106	PLK2,TEK,SELP,PRCP,CXCL8,DOCK4,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,MEF2C,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,JAG1,RAPGEF2,HMGB1,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC

GO:0016477	4.94E-09	1	71	426	cell migration	BP	0.0000133	EPHB1,PLK2,EDNRB,TEK,SELP,KIT,SELE,PRCP,CXCL8,DOCK4,CLEC14A,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,SOX18,PIK3C2A,PPP3CA,EPHB4,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,ELMO1,PAK2,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,FMNL3,PRAG1,HMGB1,ARPC5L,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,TNFAIP1,PTP4A1,JCAD,ARHGEF2,FSCN1,FBXO5,ZNF609	up_VCAV_EC
GO:0051726	7.2E-09	1	67	393	regulation of cell cycle	BP	0.0000027	SMC1A,HINFP,WDR76,ZW10,INTS7,SLC29A1,PPM1G,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,NF2,AURKB,CDKN2C,TOPBP1,EZH2,MAP3K20,NEK2,CLIC1,FEN1,CDK4,TRIM35,RNASEH2B,PLK3,RCC1,CKS2,GMNN,POC1A,BRCA1,E2F8,CDC6,NDC80,NUP62,DTL,PDXP,PRR11,PLK4,IQGAP1,SMC3,CDK2,DDX39B,ENSCAFG00000030087,STAG1,ENSCAFG00000005299,CLSPN,BUB1,RBM14,RAD23A,PHACTR4,CDC20,TTK,BAP1,ASPM,CDC25A,KIF11,GLI1,H2AFX,CDC5L,ATRIP,CCNB3,UBE2C,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0045786	8.62E-09	1	42	195	negative regulation of cell cycle	BP	0.00000316	SMC1A,HINFP,WDR76,ZW10,INTS7,SLC29A1,PPM1G,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,AURKB,CDKN2C,TOPBP1,EZH2,MAP3K20,NEK2,CDK4,TRIM35,RNASEH2B,GMNN,BRCA1,E2F8,NDC80,DTL,PRR11,SMC3,DDX39B,ENSCAFG00000005299,CLSPN,BUB1,RBM14,TTK,H2AFX,CDC5L,ATRIP,CDKN3,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0007165	8.97E-09	1	179	1496	signal transduction	BP	0.0000194	GNGT2,ACKR1,EPHB1,EDNRB,TEK,RASGRP3,HCLS1,IL7R,NPR1,ADGRF5,SELP,RGS16,KIT,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,TNFAIP3,ADGRL2,MAP3K11,TNIP1,LRRC8D,AMOT,PDGFB,STK10,SH2D3C,BAIAP2L1,TSPAN8,RELN,FGD6,KDR,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,TSPAN15,EIF2B2,GATA3,EDN1,RALB,APLNR,ARAP3,SMAD1,HOMER3,IGSF3,ARHGAP28,PIK3C2A,EGFL7,FIGNL1,PELI1,PPP3CA,RAPGEF3,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,LRRC8C,PDE7B,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,HHEX,SPNS3,CHN2,CAV2,PREX2,SLK,BMP2K,SH3BP5,RALBP1,PDZD8,GNG11,ARHGAP29,DOCK6,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNGR1,RIOK3,ANGPT2,ARHGEF12,IQGAP2,ENSCAFG00000010224,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,TSPAN12,RAP1A,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,TSPAN9,NCK1,OTUD4,WSB1,NET1,FES,JAG1,PITPNM2,GUCY1B1,GRM8,PTGS2,RAPGEF2,PLCG2,CTDSPL2,BCL10,USP28,TAOK1,CTNNA1,CNOT7,RPS6KL1,ADIPOR2,HMGB1,NO	up_VCAV_EC
GO:0007264	9.61E-09	1	39	164	small GTPase mediated signal transduction	BP	0.0000194	RASGRP3,ARHGEF15,FGD5,DOCK4,AMOT,SH2D3C,RELN,FGD6,RAPGEF1,GPR4,RALB,ARAP3,RAPGEF3,PLEKHG1,CHN2,PREX2,RALBP1,DOCK6,ABCA1,ITPKB,NCKAP1,ARHGEF12,MADD,CTNNAL1,ELMO1,STMN1,RAP1A,PAK2,NET1,RAPGEF2,USP28,ENSCAFG00000024183,ARHGDIB,ARHGAP26,ALS2,TNFAIP1,RGL2,ARHGEF2,CDON	up_VCAV_EC
GO:0040012	1.28E-08	1	55	303	regulation of locomotion	BP	0.0000216	PLK2,TEK,SELP,PRCP,CXCL8,CXCR4,DOCK4,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,MEF2C,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,HMGB1,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC

GO:0007154	1.34E-08	1	190	1622	cell communication	BP	0.0000216	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,TEK,RASGRP3,HCLS1,PCDH12,IL7R,NPR1,ADGRF5,SELP,RGS16,KIT,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,TNFAIP3,ADGRL2,MAP3K11,TNIP1,LRRC8D,AMOT,PDGFB,STK10,SH2D3C,BAIAP2L1,TSPAN8,RELN,FGD6,KDR,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,TSPAN15,EIF2B2,GATA3,EDN1,RALB,APLNR,ARAP3,SMAD1,NTN4,SNCAIP,HOMER3,IGSF3,ARHGAP28,PIK3C2A,EGFL7,FIGNL1,PELI1,PPP3CA,RAPGEF3,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,SNAP23,LRRC8C,PDE7B,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,HHEX,SPNS3,CHN2,CAV2,PREX2,SLC12A7,SLK,BMP2K,SH3BP5,RALBP1,PDZD8,GNG11,ARHGAP29,DOCK6,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNGR1,RIOK3,ANGPT2,ARHGEF12,IQGAP2,ENSCAFG00000010224,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,TSPAN12,RAP1A,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,TSPAN9,NCK1,OTUD4,WSB1,NET1,FES,JAG1,PITPNM2,GUCY1B1,GRM8,PTGS2,RAPGEF2,PLCG2,CTDSPL2,CREB1,BCL10,USP28	up_VCAV_EC
GO:0048870	1.86E-08	1	72	451	cell motility	BP	0.0000245	EPHB1,PLK2,EDNRB,TEK,SELP,KIT,SELE,PRCP,CXCL8,DOCK4,CLEC14A,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,SOX18,PIK3C2A,PPP3CA,EPHB4,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,ELMO1,PAK2,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,FMNL3,PRAG1,HMGB1,ARPC5L,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,TNFAIP1,PTP4A1,JCAD,ARHGEF2,FSCN1,FBXO5,ZNF609	up_VCAV_EC
GO:0051674	1.86E-08	1	72	451	localization of cell	BP	0.0000245	EPHB1,PLK2,EDNRB,TEK,SELP,KIT,SELE,PRCP,CXCL8,DOCK4,CLEC14A,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,SOX18,PIK3C2A,PPP3CA,EPHB4,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,ELMO1,PAK2,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,FMNL3,PRAG1,HMGB1,ARPC5L,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,TNFAIP1,PTP4A1,JCAD,ARHGEF2,FSCN1,FBXO5,ZNF609	up_VCAV_EC
GO:0060065	0.000000025	1	3	7	uterus development	BP	0.000404	HOXA9,WNT7A,ESR1	up_AORTRT_VSMC
GO:0034501	2.72E-08	1	8	9	protein localization to kinetochore	BP	0.00000913	ZW10,CDK1,AURKB,NDC80,HASPIN,TTK,KNL1,MTBP	down_ACOR_VSMC
GO:0044770	2.96E-08	1	36	161	cell cycle phase transition	BP	0.00000975	HINFP,UBE2S,ZW10,TRIP13,POLE,FBXO5,BIRC5,CDK1,CASP2,FANCI,TIMELESS,CDKN2C,TOPBP1,EZH2,CDK4,RNASEH2B,PLK3,RCC1,CKS2,CDC6,NDC80,DTL,CDK2,CCNA2,ENSCAFG00000005299,RBBP8,CLSPN,BUB1,TTK,CDC25A,GLI1,CCNB3,UBE2C,CDKN3,MTBP,GEN1	down_ACOR_VSMC

GO:0051179	3.96E-08	1	152	1747	localization	BP	0.000213	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,SLC39A7,SHROOM2,NR1H4,FMNL3,PLK3,HSPA5,SERPINE1,ACTN1,HM13,SPARC,ANKRD50,GOLT1B,TRAM1,ERO1A,PTPN14,SLC7A5,ENPP1,ITGA2,SEC24D,JCAD,ENSCAFG00000003477,HYOU1,PTPN11,EXOC5,ATP2B1,FSCN1,SEC23A,MZT1,DPYSL3,LRRC8A,HOOK3,SLC38A1,TRIB3,ILK,PPP1R12A,PRCP,SESN2,SRP54,TMEM87B,REM1,WDR1,MYO1C,ENSCAFG00000031588,CANX,PIK3C2A,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,NDUFA4L2,CX3CL1,DYNLL1,TRAK1,SSR1,SLC20A1,IWS1,YIPF5,SLC2A1,TNIK,OSBPL9,ZPR1,PTPN2,STAM2,YES1,SMG7,SDC3,XPOT,USO1,SRPRA,SLC25A16,DDX39B,COPG1,ADAM17,AGRN,PALLD,CTNNB1,KPNB1,ANLN,COPB2,SRP72,CRYAB,STARD13,ENSCAFG00000002015,TFRC,APOE,PTP4A1,KPNA4,PLOD3,MMP28,LYN,BNIP3,STRAP,DDIT3,PDS5B,CCNYL1,SLC2A3,TLN1,MMD,CLCN3,OSBPL6,GPR107,SLC7A11,GSK3B,NKAIN1,NEXN,ARMCX3,GBP5,SH3GLB1,TAX1BP3,SLC20A2,MYO1E,SDC4,KPNA1,HTT,REST,ABHD5,CLINT1,ZMYND8,SCAMP1,CALM1,RAB11FIP1,DISC1,KDELR2,AP3S1,PAK2,CLTC,CREB3L2,LRRTM2,INHBA,STX6,ICAM5,ESYT3,SIX4,CDKN1A,NRP1,RHBDF2,ARF4,YWHAH,BLZF1,TNFAIP1,	down_VSAP_EC
GO:1901360	4.42E-08	1	226	2016	organic cyclic compound metabolic process	BP	0.000014	ELK3,PRPSAP1,SQLE,HMGB1,MCM6,RNPS1,LSS,SREBF1,ACLY,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,SNRPB2,TOP3A,TRIP13,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,RAN,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,DHCR24,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,E2F8,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,CYCS,NCL,NUP62,DTL,DDX28,PDXP,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,SMC6,SF3A2,ELOVL	down_ACOR_VSMC
GO:0006139	5.29E-08	1	216	1909	nucleobase-containing compound metabolic process	BP	0.0000164	ELK3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,SNRPB2,TOP3A,TRIP13,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,RAN,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,E2F8,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,CYCS,NCL,NUP62,DTL,DDX28,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,SMC6,SF3A2,ELOVL6,DHX38,RBM14,RBM17,RAD23A,OSGEP,CYC1,	down_ACOR_VSMC

GO:0010564	5.65E-08	1	43	217	regulation of cell cycle process	BP	0.0000171	SMC1A,ZW10,SLC29A1,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,AURKB,TOPBP1,EZH2,NEK2,FEN1,CDK4,RNASEH2B,PLK3,RCC1,POC1A,BRCA1,E2F8,CDC6,NDC80,NUP62,DTL,PDXP,PLK4,SMC3,CDK2,STAG1,ENSCAFG00000005299,CLSPN,BUB1,RBM14,CDC20,TTK,CDC25A,KIF11,GLI1,CCNB3,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:1903046	5.77E-08	1	19	55	meiotic cell cycle process	BP	0.0000171	NCAPD2,SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,PSMD13,RAD51,DSN1,MND1,CKS2,NCAPH,SMC2,ESPL1,CDC20,TTK,ASPM,SGO2	down_ACOR_VSMC
GO:0044772	5.81E-08	1	33	144	mitotic cell cycle phase transition	BP	0.0000171	HINFP,UBE2S,ZW10,TRIP13,POLE,FBXO5,BIRC5,CDK1,CASP2,FANCI,CDKN2C,TOPBP1,EZH2,CDK4,RNASEH2B,PLK3,RCC1,CKS2,CDC6,NDC80,DTL,CDK2,CCNA2,ENSCAFG00000005299,RBBP8,CLSPN,BUB1,TTK,CCNB3,UBE2C,CDKN3,MTBP,GEN1	down_ACOR_VSMC
GO:0140013	6.19E-08	1	18	50	meiotic nuclear division	BP	0.0000178	SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,FBXO5,PSMD13,RAD51,DSN1,MND1,CKS2,NCAPH,SMC2,ESPL1,CDC20,TTK,ASPM,SGO2	down_ACOR_VSMC
GO:0046483	6.56E-08	1	219	1948	heterocycle metabolic process	BP	0.0000186	ELK3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,SNRPB2,TOP3A,TRIP13,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,RAN,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,E2F8,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,CYCS,NCL,NUP62,DTL,DDX28,PDXP,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,SMC6,SF3A2,ELOVL6,DHX38,RBM14,RBM17,RAD23A,OSGEP	down_ACOR_VSMC
GO:0030326	6.73E-08	1	6	51	embryonic limb morphogenesis	BP	0.000517	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC
GO:0035113	6.73E-08	1	6	51	embryonic appendage morphogenesis	BP	0.000517	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC
GO:0006270	7.38E-08	1	11	19	DNA replication initiation	BP	0.0000204	MCM6,MCM4,MCM7,MCM3,POLA2,GINS4,TOPBP1,MCM10,CDC6,CDK2,CDC45	down_ACOR_VSMC
GO:0090304	7.57E-08	1	196	1694	nucleic acid metabolic process	BP	0.0000204	ELK3,HMGB1,MCM6,RNPS1,SREBF1,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HNRNPUL1,EDC3,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,SNRPB2,TOP3A,TRIP13,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,WDR62,FASTKD3,NOC2L,E2F8,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,NCL,NUP62,DTL,DDX28,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,SMC6,SF3A2,DHX38,RBM14,RBM17,RAD23A,OSGEP,POLR3F,HOXA10,ERF,ENSCAFG00000019620,TCERG1,RARS,CDC45,METT	down_ACOR_VSMC

GO:0006281	7.58E-08	1	42	208	DNA repair	BP	0.0000204	HMGB1,USP1,RPA1,HMGA1,SMC1A,HINFP,POLA1,TRIP13,PARPBP,GINS4,RAD54L,POLE,UBE2T,RFC2,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,TIMELESS,RFC4,FEN1,MND1,PCNA,TONSL,BRCA1,POLH,NEIL3,DTL,DMAP1,SMARCB1,RBBP8,SMC6,RBM17,RAD23A,SMARCAL1,H2AFX,NUDT1,HMGN1,APEX1,GEN1	down_ACOR_VSMC
GO:0032501	7.96E-08	1	202	1782	multicellular organismal process	BP	0.0000918	ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,PCDH12,IL7R,GBP5,ADGRF5,SELP,KIT,PRCP,CXCL8,F8,PTCHD1,PRKCH,ARHGEF15,IFRD1,EMCN,DOCK4,CLEC14A,IL6,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,ATP8A1,AMOT,PDGFB,MALL,PODXL,TMEM173,TSPAN8,RELN,VWF,CD34,LAMC2,PDE4D,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,CDH5,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,RAB27A,TCF4,SMAD1,NTN4,FOXN2,HOMER3,PTGS1,TFPI,IGSF3,PSME4,ENSCAFG00000003530,IRF8,SOX18,PIK3C2A,TMOD1,FIGNL1,PELI1,PPP3CA,PTPRB,SERINC5,MTSS1,GUCY1A1,TMEM150C,ODC1,ARG2,CASP8,EPHB4,NECTIN2,B3GNT5,MTOR,NAV2,ACPP,TENT2,HOOK3,SNAP23,MMRN1,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,CAV2,PREX2,BMP2K,ENC1,ABCA1,MAPK13,ITPKB,GDPD5,RIOK3,ANGPT2,PROX1,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,TSPAN12,MMP24,PAK2,MCC,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,APOD,BTBD7,PROCR,NCK1,KCNJ2,EXOC5,TIMELESS,HOXB5,LDB2,CD200,SLC25A25,FES,JAG1,HIST1H1A,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,BCL10,BASP1,ZC4H2,TAOK1,CT	up_VCAV_EC
GO:0000075	8.17E-08	1	25	91	cell cycle checkpoint	BP	0.0000216	HINFP,WDR76,ZW10,INTS7,TRIP13,BIRC5,CDK1,CASP2,FANCI,AURKB,TOPBP1,MAP3K20,RNASEH2B,NDC80,DTL,DDX39B,ENSCAFG00000005299,CLSPN,BUB1,TTK,H2AFX,CDC5L,ATRIP,ZWINT,GEN1	down_ACOR_VSMC
GO:0006725	0.000000092	1	219	1956	cellular aromatic compound metabolic process	BP	0.0000232	ELK3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,SNRPB2,TOP3A,TRIP13,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,RAN,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,E2F8,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,CYCS,NCL,NUP62,DTL,DDX28,PDXP,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,SMC6,SF3A2,ELOVL6,DHX38,RBM14,RBM17,RAD23A,OSGEP	down_ACOR_VSMC
GO:0000375	0.000000103	1	29	120	RNA splicing, via transesterification reactions	BP	0.0000255	RNPS1,DDX39A,USP4,SF3B2,SRSF2,U2AF2,SNRPB2,SF1,DDX23,U2AF1,THRAP3,NONO,HNRNPL,SF3B4,PHF5A,ENSCAFG00000015065,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,PRMT5,WTAP,JMJD6,ENSCAFG00000003222,CDC5L,GEMIN7,SF3A1	down_ACOR_VSMC
GO:0007088	0.000000112	1	20	64	regulation of mitotic nuclear division	BP	0.0000273	SMC1A,ZW10,TRIP13,FBXO5,BIRC5,NEK2,RCC1,CDC6,NDC80,NUP62,PDXP,SMC3,STAG1,ENSCAFG00000005299,BUB1,TTK,KIF11,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:1902850	0.000000117	1	18	52	microtubule cytoskeleton organization involved in mitosis	BP	0.0000282	SMC1A,ZW10,CENPA,BIRC5,AURKB,STMN1,NEK2,RCC1,POC1A,WDR62,SPC25,NDC80,NUP62,SMC3,STAG1,ENSCAFG00000005299,CDC20,KIF11	down_ACOR_VSMC

GO:0007052	0.000000123	1	16	42	mitotic spindle organization	BP	0.0000293	SMC1A,BIRC5,AURKB,STMN1,NEK2,RCC1,POC1A,WDR62,SPC25,NDC80,NUP62,SMC3,STAG1,ENSCAFG00000005299,CDC20,KIF11	down_ACOR_VSMC
GO:0008380	0.000000131	1	33	149	RNA splicing	BP	0.0000307	RNPS1,DDX39A,USP4,SF3B2,EIF4A3,SRSF2,U2AF2,SNRPB2,SF1,DDX23,U2AF1,THRAP3,NONO,HNRNPL,SF3B4,PHF5A,WDR62,ENSCAFG00000015065,HNRNPF,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,PRMT5,WTAP,JMJD6,ENSCAFG00000003222,CDC5L,RTCB,GEMIN7,SF3A1	down_ACOR_VSMC
GO:0048598	0.000000141	1	9	207	embryonic morphogenesis	BP	0.000517	HOXA11,TBX15,HOXA9,PITX1,SALL1,HOXC10,IRX5,SHOX2,GJB5	up_VSAP_VSMC
GO:0050896	0.000000149	1	249	2346	response to stimulus	BP	0.00016	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,TEK,RASGRP3,HCLS1,IL7R,GBP5,NPR1,ADGRF5,SELP,RGS16,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,F8,PTCHD1,PRKCH,ARHGEF15,IFRD1,LAPTM5,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,IL6,CALCRL,TIE1,TNFAIP3,ADAMTS9,PPARG,ADGRL2,MAP3K11,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,P2RX7,STK10,SH2D3C,BAIAP2L1,TMEM173,TSPAN8,RELN,VWF,CD34,SELL,FGD6,KDR,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,TSPAN15,EIF2B2,GATA3,MMP28,EDN1,RALB,APLNR,ARAP3,RAB27A,SMAD1,HOMER3,PTGS1,TFPI,IGSF3,PSME4,IRF8,ARHGAP28,PIK3C2A,EGFL7,FIGNL1,PELI1,PPP3CA,SERINC5,YES1,RAPGEF3,MTSS1,GUCY1A1,TMEM150C,ODC1,ARG2,CASP8,NECTIN2,MTOR,ACPP,SNAP23,MMRN1,LRRC8C,PDE7B,ELF4,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,TJP1,HHEX,SPNS3,CHN2,CAV2,PREX2,SLK,BMP2K,SH3BP5,RALBP1,PDZD8,ST3GAL6,GNG11,ARHGAP29,DOCK6,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNGR1,RIOK3,ANGPT2,ARHGEF12,IQGAP2,ENSCAFG00000010224,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,FLNB,TSPAN	up_VCAV_EC
GO:0048706	0.000000158	1	6	59	embryonic skeletal system development	BP	0.00255	TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0035107	0.00000016	1	6	60	appendage morphogenesis	BP	0.000517	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC
GO:0035108	0.00000016	1	6	60	limb morphogenesis	BP	0.000517	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC
GO:0006996	0.000000168	1	156	1301	organelle organization	BP	0.0000388	FSCN1,HMGB1,MCM6,SREBF1,MCM4,FLNB,POLE3,MCM7,RPA1,NCAPD2,STXBP6,FMNL3,ATAD2,HMGA1,EDC3,HNRNPD,SMC1A,UBE2S,ZW10,ENSCAFG00000016482,CAPG,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,CENPN,TOP3A,TRIP13,SLC25A5,TIMM44,SF1,SGO1,GINS4,SDC1,CTDNEP1,FBXO5,RAN,CFAP298,PRELID1,PSMD13,BIRC5,INSIG1,PRMT1,CAV1,CDK1,RAD51,LIMA1,NF2,AURKB,DSN1,EZH2,STMN1,CENPO,HAUS8,NCAPD3,MAP3K20,NEK2,CHCHD3,FBL,FEN1,SMARCC1,MND1,GAS2L3,PLK3,HMGB3,RCC1,KIF22,UHRF1,CKS2,CDCA8,CENPH,NCAPH,POC1A,BRCA1,WDR62,CENPI,FASTKD3,NOC2L,SMC2,PREB,ESPL1,SPC25,CDC6,NDC80,OIP5,IPO4,HIST1H1A,RAC1,NUP62,EMP2,DDX28,PDXP,PLK4,SUV39H1,HASPIN,TOMM34,IQGAP2,SAMM50,REEP4,HMGB2,DMAP1,CDC42EP4,HIST1H2BB,SMC3,CDK2,SMARCB1,CCNA2,STAG1,ENSCAFG00000005299,EZR,SMC6,SASS6,BUB1,RBM14,CORO1A,NOLC1,CENPW,FOXRED1,PHACTR4,CDC20,TTK,BAP1,ASPM,SGO2,MAST2,ARPC1B,CENPP,GRWD1,ENSCAFG00000010224,PRMT5,ARHGEF2,TRAPPC6A,ENSCAFG00000015189,SUPT16H,KIF11,TADA2A,PMPCA,HAT1,HIST2H2AC,TINF2,H2AFX,EMG1,RTTN,UBE	down_ACOR_VSMC
GO:0007051	0.00000018	1	21	70	spindle organization	BP	0.0000409	SMC1A,FBXO5,BIRC5,AURKB,STMN1,HAUS8,NEK2,RCC1,POC1A,WDR62,ESPL1,SPC25,NDC80,NUP62,SMC3,STAG1,ENSCAFG00000005299,EZR,CDC20,ASPM,KIF11	down_ACOR_VSMC

GO:0035556	0.000000189	1	111	845	intracellular signal transduction	BP	0.00019	EPHB1,EDNRB,TEK,RASGRP3,HCLS1,IL7R,NPR1,SELP,KIT,CXCL8,PRKCH,ARHGEF15,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,STK10,SH2D3C,RELN,FGD6,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,GPR4,GATA3,EDN1,RALB,APLNR,ARAP3,HOMER3,PIK3C2A,FIGNL1,PELI1,PPP3CA,RAPGEF3,GUCY1A1,CASP8,MTOR,ASB9,PLEKHG1,MAP3K3,BMP2,CHN2,PREX2,SLK,SH3BP5,RALBP1,PDZD8,ARHGAP29,DOCK6,ABCA1,ERC1,MAPK13,ITPKB,NCKAP1,RIOK3,ARHGEF12,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,RAP1A,PAK2,PRKD2,TLR3,AKAP12,NCK1,WSB1,NET1,PITPNM2,GUCY1B1,PTGS2,RAPGEF2,PLCG2,BCL10,USP28,TAOK1,CNOT7,HMGB1,NOS2,PMAIP1,RIPK1,LSM14A,SKIL,ENSCAFG00000024183,MCU,PDGFD,ARHGDIB,BMX,HIF1A,ARHGAP26,ALS2,ATRX,ENSCAFG00000002015,TNFAIP1,IVNS1ABP,RGL2,JCAD,ATP2A1,ARHGEF2,PEAR1,CDON	up_VCAV_EC
GO:0050789	0.000000213	1	327	3295	regulation of biological process	BP	0.000202	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,RASGRP3,HCLS1,IL7R,GBP5,NPR1,ADGRF5,SELP,RGS16,KIT,SELE,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,SHE,CXCR4,EMCN,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,FLI1,TIE1,CDA,TNFAIP3,ADAMTS9,PPARG,ADGRL2,MAP3K11,ATP8A1,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,PODXL,STK10,SH2D3C,BAIAP2L1,TMEM173,TSPAN8,RELN,CD34,FGD6,KDR,CXHXorf36,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GPR4,TSPAN15,STC1,EIF2B2,GATA3,MMP28,EDN1,HOXB8,RAB11A,RALB,APLNR,ARAP3,RAB27A,TCF4,SMAD1,CTTNBP2NL,NTN4,SNCAIP,FOXN2,MEOX1,HOMER3,PTGS1,TNFAIP8,TFPI,ENSCAFG00000017103,IGSF3,NEDD9,IRF8,ARHGAP28,SOX18,PIK3C2A,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,YES1,RAPGEF3,FAM3C,MTSS1,GUCY1A1,ODC1,SPTLC2,ARG2,CASP8,NECTIN2,MTOR,ACPP,TENT2,SAMD8,HOOK3,LRRC8C,PDE7B,ELF4,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,SPNS3,CREM,CHN2,CAV2,PREX2,TUT7,SLK,BMP2K,SH3BP5,RALBP1,CNOT6,DEPP1,RSC1A1,PDZD8,ENC1,GNG11,ARHGAP29,DOCK6,C	up_VCAV_EC
GO:0051783	0.000000216	1	21	72	regulation of nuclear division	BP	0.0000479	SMC1A,ZW10,TRIP13,FBXO5,BIRC5,NEK2,RCC1,CDC6,NDC80,NUP62,PDXP,SMC3,STAG1,ENSCAFG00000005299,BUB1,CDC20,TTK,KIF11,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:0051716	0.000000253	1	219	2001	cellular response to stimulus	BP	0.000227	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,TEK,RASGRP3,HCLS1,IL7R,GBP5,NPR1,ADGRF5,SELP,RGS16,KIT,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,LAPTM5,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,TNFAIP3,PPARG,ADGRL2,MAP3K11,TNIP1,LRRC8D,AMOT,PDGFB,STK10,SH2D3C,BAIAP2L1,TMEM173,TSPAN8,RELN,CD34,FGD6,KDR,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,TSPAN15,EIF2B2,GATA3,MMP28,EDN1,RALB,APLNR,ARAP3,SMAD1,HOMER3,TFPI,IGSF3,PSME4,IRF8,ARHGAP28,PIK3C2A,EGFL7,FIGNL1,PELI1,PPP3CA,YES1,RAPGEF3,MTSS1,GUCY1A1,TMEM150C,ARG2,CASP8,NECTIN2,MTOR,ACPP,LRRC8C,PDE7B,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,TJP1,HHEX,SPNS3,CHN2,CAV2,PREX2,SLK,BMP2K,SH3BP5,RALBP1,PDZD8,ST3GAL6,GNG11,ARHGAP29,DOCK6,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNGR1,RIOK3,ANGPT2,ARHGEF12,IQGAP2,ENSCAFG00000010224,ENSCAFG00000010596,MADD,CTNNAL1,ELMO1,STMN1,FLNB,TSPAN12,RAP1A,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,MFNG,AKAP12,APOD,TSPAN9,NCK1,TIMELESS,OTUD4,PDIA5,WS	up_VCAV_EC
GO:0048736	0.000000279	1	6	66	appendage development	BP	0.000643	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC

GO:0060173	0.000000279	1	6	66	limb development	BP	0.000643	HOXA11,HOXA9,PITX1,SALL1,HOXC10,SHOX2	up_VSAP_VSMC
GO:0000377	0.000000306	1	28	119	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	BP	0.0000659	RNPS1,DDX39A,USP4,SF3B2,SRSF2,U2AF2,SNRPB2,SF1,U2AF1,THRAP3,NONO,HNRNPL,SF3B4,PHF5A,ENSCAFG00000015065,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,PRMT5,WTAP,JMJD6,ENSCAFG00000003222,CDC5L,GEMIN7,SF3A1	down_ACOR_VSMC
GO:0000398	0.000000306	1	28	119	mRNA splicing, via spliceosome	BP	0.0000659	RNPS1,DDX39A,USP4,SF3B2,SRSF2,U2AF2,SNRPB2,SF1,U2AF1,THRAP3,NONO,HNRNPL,SF3B4,PHF5A,ENSCAFG00000015065,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,PRMT5,WTAP,JMJD6,ENSCAFG00000003222,CDC5L,GEMIN7,SF3A1	down_ACOR_VSMC
GO:0048706	0.000000344	1	5	59	embryonic skeletal system development	BP	0.00555	EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0034508	0.000000347	1	9	15	centromere complex assembly	BP	0.0000736	CENPA,CENPN,CENPO,CENPH,CENPI,OIP5,CENPW,CENPP,MIS18A	down_ACOR_VSMC
GO:0040011	0.00000037	1	74	505	locomotion	BP	0.000314	EPHB1,PLK2,EDNRB,TEK,SELP,KIT,SELE,PRCP,CXCL8,CXCR4,DOCK4,CLEC14A,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,PODXL,STK10,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,ARAP3,NEDD9,SOX18,PIK3C2A,PPP3CA,EPHB4,MTOR,MAP3K3,BMP2,SPNS3,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,ELMO1,PAK2,MCC,PRKD2,SWAP70,APOD,NCK1,LDB2,FES,JAG1,RAPGEF2,CTNNA1,FMNL3,PRAG1,HMGB1,ARPC5L,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,TNFAIP1,PTP4A1,JCAD,ARHGEF2,FSCN1,FBXO5,ZNF609	up_VCAV_EC
GO:0034502	0.00000037	1	13	30	protein localization to chromosome	BP	0.0000776	RPA1,ZW10,CENPA,CDK1,AURKB,EZH2,NDC80,HASPIN,TTK,KNL1,TINF2,CCT4,MTBP	down_ACOR_VSMC
GO:0001501	0.000000466	1	8	178	skeletal system development	BP	0.00376	HOXC10,TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0051239	0.000000504	1	110	859	regulation of multicellular organismal process	BP	0.000407	ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,IL7R,GBP5,SELP,KIT,PRCP,CXCL8,PRKCH,ARHGEF15,IFRD1,DOCK4,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,TMEM173,RELN,CD34,PDE4D,MEF2C,FERMT1,CHD7,KLKB1,DLL4,RAPGEF1,TLR4,GPR4,STC1,GATA3,EDN1,HOXB8,RAB11A,APLNR,TCF4,SMAD1,NTN4,HOMER3,TFPI,IRF8,PIK3C2A,PELI1,PPP3CA,GUCY1A1,ARG2,CASP8,MTOR,ACPP,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,BMP2K,MAPK13,ITPKB,GDPD5,RIOK3,ANGPT2,PROX1,TSPAN12,MCC,PRKD2,THOC1,TLR3,APOD,BTBD7,PROCR,NCK1,KCNJ2,CD200,FES,JAG1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BCL10,ZC4H2,CTNNA1,GCH1,ADIPOR2,HMGB1,NOS2,SPTBN4,RIPK1,LSM14A,ATP11C,ARHGDIB,CUL4A,NR1D2,HIF1A,KDM3A,VASH1,ZC3H13,JCAD,ATP2A1,ZEB1,ARHGEF2,FBXO5,CDON,TJP2,ZNF609	up_VCAV_EC
GO:0006323	0.000000531	1	18	58	DNA packaging	BP	0.000107	NCAPD2,HMGA1,SMC4,CENPA,NCAPD3,NCAPH,NOC2L,SMC2,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,CENPP,GRWD1,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:0034976	0.000000534	1	22	112	response to endoplasmic reticulum stress	BP	0.00144	P4HB,ENSCAFG00000013214,HSPA5,HM13,ERO1A,HSP90B1,ENSCAFG00000003477,HYOU1,SESN2,SEL1L,DNAJC10,PTPN2,PDIA4,DNAJB9,UBA5,DDIT3,ATF3,GSK3B,EIF2S1,CREB3L2,TMTC3,USP14	down_VSAP_EC
GO:0001501	0.000000644	1	8	178	skeletal system development	BP	0.0013	HOXA11,TBX15,HOXA9,PITX1,HOXC10,IRX5,SHOX2,HAPLN1	up_VSAP_VSMC
GO:0071824	0.000000879	1	23	92	protein-DNA complex subunit organization	BP	0.000175	HMGB1,CENPA,CENPN,RAD51,CENPO,SMARCC1,GMNN,CENPH,CENPI,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,SMARCB1,CENPW,CENPP,GRWD1,PSMC1,SUPT16H,HAT1,MIS18A,H3F3B	down_ACOR_VSMC

GO:0050794	0.000000886	1	306	3075	regulation of cellular process	BP	0.000658	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,TEK,RASGRP3,HCLS1,IL7R,GBP5,NPR1,ADGRF5,SELP,RGS16,KIT,SELE,PRCP,PPP2R5A,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,SHE,CXCR4,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,FLI1,TIE1,CDA,TNFAIP3,ADAMTS9,PPARG,ADGRL2,MAP3K11,ATP8A1,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,PODXL,STK10,SH2D3C,BAIAP2L1,TMEM173,TSPAN8,RELN,CD34,FGD6,KDR,CXHXorf36,PDE4D,IWS1,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GPR4,TSPAN15,STC1,EIF2B2,GATA3,MMP28,EDN1,HOXB8,RAB11A,RALB,APLNR,ARAP3,RAB27A,TCF4,SMAD1,SNCAIP,FOXN2,MEOX1,HOMER3,PTGS1,TNFAIP8,ENSCAFG00000017103,IGSF3,NEDD9,IRF8,ARHGAP28,SOX18,PIK3C2A,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,YES1,RAPGEF3,FAM3C,MTSS1,GUCY1A1,ODC1,SPTLC2,ARG2,CASP8,NECTIN2,MTOR,ACPP,TENT2,SAMD8,HOOK3,LRRC8C,PDE7B,ELF4,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,SPNS3,CREM,CHN2,CAV2,PREX2,SLK,BMP2K,SH3BP5,RALBP1,CNOT6,DEPP1,RSC1A1,PDZD8,ENC1,GNG11,ARHGAP29,DOCK6,CCAR1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,NCKAP1,GDPD5,IFNG	up_VCAV_EC
GO:0045132	0.00000089	1	11	23	meiotic chromosome segregation	BP	0.000175	SMC4,ENSCAFG00000017264,NDC1,TRIP13,SGO1,DSN1,NCAPH,SMC2,ESPL1,TTK,SGO2	down_ACOR_VSMC
GO:0043542	0.000000897	1	22	86	endothelial cell migration	BP	0.000658	PLK2,TEK,PRCP,CLEC14A,ADAMTS9,AMOT,PDGFB,MEF2C,DLL4,STC1,GATA3,SOX18,PIK3C2A,EPHB4,MAP3K3,ANGPT2,PROX1,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0010948	0.000000975	1	24	96	negative regulation of cell cycle process	BP	0.00019	SMC1A,ZW10,SLC29A1,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,NEK2,CDK4,E2F8,NDC80,DTL,SMC3,ENSCAFG00000005299,CLSPN,BUB1,RBM14,TTK,MTBP,GEN1	down_ACOR_VSMC
GO:0002376	0.000000985	1	84	622	immune system process	BP	0.000661	EDNRB,HOXB7,HCLS1,IL7R,GBP5,ADGRF5,SELP,KIT,SELE,CXCL8,PRKCH,IL6,FLI1,TNFAIP3,TNIP1,MX2,PDGFB,BCL6B,STK10,TMEM173,CD34,SELL,PDE4D,MEF2C,CHD7,TIPARP,DLL4,TLR4,NLRC5,EIF2B2,GATA3,MMP28,HOXB8,RAB27A,ENSCAFG00000003530,IRF8,PELI1,SERINC5,ARG2,CASP8,NECTIN2,MTOR,TENT2,SNAP23,ELF4,HHEX,ITPKB,RIOK3,FLNB,PRKD2,THOC1,SWAP70,TLR3,MFNG,OAS3,APOD,NCK1,OTUD4,CD200,FES,JAG1,PLCG2,CREB1,BCL10,CNOT7,GCH1,HMGB1,PMAIP1,RIPK1,CRIP2,LSM14A,ITGA6,ATP11C,SKIL,CUL4A,BMX,HIF1A,TNFAIP1,PSMB9,TMOD3,ZEB1,TET2,ARHGEF2,TJP2	up_VCAV_EC
GO:0048706	0.00000103	1	4	59	embryonic skeletal system development	BP	0.0166	TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:0051240	0.00000105	1	71	489	positive regulation of multicellular organismal process	BP	0.000661	EPHB1,PLK2,HOXB7,TEK,HCLS1,IL7R,GBP5,SELP,KIT,CXCL8,PRKCH,TNFAIP3,AMOT,PDGFB,TMEM173,RELN,CD34,PDE4D,MEF2C,FERMT1,CHD7,RAPGEF1,TLR4,GATA3,EDN1,RAB11A,APLNR,TCF4,SMAD1,IRF8,PIK3C2A,PELI1,PPP3CA,CASP8,MTOR,MAP3K3,BMP2,MAPK13,ITPKB,GDPD5,RIOK3,PROX1,PRKD2,TLR3,NCK1,CD200,FES,JAG1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BCL10,ZC4H2,GCH1,ADIPOR2,HMGB1,SPTBN4,RIPK1,LSM14A,ATP11C,HIF1A,KDM3A,JCAD,ATP2A1,ZEB1,ARHGEF2,FBXO5,CDON,ZNF609	up_VCAV_EC
GO:0010631	0.00000106	1	27	118	epithelial cell migration	BP	0.000661	PLK2,TEK,KIT,PRCP,CLEC14A,ADAMTS9,AMOT,PDGFB,MEF2C,FERMT1,DLL4,STC1,GATA3,RAB11A,SOX18,PIK3C2A,EPHB4,MTOR,MAP3K3,ANGPT2,PROX1,MCC,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0090132	0.00000106	1	27	118	epithelium migration	BP	0.000661	PLK2,TEK,KIT,PRCP,CLEC14A,ADAMTS9,AMOT,PDGFB,MEF2C,FERMT1,DLL4,STC1,GATA3,RAB11A,SOX18,PIK3C2A,EPHB4,MTOR,MAP3K3,ANGPT2,PROX1,MCC,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0090068	0.0000011	1	21	78	positive regulation of cell cycle process	BP	0.000206	BIRC5,CDK1,CASP2,AURKB,EZH2,FEN1,CDK4,POC1A,BRCA1,E2F8,CDC6,NDC80,NUP62,DTL,PLK4,ENSCAFG00000005299,CDC25A,GLI1,UBE2C,MTBP,GEN1	down_ACOR_VSMC

GO:0051304	0.00000115	1	14	38	chromosome separation	BP	0.000211	NCAPD2,ZW10,TRIP13,FBXO5,BIRC5,NCAPH,ESPL1,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0048665	0.00000132	1	3	6	neuron fate specification	BP	0.00402	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0048704	0.00000137	1	5	46	embryonic skeletal system morphogenesis	BP	0.00402	TBX15,EYA1,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0001944	0.00000138	1	45	263	vasculature development	BP	0.000776	EPHB1,PLK2,TEK,ADGRF5,KIT,PRCP,CXCL8,ARHGEF15,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PDGFB,CD34,MEF2C,CHD7,TIPARP,DLL4,RAPGEF1,GPR4,CDH5,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MAP3K3,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,JAG1,RAPGEF2,ADIPOR2,HIF1A,LUZP1,VASH1,JCAD,ELK3	up_VCAV_EC
GO:0007265	0.0000014	1	28	121	Ras protein signal transduction	BP	0.000776	RASGRP3,ARHGEF15,FGD5,FGD6,RAPGEF1,GPR4,RALB,ARAP3,PLEKHG1,PREX2,ABCA1,ITPKB,NCKAP1,ARHGEF12,MADD,CTNNAL1,ELMO1,STMN1,RAP1A,PAK2,NET1,RAPGEF2,USP28,ARHGDIB,ALS2,TNFAIP1,RGL2,ARHGEF2	up_VCAV_EC
GO:0071897	0.00000141	1	17	54	DNA biosynthetic process	BP	0.000253	HNRNPD,SLC29A1,POLE,RFC2,RFC5,RFC3,FAM129B,AURKB,TK1,GREM1,RFC4,NEK2,PCNA,POLH,DTL,TINF2,CCT4	down_ACOR_VSMC
GO:0007389	0.00000144	1	7	137	pattern specification process	BP	0.00402	HOXC10,EYA1,HOXA9,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0065007	0.00000149	1	340	3499	biological regulation	BP	0.000803	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,RASGRP3,HCLS1,IL7R,GBP5,NPR1,ADGRF5,SELP,RGS16,KIT,SELE,PRCP,PPP2R5A,CXCL8,F8,PTCHD1,PRKCH,ARHGEF15,IFRD1,SHE,CP,CXCR4,EMCN,FGD5,ENSCAFG00000007112,DOCK4,CALCRL,FLI1,TIE1,CDA,TNFAIP3,ADAMTS9,PPARG,ADGRL2,MAP3K11,ATP8A1,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,PODXL,STK10,SH2D3C,BAIAP2L1,TMEM173,ATP2B1,TSPAN8,RELN,VWF,CD34,FGD6,KDR,CXHXorf36,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NOS3,NLRC5,QKI,GPR4,TSPAN15,STC1,EIF2B2,GATA3,MMP28,EDN1,HOXB8,RAB11A,RALB,APLNR,ARAP3,RAB27A,TCF4,SLC39A8,SMAD1,CTTNBP2NL,NTN4,SNCAIP,FOXN2,MEOX1,HOMER3,PTGS1,TNFAIP8,TFPI,ENSCAFG00000017103,IGSF3,NEDD9,IRF8,ARHGAP28,SOX18,PIK3C2A,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,YES1,RAPGEF3,FAM3C,MTSS1,GUCY1A1,ODC1,SPTLC2,ARG2,CASP8,NECTIN2,MTOR,NAV2,ACPP,TENT2,SAMD8,HOOK3,SNAP23,MMRN1,LRRC8C,PDE7B,ELF4,ASB9,TSPAN14,PLEKHG1,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,SPNS3,CREM,CHN2,CAV2,PREX2,TUT7,SLC12A7,SLK,BMP2K,SH3BP5,RALB	up_VCAV_EC
GO:0048598	0.00000149	1	8	207	embryonic morphogenesis	BP	0.00402	HOXC10,TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0034641	0.00000154	1	232	2171	cellular nitrogen compound metabolic process	BP	0.000274	ELK3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,SRSF2,RRM1,THOP1,MED17,U2AF2,INTS7,POLA1,SLC29A1,MTDH,HEY1,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,MRPS18B,RAN,UBE2T,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FBL,FEN1,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,EIF5A,E2F8,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,YBX3,HNRNPF,CYCS,NCL,NUP62,MRPL37,DTL,DDX28,PDXP,FOSL1,SUV39H1,RSL1D1,THUMPD2,RRP1,ZNF367,CACTIN,HMGB2,GSTO1,DMAP1,DHX15,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RB	down_ACOR_VSMC

GO:0006810	0.00000155	1	111	1244	transport	BP	0.00313	PRICKLE1,VEGFA,MYH9,SLC39A7,NR1H4,PLK3,HSPA5,SERPINE1,HM13,ANKRD50,GOLT1B,TRAM1,ERO1A,PTPN14,SLC7A5,ENPP1,SEC24D,ENSCAFG00000003477,HYOU1,PTPN11,EXOC5,ATP2B1,SEC23A,LRRC8A,HOOK3,SLC38A1,TRIB3,PPP1R12A,SESN2,SRP54,TMEM87B,REM1,WDR1,MYO1C,ENSCAFG00000031588,CANX,PIK3C2A,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,NDUFA4L2,DYNLL1,TRAK1,SSR1,SLC20A1,IWS1,YIPF5,SLC2A1,OSBPL9,ZPR1,STAM2,YES1,SMG7,XPOT,USO1,SRPRA,SLC25A16,DDX39B,COPG1,CTNNB1,KPNB1,COPB2,SRP72,CRYAB,TFRC,APOE,KPNA4,LYN,BNIP3,DDIT3,SLC2A3,CLCN3,OSBPL6,GPR107,SLC7A11,GSK3B,NKAIN1,GBP5,SH3GLB1,SLC20A2,MYO1E,SDC4,KPNA1,HTT,REST,CLINT1,SCAMP1,CALM1,RAB11FIP1,KDELR2,AP3S1,CLTC,CREB3L2,LRRTM2,INHBA,STX6,ICAM5,ESYT3,CDKN1A,NRP1,RHBDF2,ARF4,YWHAH,BLZF1,SEC13,RINT1,HOMER1	down_VSAP_EC
GO:0090130	0.00000164	1	27	121	tissue migration	BP	0.00083	PLK2,TEK,KIT,PRCP,CLEC14A,ADAMTS9,AMOT,PDGFB,MEF2C,FERMT1,DLL4,STC1,GATA3,RAB11A,SOX18,PIK3C2A,EPHB4,MTOR,MAP3K3,ANGPT2,PROX1,MCC,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0051056	0.00000165	1	24	87	regulation of small GTPase mediated signal transduction	BP	0.00083	ARHGEF15,FGD5,AMOT,RELN,FGD6,RAPGEF1,GPR4,ARAP3,PLEKHG1,CHN2,PREX2,ABCA1,ITPKB,ARHGEF12,MADD,STMN1,NET1,ARHGDIB,ARHGAP26,ALS2,TNFAIP1,RGL2,ARHGEF2,CDON	up_VCAV_EC
GO:1901987	0.0000018	1	25	107	regulation of cell cycle phase transition	BP	0.000312	ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,CDK4,RNASEH2B,CDC6,NDC80,DTL,CDK2,ENSCAFG00000005299,CLSPN,BUB1,TTK,CDC25A,GLI1,CCNB3,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:0048731	0.00000198	1	147	1247	system development	BP	0.000943	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,PCDH12,IL7R,ADGRF5,KIT,PRCP,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,EMCN,CLEC14A,IL6,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,MALL,PODXL,RELN,CD34,LAMC2,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,GPR4,STC1,CDH5,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,TCF4,SMAD1,NTN4,FOXN2,IGSF3,ENSCAFG00000003530,IRF8,SOX18,PIK3C2A,TMOD1,PPP3CA,PTPRB,SERINC5,MTSS1,ODC1,ARG2,CASP8,EPHB4,B3GNT5,MTOR,NAV2,TENT2,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,CAV2,PREX2,BMP2K,ENC1,ITPKB,GDPD5,ANGPT2,PROX1,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,TSPAN12,MMP24,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,APOD,BTBD7,NCK1,TIMELESS,HOXB5,LDB2,SLC25A25,FES,JAG1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BCL10,BASP1,ZC4H2,TAOK1,CTNNA1,ADIPOR2,HMGB1,NUP133,SPTBN4,RIPK1,CRIP2,ITGA6,ATP11C,SKIL,CUL4A,BMX,NR1D2,HIF1A,ALS2,ATRX,ALDH1A3,P2RX2,LUZP1,RBBP6,VASH1,JCAD,TMOD3,ZEB1,TET2,ARHGEF2,FBXO5,CDON,ELK3,TJP2,ZNF609	up_VCAV_EC
GO:1901990	0.00000199	1	23	94	regulation of mitotic cell cycle phase transition	BP	0.000341	ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,CDK4,RNASEH2B,CDC6,NDC80,DTL,CDK2,ENSCAFG00000005299,CLSPN,BUB1,TTK,CCNB3,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:0043534	0.00000199	1	17	57	blood vessel endothelial cell migration	BP	0.000943	PLK2,PRCP,CLEC14A,AMOT,PDGFB,MEF2C,DLL4,SOX18,PIK3C2A,EPHB4,MAP3K3,ANGPT2,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0001501	0.00000216	1	5	178	skeletal system development	BP	0.0174	HOXC10,TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC

GO:0051234	0.00000222	1	113	1283	establishment of localization	BP	0.00326	PRICKLE1,VEGFA,MYH9,SLC39A7,SHROOM2,NR1H4,PLK3,HSPA5,SERPINE1,HM13,ANKRD50,GOLT1B,TRAM1,ERO1A,PTPN14,SLC7A5,ENPP1,SEC24D,ENSCAFG00000003477,HYOU1,PTPN11,EXOC5,ATP2B1,SEC23A,LRRC8A,HOOK3,SLC38A1,TRIB3,PPP1R12A,SESN2,SRP54,TMEM87B,REM1,WDR1,MYO1C,ENSCAFG00000031588,CANX,PIK3C2A,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,NDUFA4L2,DYNLL1,TRAK1,SSR1,SLC20A1,IWS1,YIPF5,SLC2A1,OSBPL9,ZPR1,STAM2,YES1,SMG7,XPOT,USO1,SRPRA,SLC25A16,DDX39B,COPG1,CTNNB1,KPNB1,COPB2,SRP72,CRYAB,ENSCAFG00000002015,TFRC,APOE,KPNA4,LYN,BNIP3,DDIT3,SLC2A3,CLCN3,OSBPL6,GPR107,SLC7A11,GSK3B,NKAIN1,GBP5,SH3GLB1,SLC20A2,MYO1E,SDC4,KPNA1,HTT,REST,CLINT1,SCAMP1,CALM1,RAB11FIP1,KDELR2,AP3S1,CLTC,CREB3L2,LRRTM2,INHBA,STX6,ICAM5,ESYT3,CDKN1A,NRP1,RHBDF2,ARF4,YWHAH,BLZF1,SEC13,RINT1,HOMER1	down_VSAP_EC
GO:0048705	0.00000245	1	6	95	skeletal system morphogenesis	BP	0.00566	TBX15,EYA1,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0072358	0.00000253	1	45	268	cardiovascular system development	BP	0.00112	EPHB1,PLK2,TEK,ADGRF5,KIT,PRCP,CXCL8,ARHGEF15,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PDGFB,CD34,MEF2C,CHD7,TIPARP,DLL4,RAPGEF1,GPR4,CDH5,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MAP3K3,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,JAG1,RAPGEF2,ADIPOR2,HIF1A,LUZP1,VASH1,JCAD,ELK3	up_VCAV_EC
GO:0007155	0.00000256	1	54	324	cell adhesion	BP	0.00112	EPHB1,TEK,PCDH12,IL7R,SELP,KIT,SELE,CXCL8,EMCN,PCDH1,ADAMTS9,TNIP1,PODXL,STK10,DSC2,VWF,CD34,SELL,FERMT1,RAPGEF1,LYVE1,CDH5,ESAM,GATA3,COL4A5,NEDD9,PELI1,PPP3CA,ARG2,EPHB4,NECTIN2,BMP2,SLK,DSG2,ITPKB,ANGPT2,CTNNAL1,MMP24,PRKD2,SWAP70,APOD,CDH24,NCK1,CD200,FES,JAG1,BCL10,CTNNA1,PPP1CB,HMGB1,ITGA6,ITGB3,ENSCAFG00000002015,PEAR1	up_VCAV_EC
GO:0001568	0.00000256	1	43	252	blood vessel development	BP	0.00112	EPHB1,PLK2,TEK,ADGRF5,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PDGFB,CD34,MEF2C,CHD7,TIPARP,DLL4,RAPGEF1,GPR4,CDH5,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MAP3K3,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,JAG1,RAPGEF2,ADIPOR2,HIF1A,LUZP1,VASH1,JCAD,ELK3	up_VCAV_EC
GO:0031577	0.00000264	1	9	17	spindle checkpoint	BP	0.000448	ZW10,TRIP13,BIRC5,AURKB,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0030071	0.00000276	1	11	26	regulation of mitotic metaphase/anaphase transition	BP	0.000459	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:1902099	0.00000276	1	11	26	regulation of metaphase/anaphase transition of cell cycle	BP	0.000459	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0051272	0.00000287	1	33	170	positive regulation of cellular component movement	BP	0.00122	PLK2,TEK,SELP,CXCL8,DOCK4,ATP8A1,PDGFB,PODXL,RELN,GATA3,EDN1,RAB11A,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,CCAR1,PROX1,STMN1,PRKD2,SWAP70,RAPGEF2,HMGB1,ITGA6,PDGFD,HIF1A,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0022610	0.00000308	1	54	326	biological adhesion	BP	0.00127	EPHB1,TEK,PCDH12,IL7R,SELP,KIT,SELE,CXCL8,EMCN,PCDH1,ADAMTS9,TNIP1,PODXL,STK10,DSC2,VWF,CD34,SELL,FERMT1,RAPGEF1,LYVE1,CDH5,ESAM,GATA3,COL4A5,NEDD9,PELI1,PPP3CA,ARG2,EPHB4,NECTIN2,BMP2,SLK,DSG2,ITPKB,ANGPT2,CTNNAL1,MMP24,PRKD2,SWAP70,APOD,CDH24,NCK1,CD200,FES,JAG1,BCL10,CTNNA1,PPP1CB,HMGB1,ITGA6,ITGB3,ENSCAFG00000002015,PEAR1	up_VCAV_EC
GO:0001501	0.00000321	1	6	178	skeletal system development	BP	0.0139	HOXC10,EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006333	0.00000344	1	17	59	chromatin assembly or disassembly	BP	0.000555	HMGA1,ENSCAFG00000016482,CENPA,SMARCC1,NOC2L,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,SMARCB1,CENPP,GRWD1,SUPT16H,HAT1,MIS18A,H3F3B	down_ACOR_VSMC

GO:0035115	0.00000363	1	3	12	embryonic forelimb morphogenesis	BP	0.0139	HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0098609	0.00000369	1	35	181	cell-cell adhesion	BP	0.00149	PCDH12,IL7R,SELP,KIT,SELE,EMCN,PCDH1,TNIP1,PODXL,STK10,DSC2,CD34,SELL,RAPGEF1,CDH5,ESAM,GATA3,PELI1,ARG2,NECTIN2,BMP2,DSG2,ITPKB,MMP24,SWAP70,CDH24,NCK1,CD200,JAG1,BCL10,CTNNA1,HMGB1,ITGA6,ITGB3,PEAR1	up_VCAV_EC
GO:0001944	0.00000371	1	9	263	vasculature development	BP	0.0354	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0035295	0.00000404	1	55	356	tube development	BP	0.00159	EPHB1,PLK2,EDNRB,HOXB7,TEK,ADGRF5,KIT,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PODXL,CD34,MEF2C,CHD7,TIPARP,DLL4,GPR4,GATA3,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,MTSS1,ARG2,EPHB4,MAP3K3,BMP2,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,TIMELESS,JAG1,RAPGEF2,CREB1,BCL10,ADIPOR2,NUP133,ITGA6,HIF1A,ATRX,LUZP1,VASH1,JCAD,ZEB1,ELK3	up_VCAV_EC
GO:0048514	0.00000435	1	38	214	blood vessel morphogenesis	BP	0.00167	EPHB1,PLK2,TEK,ADGRF5,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,CD34,CHD7,TIPARP,DLL4,GPR4,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MAP3K3,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,JAG1,RAPGEF2,ADIPOR2,HIF1A,VASH1,JCAD,ELK3	up_VCAV_EC
GO:0072358	0.00000439	1	9	268	cardiovascular system development	BP	0.0354	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0030335	0.00000444	1	32	165	positive regulation of cell migration	BP	0.00167	PLK2,TEK,SELP,CXCL8,DOCK4,ATP8A1,PDGFB,PODXL,RELN,GATA3,EDN1,RAB11A,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,CCAR1,PROX1,PRKD2,SWAP70,RAPGEF2,HMGB1,ITGA6,PDGFD,HIF1A,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0007091	0.00000444	1	11	27	metaphase/anaphase transition of mitotic cell cycle	BP	0.000683	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0010965	0.00000444	1	11	27	regulation of mitotic sister chromatid separation	BP	0.000683	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0044784	0.00000444	1	11	27	metaphase/anaphase transition of cell cycle	BP	0.000683	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0065004	0.00000454	1	20	81	protein-DNA complex assembly	BP	0.000691	HMGB1,CENPA,CENPN,RAD51,CENPO,GMNN,CENPH,CENPI,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,CENPW,CENPP,GRWD1,PSMC1,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:0048598	0.00000457	1	5	207	embryonic morphogenesis	BP	0.0246	HOXC10,TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:0036294	0.00000484	1	11	37	cellular response to decreased oxygen levels	BP	0.00492	VEGFA,P4HB,PLK3,HYOU1,PGK1,PTGS2,HIF1A,BNIP3,FAM162A,BACH1,HIF1AN	down_VSAP_EC
GO:0071456	0.00000484	1	11	37	cellular response to hypoxia	BP	0.00492	VEGFA,P4HB,PLK3,HYOU1,PGK1,PTGS2,HIF1A,BNIP3,FAM162A,BACH1,HIF1AN	down_VSAP_EC
GO:0045841	0.00000499	1	9	18	negative regulation of mitotic	BP	0.000732	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:1902100	0.00000499	1	9	18	negative regulation of metaphase/anaphase transition of cell cycle	BP	0.000732	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:1905819	0.00000499	1	9	18	negative regulation of chromosome separation	BP	0.000732	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:2000816	0.00000499	1	9	18	negative regulation of mitotic sister chromatid	BP	0.000732	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0018126	0.00000531	1	7	14	protein hydroxylation	BP	0.00492	P4HB,PLOD2,P4HA1,PLOD3,ASPH,P3H4,HIF1AN	down_VSAP_EC
GO:0001775	0.0000055	1	39	219	cell activation	BP	0.00202	EPHB1,IL7R,ADGRF5,SELP,KIT,CXCL8,F8,IL6,TNFAIP3,PDGFB,VWF,MEF2C,CHD7,DLL4,TLR4,GATA3,RAB27A,PELI1,ARG2,NECTIN2,MTOR,SNAP23,ELF4,HHEX,ITPKB,THOC1,SWAP70,MFNG,NCK1,CD200,FES,PLCG2,BCL10,HMGB1,ATP11C,BMX,ITGB3,ZEB1,PEAR1	up_VCAV_EC
GO:0048704	0.00000563	1	4	46	embryonic skeletal system morphogenesis	BP	0.0139	EYA1,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0001666	0.0000058	1	15	67	response to hypoxia	BP	0.00492	VEGFA,P4HB,PLOD2,PLK3,HYOU1,PGK1,PTGS2,HIF1A,ADAM17,CRYAB,BNIP3,FAM162A,BACH1,REST,HIF1AN	down_VSAP_EC
GO:0036293	0.0000058	1	15	67	response to decreased oxygen levels	BP	0.00492	VEGFA,P4HB,PLOD2,PLK3,HYOU1,PGK1,PTGS2,HIF1A,ADAM17,CRYAB,BNIP3,FAM162A,BACH1,REST,HIF1AN	down_VSAP_EC

GO:0048706	0.000006	1	5	59	embryonic skeletal system development	BP	0.00968	HOXA11,TBX15,HOXA9,IRX5,SHOX2	up_VSAP_VSMC
GO:0006952	0.00000601	1	49	319	defense response	BP	0.00215	ACKR1,GBP5,SELP,KIT,LYZ,PRCP,CXCL8,F8,IL6,TNFAIP3,TNIP1,MX2,BCL6B,TMEM173,MEF2C,TLR4,NLRC5,GATA3,RAB27A,PTGS1,IRF8,PELI1,SERINC5,ARG2,NECTIN2,SNAP23,ELF4,BMP2,RIOK3,FLNB,TLR3,OAS3,APOD,OTUD4,FES,PTGS2,BCL10,CNOT7,GCH1,HMGB1,NOS2,PMAIP1,LSM14A,BMX,NR1D2,ENSCAFG00000025410,HIF1A,ALS2,ARHGEF2	up_VCAV_EC
GO:0006396	0.00000611	1	56	368	RNA processing	BP	0.000888	RNPS1,PTBP1,DDX39A,USP4,SF3B2,EIF4A3,HNRNPUL1,SRSF2,U2AF2,INTS7,SNRPB2,SF1,SRRT,NOP56,DDX23,U2AF1,THRAP3,TRUB2,NONO,HNRNPL,FBL,SFSWAP,DHX33,SF3B4,PHF5A,DIS3,NOC4L,WDR62,ENSCAFG00000015065,HNRNPF,RSL1D1,THUMPD2,RRP1,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,OSGEP,ENSCAFG00000019620,NOP14,PRMT5,NOP58,ENSCAFG00000015189,WTAP,JMJD6,WDR33,ENSCAFG00000003222,CDC5L,EMG1,RTCB,EXOSC5,GEMIN7,SF3A1,NOB1	down_ACOR_VSMC
GO:0001667	0.00000667	1	29	146	ameboidal-type cell migration	BP	0.00229	PLK2,EDNRB,TEK,KIT,PRCP,CLEC14A,ADAMTS9,AMOT,PDGFB,MEF2C,FERMT1,DLL4,STC1,GATA3,RAB11A,SOX18,PIK3C2A,EPHB4,MTOR,MAP3K3,ANGPT2,PROX1,MCC,PRKD2,HMGB1,ARHGDIB,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:1905818	0.0000067	1	11	28	regulation of chromosome separation	BP	0.000965	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0035239	0.0000068	1	48	299	tube morphogenesis	BP	0.00229	EPHB1,PLK2,HOXB7,TEK,ADGRF5,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PODXL,CD34,MEF2C,CHD7,TIPARP,DLL4,GPR4,GATA3,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,MTSS1,EPHB4,MAP3K3,BMP2,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,TIMELESS,JAG1,RAPGEF2,BCL10,ADIPOR2,HIF1A,LUZP1,VASH1,JCAD,ZEB1,ELK3	up_VCAV_EC
GO:0030326	0.00000691	1	4	51	embryonic limb morphogenesis	BP	0.0139	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0035113	0.00000691	1	4	51	embryonic appendage morphogenesis	BP	0.0139	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:2000147	0.00000713	1	32	169	positive regulation of cell motility	BP	0.00235	PLK2,TEK,SELP,CXCL8,DOCK4,ATP8A1,PDGFB,PODXL,RELN,GATA3,EDN1,RAB11A,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,CCAR1,PROX1,PRKD2,SWAP70,RAPGEF2,HMGB1,ITGA6,PDGFD,HIF1A,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0009790	0.00000738	1	9	335	embryo development	BP	0.0108	HOXA11,TBX15,HOXA9,PITX1,SALL1,HOXC10,IRX5,SHOX2,GJB5	up_VSAP_VSMC
GO:0009954	0.0000074	1	3	16	proximal/distal pattern formation	BP	0.0139	HOXC10,HOXA9,HOXA11	up_VFEM_VSMC
GO:0048598	0.00000756	1	6	207	embryonic morphogenesis	BP	0.0139	HOXC10,EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0035136	0.00000776	1	3	16	forelimb morphogenesis	BP	0.0139	HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048514	0.00000777	1	8	214	blood vessel morphogenesis	BP	0.0418	ACVRL1,HOXA3,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0000226	0.00000801	1	36	197	microtubule cytoskeleton organization	BP	0.00112	SMC1A,ZW10,CENPA,FBXO5,BIRC5,CDK1,AURKB,STMN1,HAUS8,NEK2,GAS2L3,PLK3,RCC1,POC1A,WDR62,ESPL1,SPC25,NDC80,RAC1,NUP62,PLK4,SMC3,CDK2,STAG1,ENSCAFG00000005299,EZR,SASS6,RBM14,CDC20,ASPM,ENSCAFG00000010224,ARHGEF2,KIF11,TTLL1,GEN1,KIF24	down_ACOR_VSMC
GO:0001525	0.00000837	1	32	173	angiogenesis	BP	0.00265	EPHB1,PLK2,TEK,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,CD34,DLL4,GPR4,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MAP3K3,HHEX,ANGPT2,TSPAN12,PRKD2,TLR3,ADIPOR2,HIF1A,VASH1,JCAD,ELK3	up_VCAV_EC

GO:0051094	0.00000909	1	57	388	positive regulation of developmental process	BP	0.00282	EPHB1,PLK2,HOXB7,TEK,HCLS1,IL7R,KIT,CXCL8,PRKCH,TNFAIP3,ADAMTS9,PPARG,AMOT,PDGFB,RELN,CD34,MEF2C,CHD7,RAPGEF1,GATA3,EDN1,RAB11A,APLNR,TCF4,SMAD1,NEDD9,PIK3C2A,ARG2,CASP8,MTOR,MAP3K3,BMP2,ITPKB,GDPD5,PROX1,PRKD2,TLR3,NCK1,FES,JAG1,PTGS2,MMD,RAPGEF2,CREB1,ZC4H2,HMGB1,SPTBN4,RIPK1,ATP11C,HIF1A,ENSCAFG00000002015,JCAD,ZEB1,ARHGEF2,FBXO5,CDON,ZNF609	up_VCAV_EC
GO:0007165	9.27579E-06	1	65	1496	signal transduction	BP	0.0566569	SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,CALY,SOX9,RHOU,ARHGAP6,PTH1R,RGS1,NDRG2,AQP1,PORCN,ENSCAFG00000004331,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,RGMA,PDE4A,INSYN1,SMAD6,PLCE1,ACTN2,ARHGAP28,ESM1,PAK3,GUCY1B1,GRK7,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,PRKACA,STK32C,NRP1,ARHGEF26,PRKCD,GNAZ,RIN2,PYGO2,ADGRL1	up_ACOR_EC
GO:0003002	0.00000935	1	6	118	regionalization	BP	0.0189	HOXC10,HOXA9,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0010594	0.00000947	1	18	71	regulation of endothelial cell migration	BP	0.00288	PLK2,TEK,PRCP,ADAMTS9,PDGFB,MEF2C,DLL4,STC1,GATA3,PIK3C2A,MAP3K3,ANGPT2,PROX1,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:1901342	0.0000101	1	24	114	regulation of vasculature development	BP	0.00302	PLK2,TEK,KIT,CXCL8,TIE1,ADAMTS9,AMOT,PDGFB,CD34,DLL4,GPR4,APLNR,SMAD1,PIK3C2A,MAP3K3,HHEX,ANGPT2,TSPAN12,PRKD2,TLR3,RAPGEF2,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0051306	0.0000101	1	11	29	mitotic sister chromatid separation	BP	0.00138	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0045787	0.0000108	1	25	117	positive regulation of cell cycle	BP	0.00146	SLC29A1,BIRC5,CDK1,CASP2,AURKB,EZH2,FEN1,CDK4,CKS2,POC1A,BRCA1,E2F8,CDC6,NDC80,NUP62,DTL,PLK4,DDX39B,ENSCAFG00000005299,RAD23A,CDC25A,GLI1,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:2001199	0.000011	1	2	3	negative regulation of dendritic cell	BP	0.176	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0022414	0.0000114	1	47	294	reproductive process	BP	0.00153	NCAPD2,ACSL4,SMC1A,SMC4,SLC29A1,ENSCAFG00000017264,NDC1,TRIP13,SF1,SGO1,CTDNEP1,FBXO5,PSMD13,CDK1,RAD51,CASP2,AAAS,DSN1,MND1,CKS2,DHCR24,NCAPH,POC1A,E2F8,B4GALT1,SMC2,PPARD,ESPL1,HIST1H1A,EMP2,FOSL1,PLK4,HMGB2,SMC3,SGPL1,CDC20,TTK,ASPM,SGO2,HOXA9,GLI1,H2AFX,RTCB,CCNB3,CCT4,SIX4,TTLL1	down_ACOR_VSMC
GO:0023052	1.14358E-05	0.99999	68	1602	signaling	BP	0.0566569	CNTNAP4,SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,CALY,SOX9,RHOU,ARHGAP6,PTH1R,RGS1,NDRG2,AQP1,PORCN,ENSCAFG00000004331,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,RGMA,PDE4A,INSYN1,SMAD6,PLCE1,ACTN2,ARHGAP28,ESM1,PAK3,GUCY1B1,GRK7,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,TBX5,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,PRKACA,STK32C,NRP1,ARHGEF26,PRKCD,GNAZ,RIN2,PYGO2,ADGRL1	up_ACOR_EC
GO:0035107	0.000012	1	4	60	appendage morphogenesis	BP	0.0177	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0035108	0.000012	1	4	60	limb morphogenesis	BP	0.0177	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0061333	0.0000121	1	4	35	renal tubule morphogenesis	BP	0.0217	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0000003	0.0000125	1	47	295	reproduction	BP	0.00167	NCAPD2,ACSL4,SMC1A,SMC4,SLC29A1,ENSCAFG00000017264,NDC1,TRIP13,SF1,SGO1,CTDNEP1,FBXO5,PSMD13,CDK1,RAD51,CASP2,AAAS,DSN1,MND1,CKS2,DHCR24,NCAPH,POC1A,E2F8,B4GALT1,SMC2,PPARD,ESPL1,HIST1H1A,EMP2,FOSL1,PLK4,HMGB2,SMC3,SGPL1,CDC20,TTK,ASPM,SGO2,HOXA9,GLI1,H2AFX,RTCB,CCNB3,CCT4,SIX4,TTLL1	down_ACOR_VSMC

GO:0002764	0.0000128	1	19	80	immune response-regulating signaling pathway	BP	0.00368	KIT,PRKCH,TNFAIP3,TNIP1,PDE4D,MEF2C,TLR4,EIF2B2,GATA3,PELI1,NECTIN2,RIOK3,PRKD2,TLR3,OTUD4,PLCG2,BCL10,HMGB1,LSM14A	up_VCAV_EC
GO:0016126	0.0000129	1	9	20	sterol biosynthetic process	BP	0.00171	SQLE,LSS,SREBF1,HMGCR,INSIG1,ENSCAFG00000018572,DHCR24,MVD,FDFT1	down_ACOR_VSMC
GO:0035023	0.0000132	1	15	46	regulation of Rho protein signal transduction	BP	0.00372	ARHGEF15,FGD5,FGD6,GPR4,ARAP3,PLEKHG1,PREX2,ABCA1,ARHGEF12,STMN1,NET1,ARHGDIB,ALS2,TNFAIP1,ARHGEF2	up_VCAV_EC
GO:0001708	0.0000138	1	3	20	cell fate specification	BP	0.0185	HOXC10,EYA1,HOXA11	up_VFEM_VSMC
GO:0006928	0.000014	1	76	557	movement of cell or subcellular component	BP	0.00389	EPHB1,PLK2,EDNRB,TEK,SELP,KIT,SELE,PRCP,CXCL8,DOCK4,CLEC14A,TIE1,ADAMTS9,ATP8A1,AMOT,PDGFB,KIF21B,PODXL,STK10,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,DLL4,STC1,GATA3,MMP28,EDN1,RAB11A,KIF3C,ARAP3,NEDD9,SOX18,PIK3C2A,PPP3CA,EPHB4,MTOR,MAP3K3,BMP2,SLK,CCAR1,ANGPT2,PROX1,ENSCAFG00000010224,ELMO1,STMN1,PAK2,MCC,PRKD2,SWAP70,APOD,NCK1,KCNJ2,LDB2,FES,JAG1,RAPGEF2,CTNNA1,FMNL3,PRAG1,HMGB1,ARPC5L,ITGA6,PDGFD,ARHGDIB,HIF1A,VASH1,TNFAIP1,PTP4A1,JCAD,ARHGEF2,FSCN1,FBXO5,ZNF609	up_VCAV_EC
GO:0051383	0.0000142	1	7	12	kinetochore organization	BP	0.00186	SMC4,CENPA,CENPN,CENPH,SMC2,NDC80,CENPW	down_ACOR_VSMC
GO:0042391	0.0000143	1	21	81	regulation of membrane potential	BP	0.0384	FGF13,ACTN2,SLC26A7,KCNE3,TPC3,GJA1,SCARB2,PTPN3,TMEM108,USP53,BNIP3,AKAP6,DMPK,APP,PSEN1,JUP,INSYN1,FXYD1,GNAQ,PARK7,BVES	up_ACOR_VSMC
GO:0001525	0.0000167	1	7	173	angiogenesis	BP	0.0636	ACVRL1,HOXA3,NRP2,HOXA7,ANPEP,SULF1,ELK3	down_ACOR_EC
GO:1903522	0.0000168	1	17	58	regulation of blood circulation	BP	0.0387	TNNT2,FGF13,ADRA1B,KCNE3,GJA1,HRH1,PDE5A,F2RL1,HRH2,DMPK,RNLS,JUP,EDN1,GAA,DOCK5,SLC8A1,BVES	up_ACOR_VSMC
GO:0007094	0.000017	1	8	16	mitotic spindle assembly checkpoint	BP	0.00216	ZW10,TRIP13,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0071173	0.000017	1	8	16	spindle assembly checkpoint	BP	0.00216	ZW10,TRIP13,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0071174	0.000017	1	8	16	mitotic spindle checkpoint	BP	0.00216	ZW10,TRIP13,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0048736	0.0000172	1	4	66	appendage development	BP	0.0198	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060173	0.0000172	1	4	66	limb development	BP	0.0198	HOXC10,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0007154	1.7555E-05	0.99999	68	1622	cell communication	BP	0.0566569	CNTNAP4,SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,CALY,SOX9,RHOU,ARHGAP6,PTH1R,RGS1,NDRG2,AQP1,PORCN,ENSCAFG00000004331,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,RGMA,PDE4A,INSYN1,SMAD6,PLCE1,ACTN2,ARHGAP28,ESM1,PAK3,GUCY1B1,GRK7,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,TBX5,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,PRKACA,STK32C,NRP1,ARHGEF26,PRKCD,GNAZ,RIN2,PYGO2,ADGRL1	up_ACOR_EC
GO:2000026	0.0000176	1	75	560	regulation of multicellular organismal development	BP	0.00468	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,IL7R,KIT,CXCL8,PRKCH,ARHGEF15,IFRD1,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,RELN,CD34,MEF2C,FERMT1,CHD7,DLL4,RAPGEF1,GPR4,GATA3,EDN1,HOXB8,RAB11A,APLNR,TCF4,SMAD1,NTN4,PIK3C2A,PPP3CA,CASP8,MTOR,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,BMP2K,ITPKB,GDPD5,ANGPT2,PROX1,TSPAN12,PRKD2,THOC1,TLR3,BTBD7,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,HMGB1,RIPK1,ATP11C,ARHGDIB,CUL4A,NR1D2,HIF1A,VASH1,JCAD,ZEB1,ARHGEF2,FBXO5,CDON,TJP2,ZNF609	up_VCAV_EC
GO:0045839	0.0000183	1	10	25	negative regulation of mitotic nuclear division	BP	0.0023	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,MTBP,GEN1	down_ACOR_VSMC
GO:0070192	0.0000191	1	9	20	chromosome organization involved in meiotic cell	BP	0.0024	NCAPD2,SMC4,NDC1,TRIP13,RAD51,DSN1,NCAPH,SMC2,SGO2	down_ACOR_VSMC
GO:0035115	0.0000193	1	3	12	embryonic forelimb morphogenesis	BP	0.0259	HOXA11,HOXA9,SHOX2	up_VSAP_VSMC

GO:0051983	0.0000201	1	14	47	regulation of chromosome segregation	BP	0.0025	ZW10,TRIP13,FBXO5,BIRC5,NEK2,FEN1,CDC6,NDC80,ENSCAFG00000005299,SMC6,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0007389	0.0000201	1	5	137	pattern specification process	BP	0.0208	HOXC10,EYA1,HOXA9,EMX2,HOXA11	up_VFEM_VSMC
GO:0007017	0.0000203	1	44	273	microtubule-based process	BP	0.0025	SMC1A,KIF2A,ZW10,CENPA,FBXO5,CFAP298,BIRC5,CDK1,CENPE,AURKB,STMN1,HAUS8,NEK2,GAS2L3,PLK3,RCC1,KIF22,POC1A,WDR62,ESPL1,SPC25,NDC80,RAC1,NUP62,PLK4,TRAK1,KIF4A,SMC3,CDK2,KIF15,STAG1,ENSCAFG00000005299,EZR,SASS6,RBM14,CDC20,ASPM,ENSCAFG00000010224,ARHGEF2,KIF11,TTLL1,KIF21B,GEN1,KIF24	down_ACOR_VSMC
GO:0007266	0.0000203	1	17	64	Rho protein signal transduction	BP	0.0052	ARHGEF15,FGD5,FGD6,GPR4,ARAP3,PLEKHG1,PREX2,ABCA1,ARHGEF12,CTNNAL1,STMN1,PAK2,NET1,ARHGDIB,ALS2,TNFAIP1,ARHGEF2	up_VCAV_EC
GO:0009887	0.0000209	1	9	314	animal organ morphogenesis	BP	0.0636	ACVRL1,HOXA3,NRP2,HOXA7,SULF1,HOXA1,CSGALNACT1,HOXC4,ASPN	down_ACOR_EC
GO:0010632	0.0000211	1	21	95	regulation of epithelial cell migration	BP	0.00531	PLK2,TEK,PRCP,ADAMTS9,PDGFB,MEF2C,DLL4,STC1,GATA3,RAB11A,PIK3C2A,MTOR,MAP3K3,ANGPT2,PROX1,MCC,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0048663	0.0000211	1	3	13	neuron fate commitment	BP	0.0308	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0048583	0.0000214	1	127	1095	regulation of response to stimulus	BP	0.00531	EPHB1,PLK2,TEK,HCLS1,IL7R,GBP5,SELP,KIT,PRCP,CXCL8,PRKCH,ARHGEF15,CXCR4,FGD5,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,BCL6B,BAIAP2L1,TMEM173,RELN,CD34,FGD6,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,KLKB1,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,EIF2B2,GATA3,MMP28,EDN1,APLNR,ARAP3,HOMER3,TFPI,EGFL7,FIGNL1,PELI1,PPP3CA,GUCY1A1,ARG2,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,PLEKHG1,MAP3K3,BMP2,HHEX,CHN2,CAV2,PREX2,BMP2K,ABCA1,PPP1R2,ITPKB,GDPD5,RIOK3,ANGPT2,ARHGEF12,MADD,STMN1,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,MFNG,AKAP12,APOD,NCK1,TIMELESS,OTUD4,CD200,NET1,FES,JAG1,PTGS2,ETAA1,RAPGEF2,PLCG2,CTDSPL2,BCL10,TAOK1,CTNNA1,CNOT7,GCH1,HMGB1,NOS2,PMAIP1,RIPK1,LSM14A,ITGA6,RGS2,SKIL,PDGFD,ARHGDIB,CUL4A,NR1D2,UFSP2,ENSCAFG00000025410,HIF1A,ARHGAP26,ALS2,ENSCAFG00000002015,VASH1,TNFAIP1,IVNS1ABP,RGL2,JCAD,ZEB1,ARHGEF2,PEAR1,CDON	up_VCAV_EC
GO:2001198	0.0000219	1	2	4	regulation of dendritic cell differentiation	BP	0.176	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0061326	0.0000229	1	4	41	renal tubule development	BP	0.0308	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0072080	0.0000229	1	4	41	nephron tubule development	BP	0.0308	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0009952	0.0000236	1	4	66	anterior/posterior pattern specification	BP	0.0224	HOXC10,HOXA9,EMX2,HOXA11	up_VFEM_VSMC
GO:0033046	0.0000243	1	9	21	negative regulation of sister chromatid	BP	0.00292	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0033048	0.0000243	1	9	21	negative regulation of mitotic sister chromatid	BP	0.00292	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0051985	0.0000243	1	9	21	negative regulation of chromosome segregation	BP	0.00292	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0001568	0.0000244	1	8	252	blood vessel development	BP	0.0636	ACVRL1,HOXA3,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0030326	0.0000245	1	3	51	embryonic limb morphogenesis	BP	0.101	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0035113	0.0000245	1	3	51	embryonic appendage morphogenesis	BP	0.101	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0070482	0.0000247	1	15	75	response to oxygen levels	BP	0.0143	VEGFA,P4HB,PLOD2,PLK3,HYOU1,PGK1,PTGS2,HIF1A,ADAM17,CRYAB,BNIP3,FAM162A,BACH1,REST,HIF1AN	down_VSAP_EC
GO:0043627	0.000025	1	2	8	response to estrogen	BP	0.101	WNT7A,ESR1	up_AORTRT_VSMC
GO:0009954	0.0000251	1	5	16	proximal/distal pattern formation	BP	0.241	HOXA9,IRX3,HOXC10,DLL1,GREM1	up_AFEM_EC

GO:0009605	0.0000254	1	71	538	response to external stimulus	BP	0.0062	EPHB1,EDNRB,GBP5,SELP,KIT,LYZ,CXCL8,CXCR4,DOCK4,TNFAIP3,ADAMTS9,TNIP1,MX2,AMOT,PDGFB,BCL6B,P2RX7,BAIAP2L1,TMEM173,RELN,CD34,SELL,PDE4D,MEF2C,ATF3,CHD7,KLKB1,TLR4,NLRC5,GATA3,MMP28,RALB,TFPI,IRF8,PELI1,SERINC5,GUCY1A1,TMEM150C,ODC1,ARG2,CASP8,MTOR,ABCA1,RIOK3,ANGPT2,ENSCAFG00000010596,STMN1,MMP24,PRKD2,SWAP70,TLR3,OAS3,APOD,NCK1,SLC25A25,FES,PTGS2,PLCG2,BCL10,CNOT7,GCH1,HMGB1,NOS2,PMAIP1,LSM14A,ITGA6,NR1D2,ENSCAFG00000025410,ALDH1A3,P2RX2,IVNS1ABP	up_VCAV_EC
GO:0048665	0.0000269	1	2	6	neuron fate specification	BP	0.109	HOXC10,EYA1	up_AFEM_VSMC
GO:0021675	0.0000276	1	4	29	nerve development	BP	0.0636	HOXA3,NRP2,SULF1,HOXA1	down_ACOR_EC
GO:0040017	0.0000288	1	32	180	positive regulation of locomotion	BP	0.00685	PLK2,TEK,SELP,CXCL8,DOCK4,ATP8A1,PDGFB,PODXL,RELN,GATA3,EDN1,RAB11A,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,CCAR1,PROX1,PRKD2,SWAP70,RAPGEF2,HMGB1,ITGA6,PDGFD,HIF1A,PTP4A1,JCAD,ARHGEF2,FBXO5,ZNF609	up_VCAV_EC
GO:0007346	0.0000293	1	36	210	regulation of mitotic cell cycle	BP	0.00348	SMC1A,ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,MAP3K20,NEK2,CDK4,TRIM35,RNASEH2B,RCC1,CKS2,CDC6,NDC80,NUP62,DTL,PDXP,IQGAP1,SMC3,CDK2,STAG1,ENSCAFG00000005299,CLSPN,BUB1,TTK,KIF11,CCNB3,UBE2C,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0002757	0.0000306	1	18	78	immune response-activating signal transduction	BP	0.00709	PRKCH,TNFAIP3,TNIP1,PDE4D,MEF2C,TLR4,EIF2B2,GATA3,PELI1,NECTIN2,RIOK3,PRKD2,TLR3,OTUD4,PLCG2,BCL10,HMGB1,LSM14A	up_VCAV_EC
GO:0008217	0.0000308	1	12	38	regulation of blood pressure	BP	0.00709	EDNRB,PRCP,PDGFB,CD34,EDN1,PTGS1,GUCY1A1,NAV2,PTGS2,GCH1,NOS2,P2RX2	up_VCAV_EC
GO:0009653	0.0000312	1	12	773	anatomical structure morphogenesis	BP	0.0365	HOXC10,TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1,RADIL,CYP26B1,CDC42EP5,MTSS1,CA9	up_VFEM_EC
GO:0048468	0.0000313	1	58	553	cell development	BP	0.0174	ARHGEF2,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,ACTN1,SGK1,PTPN11,FLNB,DPYSL3,HOOK3,IFRD1,ILK,FHL2,WDR1,CHSY1,MSN,KIF5B,HIF1A,SLC45A3,TNIK,UBA6,ZPR1,EIF2B1,NEO1,ACTA2,UST,CDH11,CTNNB1,ENSCAFG00000002015,APOE,PLOD3,KLF5,LYN,MMD,GSK3B,VLDLR,NEXN,MYO1E,SDC4,REST,MAPK10,PRMT1,EXT1,DISC1,CDYL,PAK2,INHBA,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0048513	0.0000316	1	13	906	animal organ development	BP	0.0365	HOXC10,TBX15,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,CYP26B1,MTSS1	up_VFEM_EC
GO:2000278	0.0000321	1	12	37	regulation of DNA biosynthetic process	BP	0.00375	HNRNPD,SLC29A1,RFC2,RFC5,RFC3,FAM129B,AURKB,GREM1,RFC4,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0048704	0.0000339	1	3	46	embryonic skeletal system morphogenesis	BP	0.109	TBX15,EYA1,IRX5	up_AFEM_VSMC
GO:0048645	0.0000343	1	3	33	animal organ formation	BP	0.184	HOXA3,TBX5,GATA5	up_VPUL_VSMC
GO:0009607	0.0000344	1	37	232	response to biotic stimulus	BP	0.00742	GBP5,LYZ,CXCL8,TNFAIP3,ADAMTS9,TNIP1,MX2,BAIAP2L1,TMEM173,PDE4D,MEF2C,CHD7,TLR4,NLRC5,GATA3,IRF8,PELI1,SERINC5,GUCY1A1,ODC1,ARG2,NECTIN2,ABCA1,RIOK3,STMN1,TLR3,OAS3,NCK1,PLCG2,BCL10,CNOT7,GCH1,HMGB1,NOS2,PMAIP1,LSM14A,IVNS1ABP	up_VCAV_EC
GO:0098742	0.0000346	1	14	44	cell-cell adhesion via plasma-membrane adhesion molecules	BP	0.00742	PCDH12,SELP,SELE,PCDH1,DSC2,SELL,CDH5,ESAM,NECTIN2,BMP2,DSG2,MMP24,CDH24,CD200	up_VCAV_EC
GO:0043207	0.000035	1	35	216	response to external biotic stimulus	BP	0.00742	GBP5,LYZ,CXCL8,TNFAIP3,ADAMTS9,TNIP1,MX2,BAIAP2L1,TMEM173,PDE4D,MEF2C,CHD7,TLR4,NLRC5,GATA3,IRF8,PELI1,SERINC5,GUCY1A1,ODC1,ARG2,ABCA1,RIOK3,STMN1,TLR3,OAS3,NCK1,PLCG2,BCL10,CNOT7,GCH1,NOS2,PMAIP1,LSM14A,IVNS1ABP	up_VCAV_EC
GO:0051707	0.000035	1	35	216	response to other organism	BP	0.00742	GBP5,LYZ,CXCL8,TNFAIP3,ADAMTS9,TNIP1,MX2,BAIAP2L1,TMEM173,PDE4D,MEF2C,CHD7,TLR4,NLRC5,GATA3,IRF8,PELI1,SERINC5,GUCY1A1,ODC1,ARG2,ABCA1,RIOK3,STMN1,TLR3,OAS3,NCK1,PLCG2,BCL10,CNOT7,GCH1,NOS2,PMAIP1,LSM14A,IVNS1ABP	up_VCAV_EC

GO:0031331	0.0000362	1	19	110	positive regulation of cellular catabolic process	BP	0.0188	PRICKLE1,PLK3,SOCS5,TRIB3,SESN2,MSN,HIF1A,MTDH,CNOT7,APOE,BNIP3,GSK3B,CDC37,SH3GLB1,HTT,ABHD5,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:0009954	0.0000368	1	3	16	proximal/distal pattern formation	BP	0.0395	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0048568	0.000037	1	6	148	embryonic organ development	BP	0.0458	HOXA11,TBX15,SALL1,IRX5,SHOX2,GJB5	up_VSAP_VSMC
GO:0043535	0.0000387	1	13	45	regulation of blood vessel endothelial cell migration	BP	0.00801	PLK2,PRCP,PDGFB,MEF2C,DLL4,PIK3C2A,MAP3K3,ANGPT2,PRKD2,HMGB1,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0033045	0.0000402	1	12	38	regulation of sister chromatid segregation	BP	0.0046	ZW10,TRIP13,FBXO5,BIRC5,FEN1,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:0051052	0.0000405	1	28	145	regulation of DNA metabolic process	BP	0.00461	HMGB1,USP1,HNRNPD,SMC1A,SLC29A1,PARPBP,RFC2,RFC5,RFC3,RAD51,TIMELESS,FAM129B,AURKB,GREM1,RFC4,NEK2,PCNA,UHRF1,GMNN,E2F8,TFRC,SMC3,CDK2,AIFM1,GLI1,TINF2,MIS18A,CCT4	down_ACOR_VSMC
GO:0072009	0.0000408	1	4	48	nephron epithelium development	BP	0.0395	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:1901991	0.000041	1	15	56	negative regulation of mitotic cell cycle phase transition	BP	0.00462	ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,NDC80,ENSCAFG00000005299,CLSPN,BUB1,TTK,GEN1	down_ACOR_VSMC
GO:0001822	0.0000416	1	5	98	kidney development	BP	0.0395	EYA1,MME,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0035107	0.0000419	1	3	60	appendage morphogenesis	BP	0.113	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0035108	0.0000419	1	3	60	limb morphogenesis	BP	0.113	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0009954	0.0000419	1	3	16	proximal/distal pattern formation	BP	0.0458	HOXA11,HOXA9,HOXC10	up_VSAP_VSMC
GO:0035136	0.0000426	1	3	16	forelimb morphogenesis	BP	0.0458	HOXA11,HOXA9,SHOX2	up_VSAP_VSMC
GO:1900122	0.0000427	1	2	3	positive regulation of receptor binding	BP	0.689	HOXA3,PLCL1	up_APUL_EC
GO:0033047	0.0000443	1	11	33	regulation of mitotic sister chromatid segregation	BP	0.0049	ZW10,TRIP13,FBXO5,BIRC5,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,UBE2C,GEN1	down_ACOR_VSMC
GO:1900262	0.0000443	1	4	4	regulation of DNA-directed DNA polymerase	BP	0.0049	RFC2,RFC5,RFC3,RFC4	down_ACOR_VSMC
GO:1900264	0.0000443	1	4	4	positive regulation of DNA-directed DNA polymerase	BP	0.0049	RFC2,RFC5,RFC3,RFC4	down_ACOR_VSMC
GO:0071453	0.0000449	1	11	46	cellular response to oxygen levels	BP	0.0226	VEGFA,P4HB,PLK3,HYOU1,PGK1,PTGS2,HIF1A,BNIP3,FAM162A,BACH1,HIF1AN	down_VSAP_EC
GO:0016071	0.0000459	1	40	248	mRNA metabolic process	BP	0.00504	RNPS1,SREBF1,PTBP1,DDX39A,USP4,SF3B2,EIF4A3,EDC3,HNRNPD,SRSF2,U2AF2,SNRPB2,SF1,U2AF1,THRAP3,EDC4,NONO,HNRNPL,SMG9,SF3B4,PHF5A,FASTKD3,ENSCAFG00000015065,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,ENSCAFG00000019620,PRMT5,ENSCAFG00000015189,WTAP,JMJD6,WDR33,ENSCAFG00000003222,CDC5L,EXOSC5,GEMIN7,SF3A1	down_ACOR_VSMC
GO:0009790	0.0000463	1	5	335	embryo development	BP	0.125	HOXC10,TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:1901988	0.0000467	1	16	63	negative regulation of cell cycle phase transition	BP	0.0051	ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,NDC80,DTL,ENSCAFG00000005299,CLSPN,BUB1,TTK,GEN1	down_ACOR_VSMC

GO:0048856	0.0000474	1	167	1533	anatomical structure development	BP	0.00953	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,PCDH12,IL7R,ADGRF5,KIT,PRCP,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,EMCN,CLEC14A,IL6,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,MALL,PODXL,RELN,CD34,LAMC2,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,CDH5,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,ARAP3,TCF4,SMAD1,NTN4,FOXN2,IGSF3,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SOX18,PIK3C2A,TMOD1,PPP3CA,PTPRB,SERINC5,MTSS1,ODC1,ARG2,CASP8,EPHB4,NECTIN2,B3GNT5,MTOR,NAV2,TENT2,HOOK3,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CAV2,PREX2,BMP2K,PDZD8,ENC1,ITPKB,GDPD5,ANGPT2,PROX1,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,SNX2,TSPAN12,MMP24,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,APOD,BTBD7,NCK1,EXOC5,TIMELESS,HOXB5,LDB2,SLC25A25,FES,JAG1,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,BCL10,BASP1,ZC4H2,TAOK1,CTNNA1,FMNL3,ASF1A,ADIPOR2,HMGB1,NUP133,SPTBN4,RIPK1,CRIP2,AFF4,ITGA6,ATP11C,SKIL,ARHGDIB,CUL4A,BMX,NR1D2,HIF1A,KDM3A,ALS2,ATRX,ALDH1A3,ENSCAFG00000002015,P2RX2,LUZP	up_VCAV_EC
GO:0048869	0.0000476	1	129	1119	cellular developmental process	BP	0.00953	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,IL7R,ADGRF5,KIT,PRKCH,IFRD1,IL6,FLI1,ADAMTS9,PPARG,AMOT,PDGFB,BCL6B,PODXL,RELN,CD34,PDE4D,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,ARAP3,RAB27A,TCF4,NTN4,FOXN2,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SOX18,TMOD1,FIGNL1,PPP3CA,MTSS1,ARG2,CASP8,NECTIN2,MTOR,NAV2,TENT2,HOOK3,LRRC8C,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CAV2,PREX2,PDZD8,ITPKB,GDPD5,ANGPT2,PROX1,UHRF2,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,SNX2,MMP24,PAK2,MFNG,APOD,NCK1,HOXB5,FES,JAG1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BASP1,ZC4H2,CTNNA1,FMNL3,ASF1A,HMGB1,NUP133,SPTBN4,RIPK1,SMC5,AFF4,ITGA6,ATP11C,SKIL,CUL4A,BMX,NR1D2,HIF1A,KDM3A,ALS2,ATRX,NR4A1,ENSCAFG00000002015,P2RX2,VASH1,TMOD3,ZEB1,TET2,ARHGEF2,FBXO5,CDON,ELK3,TJP2,ZMYM2,ZNF609	up_VCAV_EC
GO:0007166	0.0000478	1	86	686	cell surface receptor signaling pathway	BP	0.00953	ACKR1,TEK,NPR1,ADGRF5,KIT,CXCL8,PTCHD1,PRKCH,CXCR4,CALCRL,TNFAIP3,ADGRL2,PDGFB,BAIAP2L1,TSPAN8,RELN,KDR,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,NLRC5,TSPAN15,EIF2B2,GATA3,EDN1,SMAD1,IGSF3,EGFL7,PELI1,PPP3CA,CASP8,NECTIN2,ACPP,TSPAN14,HHAT,BMP2,HHEX,BMP2K,ITPKB,GDPD5,IFNGR1,ANGPT2,MADD,STMN1,TSPAN12,PAK2,MCC,PRKD2,SMARCA4,TLR3,MFNG,APOD,TSPAN9,NCK1,OTUD4,FES,JAG1,GRM8,RAPGEF2,PLCG2,CTDSPL2,BCL10,CTNNA1,CNOT7,ADIPOR2,PMAIP1,RIPK1,LSM14A,ITGA6,SKIL,PDGFD,BMX,HIF1A,IQUB,ITGB3,ENSCAFG00000002015,JCAD,ZEB1,ARHGEF2,PEAR1,CDON,TJP2	up_VCAV_EC
GO:0051641	0.0000488	1	79	858	cellular localization	BP	0.0238	PRICKLE1,MYH9,SHROOM2,NR1H4,PLK3,HSPA5,HM13,ANKRD50,TRAM1,ERO1A,PTPN14,SEC24D,HYOU1,PTPN11,EXOC5,SEC23A,MZT1,HOOK3,PPP1R12A,SESN2,SRP54,TMEM87B,MYO1C,CANX,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TRAK1,SSR1,IWS1,YIPF5,TNIK,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,AGRN,CTNNB1,KPNB1,COPB2,SRP72,CRYAB,APOE,KPNA4,LYN,DDIT3,TLN1,GSK3B,ARMCX3,GBP5,SH3GLB1,TAX1BP3,KPNA1,HTT,CALM1,DISC1,KDELR2,AP3S1,CLTC,CREB3L2,STX6,ESYT3,SIX4,CDKN1A,NRP1,ARF4,YWHAH,BLZF1,SEC13,MID1	down_VSAP_EC
GO:0035295	0.0000497	1	9	356	tube development	BP	0.0898	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC

GO:0048646	0.0000501	1	9	349	anatomical structure formation involved in	BP	0.0898	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0009790	0.0000517	1	8	335	embryo development	BP	0.0451	HOXC10,TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0050817	0.0000521	1	14	50	coagulation	BP	0.0102	SELP,F8,PDGFB,VWF,CD34,KLKB1,TLR4,RAB27A,TFPI,MMRN1,PROCR,PDGFD,ITGB3,PEAR1	up_VCAV_EC
GO:0048704	0.0000526	1	4	46	embryonic skeletal system morphogenesis	BP	0.053	HOXA11,TBX15,IRX5,SHOX2	up_VSAP_VSMC
GO:0001936	0.0000538	1	13	49	regulation of endothelial cell proliferation	BP	0.0105	PDGFB,MEF2C,DLL4,APLNR,EGFL7,BMP2,CAV2,PROX1,PRKD2,HMGB1,NRAS,VASH1,JCAD	up_VCAV_EC
GO:0072513	0.0000546	1	2	3	positive regulation of secondary heart field cardioblast proliferation	BP	0.0451	EYA1,SIX1	up_VFEM_EC
GO:2000573	0.000055	1	10	28	positive regulation of DNA biosynthetic process	BP	0.00588	HNRNPD,SLC29A1,RFC2,RFC5,RFC3,AURKB,GREM1,RFC4,NEK2,CCT4	down_ACOR_VSMC
GO:0008015	0.0000551	1	26	120	blood circulation	BP	0.111	TNNT2,ADRA1B,KCNE3,HTR2B,NPPB,GJA1,HRH1,PDE5A,SLC2A5,ADCY6,F2RL1,HRH2,CLSTN1,DMPK,PTGDR,TBX20,RNLS,CHD7,JUP,EDN1,NCALD,GAA,DOCK5,ERAP1,SLC8A1,BVES	up_ACOR_VSMC
GO:0090257	0.0000551	1	2	52	regulation of muscle system process	BP	0.438	JUP,GATA5	down_VFEM_VSMC
GO:0044057	0.0000554	1	11	110	regulation of system process	BP	0.244	IRX5,LEP,CRY2,LMCD1,CHRM2,THRB,TMEM100,AVPR1A,TBXA2R,BVES,DMPK	up_AFEM_EC
GO:0072001	0.0000559	1	5	104	renal system development	BP	0.0451	EYA1,MME,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0007275	0.0000564	1	152	1370	multicellular organism development	BP	0.0107	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,PCDH12,IL7R,ADGRF5,KIT,PRCP,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,EMCN,CLEC14A,IL6,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,MALL,PODXL,RELN,CD34,LAMC2,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,CDH5,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,TCF4,SMAD1,NTN4,FOXN2,IGSF3,ENSCAFG00000003530,IRF8,SOX18,PIK3C2A,TMOD1,PPP3CA,PTPRB,SERINC5,MTSS1,ODC1,ARG2,CASP8,EPHB4,B3GNT5,MTOR,NAV2,TENT2,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,CAV2,PREX2,BMP2K,ENC1,ITPKB,GDPD5,ANGPT2,PROX1,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,TSPAN12,MMP24,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,APOD,BTBD7,NCK1,TIMELESS,HOXB5,LDB2,SLC25A25,FES,JAG1,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,BCL10,BASP1,ZC4H2,TAOK1,CTNNA1,ADIPOR2,HMGB1,NUP133,SPTBN4,RIPK1,CRIP2,ITGA6,ATP11C,SKIL,ARHGDIB,CUL4A,BMX,NR1D2,HIF1A,ALS2,ATRX,ALDH1A3,P2RX2,LUZP1,RBBP6,VASH1,JCAD,TMOD3,ZEB1,TET2,ARHGEF2,FBXO5,CDON,ELK3,TJP2,ZMYM2,ZNF609,GINS4	up_VCAV_EC
GO:0010720	0.0000566	1	23	110	positive regulation of cell development	BP	0.0107	PRKCH,RELN,MEF2C,RAPGEF1,EDN1,RAB11A,TCF4,NEDD9,MTOR,BMP2,GDPD5,PROX1,NCK1,FES,MMD,RAPGEF2,ZC4H2,HIF1A,ENSCAFG00000002015,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0048736	0.0000569	1	3	66	appendage development	BP	0.115	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0060173	0.0000569	1	3	66	limb development	BP	0.115	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0051784	0.000059	1	10	28	negative regulation of nuclear division	BP	0.00619	ZW10,TRIP13,FBXO5,BIRC5,NDC80,ENSCAFG00000005299,BUB1,TTK,MTBP,GEN1	down_ACOR_VSMC
GO:0006397	0.0000591	1	30	168	mRNA processing	BP	0.00619	RNPS1,PTBP1,DDX39A,USP4,SF3B2,SRSF2,U2AF2,SNRPB2,SF1,U2AF1,THRAP3,NONO,HNRNPL,SF3B4,PHF5A,ENSCAFG00000015065,DHX15,DDX39B,SF3A2,DHX38,RBM14,RBM17,PRMT5,WTAP,JMJD6,WDR33,ENSCAFG00000003222,CDC5L,GEMIN7,SF3A1	down_ACOR_VSMC

GO:0050793	0.0000597	1	90	731	regulation of developmental process	BP	0.0112	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,IL7R,KIT,CXCL8,PRKCH,ARHGEF15,IFRD1,TIE1,TNFAIP3,ADAMTS9,PPARG,AMOT,PDGFB,BCL6B,RELN,CD34,MEF2C,FERMT1,CHD7,DLL4,RAPGEF1,GPR4,GATA3,EDN1,HOXB8,RAB11A,APLNR,ARAP3,TCF4,SMAD1,NTN4,NEDD9,PIK3C2A,PPP3CA,ARG2,CASP8,MTOR,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,BMP2K,PDZD8,ITPKB,GDPD5,ANGPT2,PROX1,ENSCAFG00000010596,TSPAN12,PRKD2,THOC1,TLR3,BTBD7,NCK1,FES,JAG1,PTGS2,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,FMNL3,HMGB1,SPTBN4,RIPK1,ATP11C,SKIL,ARHGDIB,CUL4A,NR1D2,HIF1A,KDM3A,ENSCAFG00000002015,VASH1,ZC3H13,JCAD,ZEB1,ARHGEF2,FBXO5,CDON,TJP2,ZMYM2,ZNF609	up_VCAV_EC
GO:0032501	0.0000604	1	65	1782	multicellular organismal process	BP	0.244	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXC10,LEP,LBH,CRY2,XYLT1,F5,ANGPT4,HOXA7,COL8A2,CD40,DLL1,CRYAB,F3,VXN,PLXNA4,BPI,GPAM,NEFH,LMCD1,CHRM2,TWIST2,MAB21L1,THRB,LGI4,TMEM100,PLAGL2,GREM1,HTR1D,NFE2L1,OVOL1,AVPR1A,CAMK2A,GREM2,HOXA6,CYLD,LUZP1,RECK,PTHLH,TBXA2R,EVI2B,CNNM4,TFPI2,REEP2,BVES,PTPRB,AXIN2,ACACB,NAPEPLD,PPARGC1A,SPATA6,FAP,DMPK,ADAM17,CLIC4,LRRN2,AGPAT2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0097435	0.0000615	1	30	230	supramolecular fiber organization	BP	0.0292	ARHGEF2,SERPINH1,PLK3,ACTN1,VASP,P4HA1,TPM4,FSCN1,MZT1,DPYSL3,HOOK3,WDR1,TMSB10,ACTR3,KPNB1,CRYAB,APOE,PLOD3,TWF1,PLEKHG2,PLS3,P3H4,CAPG,SIX4,NRP1,COL12A1,ENSCAFG00000030508,TNFAIP1,MYBPC2,MID1	down_VSAP_EC
GO:0032879	0.0000618	1	93	767	regulation of localization	BP	0.0115	PLK2,TEK,HCLS1,SELP,SELE,PRCP,PPP2R5A,CXCL8,DOCK4,TIE1,ADAMTS9,ATP8A1,MX2,AMOT,PDGFB,PODXL,STK10,TMEM173,RELN,PDE4D,IWS1,MEF2C,FERMT1,CHD7,DLL4,TLR4,STC1,GATA3,MMP28,EDN1,RAB11A,APLNR,ARAP3,RAB27A,CTTNBP2NL,SNCAIP,NEDD9,PIK3C2A,PPP3CA,YES1,ARG2,MTOR,MAP3K3,BMP2,SLK,BMP2K,RSC1A1,CCAR1,ABCA1,KCNJ3,ANGPT2,PROX1,ENSCAFG00000010224,EPB41,STMN1,MCC,PRKD2,SH3GLB1,SWAP70,APOD,NCK1,KCNJ2,LDB2,CD200,FES,JAG1,HIST1H1A,MMD,RAPGEF2,PLCG2,CTDSPL2,CREB1,GCC2,CTNNA1,HMGB1,TBC1D1,SPTBN4,RIPK1,ITGA6,MCU,DNAJC13,PDGFD,ARHGDIB,HIF1A,VASH1,DCP2,PTP4A1,JCAD,RABGAP1,ARHGEF2,FBXO5,USP6NL,ZNF609	up_VCAV_EC
GO:0007501	0.0000624	1	2	5	mesodermal cell fate specification	BP	0.0559	EYA1,HOXA11	up_VFEM_VSMC
GO:0048562	0.0000628	1	5	102	embryonic organ morphogenesis	BP	0.0483	TBX15,EYA1,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0003013	0.0000639	1	26	121	circulatory system process	BP	0.115	TNNT2,ADRA1B,KCNE3,HTR2B,NPPB,GJA1,HRH1,PDE5A,SLC2A5,ADCY6,F2RL1,HRH2,CLSTN1,DMPK,PTGDR,TBX20,RNLS,CHD7,JUP,EDN1,NCALD,GAA,DOCK5,ERAP1,SLC8A1,BVES	up_ACOR_VSMC
GO:0001935	0.0000642	1	13	50	endothelial cell proliferation	BP	0.0116	PDGFB,MEF2C,DLL4,APLNR,EGFL7,BMP2,CAV2,PROX1,PRKD2,HMGB1,NRAS,VASH1,JCAD	up_VCAV_EC
GO:0035115	0.0000645	1	2	12	embryonic forelimb morphogenesis	BP	0.116	HOXA9,WNT7A	up_AORTRT_VSMC
GO:0006457	0.0000712	1	14	77	protein folding	BP	0.0326	P4HB,ENSCAFG00000013214,ERO1A,HSP90B1,ENSCAFG00000003477,FKBP11,CANX,PPIB,FKBP10,DNAJC10,PDIA4,CCT8,CDC37,SH3GLB1	down_VSAP_EC

GO:0033036	0.0000727	1	78	852	macromolecule localization	BP	0.0326	PRICKLE1,MYH9,SHROOM2,NR1H4,PLK3,HSPA5,HM13,TRAM1,PTPN14,ENPP1,SEC24D,PTPN11,EXOC5,SEC23A,MZT1,HOOK3,SESN2,SRP54,MYO1C,ENSCAFG00000031588,MSN,SEL1L,KIF5B,HIF1A,SSR1,IWS1,TNIK,OSBPL9,ZPR1,PTPN2,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,AGRN,CTNNB1,KPNB1,COPB2,SRP72,ENSCAFG00000002015,TFRC,APOE,KPNA4,PLOD3,LYN,DDIT3,TLN1,MMD,OSBPL6,GSK3B,ARMCX3,GBP5,SH3GLB1,TAX1BP3,KPNA1,REST,ABHD5,SCAMP1,RAB11FIP1,DISC1,KDELR2,AP3S1,CLTC,INHBA,STX6,ESYT3,SIX4,CDKN1A,NRP1,RHBDF2,ARF4,YWHAH,BLZF1,SEC13,MID1	down_VSAP_EC
GO:0001708	0.0000729	1	3	20	cell fate specification	BP	0.0535	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0072359	0.0000733	1	9	368	circulatory system development	BP	0.102	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0048562	0.0000733	1	5	102	embryonic organ morphogenesis	BP	0.0696	HOXA11,TBX15,SALL1,IRX5,SHOX2	up_VSAP_VSMC
GO:0050789	7.35887E-05	0.99996	113	3295	regulation of biological process	BP	0.19791669	C7,CNTNAP4,SH3TC2,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TRPS1,PLCL1,PKIB,CALY,SOX9,RHOU,PKNOX2,ARHGAP6,PTH1R,RGS1,PCSK1N,FNDC4,NDRG2,AQP1,PORCN,ENSCAFG00000004331,SYNPO2,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,SEMA6D,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,IL33,RGMA,CASP10,LHX9,PDE4A,INSYN1,SMAD6,KLHL25,PLCE1,PLS1,ACTN2,ZMYND8,ARHGAP28,RNLS,ESM1,PTGDS,PAK3,MMP28,GUCY1B1,GRK7,BCL2,TRIM8,TNFRSF19,PTGER4,ARHGDIB,PREB,CST3,PIAS1,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,TBX5,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,C23H3orf58,ZNF229,CHMP4B,TP53INP2,RARRES2,VPS16,GMEB2,RIOX2,PRKACA,RNF114,STK32C,NRP1,AZIN2,AGPAT2,ARHGEF26,PRKCD,GNAZ,RIN2,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,MFAP4,ADGRL1,TUBB4A,TLE2	up_ACOR_EC
GO:0006955	0.0000738	1	47	327	immune response	BP	0.013	IL7R,GBP5,KIT,CXCL8,PRKCH,IL6,TNFAIP3,TNIP1,MX2,BCL6B,TMEM173,PDE4D,MEF2C,TLR4,NLRC5,EIF2B2,GATA3,RAB27A,IRF8,PELI1,SERINC5,ARG2,NECTIN2,MTOR,SNAP23,ELF4,RIOK3,FLNB,PRKD2,THOC1,SWAP70,TLR3,MFNG,OAS3,OTUD4,CD200,FES,JAG1,PLCG2,BCL10,CNOT7,GCH1,HMGB1,LSM14A,BMX,TNFAIP1,ARHGEF2	up_VCAV_EC
GO:0007389	0.0000739	1	3	137	pattern specification process	BP	0.398	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0106049	0.0000742	1	2	4	regulation of cellular response to osmotic	BP	0.339	PTGER2,ARHGEF2	up_VPUL_EC
GO:1902218	0.0000742	1	2	4	regulation of intrinsic apoptotic signaling pathway in response to	BP	0.339	PTGER2,ARHGEF2	up_VPUL_EC
GO:1902219	0.0000742	1	2	4	negative regulation of intrinsic apoptotic signaling pathway in	BP	0.339	PTGER2,ARHGEF2	up_VPUL_EC
GO:0002682	0.0000744	1	49	343	regulation of immune system process	BP	0.013	HCLS1,IL7R,GBP5,ADGRF5,SELP,KIT,CXCL8,PRKCH,TNFAIP3,TNIP1,STK10,TMEM173,PDE4D,MEF2C,TLR4,NLRC5,EIF2B2,GATA3,MMP28,HOXB8,PELI1,ARG2,CASP8,NECTIN2,MTOR,ITPKB,RIOK3,PRKD2,THOC1,SWAP70,TLR3,APOD,NCK1,OTUD4,CD200,FES,JAG1,PLCG2,CREB1,BCL10,CNOT7,HMGB1,RIPK1,LSM14A,ATP11C,CUL4A,HIF1A,ZEB1,TJP2	up_VCAV_EC
GO:0010032	0.0000744	1	4	4	meiotic chromosome condensation	BP	0.00775	NCAPD2,SMC4,NCAPH,SMC2	down_ACOR_VSMC
GO:0045597	0.0000782	1	39	253	positive regulation of cell differentiation	BP	0.0136	HCLS1,IL7R,KIT,PRKCH,ADAMTS9,PPARG,RELN,CD34,MEF2C,RAPGEF1,GATA3,EDN1,RAB11A,TCF4,NEDD9,CASP8,MTOR,BMP2,ITPKB,GDPD5,PROX1,NCK1,FES,JAG1,PTGS2,MMD,RAPGEF2,CREB1,ZC4H2,HMGB1,RIPK1,ATP11C,HIF1A,ENSCAFG00000002015,ZEB1,ARHGEF2,FBXO5,CDON,ZNF609	up_VCAV_EC
GO:0009653	0.0000802	1	13	773	anatomical structure morphogenesis	BP	0.102	ACVRL1,HOXA3,SPG11,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,HOXC4,ASPN	down_ACOR_EC

GO:0007093	0.0000813	1	15	59	mitotic cell cycle checkpoint	BP	0.00835	ZW10,TRIP13,BIRC5,CDK1,CASP2,FANCI,TOPBP1,MAP3K20,NDC80,ENSCAFG00000005299,CLSPN,BUB1,TTK,ZWINT,GEN1	down_ACOR_VSMC
GO:0044057	0.0000832	1	24	110	regulation of system process	BP	0.128	TNNT2,FGF13,ADRA1B,LEP,KCNE3,GATA5,GJA1,HRH1,WASF3,PDE5A,TMEM108,F2RL1,HRH2,DMPK,NPNT,RNLS,APP,JUP,EDN1,GAA,INPP5K,DOCK5,SLC8A1,BVES	up_ACOR_VSMC
GO:0045765	0.0000835	1	21	105	regulation of angiogenesis	BP	0.0143	PLK2,TEK,CXCL8,TIE1,ADAMTS9,AMOT,CD34,DLL4,GPR4,APLNR,SMAD1,PIK3C2A,MAP3K3,HHEX,ANGPT2,TSPAN12,PRKD2,TLR3,HIF1A,VASH1,JCAD	up_VCAV_EC
GO:0021602	0.0000836	1	3	16	cranial nerve morphogenesis	BP	0.102	HOXA3,NRP2,HOXA1	down_ACOR_EC
GO:0030036	0.0000846	1	29	223	actin cytoskeleton organization	BP	0.0369	ARHGEF2,SIPA1L1,MYH9,FMNL3,ACTN1,VASP,TPM4,CORO1C,FSCN1,FLNB,DPYSL3,WDR1,TNIK,TMSB10,ACTR3,PALLD,TWF1,PLEKHG2,TLN1,PLS3,DAAM1,ENSCAFG00000017326,PAK2,CAPG,SIX4,NRP1,ENSCAFG00000030508,TNFAIP1,MYBPC2	down_VSAP_EC
GO:0048665	0.0000856	1	2	6	neuron fate specification	BP	0.0704	HOXC10,EYA1	up_VFEM_VSMC
GO:0048705	0.0000873	1	4	95	skeletal system morphogenesis	BP	0.0704	EYA1,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0007200	0.0000874	1	8	18	phospholipase C-activating G protein-coupled receptor signaling	BP	0.128	ADRA1B,ACTN2,HTR2B,HRH1,F2RL1,GNA14,EDN1,GNAQ	up_ACOR_VSMC
GO:0048705	0.0000878	1	5	95	skeletal system morphogenesis	BP	0.102	HOXA3,HOXA7,SULF1,HOXA1,CSGALNACT1	down_ACOR_EC
GO:0032502	0.0000883	1	177	1661	developmental process	BP	0.0148	EPHB1,PLK2,EDNRB,HOXB7,TEK,HCLS1,PCDH12,IL7R,ADGRF5,KIT,PRCP,CXCL8,PTCHD1,PRKCH,ARHGEF15,IFRD1,EMCN,CLEC14A,IL6,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,PPARG,AMOT,PDGFB,BCL6B,MALL,PODXL,RELN,CD34,LAMC2,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,CDH5,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,ARAP3,RAB27A,TCF4,SMAD1,NTN4,FOXN2,IGSF3,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SOX18,PIK3C2A,TMOD1,FIGNL1,PPP3CA,PTPRB,SERINC5,MTSS1,ODC1,ARG2,CASP8,EPHB4,NECTIN2,B3GNT5,MTOR,NAV2,TENT2,HOOK3,LRRC8C,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CAV2,PREX2,BMP2K,PDZD8,ENC1,ITPKB,GDPD5,ANGPT2,PROX1,UHRF2,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,SNX2,TSPAN12,MMP24,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,APOD,BTBD7,NCK1,EXOC5,TIMELESS,HOXB5,LDB2,SLC25A25,FES,JAG1,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,BCL10,BASP1,ZC4H2,TAOK1,CTNNA1,FMNL3,ASF1A,ADIPOR2,HMGB1,NUP133,SPTBN4,RIPK1,CRIP2,SMC5,AFF4,ITGA6,ATP11C,SKIL,ARHGDIB,CUL4A,BMX,NR1D2,HIF1A,KDM3A,AL	up_VCAV_EC
GO:0046578	0.0000886	1	19	77	regulation of Ras protein signal transduction	BP	0.0148	ARHGEF15,FGD5,FGD6,RAPGEF1,GPR4,ARAP3,PLEKHG1,PREX2,ABCA1,ITPKB,ARHGEF12,MADD,STMN1,NET1,ARHGDIB,ALS2,TNFAIP1,RGL2,ARHGEF2	up_VCAV_EC
GO:0030029	0.000089	1	38	239	actin filament-based process	BP	0.0148	TEK,HCLS1,KIT,SELE,ARHGEF15,ENSCAFG00000007112,AMOT,BAIAP2L1,PDE4D,MEF2C,STC1,EDN1,ARHGAP28,TMOD1,MTSS1,MTOR,NCKAP1,PROX1,IQGAP2,EPB41,ELMO1,STMN1,FLNB,PAK2,SWAP70,NCK1,KCNJ2,FES,CTNNA1,FMNL3,ARPC5L,ARHGDIB,ARHGAP26,GAS2L3,TNFAIP1,TMOD3,ARHGEF2,FSCN1	up_VCAV_EC
GO:0008104	0.0000903	1	71	763	protein localization	BP	0.0373	PRICKLE1,MYH9,SHROOM2,NR1H4,PLK3,HSPA5,HM13,TRAM1,PTPN14,SEC24D,PTPN11,EXOC5,SEC23A,MZT1,HOOK3,SESN2,SRP54,MYO1C,ENSCAFG00000031588,MSN,SEL1L,KIF5B,HIF1A,SSR1,IWS1,TNIK,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,AGRN,CTNNB1,KPNB1,COPB2,SRP72,ENSCAFG00000002015,TFRC,APOE,KPNA4,PLOD3,LYN,DDIT3,TLN1,MMD,GSK3B,ARMCX3,GBP5,SH3GLB1,TAX1BP3,KPNA1,REST,SCAMP1,RAB11FIP1,DISC1,KDELR2,AP3S1,CLTC,STX6,SIX4,CDKN1A,NRP1,RHBDF2,ARF4,YWHAH,BLZF1,SEC13,MID1	down_VSAP_EC

GO:0072006	0.0000903	1	4	59	nephron development	BP	0.0603	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0032392	0.0000928	1	8	19	DNA geometric change	BP	0.00936	HMGB1,MCM6,MCM4,MCM7,GINS4,RAD51,HMGB3,HMGB2	down_ACOR_VSMC
GO:0043062	0.0000932	1	15	99	extracellular structure organization	BP	0.251	ADAMTS2,FBLN2,LUM,SDC4,LOX,RECK,LCAT,CRISPLD2,B4GALT1,ADAMTSL4,LOXL3,DDR2,GREM1,SOAT1,ECM2	down_VCAV_EC
GO:0008406	0.0000943	1	4	57	gonad development	BP	0.0801	HOXA11,HOXA9,SALL1,IRX5	up_VSAP_VSMC
GO:0045137	0.0000943	1	4	57	development of primary sexual characteristics	BP	0.0801	HOXA11,HOXA9,SALL1,IRX5	up_VSAP_VSMC
GO:0001655	0.0000959	1	5	116	urogenital system development	BP	0.0603	EYA1,MME,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0007076	0.0000964	1	5	7	mitotic chromosome condensation	BP	0.00966	NCAPD2,SMC4,NCAPD3,NCAPH,SMC2	down_ACOR_VSMC
GO:0043587	0.0000988	1	2	4	tongue morphogenesis	BP	0.0603	SIX1,CYP26B1	up_VFEM_EC
GO:0072073	0.0000994	1	4	60	kidney epithelium development	BP	0.0603	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0060836	0.0000997	1	2	4	lymphatic endothelial cell differentiation	BP	0.102	ACVRL1,PDPN	down_ACOR_EC
GO:0035239	0.000101	1	8	299	tube morphogenesis	BP	0.102	ACVRL1,HOXA3,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1	down_ACOR_EC
GO:0003263	0.000101	1	2	4	cardioblast proliferation	BP	0.0603	EYA1,SIX1	up_VFEM_EC
GO:0045321	0.000106	1	32	191	leukocyte activation	BP	0.0174	IL7R,ADGRF5,KIT,CXCL8,IL6,TNFAIP3,MEF2C,CHD7,DLL4,TLR4,GATA3,RAB27A,PELI1,ARG2,NECTIN2,MTOR,SNAP23,ELF4,HHEX,ITPKB,THOC1,SWAP70,MFNG,NCK1,CD200,FES,PLCG2,BCL10,HMGB1,ATP11C,BMX,ZEB1	up_VCAV_EC
GO:0030029	0.000108	1	30	239	actin filament-based process	BP	0.0438	ARHGEF2,SIPA1L1,MYH9,FMNL3,ACTN1,VASP,TPM4,CORO1C,FSCN1,FLNB,DPYSL3,WDR1,MYO1C,TNIK,TMSB10,ACTR3,PALLD,TWF1,PLEKHG2,TLN1,PLS3,DAAM1,ENSCAFG00000017326,PAK2,CAPG,SIX4,NRP1,ENSCAFG00000030508,TNFAIP1,MYBPC2	down_VSAP_EC
GO:0003180	0.000108	1	5	7	aortic valve morphogenesis	BP	0.145	SMAD6,GATA5,GATA4,BMP4,TBX20	up_ACOR_VSMC
GO:0009966	0.000109	1	102	868	regulation of signal transduction	BP	0.0176	EPHB1,TEK,HCLS1,IL7R,SELP,KIT,PRCP,CXCL8,PRKCH,ARHGEF15,FGD5,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,BAIAP2L1,RELN,FGD6,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,GATA3,EDN1,APLNR,ARAP3,HOMER3,EGFL7,FIGNL1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,PLEKHG1,MAP3K3,BMP2,HHEX,CHN2,CAV2,PREX2,BMP2K,ABCA1,PPP1R2,ITPKB,GDPD5,RIOK3,ARHGEF12,MADD,STMN1,PAK2,MCC,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,NCK1,OTUD4,NET1,JAG1,PTGS2,RAPGEF2,CTDSPL2,BCL10,TAOK1,CTNNA1,CNOT7,HMGB1,PMAIP1,RIPK1,LSM14A,ITGA6,RGS2,SKIL,PDGFD,ARHGDIB,UFSP2,HIF1A,ARHGAP26,ALS2,ENSCAFG00000002015,TNFAIP1,IVNS1ABP,RGL2,JCAD,ZEB1,ARHGEF2,PEAR1,CDON	up_VCAV_EC
GO:0031497	0.000109	1	13	49	chromatin assembly	BP	0.0109	HMGA1,CENPA,NOC2L,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,CENPP,GRWD1,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:0009790	0.000109	1	6	335	embryo development	BP	0.0812	HOXC10,EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048562	0.000111	1	4	102	embryonic organ morphogenesis	BP	0.0812	EYA1,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042060	0.000117	1	21	103	wound healing	BP	0.0188	SELP,PRCP,F8,IFRD1,PDGFB,VWF,CD34,KLKB1,TLR4,GPR4,RAB27A,TFPI,MTOR,MMRN1,APOD,ADIPOR2,PDGFD,HIF1A,ITGB3,PEAR1,ELK3	up_VCAV_EC
GO:0048024	0.000117	1	10	30	regulation of mRNA splicing, via spliceosome	BP	0.0116	RNPS1,SRSF2,U2AF2,THRAP3,HNRNPL,SF3B4,RBM14,WTAP,JMJD6,SF3A1	down_ACOR_VSMC

GO:0006082	0.000118	1	50	305	organic acid metabolic process	BP	0.494	PEX7,HNF4A,ACSM3,LIPC,INSIG2,ACAA1,ACACB,PEX2,GOT1,DLST,GLUL,ADHFE1,ENSCAFG00000013986,WARS2,C1QTNF2,ALDH6A1,HSD17B8,FAAH,PDK2,GALK1,PTGES,SUOX,HACD4,GCDH,ABAT,BCKDHB,ENSCAFG00000016140,AZIN2,DAGLB,MARC1,EHHADH,FARS2,LONP2,ACSS2,PC,DHRS9,ABHD16A,ENSCAFG00000002977,HPGD,PNP,QARS,ENSCAFG00000023820,IDH1,IDH3A,ENSCAFG00000006639,ASS1,CHST7,LARS2,DDIT4,IDO2	up_VSAP_EC
GO:1901989	0.000119	1	10	31	positive regulation of cell cycle phase transition	BP	0.0116	BIRC5,CDK1,EZH2,CDK4,DTL,ENSCAFG00000005299,CDC25A,GLI1,UBE2C,MTBP	down_ACOR_VSMC
GO:0048513	0.000119	1	8	906	animal organ development	BP	0.393	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0008627	0.00012	1	2	5	intrinsic apoptotic signaling pathway in response to osmotic	BP	0.339	PTGER2,ARHGEF2	up_VPUL_EC
GO:0050878	0.000121	1	17	75	regulation of body fluid levels	BP	0.0191	SELP,F8,PDGFB,VWF,CD34,KLKB1,TLR4,EDN1,RAB27A,TFPI,MMRN1,STMN1,CREB1,PDGFD,HIF1A,ITGB3,PEAR1	up_VCAV_EC
GO:0007389	0.000122	1	4	137	pattern specification process	BP	0.393	HOXA3,TBX5,GATA5,HOXB5	up_VPUL_VSMC
GO:0051241	0.000123	1	48	336	negative regulation of multicellular organismal process	BP	0.0193	EPHB1,PLK2,EDNRB,TEK,ARHGEF15,IFRD1,DOCK4,TIE1,TNFAIP3,ADAMTS9,AMOT,PDGFB,CD34,PDE4D,MEF2C,FERMT1,KLKB1,DLL4,TLR4,GPR4,STC1,GATA3,HOXB8,HOMER3,TFPI,PPP3CA,GUCY1A1,ARG2,HOOK3,BMP2,HMG20A,HHEX,ITPKB,ANGPT2,MCC,THOC1,APOD,PROCR,JAG1,RAPGEF2,CTNNA1,HMGB1,SPTBN4,ARHGDIB,CUL4A,HIF1A,VASH1,TJP2	up_VCAV_EC
GO:0002253	0.000124	1	19	92	activation of immune response	BP	0.0193	PRKCH,TNFAIP3,TNIP1,TMEM173,PDE4D,MEF2C,TLR4,EIF2B2,GATA3,PELI1,NECTIN2,RIOK3,PRKD2,TLR3,OTUD4,PLCG2,BCL10,HMGB1,LSM14A	up_VCAV_EC
GO:0000077	0.000124	1	15	60	DNA damage checkpoint	BP	0.0121	HINFP,WDR76,INTS7,CDK1,CASP2,FANCI,TOPBP1,MAP3K20,RNASEH2B,DTL,DDX39B,CLSPN,H2AFX,CDC5L,ATRIP	down_ACOR_VSMC
GO:0047484	0.000126	1	2	5	regulation of response to osmotic stress	BP	0.339	PTGER2,ARHGEF2	up_VPUL_EC
GO:0007596	0.000128	1	13	47	blood coagulation	BP	0.0195	SELP,F8,PDGFB,VWF,CD34,KLKB1,TLR4,RAB27A,TFPI,MMRN1,PDGFD,ITGB3,PEAR1	up_VCAV_EC
GO:0045666	0.000129	1	16	68	positive regulation of neuron differentiation	BP	0.0195	RELN,MEF2C,RAPGEF1,RAB11A,TCF4,BMP2,GDPD5,PROX1,NCK1,FES,MMD,RAPGEF2,ZC4H2,ZEB1,ARHGEF2,CDON	up_VCAV_EC
GO:0048856	0.000129	1	16	1533	anatomical structure development	BP	0.0736	HOXC10,TBX15,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,RADIL,CYP26B1,CDC42EP5,MTSS1,CA9	up_VFEM_EC
GO:0001658	0.000132	1	3	24	branching involved in ureteric bud	BP	0.0736	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0008283	0.000133	1	68	545	cell proliferation	BP	0.0199	EPHB1,HCLS1,IL7R,KIT,CXCL8,PRKCH,CALCRL,TNFAIP3,MAP3K11,PDGFB,BCL6B,CD34,MEF2C,FERMT1,DLL4,RAPGEF1,TLR4,STC1,GATA3,EDN1,APLNR,PTGS1,SOX18,EGFL7,FIGNL1,PELI1,MTSS1,ODC1,ARG2,HOOK3,ELF4,MAP3K3,BMP2,HHEX,CAV2,CNOT6,CCAR1,ITPKB,PROX1,UHRF2,MCC,PRKD2,APOD,NCK1,FES,JAG1,PTGS2,RAPGEF2,USP28,CTNNA1,CNOT7,HMGB1,CRIP2,NRAS,USP13,PDGFD,CUL4A,BMX,HIF1A,NR4A1,HP1BP3,VASH1,JCAD,ZEB1,ARHGEF2,CDON,ZNF609,GINS4	up_VCAV_EC
GO:0030111	0.000137	1	4	108	regulation of Wnt signaling pathway	BP	0.788	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0001710	0.000137	1	2	7	mesodermal cell fate commitment	BP	0.0961	EYA1,HOXA11	up_VFEM_VSMC
GO:0035480	0.000139	1	1	1	regulation of Notch signaling pathway involved in heart	BP	0.32	GATA5	down_AFEM_VSMC
GO:0035481	0.000139	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	0.32	GATA5	down_AFEM_VSMC
GO:0003137	0.000139	1	1	1	Notch signaling pathway involved in heart	BP	0.32	GATA5	down_AFEM_VSMC
GO:0061999	0.000139	1	1	1	regulation of cardiac endothelial to	BP	0.32	GATA5	down_AFEM_VSMC
GO:0062000	0.000139	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	0.32	GATA5	down_AFEM_VSMC

GO:0090381	0.000139	1	1	1	regulation of heart induction	BP	0.32	GATA5	down_AFEM_VSMC
GO:1901321	0.000139	1	1	1	positive regulation of heart induction	BP	0.32	GATA5	down_AFEM_VSMC
GO:0035136	0.00014	1	2	16	forelimb morphogenesis	BP	0.217	HOXA9,WNT7A	up_AORTRT_VSMC
GO:0048706	0.000141	1	4	59	embryonic skeletal system development	BP	0.133	HOXA3,HOXA7,SULF1,HOXA1	down_ACOR_EC
GO:0034728	0.000144	1	14	56	nucleosome organization	BP	0.0137	CENPA,SMARCC1,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,SMARCB1,CENPP,GRWD1,SUPT16H,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:0006695	0.000147	1	7	16	cholesterol biosynthetic process	BP	0.0138	LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1	down_ACOR_VSMC
GO:1902653	0.000147	1	7	16	secondary alcohol biosynthetic process	BP	0.0138	LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1	down_ACOR_VSMC
GO:0048856	0.000148	1	8	1533	anatomical structure development	BP	0.69	HOXC6,SLITRK5,LIMK1,GATA5,CA2,LRRC17,C6,TGFBI	up_VCAV_VSMC
GO:0045165	0.000148	1	4	65	cell fate commitment	BP	0.0794	HOXC10,EYA1,SIX1,CYP26B1	up_VFEM_EC
GO:0009954	0.000148	1	2	16	proximal/distal pattern formation	BP	0.217	HOXC10,HOXA9	up_AORTRT_VSMC
GO:0030154	0.00015	1	91	1040	cell differentiation	BP	0.0539	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,TAGLN2,SERPINE1,ACTN1,SOCS5,ETV6,SGK1,ERO1A,ENPP1,ERRFI1,ITGA2,CASP3,PGK1,PTPN11,FLNB,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,FHL2,TGFBR1,PTGS2,WDR1,CHSY1,MSN,HOXB7,KIF5B,HIF1A,FOXP4,SLC45A3,TNIK,UBA6,ZPR1,PTPN2,EIF2B1,EVI2B,NEO1,ACTA2,UST,CDH11,CTNNB1,ANLN,ENSCAFG00000002015,TFRC,APOE,PLOD3,KLF5,LYN,BNIP3,STRAP,DDIT3,MMD,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,REST,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,CDYL,PAK2,CREB3L2,A2M,INHBA,CAMK2D,NR4A1,HIF1AN,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,COL12A1,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0030154	0.000151	1	119	1040	cell differentiation	BP	0.0223	EPHB1,EDNRB,HOXB7,TEK,HCLS1,IL7R,ADGRF5,KIT,PRKCH,IFRD1,IL6,FLI1,ADAMTS9,PPARG,AMOT,PDGFB,BCL6B,PODXL,RELN,CD34,PDE4D,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,QKI,GPR4,STC1,EIF2B2,GATA3,EDN1,HOXB8,RAB11A,APLNR,RAB27A,TCF4,NTN4,FOXN2,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SOX18,TMOD1,FIGNL1,PPP3CA,MTSS1,CASP8,NECTIN2,MTOR,NAV2,TENT2,HOOK3,LRRC8C,ELF4,BMP2,CDYL,HMG20A,HHEX,CAV2,PREX2,ITPKB,GDPD5,ANGPT2,PROX1,UHRF2,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,MMP24,PAK2,MFNG,APOD,NCK1,HOXB5,FES,JAG1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BASP1,ZC4H2,CTNNA1,ASF1A,HMGB1,NUP133,SPTBN4,RIPK1,AFF4,ITGA6,ATP11C,SKIL,CUL4A,BMX,NR1D2,HIF1A,KDM3A,ALS2,ATRX,NR4A1,ENSCAFG00000002015,P2RX2,TMOD3,ZEB1,TET2,ARHGEF2,FBXO5,CDON,ELK3,TJP2,ZNF609	up_VCAV_EC
GO:0006325	0.000151	1	37	234	chromatin organization	BP	0.014	SREBF1,POLE3,ATAD2,HMGA1,ENSCAFG00000016482,CENPA,PRMT1,CDK1,AURKB,EZH2,FBL,SMARCC1,UHRF1,BRCA1,NOC2L,OIP5,IPO4,HIST1H1A,SUV39H1,HASPIN,HMGB2,DMAP1,HIST1H2BB,SMARCB1,CCNA2,RBM14,BAP1,CENPP,GRWD1,SUPT16H,TADA2A,HAT1,HIST2H2AC,H2AFX,MIS18A,HMGN1,H3F3B	down_ACOR_VSMC
GO:0003002	0.000151	1	4	118	regionalization	BP	0.788	HOXA3,BARX1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0031570	0.000152	1	15	61	DNA integrity checkpoint	BP	0.014	HINFP,WDR76,INTS7,CDK1,CASP2,FANCI,TOPBP1,MAP3K20,RNASEH2B,DTL,DDX39B,CLSPN,H2AFX,CDC5L,ATRIP	down_ACOR_VSMC
GO:0048663	0.000152	1	2	13	neuron fate commitment	BP	0.306	HOXC10,EYA1	up_AFEM_VSMC
GO:0060065	0.000152	1	2	7	uterus development	BP	0.102	HOXA9,HOXA11	up_VFEM_VSMC

GO:0065007	0.000155308	0.99991	117	3499	biological regulation	BP	0.35802952	C7,CNTNAP4,SH3TC2,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TRPS1,PLCL1,PKIB,CALY,SOX9,RHOU,PKNOX2,ARHGAP6,PTH1R,RGS1,PCSK1N,FNDC4,NDRG2,AQP1,PORCN,ENSCAFG00000004331,SYNPO2,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,SEMA6D,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,IL33,RGMA,CASP10,LHX9,PDE4A,INSYN1,SMAD6,DYNC1I1,KLHL25,PLCE1,PLS1,ACTN2,ZMYND8,ARHGAP28,RNLS,ESM1,PTGDS,PAK3,MMP28,GUCY1B1,GRK7,BCL2,TRIM8,TNFRSF19,PTGER4,ARHGDIB,PREB,CST3,PIAS1,DCLK2,ADAMTSL2,USP53,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,TBX5,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SLC9A9,SFMBT2,C23H3orf58,ZNF229,CHMP4B,TP53INP2,TMTC2,RARRES2,VPS16,GMEB2,RIOX2,PRKACA,RNF114,STK32C,NRP1,AZIN2,AGPAT2,ARHGEF26,PRKCD,GNAZ,RIN2,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,MFAP4,ADGRL1,TUBB4A,TLE2	up_ACOR_EC
GO:0090329	0.000156	1	9	25	regulation of DNA-dependent DNA	BP	0.0143	SMC1A,RFC2,RFC5,RFC3,RFC4,GMNN,E2F8,SMC3,CDK2	down_ACOR_VSMC
GO:0007599	0.000157	1	13	48	hemostasis	BP	0.0231	SELP,F8,PDGFB,VWF,CD34,KLKB1,TLR4,RAB27A,TFPI,MMRN1,PDGFD,ITGB3,PEAR1	up_VCAV_EC
GO:0043484	0.000157	1	12	43	regulation of RNA splicing	BP	0.0143	RNPS1,SRSF2,U2AF2,THRAP3,HNRNPL,SF3B4,HNRNPF,RBM14,RBM17,WTAP,JMJD6,SF3A1	down_ACOR_VSMC
GO:0060272	0.00016	1	2	7	embryonic skeletal joint morphogenesis	BP	0.104	HOXA11,SHOX2	up_VFEM_VSMC
GO:0007275	0.000161	1	17	1370	multicellular organism development	BP	0.144	ACVRL1,LYN,HOXA3,ACSL4,SPG11,PDPN,NRP2,HIVEP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,HOXC4,ASPN,NEDD4	down_ACOR_EC
GO:0051225	0.000162	1	13	49	spindle assembly	BP	0.0146	SMC1A,FBXO5,BIRC5,AURKB,HAUS8,NEK2,RCC1,SMC3,STAG1,ENSCAFG00000005299,CDC20,ASPM,KIF11	down_ACOR_VSMC
GO:0051649	0.000163	1	60	630	establishment of localization in cell	BP	0.0548	PRICKLE1,MYH9,SHROOM2,NR1H4,PLK3,HM13,ANKRD50,TRAM1,ERO1A,PTPN14,SEC24D,HYOU1,PTPN11,SEC23A,HOOK3,PPP1R12A,SRP54,TMEM87B,MYO1C,CANX,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TRAK1,SSR1,IWS1,YIPF5,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,CTNNB1,KPNB1,COPB2,SRP72,CRYAB,KPNA4,LYN,DDIT3,GSK3B,SH3GLB1,KPNA1,HTT,CALM1,AP3S1,CLTC,CREB3L2,STX6,CDKN1A,YWHAH,SEC13	down_VSAP_EC
GO:0050769	0.000164	1	20	95	positive regulation of neurogenesis	BP	0.0238	PRKCH,RELN,MEF2C,RAPGEF1,RAB11A,TCF4,MTOR,BMP2,GDPD5,PROX1,NCK1,FES,MMD,RAPGEF2,ZC4H2,HIF1A,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0090307	0.000168	1	9	26	mitotic spindle assembly	BP	0.0151	SMC1A,BIRC5,AURKB,NEK2,SMC3,STAG1,ENSCAFG00000005299,CDC20,KIF11	down_ACOR_VSMC
GO:0003012	0.000168	1	2	90	muscle system process	BP	0.438	JUP,GATA5	down_VFEM_VSMC
GO:0003264	0.00017	1	2	5	regulation of cardioblast proliferation	BP	0.0857	EYA1,SIX1	up_VFEM_EC
GO:0003266	0.00017	1	2	5	regulation of secondary heart field cardioblast	BP	0.0857	EYA1,SIX1	up_VFEM_EC
GO:0010639	0.000172	1	24	128	negative regulation of organelle organization	BP	0.0154	ATAD2,ZW10,CAPG,TRIP13,SLC25A5,FBXO5,PRELID1,BIRC5,INSIG1,LIMA1,STMN1,NEK2,BRCA1,NOC2L,NDC80,ENSCAFG00000005299,BUB1,RBM14,CORO1A,TTK,ARHGEF2,TINF2,MTBP,GEN1	down_ACOR_VSMC

GO:0023051	0.000175	1	109	954	regulation of signaling	BP	0.0252	EPHB1,PLK2,TEK,HCLS1,IL7R,SELP,KIT,PRCP,CXCL8,PRKCH,ARHGEF15,FGD5,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,BAIAP2L1,RELN,FGD6,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,CHD7,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,GATA3,EDN1,APLNR,ARAP3,SNCAIP,HOMER3,EGFL7,FIGNL1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,PLEKHG1,MAP3K3,BMP2,HHEX,CHN2,CAV2,PREX2,BMP2K,ABCA1,PPP1R2,ITPKB,GDPD5,RIOK3,ARHGEF12,MADD,STMN1,PAK2,MCC,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,NCK1,OTUD4,NET1,JAG1,GRM8,PTGS2,RAPGEF2,CTDSPL2,CREB1,BCL10,TAOK1,CTNNA1,CNOT7,HMGB1,PMAIP1,RIPK1,LSM14A,ITGA6,RGS2,SKIL,MCU,PDGFD,ARHGDIB,UFSP2,HIF1A,ARHGAP26,ALS2,LMTK2,ENSCAFG00000002015,TNFAIP1,IVNS1ABP,RGL2,JCAD,ZEB1,ARHGEF2,PEAR1,CDON	up_VCAV_EC
GO:0048731	0.000178	1	105	1247	system development	BP	0.0587	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,SERPINH1,MYH9,NR1H4,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,SGK1,PRKACB,PTPN14,ERRFI1,JCAD,CASP3,PGK1,BCAR3,PTPN11,AARS,FLNB,ENSCAFG00000032470,DPYSL3,HOOK3,IFRD1,TMED2,ILK,FHL2,PRCP,SMARCA4,TGFBR1,PTGS2,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,HIF1A,SLC45A3,SLC20A1,THBS2,ACTG2,TNIK,NXN,UBA6,ZPR1,PTPN2,UCHL5,EIF2B1,EVI2B,NEO1,MTDH,ESM1,ACTA2,ADAMTS6,UST,CDH11,MAGED1,CTNNB1,ANLN,CRYAB,STARD13,TFRC,APOE,PLOD3,KLF5,LYN,STRAP,DDIT3,PDS5B,MMD,PLS3,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,HTT,REST,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,RTCB,HOMER1	down_VSAP_EC
GO:0009952	0.000183	1	4	66	anterior/posterior pattern specification	BP	0.0897	HOXC10,HOXA9,HOXB7,HOXA7	up_VFEM_EC
GO:0031333	0.000183612	0.99998	7	46	negative regulation of protein complex assembly	BP	0.3703682	TMOD1,SMAD6,PTGER4,CLSTN1,CLU,PRKCD,TUBB4A	up_ACOR_EC
GO:0010646	0.000185	1	108	945	regulation of cell communication	BP	0.0264	EPHB1,PLK2,TEK,HCLS1,IL7R,SELP,KIT,PRCP,CXCL8,PRKCH,ARHGEF15,FGD5,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,BAIAP2L1,RELN,FGD6,CXHXorf36,PDE4D,MEF2C,FERMT1,ATF3,CHD7,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,GATA3,EDN1,APLNR,ARAP3,SNCAIP,HOMER3,EGFL7,FIGNL1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,PLEKHG1,MAP3K3,BMP2,HHEX,CHN2,CAV2,PREX2,BMP2K,ABCA1,PPP1R2,ITPKB,GDPD5,RIOK3,ARHGEF12,MADD,STMN1,PAK2,MCC,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,APOD,NCK1,OTUD4,NET1,JAG1,GRM8,PTGS2,RAPGEF2,CTDSPL2,CREB1,BCL10,TAOK1,CTNNA1,CNOT7,HMGB1,PMAIP1,RIPK1,LSM14A,ITGA6,RGS2,SKIL,MCU,PDGFD,ARHGDIB,UFSP2,HIF1A,ARHGAP26,ALS2,ENSCAFG00000002015,TNFAIP1,IVNS1ABP,RGL2,JCAD,ZEB1,ARHGEF2,PEAR1,CDON	up_VCAV_EC
GO:0043009	0.000185	1	5	227	chordate embryonic development	BP	0.115	EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0043009	0.000185	1	4	227	chordate embryonic development	BP	0.306	TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:0007548	0.000185	1	4	68	sex differentiation	BP	0.149	HOXA11,HOXA9,SALL1,IRX5	up_VSAP_VSMC
GO:0022603	0.000188	1	44	301	regulation of anatomical structure morphogenesis	BP	0.0266	PLK2,HOXB7,TEK,KIT,CXCL8,IFRD1,TIE1,TNFAIP3,ADAMTS9,AMOT,RELN,CD34,MEF2C,DLL4,GPR4,GATA3,EDN1,RAB11A,APLNR,ARAP3,SMAD1,NTN4,NEDD9,PIK3C2A,PPP3CA,MTOR,MAP3K3,BMP2,HHEX,PDZD8,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,BTBD7,FES,RAPGEF2,FMNL3,HIF1A,ENSCAFG00000002015,VASH1,JCAD,ZMYM2	up_VCAV_EC
GO:0090330	0.000188	1	2	5	regulation of platelet aggregation	BP	0.16	LYN,PDPN	down_ACOR_EC

GO:0032502	0.000189	1	60	1661	developmental process	BP	0.509	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXC10,LEP,LBH,XYLT1,GAS1,ANGPT4,HOXA7,COL8A2,CD40,DLL1,CRYAB,F3,VXN,PLXNA4,GPAM,NEFH,TWIST2,MAB21L1,THRB,LGI4,HCK,TMEM100,PLAGL2,GREM1,NFE2L1,OVOL1,CAMK2A,GREM2,HOXA6,CYLD,POSTN,LUZP1,MYBL1,RECK,PTHLH,TBXA2R,EVI2B,CNNM4,BVES,LGR6,PTPRB,AXIN2,ACACB,NAPEPLD,PPARGC1A,CDC42EP5,DMPK,ADAM17,CLIC4,LRRN2,HSPB2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC
GO:2001251	0.000189	1	13	49	negative regulation of chromosome organization	BP	0.0166	ATAD2,ZW10,TRIP13,FBXO5,BIRC5,BRCA1,NOC2L,NDC80,ENSCAFG00000005299,BUB1,TTK,TINF2,GEN1	down_ACOR_VSMC
GO:0007186	0.000191	1	25	124	G protein-coupled receptor signaling pathway	BP	0.237	ADRA1B,ATRNL1,ACTN2,LGR6,PLCL1,ADGRD1,HTR2B,ABCA1,HRH1,GLRB,PTGIR,ADCY6,F2RL1,GNA14,APLP1,AGRN,SCG5,RGS2,SENP7,CCL5,EDN1,HPGD,USP20,GNAQ,INPP5K	up_ACOR_VSMC
GO:0043436	0.000194	1	49	303	oxoacid metabolic process	BP	0.494	PEX7,HNF4A,ACSM3,LIPC,INSIG2,ACAA1,ACACB,PEX2,GOT1,DLST,GLUL,ADHFE1,ENSCAFG00000013986,WARS2,C1QTNF2,ALDH6A1,HSD17B8,FAAH,PDK2,GALK1,PTGES,SUOX,HACD4,GCDH,ABAT,BCKDHB,ENSCAFG00000016140,AZIN2,DAGLB,MARC1,EHHADH,FARS2,LONP2,ACSS2,PC,DHRS9,ABHD16A,ENSCAFG00000002977,HPGD,QARS,ENSCAFG00000023820,IDH1,IDH3A,ENSCAFG00000006639,ASS1,CHST7,LARS2,DDIT4,IDO2	up_VSAP_EC
GO:0048856	0.000195	1	124	1533	anatomical structure development	BP	0.0619	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,TAGLN2,NR1H4,FMNL3,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,SGK1,PRKACB,PTPN14,PTK7,ERRFI1,ITGA2,SEC24D,JCAD,CASP3,PGK1,AKAP2,BCAR3,PTPN11,EXOC5,FSCN1,AARS,FLNB,ENSCAFG00000032470,DPYSL3,HOOK3,IFRD1,TMED2,ILK,FHL2,PRCP,SMARCA4,TGFBR1,PTGS2,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,HIF1A,FOXP4,SLC45A3,SLC20A1,THBS2,ACTG2,TNIK,NXN,UBA6,ZPR1,PTPN2,UCHL5,EIF2B1,EVI2B,NEO1,MTDH,ESM1,ADAM17,ACTA2,ADAMTS6,UST,CDH11,MAGED1,CTNNB1,ANLN,CRYAB,STARD13,ENSCAFG00000002015,TFRC,APOE,PLOD3,KLF5,LYN,BNIP3,STRAP,DDIT3,PDS5B,MMD,PLS3,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,HTT,REST,RBBP8,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,CDYL,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,HIF1AN,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,COL12A1,RTCB,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0048869	0.000197	1	96	1119	cellular developmental process	BP	0.0619	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,TAGLN2,FMNL3,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,SGK1,ERO1A,ENPP1,ERRFI1,ITGA2,CASP3,PGK1,AKAP2,NUAK1,PTPN11,FLNB,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,FHL2,TGFBR1,PTGS2,WDR1,CHSY1,MSN,HOXB7,KIF5B,HIF1A,FOXP4,SLC45A3,TNIK,UBA6,ZPR1,PTPN2,EIF2B1,EVI2B,NEO1,ACTA2,UST,CDH11,CTNNB1,ANLN,ENSCAFG00000002015,TFRC,APOE,PLOD3,KLF5,LYN,BNIP3,STRAP,DDIT3,MMD,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,REST,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,CDYL,PAK2,CREB3L2,A2M,INHBA,CAMK2D,NR4A1,HIF1AN,BTK,SIX4,CDKN1A,NRP1,SPINK2,ARF4,YWHAH,COL12A1,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0048731	0.000198	1	16	1247	system development	BP	0.16	ACVRL1,LYN,HOXA3,ACSL4,SPG11,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,HOXC4,ASPN,NEDD4	down_ACOR_EC
GO:0009792	0.000199	1	4	231	embryo development ending in birth or egg	BP	0.306	TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:0002684	0.0002	1	36	239	positive regulation of immune system process	BP	0.028	HCLS1,IL7R,GBP5,SELP,CXCL8,PRKCH,TNFAIP3,TNIP1,TMEM173,PDE4D,MEF2C,TLR4,NLRC5,EIF2B2,GATA3,PELI1,CASP8,NECTIN2,ITPKB,RIOK3,PRKD2,SWAP70,TLR3,NCK1,OTUD4,CD200,FES,JAG1,PLCG2,CREB1,BCL10,HMGB1,RIPK1,LSM14A,ATP11C,HIF1A	up_VCAV_EC

GO:0097028	0.000201	1	2	11	dendritic cell differentiation	BP	0.487	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0009792	0.000203	1	5	231	embryo development ending in birth or egg	BP	0.118	EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0034613	0.000206	1	56	576	cellular protein localization	BP	0.0626	PRICKLE1,PLK3,HSPA5,HM13,TRAM1,PTPN14,SEC24D,PTPN11,EXOC5,SEC23A,MZT1,HOOK3,SESN2,SRP54,MYO1C,MSN,SEL1L,KIF5B,SSR1,IWS1,TNIK,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,AGRN,CTNNB1,KPNB1,COPB2,SRP72,APOE,KPNA4,DDIT3,TLN1,GSK3B,ARMCX3,GBP5,SH3GLB1,TAX1BP3,KPNA1,DISC1,KDELR2,AP3S1,CLTC,STX6,SIX4,CDKN1A,NRP1,ARF4,YWHAH,BLZF1,MID1	down_VSAP_EC
GO:1902531	0.000208	1	69	536	regulation of intracellular signal transduction	BP	0.0289	EPHB1,TEK,HCLS1,IL7R,SELP,KIT,ARHGEF15,FGD5,TNFAIP3,MAP3K11,TNIP1,AMOT,PDGFB,RELN,FGD6,PDE4D,ATF3,RAPGEF1,TLR4,GPR4,GATA3,EDN1,APLNR,ARAP3,HOMER3,FIGNL1,PELI1,PPP3CA,GUCY1A1,CASP8,MTOR,PLEKHG1,MAP3K3,BMP2,CHN2,PREX2,ABCA1,ITPKB,RIOK3,ARHGEF12,MADD,STMN1,PAK2,PRKD2,TLR3,AKAP12,NCK1,NET1,PTGS2,RAPGEF2,BCL10,TAOK1,CNOT7,HMGB1,PMAIP1,RIPK1,SKIL,PDGFD,ARHGDIB,HIF1A,ARHGAP26,ALS2,ENSCAFG00000002015,TNFAIP1,IVNS1ABP,RGL2,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0034724	0.000208	1	6	12	DNA replication-independent nucleosome	BP	0.0181	OIP5,IPO4,CENPP,SUPT16H,HAT1,MIS18A	down_ACOR_VSMC
GO:0009954	0.000209	1	2	16	proximal/distal pattern formation	BP	0.306	HOXC10,HOXA9	up_AFEM_VSMC
GO:0003002	0.00021	1	4	118	regionalization	BP	0.118	HOXC10,HOXA9,EMX2,HOXA11	up_VFEM_VSMC
GO:0060914	0.000211	1	2	11	heart formation	BP	0.487	TBX5,GATA5	up_VPUL_VSMC
GO:0048513	0.000213	1	12	906	animal organ development	BP	0.152	HOXA11,TBX15,HOXA9,PITX1,EMX2,SALL1,HOXC10,IRX5,MAB21L1,CAV1,SHOX2,GJB5	up_VSAP_VSMC
GO:0048608	0.000213	1	5	129	reproductive structure development	BP	0.152	HOXA11,HOXA9,SALL1,IRX5,GJB5	up_VSAP_VSMC
GO:0072498	0.000213	1	2	8	embryonic skeletal joint development	BP	0.118	HOXA11,SHOX2	up_VFEM_VSMC
GO:0009952	0.000216	1	4	66	anterior/posterior pattern specification	BP	0.152	HOXA11,HOXA9,EMX2,HOXC10	up_VSAP_VSMC
GO:0048645	0.00022	1	2	33	animal organ formation	BP	0.64	HOXA3,TBX5	up_APUL_VSMC
GO:0030318	0.000224	1	5	8	melanocyte differentiation	BP	0.0309	EDNRB,KIT,ADAMTS9,MEF2C,RAB27A	up_VCAV_EC
GO:0060675	0.000226	1	3	29	ureteric bud morphogenesis	BP	0.107	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0061458	0.000227	1	5	131	reproductive system development	BP	0.152	HOXA11,HOXA9,SALL1,IRX5,GJB5	up_VSAP_VSMC
GO:0003002	0.000227	1	3	118	regionalization	BP	0.306	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0070727	0.000234	1	56	579	cellular macromolecule localization	BP	0.0691	PRICKLE1,PLK3,HSPA5,HM13,TRAM1,PTPN14,SEC24D,PTPN11,EXOC5,SEC23A,MZT1,HOOK3,SESN2,SRP54,MYO1C,MSN,SEL1L,KIF5B,SSR1,IWS1,TNIK,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,AGRN,CTNNB1,KPNB1,COPB2,SRP72,APOE,KPNA4,DDIT3,TLN1,GSK3B,ARMCX3,GBP5,SH3GLB1,TAX1BP3,KPNA1,DISC1,KDELR2,AP3S1,CLTC,STX6,SIX4,CDKN1A,NRP1,ARF4,YWHAH,BLZF1,MID1	down_VSAP_EC
GO:0043586	0.000237	1	2	6	tongue development	BP	0.109	SIX1,CYP26B1	up_VFEM_EC
GO:0048598	0.000238	1	3	207	embryonic morphogenesis	BP	0.64	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0009790	0.000242	1	8	335	embryo development	BP	0.18	ACVRL1,HOXA3,ACSL4,NRP2,HOXA7,SULF1,HOXA1,HOXC4	down_ACOR_EC

GO:0032502	0.000243	1	132	1661	developmental process	BP	0.0691	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,TAGLN2,NR1H4,FMNL3,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,SGK1,ERO1A,PRKACB,PTPN14,PTK7,ENPP1,ERRFI1,ITGA2,SEC24D,JCAD,CASP3,PGK1,AKAP2,BCAR3,NUAK1,PTPN11,EXOC5,FSCN1,AARS,FLNB,ENSCAFG00000032470,DPYSL3,HOOK3,TRIB3,IFRD1,TMED2,ILK,FHL2,PRCP,SMARCA4,TGFBR1,PTGS2,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,HIF1A,FOXP4,SLC45A3,SLC20A1,THBS2,ACTG2,TNIK,NXN,UBA6,ZPR1,PTPN2,UCHL5,EIF2B1,EVI2B,NEO1,MTDH,ESM1,ADAM17,ACTA2,ADAMTS6,UST,CDH11,MAGED1,CTNNB1,ANLN,CRYAB,STARD13,ENSCAFG00000002015,TFRC,APOE,WWC3,PLOD3,KLF5,LYN,BNIP3,STRAP,DDIT3,PDS5B,MMD,PLS3,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,HTT,REST,RBBP8,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,CDYL,PAK2,CREB3L2,LRRTM2,A2M,INHBA,CAMK2D,NR4A1,HIF1AN,BTK,SIX4,CDKN1A,NRP1,SPINK2,ARF4,YWHAH,COL12A1,RTCB,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0009653	0.000243	1	6	773	anatomical structure morphogenesis	BP	0.69	SLITRK5,LIMK1,GATA5,CA2,C6,TGFBI	up_VCAV_VSMC
GO:0051094	0.000245	1	7	388	positive regulation of developmental process	BP	0.493	TBX5,NR1H4,EVI2B,WIF1,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0031960	0.000245	1	7	15	response to corticosteroid	BP	0.494	FAM107A,SLIT2,GOT1,ZFP36L1,CREBRF,ZFP36L2,DDIT4	up_VSAP_EC
GO:0051384	0.000245	1	7	15	response to glucocorticoid	BP	0.494	FAM107A,SLIT2,GOT1,ZFP36L1,CREBRF,ZFP36L2,DDIT4	up_VSAP_EC
GO:0030261	0.000246	1	5	8	chromosome condensation	BP	0.021	NCAPD2,SMC4,NCAPD3,NCAPH,SMC2	down_ACOR_VSMC
GO:0009653	0.000247	1	71	773	anatomical structure morphogenesis	BP	0.0691	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,SERPINH1,MYH9,FMNL3,HSPA5,SERPINE1,ACTN1,SPARC,SGK1,PRKACB,PTPN14,PTK7,ERRFI1,ITGA2,JCAD,PGK1,AKAP2,BCAR3,PTPN11,EXOC5,FSCN1,FLNB,ENSCAFG00000032470,IFRD1,TMED2,ILK,FHL2,PRCP,TGFBR1,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,HIF1A,FOXP4,THBS2,ACTG2,TNIK,UCHL5,NEO1,MTDH,ESM1,ADAM17,ACTA2,UST,CDH11,MAGED1,CTNNB1,CRYAB,STARD13,ENSCAFG00000002015,APOE,PLOD3,KLF5,BNIP3,VLDLR,MYO1E,SDC4,EXT1,INHBA,SIX4,NRP1,YWHAH,COL12A1,MYBPC2	down_VSAP_EC
GO:0044057	0.000248	1	2	110	regulation of system process	BP	0.438	JUP,GATA5	down_VFEM_VSMC
GO:0032956	0.000250732	0.99994	11	116	regulation of actin cytoskeleton organization	BP	0.44956164	TMOD1,ARHGAP6,SYNPO2,DIXDC1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,NRP1,PRKCD	up_ACOR_EC
GO:0045944	0.000254	1	43	287	positive regulation of transcription by RNA polymerase II	BP	0.0347	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,ENSCAFG00000017103,IRF8,PPP3CA,YES1,BMP2,HHEX,CREM,PROX1,ARID4B,PRKD2,SMARCA4,TLR3,NCK1,LDB2,JAG1,CNOT7,HMGB1,AHR,RIPK1,ITGA6,MTA2,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0072171	0.000254	1	3	30	mesonephric tubule morphogenesis	BP	0.114	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0006271	0.000256	1	4	5	DNA strand elongation involved in DNA	BP	0.0217	POLA1,POLE,FEN1,PCNA	down_ACOR_VSMC
GO:0043410	0.000263	1	28	144	positive regulation of MAPK cascade	BP	0.288	ADRA1B,LEP,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,F2RL1,NRP1,PTPN22,NPNT,PRKCE,FRS2,APP,PSEN1,CCL5,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0009896	0.000264	1	19	127	positive regulation of catabolic process	BP	0.0698	PRICKLE1,PLK3,SOCS5,TRIB3,SESN2,MSN,HIF1A,MTDH,CNOT7,APOE,BNIP3,GSK3B,CDC37,SH3GLB1,HTT,ABHD5,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:2001257	0.000268	1	3	30	regulation of cation channel activity	BP	0.173	NETO1,STIM1,CAV1	up_VSAP_VSMC

GO:0019752	0.00027	1	46	283	carboxylic acid metabolic process	BP	0.494	PEX7,HNF4A,ACSM3,LIPC,INSIG2,ACAA1,ACACB,PEX2,GOT1,DLST,GLUL,ADHFE1,ENSCAFG00000013986,WARS2,C1QTNF2,ALDH6A1,HSD17B8,FAAH,PDK2,GALK1,PTGES,HACD4,GCDH,ABAT,BCKDHB,ENSCAFG00000016140,AZIN2,DAGLB,EHHADH,FARS2,LONP2,ACSS2,PC,DHRS9,ABHD16A,ENSCAFG00000002977,HPGD,QARS,ENSCAFG00000023820,IDH1,IDH3A,ENSCAFG00000006639,ASS1,LARS2,DDIT4,IDO2	up_VSAP_EC
GO:0032502	0.000272	1	8	1661	developmental process	BP	0.69	HOXC6,SLITRK5,LIMK1,GATA5,CA2,LRRC17,C6,TGFBI	up_VCAV_VSMC
GO:0035480	0.000272	1	1	1	regulation of Notch signaling pathway involved in heart	BP	0.438	GATA5	down_VFEM_VSMC
GO:0035481	0.000272	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	0.438	GATA5	down_VFEM_VSMC
GO:0003137	0.000272	1	1	1	Notch signaling pathway involved in heart	BP	0.438	GATA5	down_VFEM_VSMC
GO:0061999	0.000272	1	1	1	regulation of cardiac endothelial to	BP	0.438	GATA5	down_VFEM_VSMC
GO:0062000	0.000272	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	0.438	GATA5	down_VFEM_VSMC
GO:0090381	0.000272	1	1	1	regulation of heart induction	BP	0.438	GATA5	down_VFEM_VSMC
GO:1901321	0.000272	1	1	1	positive regulation of heart induction	BP	0.438	GATA5	down_VFEM_VSMC
GO:0007389	0.000274	1	4	137	pattern specification process	BP	0.788	HOXA3,BARX1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0044085	0.000276	1	120	1076	cellular component biogenesis	BP	0.0231	ACSL3,FSCN1,HMGB1,IRAK1,ANLN,STXBP6,USP4,HMGA1,HMGCR,EDC3,SMC1A,UBE2S,RRM1,ZW10,CAPG,CENPA,SLC29A1,NDC1,CENPN,TRIP13,C1QTNF6,NOP56,SDC1,FBXO5,HSPA9,RAN,CFAP298,PSMD13,BIRC5,INSIG1,PRMT1,CAV1,RAD51,LIMA1,NF2,AURKB,TK1,STMN1,CENPO,HAUS8,GREM1,NEK2,FBL,RCC1,DHX33,DIS3,GMNN,CENPH,POC1A,NOC4L,WDR62,CENPI,FASTKD3,NOC2L,B4GALT1,FARSA,PREB,OIP5,IPO4,HIST1H1A,RAC1,NUP62,EMP2,DDX28,PDXP,FOSL1,PLK4,RSL1D1,IQGAP2,SAMM50,RRP1,HMGB2,CDC42EP4,HIST1H2BB,SMC3,CDK2,DDX39B,STAG1,ENSCAFG00000005299,EZR,SF3A2,SASS6,RBM14,CORO1A,CENPW,FOXRED1,CDC20,SIGMAR1,ENSCAFG00000019620,ASPM,ARPC1B,NOP14,CENPP,GRWD1,ENSCAFG00000010224,PRMT5,PSMC1,CTH,NOP58,TRAPPC6A,ENSCAFG00000015189,KIF11,HAT1,TINF2,EMG1,EXOSC5,GEMIN7,UBE2C,MIS18A,TBCC,SIX4,H3F3B,CEP83,PDSS1,TTLL1,TPBG,SF3A1,EIF3M,NOB1,KIF24	down_ACOR_VSMC
GO:1903010	0.000276	1	4	8	regulation of bone development	BP	0.446	NOTCH2,FBN1,GLI3,GREM1	down_VCAV_EC
GO:0048705	0.000276	1	3	95	skeletal system morphogenesis	BP	0.372	TBX15,EYA1,IRX5	up_AFEM_VSMC
GO:1900120	0.000277	1	2	7	regulation of receptor binding	BP	1	HOXA3,PLCL1	up_APUL_EC
GO:1904018	0.000278	1	15	69	positive regulation of vasculature development	BP	0.0371	PLK2,TEK,KIT,CXCL8,PDGFB,CD34,APLNR,SMAD1,PIK3C2A,MAP3K3,PRKD2,TLR3,RAPGEF2,HIF1A,JCAD	up_VCAV_EC
GO:0001501	0.00028	1	6	178	skeletal system development	BP	0.185	HOXA3,HOXA7,SULF1,HOXA1,CSGALNACT1,HOXC4	down_ACOR_EC
GO:0030198	0.000281	1	19	81	extracellular matrix organization	BP	0.288	FMOD,PRDX4,RECK,FERMT1,MFAP4,SPINT1,CTSS,ERO1B,NPNT,SPINT2,P4HA1,DAG1,APP,ECM2,DDR2,NID1,SERPINB5,KIF9,TNFRSF11B	up_ACOR_VSMC
GO:0006613	0.000281	1	5	12	cotranslational protein targeting to membrane	BP	0.0733	TRAM1,SRP54,SSR1,SRPRA,SRP72	down_VSAP_EC
GO:0003274	0.000281	1	1	2	endocardial cushion fusion	BP	0.517	GATA5	down_AFEM_VSMC
GO:0009888	0.000282	1	9	545	tissue development	BP	0.12	EYA1,TOX,HOXB7,HOXA7,SIX1,TIAM1,CYP26B1,MTSS1,CA9	up_VFEM_EC
GO:0048869	0.000283	1	13	1119	cellular developmental process	BP	0.12	HOXC10,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,TIAM1,RADIL,CYP26B1,CDC42EP5,MTSS1	up_VFEM_EC
GO:0000380	0.000284	1	8	22	alternative mRNA splicing, via spliceosome	BP	0.0235	RNPS1,SRSF2,THRAP3,HNRNPL,RBM14,RBM17,WTAP,SF3A1	down_ACOR_VSMC

GO:0031536	0.000284	1	3	3	positive regulation of exit from mitosis	BP	0.0235	BIRC5,ENSCAFG00000005299,UBE2C	down_ACOR_VSMC
GO:0007154	0.000286	1	194	1622	cell communication	BP	0.288	SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TLR1,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,IFNGR1,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,ADGRD1,CD83,EFNB2,ANGPT1,ENSCAFG00000016285,HTR2B,RASSF2,MBP,ZRANB1,FBXL20,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,RERG,GLRB,ARHGAP29,ZNRF3,CD274,PLPP2,AR,PTGIR,SASH1,STX11,GPR155,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ADCY6,ITPR1,GRK7,LIMS2,BLNK,ANKRD1,F2RL1,ADGRL1,CAMK2D,PSEN2,PPP2R5E,GABARAPL1,DAPK1,ARHGAP5,BNIP3,EGLN1,CACNB3,NCEH1,SLC12A7,AKAP6,CDKN1A,JMY,GNA14,CRLF3,ENSCAFG00000006238,CLSTN1,LRRC8C,CREBRF,NRP1,UBR1,PDE1A,PTPN22,DMPK,NPNT,UNC5B,SMPD1,RCAN2,APLP1,SLITRK5,TBX20,SESN3,SH3RF1,TBX5,CCDC3,PRKCE,FZD3,FRS2,AGRN,RNF19A,RND1,SCG5,RGS2,DAG1,FUT8,PARP9,APP,PSEN1,TGFBR1,SYNJ2BP,CHD7,TESK2,PIK3C3,LAMP2,JUP,SIPA1L1,SENP7,CCL5,WWC2,PERP,PSKH1,RTKN2,DUSP22,SIAH1,TIRAP,RAB11B,EDN1,SESN1,HPGD,KCNC4,DUSP26,NOD2,LRRC4,A	up_ACOR_VSMC
GO:0050776	0.000286	1	28	173	regulation of immune response	BP	0.0378	IL7R,GBP5,KIT,PRKCH,TNFAIP3,TNIP1,TMEM173,PDE4D,MEF2C,TLR4,NLRC5,EIF2B2,GATA3,PELI1,ARG2,NECTIN2,RIOK3,PRKD2,THOC1,TLR3,OTUD4,CD200,FES,PLCG2,BCL10,CNOT7,HMGB1,LSM14A	up_VCAV_EC
GO:0034110	0.000286	1	2	6	regulation of homotypic cell-cell adhesion	BP	0.185	LYN,PDPN	down_ACOR_EC
GO:0140074	0.000288	1	1	2	cardiac endothelial to mesenchymal transition	BP	0.517	GATA5	down_AFEM_VSMC
GO:0006268	0.000289	1	4	5	DNA unwinding involved in DNA replication	BP	0.0238	MCM6,MCM4,MCM7,RAD51	down_ACOR_VSMC
GO:0046907	0.000291	1	52	536	intracellular transport	BP	0.0746	PRICKLE1,PLK3,HM13,ANKRD50,TRAM1,PTPN14,SEC24D,HYOU1,PTPN11,SEC23A,HOOK3,PPP1R12A,SRP54,TMEM87B,MYO1C,MSN,RAB6A,SEL1L,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TRAK1,SSR1,IWS1,YIPF5,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,CTNNB1,KPNB1,COPB2,SRP72,CRYAB,KPNA4,LYN,GSK3B,KPNA1,HTT,AP3S1,CLTC,CREB3L2,STX6,CDKN1A,YWHAH,SEC13	down_VSAP_EC
GO:0061640	0.000291	1	8	23	cytoskeleton-dependent cytokinesis	BP	0.0238	ANLN,CENPA,BIRC5,AURKB,STMN1,NUP62,RAB35,ENSCAFG00000005299	down_ACOR_VSMC
GO:0030178	0.000294	1	3	52	negative regulation of Wnt signaling pathway	BP	0.788	BARX1,NKX2-5,ANKRD6	up_VPOR_VSMC
GO:0006275	0.000296	1	11	38	regulation of DNA replication	BP	0.0241	SMC1A,RFC2,RFC5,RFC3,RFC4,PCNA,GMNN,E2F8,SMC3,CDK2,GLI1	down_ACOR_VSMC
GO:0021545	0.0003	1	3	21	cranial nerve development	BP	0.186	HOXA3,NRP2,HOXA1	down_ACOR_EC
GO:0000281	0.000301	1	7	18	mitotic cytokinesis	BP	0.0244	ANLN,CENPA,BIRC5,STMN1,NUP62,RAB35,ENSCAFG00000005299	down_ACOR_VSMC
GO:0007267	0.000304	1	19	332	cell-cell signaling	BP	0.612	LEP,KCNC4,CRY2,DLL1,GPR1,CHRM2,SLC6A6,GREM1,HTR1D,FAM53B,CAMK2A,CYLD,RECK,LGR6,AXIN2,CCL5,DMPK,KANK1,TNC	up_AFEM_EC
GO:0007127	0.000306	1	9	28	meiosis I	BP	0.0246	ENSCAFG00000017264,NDC1,TRIP13,FBXO5,PSMD13,RAD51,MND1,CKS2,ESPL1	down_ACOR_VSMC
GO:0061982	0.000306	1	9	28	meiosis I cell cycle process	BP	0.0246	ENSCAFG00000017264,NDC1,TRIP13,FBXO5,PSMD13,RAD51,MND1,CKS2,ESPL1	down_ACOR_VSMC
GO:0048015	0.000312	1	13	48	phosphatidylinositol-mediated signaling	BP	0.0403	TEK,HCLS1,SELP,PDGFB,RELN,GATA3,EDN1,PIK3C2A,PREX2,PITPNM2,PDGFD,RGL2,PEAR1	up_VCAV_EC
GO:0048017	0.000312	1	13	48	inositol lipid-mediated signaling	BP	0.0403	TEK,HCLS1,SELP,PDGFB,RELN,GATA3,EDN1,PIK3C2A,PREX2,PITPNM2,PDGFD,RGL2,PEAR1	up_VCAV_EC
GO:0043009	0.000318	1	6	227	chordate embryonic development	BP	0.131	TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0016055	0.000322	1	4	134	Wnt signaling pathway	BP	0.788	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0198738	0.000322	1	4	134	cell-cell signaling by wnt	BP	0.788	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0032501	0.000325	1	17	1782	multicellular organismal process	BP	0.201	HOXA11,TBX15,HOXA9,PITX1,EMX2,NETO1,GATM,SALL1,HOXC10,IRX5,MAB21L1,TLR2,CAV1,SHOX2,F5,HAPLN1,GJB5	up_VSAP_VSMC

GO:0048333	0.000327	1	2	12	mesodermal cell differentiation	BP	0.176	EYA1,HOXA11	up_VFEM_VSMC
GO:0016192	0.000329	1	45	452	vesicle-mediated transport	BP	0.0805	VEGFA,MYH9,SERPINE1,ANKRD50,GOLT1B,SEC24D,ENSCAFG00000003477,HYOU1,EXOC5,SEC23A,HOOK3,TMEM87B,CANX,PIK3C2A,MSN,RAB6A,LMAN1,TRAK1,YIPF5,USO1,COPG1,CTNNB1,COPB2,TFRC,APOE,LYN,GPR107,GSK3B,MYO1E,SDC4,HTT,REST,CLINT1,SCAMP1,RAB11FIP1,AP3S1,CLTC,CREB3L2,LRRTM2,STX6,ICAM5,ARF4,BLZF1,SEC13,RINT1	down_VSAP_EC
GO:0001708	0.00033	1	2	20	cell fate specification	BP	0.39	HOXC10,EYA1	up_AFEM_VSMC
GO:0003008	0.000339	1	52	336	system process	BP	0.317	TNNT2,FGF13,ADRA1B,ACTN2,LEP,SLC26A7,KCNE3,GATA5,HTR2B,MBP,COCH,BMP4,NPPB,GJA1,HRH1,LRRN4,WASF3,PDE5A,GLRB,SLC2A5,GPR155,TMEM108,ADCY6,USP53,F2RL1,HRH2,CLSTN1,ABCA4,DMPK,NPNT,PTGDR,TBX20,RNLS,POMK,APP,PSEN1,CHD7,JUP,CLN8,EDN1,NOD2,FAM107A,INSYN1,JAM3,NCALD,GAA,INPP5K,WFS1,DOCK5,ERAP1,SLC8A1,BVES	up_ACOR_VSMC
GO:0048562	0.000339	1	3	102	embryonic organ morphogenesis	BP	0.39	TBX15,EYA1,IRX5	up_AFEM_VSMC
GO:0072078	0.000339	1	3	33	nephron tubule morphogenesis	BP	0.134	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0060351	0.000341	1	2	11	cartilage development involved in endochondral bone morphogenesis	BP	0.178	HOXA11,SHOX2	up_VFEM_VSMC
GO:0007275	0.000342	1	9	1370	multicellular organism development	BP	0.547	HOXA3,TBX5,GATA5,HOXA2,TMEM176A,TMEM176B,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0048536	0.000342	1	2	12	spleen development	BP	0.788	BARX1,NKX2-5	up_VPOR_VSMC
GO:2000826	0.000342	1	2	14	regulation of heart morphogenesis	BP	0.547	TBX5,GATA5	up_VPUL_VSMC
GO:0007096	0.000345	1	4	6	regulation of exit from mitosis	BP	0.0275	ZW10,BIRC5,ENSCAFG00000005299,UBE2C	down_ACOR_VSMC
GO:0043933	0.000348	1	83	698	protein-containing complex subunit organization	BP	0.0277	ACSL3,FSCN1,HMGB1,IRAK1,STXBP6,USP4,HMGCR,EDC3,UBE2S,RRM1,ZW10,CAPG,SMC4,CENPA,SLC29A1,NDC1,CENPN,COLGALT1,C1QTNF6,FBXO5,PSMD13,INSIG1,PRMT1,CAV1,RAD51,LIMA1,TK1,STMN1,CENPO,GREM1,SMARCC1,RCC1,DHX33,GMNN,CENPH,CENPI,FASTKD3,EIF5A,B4GALT1,SMC2,FARSA,PREB,NDC80,OIP5,IPO4,HIST1H1A,RAC1,DDX28,PDXP,FOSL1,IQGAP2,SAMM50,HMGB2,CDC42EP4,HIST1H2BB,SMARCB1,DDX39B,SF3A2,CORO1A,CENPW,FOXRED1,SIGMAR1,ARPC1B,CENPP,GRWD1,PRMT5,PSMC1,CTH,ARHGEF2,ENSCAFG00000015189,SUPT16H,HAT1,SERPINH1,LIPC,GEMIN7,UBE2C,MIS18A,TBCC,H3F3B,PDSS1,SF3A1,EIF3M,KIF24	down_ACOR_VSMC
GO:0051241	0.000349	1	4	336	negative regulation of multicellular organismal	BP	0.38	HOXC10,HOXA9,WNT7A,ARG2	up_AORTRT_VSMC
GO:0009792	0.000351	1	6	231	embryo development ending in birth or egg	BP	0.134	TBX15,EYA1,HOXA9,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0032502	0.000353	1	16	1661	developmental process	BP	0.134	HOXC10,TBX15,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,RADIL,CYP26B1,CDC42EP5,MTSS1,CA9	up_VFEM_EC
GO:0043009	0.000355	1	6	227	chordate embryonic development	BP	0.212	HOXA11,TBX15,HOXA9,IRX5,SHOX2,GJB5	up_VSAP_VSMC
GO:0007389	0.000355	1	3	137	pattern specification process	BP	0.38	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0048608	0.000356	1	3	129	reproductive structure development	BP	0.38	HOXA9,WNT7A,ESR1	up_AORTRT_VSMC
GO:0009954	0.000358	1	7	16	proximal/distal pattern formation	BP	0.494	HOXA11,HOXA9,DLL1,OSR1,IRX3,HOXC10,LRP4	up_VSAP_EC
GO:0060795	0.000358	1	2	12	cell fate commitment involved in formation of	BP	0.181	EYA1,HOXA11	up_VFEM_VSMC
GO:0060284	0.000361	1	34	212	regulation of cell development	BP	0.0462	EDNRB,PRKCH,IFRD1,RELN,MEF2C,CHD7,DLL4,RAPGEF1,GATA3,EDN1,RAB11A,TCF4,NEDD9,PPP3CA,MTOR,HOOK3,BMP2,HMG20A,GDPD5,PROX1,NCK1,FES,JAG1,MMD,RAPGEF2,ZC4H2,CTNNA1,HIF1A,ENSCAFG00000002015,ZEB1,ARHGEF2,CDON,TJP2,ZNF609	up_VCAV_EC
GO:0051241	0.000361	1	5	336	negative regulation of multicellular organismal	BP	0.547	TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC

GO:0072359	0.000362	1	7	368	circulatory system development	BP	1	TBX5,HOXA3,ZDHHC16,SLITRK5,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:2000136	0.000362	1	2	7	regulation of cell proliferation involved in	BP	0.134	EYA1,SIX1	up_VFEM_EC
GO:0048568	0.000365	1	5	148	embryonic organ development	BP	0.134	TBX15,EYA1,HOXB7,HOXA7,SIX1	up_VFEM_EC
GO:0072359	0.000366	1	50	368	circulatory system development	BP	0.0465	EPHB1,PLK2,TEK,ADGRF5,KIT,PRCP,CXCL8,ARHGEF15,EMCN,CLEC14A,CALCRL,TIE1,ADAMTS9,AMOT,PDGFB,CD34,MEF2C,CHD7,TIPARP,DLL4,RAPGEF1,GPR4,CDH5,GATA3,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,PTPRB,EPHB4,MTOR,MAP3K3,BMP2,HHEX,ANGPT2,PROX1,ENSCAFG00000010596,TSPAN12,PRKD2,TLR3,JAG1,RAPGEF2,CREB1,ADIPOR2,HIF1A,LUZP1,VASH1,JCAD,ELK3	up_VCAV_EC
GO:0051216	0.000371	1	4	70	cartilage development	BP	0.206	HOXA3,SULF1,CSGALNACT1,HOXC4	down_ACOR_EC
GO:0061323	0.000373	1	2	7	cell proliferation involved in heart morphogenesis	BP	0.134	EYA1,SIX1	up_VFEM_EC
GO:0035136	0.000374	1	7	16	forelimb morphogenesis	BP	0.494	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RECK,SHOX2	up_VSAP_EC
GO:0006469	0.000377	1	4	78	negative regulation of protein kinase activity	BP	0.206	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0061458	0.000377	1	3	131	reproductive system development	BP	0.38	HOXA9,WNT7A,ESR1	up_AORTRT_VSMC
GO:0030334	0.00038	1	7	267	regulation of cell migration	BP	0.206	ACVRL1,LYN,IGF1R,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0042058	0.000381	1	6	17	regulation of epidermal growth factor receptor	BP	0.0884	SOCS5,ERRFI1,PTPN2,ADAM17,CBLC,RHBDF2	down_VSAP_EC
GO:0008016	0.000383	1	13	48	regulation of heart contraction	BP	0.317	TNNT2,FGF13,ADRA1B,KCNE3,GJA1,PDE5A,DMPK,RNLS,JUP,EDN1,GAA,SLC8A1,BVES	up_ACOR_VSMC
GO:0032501	0.000386	1	19	1782	multicellular organismal process	BP	0.206	ACVRL1,LYN,HOXA3,IGF1R,ACSL4,SPG11,PDPN,NRP2,HIVEP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,HOXC4,ASPN,NED D4	down_ACOR_EC
GO:0035088	0.000388	1	5	12	establishment or maintenance of	BP	0.0884	FSCN1,ILK,WDR1,MSN,ARF4	down_VSAP_EC
GO:0061245	0.000388	1	5	12	establishment or maintenance of bipolar	BP	0.0884	FSCN1,ILK,WDR1,MSN,ARF4	down_VSAP_EC
GO:0097435	0.000390588	0.99988	16	230	supramolecular fiber organization	BP	0.61799576	MYOZ2,FMOD,TMOD1,ARHGAP6,SYNPO2,PDLIM3,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,FOXC2,NRP1,PRKCD,MFAP4,TUBB4A	up_ACOR_EC
GO:0045930	0.000391	1	19	97	negative regulation of mitotic cell cycle	BP	0.0308	ZW10,TRIP13,FBXO5,BIRC5,CDK1,CASP2,FANCI,TOPBP1,EZH2,MAP3K20,TRIM35,NDC80,ENSCAFG00000005299,CLSPN,BUB1,TTK,MTBP,ZWINT,GEN1	down_ACOR_VSMC
GO:0023052	0.000393	1	191	1602	signaling	BP	0.317	SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TLR1,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,IFNGR1,LEP,PLCL1,LBH,MAP3K8,MID1,KCNE3,GATA5,ADGRD1,CD83,EFNB2,ANGPT1,ENSCAFG00000016285,HTR2B,RASSF2,MBP,ZRANB1,FBXL20,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,RERG,GLRB,ARHGAP29,ZNRF3,CD274,PLPP2,AR,PTGIR,SASH1,STX11,GPR155,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ADCY6,ITPR1,GRK7,LIMS2,BLNK,ANKRD1,F2RL1,ADGRL1,CAMK2D,PSEN2,PPP2R5E,DAPK1,ARHGAP5,BNIP3,EGLN1,CACNB3,NCEH1,SLC12A7,AKAP6,CDKN1A,JMY,GNA14,CRLF3,CLSTN1,LRRC8C,CREBRF,NRP1,UBR1,PDE1A,PTPN22,DMPK,NPNT,UNC5B,SMPD1,RCAN2,APLP1,SLITRK5,TBX20,SESN3,SH3RF1,TBX5,CCDC3,PRKCE,FZD3,FRS2,AGRN,RNF19A,RND1,SCG5,RGS2,DAG1,FUT8,PARP9,APP,PSEN1,TGFBR1,SYNJ2BP,CHD7,TESK2,PIK3C3,JUP,SIPA1L1,SENP7,CCL5,WWC2,PERP,PSKH1,RTKN2,DUSP22,SIAH1,TIRAP,RAB11B,EDN1,SESN1,HPGD,KCNC4,DUSP26,NOD2,LRRC4,ARID5B,FAM107A,INSYN1,DDIT4,JAM	up_ACOR_VSMC
GO:0009792	0.000394	1	6	231	embryo development ending in birth or egg	BP	0.227	HOXA11,TBX15,HOXA9,IRX5,SHOX2,GJB5	up_VSAP_VSMC
GO:0048731	0.000395	1	7	1247	system development	BP	0.69	HOXC6,SLITRK5,LIMK1,GATA5,LRRC17,C6,TGFBI	up_VCAV_VSMC

GO:0051239	0.000396	1	36	859	regulation of multicellular organismal process	BP	0.632	HOXA9,CMKLR1,IRX3,IRX5,HOXC10,LEP,LBH,CRY2,ANGPT4,HOXA7,DLL1,F3,PLXNA4,BPI,GPAM,LMCD1,CHRM2,TWIST2,THRB,LGI4,TMEM100,GREM1,AVPR1A,CAMK2A,CYLD,PTHLH,TBXA2R,EVI2B,BVES,AXIN2,ACACB,PPARGC1A,DMPK,ADAM17,AGPAT2,KANK1	up_AFEM_EC
GO:0009888	0.000398	1	6	545	tissue development	BP	0.547	HOXA3,TBX5,GATA5,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0051054	0.00041	1	17	81	positive regulation of DNA metabolic process	BP	0.0321	HMGB1,HNRNPD,SLC29A1,RFC2,RFC5,RFC3,TIMELESS,AURKB,GREM1,RFC4,NEK2,PCNA,E2F8,TFRC,CDK2,GLI1,CCT4	down_ACOR_VSMC
GO:1903522	0.000413	1	7	58	regulation of blood circulation	BP	0.632	IRX5,CHRM2,THRB,AVPR1A,TBXA2R,BVES,DMPK	up_AFEM_EC
GO:0006954	0.000415	1	24	147	inflammatory response	BP	0.0524	ACKR1,GBP5,SELP,KIT,PRCP,CXCL8,F8,IL6,TNFAIP3,TNIP1,BCL6B,TLR4,GATA3,PTGS1,SNAP23,BMP2,TLR3,APOD,PTGS2,HMGB1,NOS2,NR1D2,ENSCAFG00000025410,HIF1A	up_VCAV_EC
GO:0030878	0.000416	1	2	13	thyroid gland development	BP	0.839	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0060429	0.000418	1	7	341	epithelium development	BP	0.14	EYA1,HOXB7,HOXA7,SIX1,CYP26B1,MTSS1,CA9	up_VFEM_EC
GO:0003129	0.000421	1	1	3	heart induction	BP	0.628	GATA5	down_AFEM_VSMC
GO:2001224	0.000422	1	2	5	positive regulation of neuron migration	BP	1	ARHGEF2,SEMA3A	up_VPOR_EC
GO:0061343	0.000428	1	1	3	cell adhesion involved in heart morphogenesis	BP	0.628	GATA5	down_AFEM_VSMC
GO:0032501	0.000429	1	10	1782	multicellular organismal process	BP	0.547	HOXA3,TBX5,GATA5,HOXA2,TMEM176A,TMEM176B,LRRN4,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0072088	0.000431	1	3	36	nephron epithelium morphogenesis	BP	0.142	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0060065	0.000434	1	2	7	uterus development	BP	0.242	HOXA11,HOXA9	up_VSAP_VSMC
GO:0003197	0.00044	1	2	16	endocardial cushion development	BP	0.547	TBX5,GATA5	up_VPUL_VSMC
GO:0048704	0.000445	1	2	46	embryonic skeletal system morphogenesis	BP	0.898	HOXA3,HOXB5	up_APUL_VSMC
GO:0044843	0.000446	1	14	62	cell cycle G1/S phase transition	BP	0.0347	HINFP,POLE,CASP2,CDKN2C,EZH2,CDK4,PLK3,RCC1,CDK2,CCNA2,RBBP8,GLI1,CDKN3,MTBP	down_ACOR_VSMC
GO:0002768	0.000449	1	10	37	immune response-regulating cell surface receptor signaling	BP	0.0562	KIT,PRKCH,PDE4D,MEF2C,EIF2B2,GATA3,NECTIN2,PRKD2,PLCG2,BCL10	up_VCAV_EC
GO:0019935	0.000450587	0.99995	6	38	cyclic-nucleotide-mediated signaling	BP	0.61799576	SOX9,PTH1R,AQP1,PTGIR,PDE4A,GUCY1B1	up_ACOR_EC
GO:0035115	0.000457	1	6	12	embryonic forelimb morphogenesis	BP	0.494	HOXA11,HOXA9,OSR2,OSR1,RECK,SHOX2	up_VSAP_EC
GO:0050794	0.000459562	0.99973	104	3075	regulation of cellular process	BP	0.61799576	CNTNAP4,SH3TC2,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TRPS1,PLCL1,PKIB,CALY,SOX9,RHOU,PKNOX2,ARHGAP6,PTH1R,RGS1,PCSK1N,NDRG2,AQP1,PORCN,ENSCAFG00000004331,SYNPO2,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,SEMA6D,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,RGMA,CASP10,LHX9,PDE4A,INSYN1,SMAD6,KLHL25,PLCE1,PLS1,ACTN2,ZMYND8,ARHGAP28,ESM1,PAK3,MMP28,GUCY1B1,GRK7,BCL2,TNFRSF19,PTGER4,ARHGDIB,PREB,CST3,PIAS1,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,TBX5,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,C23H3orf58,ZNF229,CHMP4B,TP53INP2,RARRES2,VPS16,GMEB2,RIOX2,PRKACA,RNF114,STK32C,NRP1,ARHGEF26,PRKCD,GNAZ,RIN2,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,ADGRL1,TUBB4A,TLE2	up_ACOR_EC
GO:0048568	0.000464	1	4	148	embryonic organ development	BP	0.227	EYA1,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006631	0.000466	1	20	93	fatty acid metabolic process	BP	0.494	PEX7,ACSM3,LIPC,INSIG2,ACAA1,ACACB,PEX2,C1QTNF2,HSD17B8,FAAH,PDK2,PTGES,HACD4,GCDH,DAGLB,EHHADH,LONP2,ABHD16A,HPGD,ENSCAFG00000023820	up_VSAP_EC
GO:2001014	0.000467	1	2	8	regulation of skeletal muscle cell differentiation	BP	0.143	SIX1,CYP26B1	up_VFEM_EC
GO:0051239	0.000468	1	11	859	regulation of multicellular organismal process	BP	0.143	HOXC10,EYA1,HOXA9,TOX,MAP2K6,AVPR1A,HOXB7,HOXA7,SIX1,TIAM1,CYP26B1	up_VFEM_EC
GO:0072028	0.000471	1	3	37	nephron morphogenesis	BP	0.143	EYA1,HOXB7,SIX1	up_VFEM_EC

GO:0060272	0.000473	1	2	7	embryonic skeletal joint morphogenesis	BP	0.246	HOXA11,SHOX2	up_VSAP_VSMC
GO:0016042	0.000475	1	18	80	lipid catabolic process	BP	0.494	PEX7,LIPC,ENPP2,PLBD1,ACAA1,ACACB,PEX2,HSD17B14,PAFAH2,FAAH,LPL,PLA2G6,GCDH,EHHADH,LONP2,ABHD16A,LIPE,IDH1	up_VSAP_EC
GO:0048584	0.000477	1	71	592	positive regulation of response to stimulus	BP	0.0592	TEK,HCLS1,IL7R,GBP5,SELP,KIT,CXCL8,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,TMEM173,RELN,PDE4D,MEF2C,FERMT1,ATF3,DLL4,TLR4,NLRC5,GPR4,EIF2B2,GATA3,EDN1,PELI1,PPP3CA,GUCY1A1,ARG2,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CAV2,BMP2K,ITPKB,RIOK3,MADD,PAK2,PRKD2,SH3GLB1,SWAP70,SMARCA4,TLR3,MFNG,AKAP12,NCK1,TIMELESS,OTUD4,JAG1,PTGS2,RAPGEF2,PLCG2,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,LSM14A,SKIL,PDGFD,HIF1A,ENSCAFG00000002015,RGL2,JCAD,CDON	up_VCAV_EC
GO:0032268	0.000477	1	69	778	regulation of cellular protein metabolic process	BP	0.101	ARHGEF2,PRICKLE1,VEGFA,MYH9,PLK3,HSPA5,SERPINE1,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PUM3,PM20D2,ILK,PPP1R12A,SESN2,PTGS2,MSN,IWS1,DNAJC10,TNIK,NXN,PTPN2,UCHL5,SPOPL,YES1,PLCL1,ADAM17,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,APOE,LYN,STRAP,FAM162A,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,HTT,REST,EIF2S1,CALM1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,MADD,KDM3A,MID1	down_VSAP_EC
GO:0033044	0.000477	1	23	127	regulation of chromosome organization	BP	0.0367	SREBF1,ATAD2,HNRNPD,ZW10,TRIP13,FBXO5,BIRC5,AURKB,NEK2,FEN1,UHRF1,BRCA1,NOC2L,CDC6,NDC80,ENSCAFG00000005299,BUB1,TTK,TADA2A,TINF2,UBE2C,CCT4,GEN1	down_ACOR_VSMC
GO:0090103	0.00048	1	2	8	cochlea morphogenesis	BP	0.143	EYA1,SIX1	up_VFEM_EC
GO:0048468	0.000481	1	70	553	cell development	BP	0.0592	EPHB1,EDNRB,TEK,ADGRF5,KIT,PRKCH,IFRD1,FLI1,PDGFB,PODXL,RELN,PDE4D,MEF2C,CHD7,DLL4,RAPGEF1,TLR4,GPR4,STC1,EIF2B2,GATA3,EDN1,RAB11A,TCF4,NTN4,PSME4,NEDD9,SOX18,TMOD1,PPP3CA,NECTIN2,MTOR,HOOK3,BMP2,CDYL,HMG20A,CAV2,PREX2,GDPD5,PROX1,ENSCAFG00000010224,ARID4B,STMN1,FLNB,PAK2,APOD,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,SPTBN4,AFF4,SKIL,HIF1A,KDM3A,ALS2,ATRX,ENSCAFG00000002015,P2RX2,TMOD3,ZEB1,ARHGEF2,FBXO5,CDON,TJP2,ZNF609	up_VCAV_EC
GO:2000145	0.000484	1	7	279	regulation of cell motility	BP	0.227	ACVRL1,LYN,IGF1R,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0033673	0.000492	1	4	84	negative regulation of kinase activity	BP	0.227	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0003231	0.000499	1	13	48	cardiac ventricle development	BP	0.361	TNNT2,SMAD6,BMP4,FGFR2,CITED2,LMO4,EGLN1,SMARCD3,TBX20,TBX5,FRS2,CHD7,AP2B1	up_ACOR_VSMC
GO:0009611	0.000504	1	22	122	response to wounding	BP	0.0616	SELP,PRCP,F8,IFRD1,PDGFB,VWF,CD34,KLKB1,TLR4,GPR4,RAB27A,TFPI,MTOR,MMRN1,APOD,ADIPOR2,PDGFD,HIF1A,ITGB3,VASH1,PEAR1,ELK3	up_VCAV_EC
GO:0014065	0.000509	1	11	39	phosphatidylinositol 3-kinase signaling	BP	0.0618	TEK,HCLS1,SELP,PDGFB,RELN,GATA3,EDN1,PREX2,PDGFD,RGL2,PEAR1	up_VCAV_EC
GO:0009653	0.00051	1	33	773	anatomical structure morphogenesis	BP	0.632	TBX15,HOXA9,IRX3,IRX5,HOXC10,LEP,ANGPT4,HOXA7,COL8A2,DLL1,CRYAB,F3,PLXNA4,THRB,TMEM100,GREM1,CAMK2A,GREM2,HOXA6,LUZP1,RECK,TBXA2R,CNNM4,BVES,PTPRB,AXIN2,CDC42EP5,ADAM17,CLIC4,LRRN2,GCNT4,KANK1,TNC	up_AFEM_EC
GO:0048598	0.000511	1	35	207	embryonic morphogenesis	BP	0.494	TBX15,HOXA11,FZD1,HOXA7,HOXA9,CDON,WNT11,HNF4A,OSR2,INSIG2,GJB5,LRIG3,IRX5,HOXD3,ABL1,DLL1,HOXA6,OSR1,FUZ,ZBTB16,RARG,HOXC4,RECK,PLPP3,ZFP36L1,IRX3,ZEB1,FBXW4,SHOX2,HOXC10,LRP4,KDM2B,TGFBR2,CITED2,LATS2	up_VSAP_EC
GO:0003279	0.000512	1	13	48	cardiac septum development	BP	0.361	SMAD6,GATA4,BMP4,FGFR2,CITED2,LMO4,EGLN1,NRP1,TBX20,TBX5,FRS2,CHD7,AP2B1	up_ACOR_VSMC
GO:0048663	0.000517	1	2	13	neuron fate commitment	BP	0.241	HOXC10,EYA1	up_VFEM_VSMC

GO:0016054	0.00052	1	15	61	organic acid catabolic process	BP	0.494	PEX7,ACAA1,ACACB,PEX2,GOT1,ADHFE1,ALDH6A1,FAAH,GCDH,BCKDHB,EHHADH,LONP2,ABHD16A,ENSCAFG00000002977,IDO2	up_VSAP_EC
GO:0046395	0.00052	1	15	61	carboxylic acid catabolic process	BP	0.494	PEX7,ACAA1,ACACB,PEX2,GOT1,ADHFE1,ALDH6A1,FAAH,GCDH,BCKDHB,EHHADH,LONP2,ABHD16A,ENSCAFG00000002977,IDO2	up_VSAP_EC
GO:1905114	0.000522	1	4	150	cell surface receptor signaling pathway involved in cell-cell	BP	0.935	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0045165	0.000522	1	3	65	cell fate commitment	BP	0.241	HOXC10,EYA1,HOXA11	up_VFEM_VSMC
GO:0051962	0.00053	1	21	112	positive regulation of nervous system development	BP	0.0638	EPHB1,PRKCH,RELN,MEF2C,RAPGEF1,RAB11A,TCF4,MTOR,BMP2,GDPD5,PROX1,NCK1,FES,MMD,RAPGEF2,ZC4H2,HIF1A,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0006520	0.000531	1	17	114	cellular amino acid metabolic process	BP	0.11	P4HB,ASNS,CARS,PLOD2,NR1H4,ERO1A,P4HA1,SARS,AARS,NMNAT2,ALDH18A1,YARS,TARS,NARS,PLOD3,RAB11FIP1,BCAT1	down_VSAP_EC
GO:0008015	0.000534	1	10	120	blood circulation	BP	0.632	IRX5,F5,DLL1,CHRM2,THRB,HTR1D,AVPR1A,TBXA2R,BVES,DMPK	up_AFEM_EC
GO:0030220	0.000534	1	4	7	platelet formation	BP	0.11	MYH9,ACTN1,PTPN11,WDR1	down_VSAP_EC
GO:0060537	0.000539	1	21	117	muscle tissue development	BP	0.0645	EPHB1,IFRD1,ADAMTS9,MEF2C,ATF3,CHD7,TIPARP,DLL4,EDN1,FOXN2,PPP3CA,MTOR,BMP2,CAV2,PROX1,ENSCAFG00000010596,FLNB,CREB1,NR1D2,P2RX2,CDON	up_VCAV_EC
GO:0030198	0.00054	1	12	81	extracellular matrix organization	BP	0.583	ADAMTS2,FBLN2,LUM,LOX,RECK,CRISPLD2,B4GALT1,ADAMTSL4,LOXL3,DDR2,GREM1,ECM2	down_VCAV_EC
GO:0051301	0.000545	1	21	117	cell division	BP	0.0417	NCAPD2,ANLN,CENPA,RAN,BIRC5,AURKB,DSN1,STMN1,PLK3,CKS2,NCAPH,E2F8,CDC6,NUP62,PDXP,FGF5,RAB35,ENSCAFG00000005299,ASPM,ARHGEF2,CCNB3	down_ACOR_VSMC
GO:0030036	0.000549	1	34	223	actin cytoskeleton organization	BP	0.0651	TEK,HCLS1,KIT,ARHGEF15,ENSCAFG00000007112,AMOT,BAIAP2L1,MEF2C,EDN1,ARHGAP28,TMOD1,MTSS1,MTOR,NCKAP1,PROX1,IQGAP2,EPB41,ELMO1,STMN1,FLNB,PAK2,SWAP70,NCK1,FES,CTNNA1,FMNL3,ARPC5L,ARHGDIB,ARHGAP26,GAS2L3,TNFAIP1,TMOD3,ARHGEF2,FSCN1	up_VCAV_EC
GO:0009952	0.000549	1	3	66	anterior/posterior pattern specification	BP	1	HOXC10,HOXA9,HOXC6	up_AORTRT_EC
GO:0042127	0.000554	1	56	452	regulation of cell proliferation	BP	0.0653	EPHB1,HCLS1,IL7R,KIT,CXCL8,PRKCH,CALCRL,TNFAIP3,PDGFB,BCL6B,MEF2C,FERMT1,DLL4,RAPGEF1,TLR4,GATA3,EDN1,APLNR,PTGS1,SOX18,EGFL7,PELI1,MTSS1,ODC1,ARG2,MAP3K3,BMP2,HHEX,CAV2,CNOT6,CCAR1,PROX1,MCC,PRKD2,APOD,NCK1,FES,JAG1,PTGS2,RAPGEF2,CTNNA1,CNOT7,HMGB1,CRIP2,NRAS,PDGFD,CUL4A,BMX,HIF1A,NR4A1,HP1BP3,VASH1,JCAD,ZEB1,CDON,ZNF609	up_VCAV_EC
GO:0043062	0.000554	1	21	99	extracellular structure organization	BP	0.373	FMOD,PRDX4,RECK,FERMT1,LCAT,MFAP4,ABCA1,SPINT1,CTSS,ERO1B,NPNT,SPINT2,P4HA1,DAG1,APP,ECM2,DDR2,NID1,SERPINB5,KIF9,TNFRSF11B	up_ACOR_VSMC
GO:0048513	0.000561	1	6	906	animal organ development	BP	0.586	HOXC10,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:1901228	0.000563	1	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	0.757	GATA5	down_AFEM_VSMC
GO:0003274	0.000564	1	1	2	endocardial cushion fusion	BP	0.61	GATA5	down_VFEM_VSMC
GO:0032101	0.000566	1	27	173	regulation of response to external stimulus	BP	0.0662	GBP5,SELP,CXCL8,CXCR4,TNFAIP3,TNIP1,PDGFB,BCL6B,TMEM173,CD34,KLKB1,TLR4,GATA3,MMP28,TFPI,ARG2,RIOK3,ANGPT2,PRKD2,SWAP70,TLR3,APOD,PTGS2,HMGB1,NOS2,NR1D2,ENSCAFG00000025410	up_VCAV_EC
GO:0007062	0.000566	1	9	29	sister chromatid cohesion	BP	0.0428	SMC1A,ENSCAFG00000017264,SGO1,FEN1,KIF22,HASPIN,SMC3,CDC20,SGO2	down_ACOR_VSMC
GO:2000026	0.000569	1	5	560	regulation of multicellular organismal development	BP	0.69	SLITRK5,LIMK1,GATA5,LRRC17,C6	up_VCAV_VSMC
GO:0003013	0.00057	1	10	121	circulatory system process	BP	0.632	IRX5,F5,DLL1,CHRM2,THRB,HTR1D,AVPR1A,TBXA2R,BVES,DMPK	up_AFEM_EC
GO:0042439	0.000573	1	2	2	ethanolamine-containing compound metabolic	BP	0.632	MOXD1,NAPEPLD	up_AFEM_EC

GO:0001819	0.000576	1	21	120	positive regulation of cytokine production	BP	0.0669	GBP5,TMEM173,CD34,PDE4D,FERMT1,TLR4,GATA3,IRF8,PELI1,MAPK13,RIOK3,PRKD2,TLR3,CD200,PLCG2,BCL10,HMGB1,RIPK1,LSM14A,HIF1A,ARHGEF2	up_VCAV_EC
GO:0043436	0.000579	1	33	303	oxoacid metabolic process	BP	0.115	P4HB,ASNS,CARS,PLOD2,NR1H4,ENSCAFG00000009211,ERO1A,ENPP1,P4HA1,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,ALDH1L2,SESN2,PTGS2,CEMIP2,CHSY1,HIF1A,SLC45A3,NMNAT2,ALDH18A1,YARS,TARS,NARS,ALDOC,PAPSS1,PLOD3,RAB11FIP1,BCAT1	down_VSAP_EC
GO:0048701	0.000581	1	2	25	embryonic cranial skeleton morphogenesis	BP	0.586	TBX15,IRX5	up_AFEM_VSMC
GO:0090383	0.000587	1	2	2	phagosome acidification	BP	0.632	RAB20,RAB7A	up_AFEM_EC
GO:0140074	0.000588	1	1	2	cardiac endothelial to mesenchymal transition	BP	0.61	GATA5	down_VFEM_VSMC
GO:0002252	0.00059	1	27	166	immune effector process	BP	0.0676	IL7R,KIT,IL6,MX2,TMEM173,TLR4,NLRC5,GATA3,RAB27A,SERINC5,NECTIN2,MTOR,SNAP23,RIOK3,THOC1,SWAP70,TLR3,MFNG,OAS3,FES,JAG1,PLCG2,BCL10,CNOT7,HMGB1,PMAIP1,LSM14A	up_VCAV_EC
GO:0030097	0.000596	1	36	244	hemopoiesis	BP	0.0678	HOXB7,HCLS1,IL7R,ADGRF5,KIT,IL6,FLI1,MEF2C,CHD7,TIPARP,DLL4,GATA3,HOXB8,ENSCAFG00000003530,IRF8,CASP8,MTOR,TENT2,HHEX,ITPKB,MFNG,FES,JAG1,PLCG2,CREB1,HMGB1,RIPK1,CRIP2,ATP11C,CUL4A,BMX,HIF1A,TMOD3,ZEB1,TET2,TJP2	up_VCAV_EC
GO:0003176	0.000596	1	5	9	aortic valve development	BP	0.385	SMAD6,GATA5,GATA4,BMP4,TBX20	up_ACOR_VSMC
GO:0045454	0.000597	1	8	35	cell redox homeostasis	BP	0.117	P4HB,ENSCAFG00000013214,ERO1A,ENSCAFG00000003477,DNAJC10,NXN,PDIA4,DDIT3	down_VSAP_EC
GO:0001938	0.000603	1	9	34	positive regulation of endothelial cell	BP	0.0681	PDGFB,APLNR,EGFL7,BMP2,PROX1,PRKD2,HMGB1,NRAS,JCAD	up_VCAV_EC
GO:0050767	0.000612	1	30	184	regulation of neurogenesis	BP	0.0683	EDNRB,PRKCH,IFRD1,RELN,MEF2C,CHD7,DLL4,RAPGEF1,GATA3,RAB11A,TCF4,PPP3CA,MTOR,HOOK3,BMP2,HMG20A,GDPD5,PROX1,NCK1,FES,JAG1,MMD,RAPGEF2,ZC4H2,CTNNA1,HIF1A,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0060037	0.000613	1	2	9	pharyngeal system development	BP	0.177	EYA1,SIX1	up_VFEM_EC
GO:0030517	0.000615	1	2	5	negative regulation of axon extension	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0009967	0.000616	1	55	435	positive regulation of signal transduction	BP	0.0683	TEK,HCLS1,IL7R,SELP,KIT,PRKCH,MAP3K11,PDGFB,RELN,FERMT1,ATF3,DLL4,TLR4,NLRC5,GPR4,GATA3,EDN1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CAV2,BMP2K,ITPKB,MADD,PAK2,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,NCK1,JAG1,RAPGEF2,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,LSM14A,SKIL,PDGFD,HIF1A,ENSCAFG00000002015,RGL2,JCAD,CDON	up_VCAV_EC
GO:1901343	0.000619	1	11	42	negative regulation of vasculature development	BP	0.0683	PLK2,TEK,TIE1,ADAMTS9,AMOT,PDGFB,DLL4,GPR4,HHEX,ANGPT2,VASH1	up_VCAV_EC
GO:0072498	0.000621	1	2	8	embryonic skeletal joint development	BP	0.313	HOXA11,SHOX2	up_VSAP_VSMC
GO:0032970	0.000621651	0.99984	11	130	regulation of actin filament-based process	BP	0.7009284	TMOD1,ARHGAP6,SYNPO2,DIXDC1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,NRP1,PRKCD	up_ACOR_EC
GO:0007186	0.000622	1	21	124	G protein-coupled receptor signaling pathway	BP	0.0683	GNGT2,EDNRB,RGS16,CXCL8,CALCRL,GPR4,EDN1,APLNR,ACPP,SPNS3,CAV2,PREX2,GNG11,ABCA1,ARHGEF12,IQGAP2,STMN1,AKAP12,GRM8,RAPGEF2,RGS2	up_VCAV_EC
GO:0048856	0.000626	1	17	1533	anatomical structure development	BP	0.258	ACVRL1,LYN,HOXA3,ACSL4,SPG11,PDPN,NRP2,HIVEP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,HOXC4,ASPN,NEDD4	down_ACOR_EC
GO:0051348	0.000628	1	4	90	negative regulation of transferase activity	BP	0.258	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC

GO:0042221	0.000631	1	85	1012	response to chemical	BP	0.121	ARHGEF2,VEGFA,P4HB,SULF1,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,HM13,SPARC,ERO1A,HSP90B1,ENPP1,JCAD,SNX25,HYOU1,PGK1,PTPN11,FLNB,DPYSL3,TRIB3,ILK,FHL2,PPP1R12A,PRCP,SMARCA4,SESN2,SRP54,TGFBR1,PTGS2,MYO1C,MSN,SEL1L,KIF5B,HIF1A,CX3CL1,DNAJC10,ZPR1,PTPN2,YES1,NEO1,MTDH,ADAM17,AGRN,CNOT7,DNAJB9,GNAQ,CTNNB1,SRP72,CRYAB,ENSCAFG00000002015,TFRC,APOE,KPNA4,ZC3H15,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,SLC7A11,ATF3,CDC37,GBP5,REST,EIF2S1,EXT1,CALM1,PAK2,CREB3L2,INHBA,NR4A1,ENSCAFG00000018360,HIF1AN,BTK,NRP1,USP14,YWHAH,KDM3A,HOMER1	down_VSAP_EC
GO:0071345	0.000631	1	5	210	cellular response to cytokine stimulus	BP	1	NR1H4,MRC1,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0003179	0.000635	1	2	19	heart valve morphogenesis	BP	0.599	TBX5,GATA5	up_VPUL_VSMC
GO:0009954	0.000636	1	2	16	proximal/distal pattern formation	BP	1	HOXC10,HOXA9	up_AORTRT_EC
GO:0060039	0.000637	1	2	11	pericardium development	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0002159	0.000639	1	1	2	desmosome assembly	BP	0.61	JUP	down_VFEM_VSMC
GO:0086042	0.000639	1	1	2	cardiac muscle cell-cardiac muscle cell	BP	0.61	JUP	down_VFEM_VSMC
GO:0086073	0.000639	1	1	2	bundle of His cell-Purkinje myocyte adhesion involved in cell	BP	0.61	JUP	down_VFEM_VSMC
GO:0006082	0.000643	1	33	305	organic acid metabolic process	BP	0.122	P4HB,ASNS,CARS,PLOD2,NR1H4,ENSCAFG00000009211,ERO1A,ENPP1,P4HA1,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,ALDH1L2,SESN2,PTGS2,CEMIP2,CHSY1,HIF1A,SLC45A3,NMNAT2,ALDH18A1,YARS,TARS,NARS,ALDOC,PAPSS1,PLOD3,RAB11FIP1,BCAT1	down_VSAP_EC
GO:1901016	0.000644	1	2	9	regulation of potassium ion transmembrane transporter activity	BP	0.315	NETO1,CAV1	up_VSAP_VSMC
GO:0000381	0.000649	1	7	19	regulation of alternative mRNA splicing, via	BP	0.0483	RNPS1,SRSF2,THRAP3,HNRNPL,RBM14,WTAP,SF3A1	down_ACOR_VSMC
GO:0071599	0.000655	1	2	9	otic vesicle development	BP	0.178	EYA1,SIX1	up_VFEM_EC
GO:0060993	0.000662	1	3	42	kidney morphogenesis	BP	0.178	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0030162	0.000665	1	24	202	regulation of proteolysis	BP	0.122	PRICKLE1,MYH9,PLK3,SERPINE1,SOCS5,PRKACB,TRIB3,PTGS2,UCHL5,SPOPL,CRYAB,APOE,LYN,FAM162A,GSK3B,REST,SPOP,DISC1,RAD23A,PAK2,A2M,TMTC3,SPINK2,USP14	down_VSAP_EC
GO:0030879	0.000665	1	2	34	mammary gland development	BP	0.434	HOXA9,ESR1	up_AORTRT_VSMC
GO:0006928	0.000666	1	53	557	movement of cell or subcellular component	BP	0.122	ARHGEF2,VEGFA,SULF1,MYH9,FMNL3,HSPA5,SERPINE1,ACTN1,SPARC,ITGA2,JCAD,PTPN11,FSCN1,DPYSL3,ILK,PRCP,WDR1,MYO1C,PIK3C2A,MSN,RPGR,KIF5B,HIF1A,CX3CL1,DYNLL1,TRAK1,NEO1,SDC3,ADAM17,PALLD,CTNNB1,KPNB1,ANLN,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,PDS5B,CCNYL1,NEXN,SDC4,HTT,ZMYND8,EXT1,DISC1,AP3S1,PAK2,SIX4,NRP1,ARF4,TNFAIP1	down_VSAP_EC
GO:0045184	0.000666	1	50	532	establishment of protein localization	BP	0.122	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SEC24D,PTPN11,SEC23A,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,ENSCAFG00000002015,TFRC,APOE,KPNA4,LYN,DDIT3,GSK3B,GBP5,SH3GLB1,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,STX6,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0051270	0.000668	1	7	296	regulation of cellular component movement	BP	0.258	ACVRL1,LYN,IGF1R,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0048534	0.00068	1	6	262	hematopoietic or lymphoid organ	BP	0.178	HOXA9,TOX,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0003007	0.000688	1	20	94	heart morphogenesis	BP	0.427	TNNT2,SMAD6,GATA5,GATA4,HTR2B,BMP4,FGFR2,GJA1,SEC24B,CITED2,ANKRD1,EGLN1,NRP1,SMARCD3,TBX20,TBX5,PSEN1,TGFBR1,CHD7,GAA	up_ACOR_VSMC

GO:0001945	0.000688	1	2	9	lymph vessel development	BP	0.258	ACVRL1,PDPN	down_ACOR_EC
GO:0001946	0.000688	1	2	9	lymphangiogenesis	BP	0.258	ACVRL1,PDPN	down_ACOR_EC
GO:0036303	0.000688	1	2	9	lymph vessel morphogenesis	BP	0.258	ACVRL1,PDPN	down_ACOR_EC
GO:0010389	0.00069	1	9	30	regulation of G2/M transition of mitotic cell	BP	0.0504	CDK1,FANCI,TOPBP1,CDK4,RNASEH2B,DTL,CDK2,CLSPN,CCNB3	down_ACOR_VSMC
GO:0010647	0.000691	1	57	460	positive regulation of cell communication	BP	0.0754	TEK,HCLS1,IL7R,SELP,KIT,PRKCH,MAP3K11,PDGFB,RELN,FERMT1,ATF3,DLL4,TLR4,NLRC5,GPR4,GATA3,EDN1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CAV2,BMP2K,ITPKB,MADD,PAK2,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,NCK1,JAG1,RAPGEF2,CREB1,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,LSM14A,SKIL,MCU,PDGFD,HIF1A,ENSCAFG00000002015,RGL2,JCAD,CDON	up_VCAV_EC
GO:0001657	0.000694	1	3	42	ureteric bud development	BP	0.178	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0072163	0.000694	1	3	42	mesonephric epithelium development	BP	0.178	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0072164	0.000694	1	3	42	mesonephric tubule development	BP	0.178	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0006272	0.000698	1	3	3	leading strand elongation	BP	0.0508	POLA1,POLE,PCNA	down_ACOR_VSMC
GO:0003156	0.000698	1	2	20	regulation of animal organ formation	BP	0.599	TBX5,GATA5	up_VPUL_VSMC
GO:0010830	0.000703	1	2	16	regulation of myotube differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0002009	0.000706	1	5	177	morphogenesis of an epithelium	BP	0.178	EYA1,HOXB7,SIX1,MTSS1,CA9	up_VFEM_EC
GO:0098609	0.000708	1	2	181	cell-cell adhesion	BP	0.635	JUP,GATA5	down_VFEM_VSMC
GO:0010614	0.000718	1	1	5	negative regulation of cardiac muscle	BP	0.827	GATA5	down_AFEM_VSMC
GO:0014741	0.000718	1	1	5	negative regulation of muscle hypertrophy	BP	0.827	GATA5	down_AFEM_VSMC
GO:0007275	0.000724	1	7	1370	multicellular organism development	BP	0.69	HOXC6,SLITRK5,LIMK1,GATA5,LRRC17,C6,TGFBI	up_VCAV_VSMC
GO:0065008	0.000726	1	41	1056	regulation of biological quality	BP	0.733	CMKLR1,IRX5,HOXC10,LEP,KCNC4,PRR16,CRY2,RAB20,F5,DLL1,CRYAB,F3,PLXNA4,GPAM,MLLT11,CHRM2,THRB,HTR1D,NFE2L1,AVPR1A,TENT5C,CAMK2A,CYLD,FXYD1,TBXA2R,MOXD1,CNNM4,TFPI2,BVES,RAB7A,AXIN2,ATP6V0B,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,DMPK,SAMD4B,GCNT4,KANK1	up_AFEM_EC
GO:0048706	0.000726	1	2	59	embryonic skeletal system development	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0007156	0.000733	1	9	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	0.0794	PCDH12,PCDH1,DSC2,CDH5,ESAM,NECTIN2,DSG2,CDH24,CD200	up_VCAV_EC
GO:0044282	0.000744	1	19	89	small molecule catabolic process	BP	0.667	PEX7,DHDH,ACAA1,ACACB,PEX2,GOT1,INPP5E,ADHFE1,ALDH6A1,FAAH,GALK1,GCDH,BCKDHB,EHHADH,LONP2,ABHD16A,ENSCAFG00000002977,PNP,IDO2	up_VSAP_EC
GO:0048856	0.000744	1	15	1533	anatomical structure development	BP	0.352	HOXA11,TBX15,HOXA9,PITX1,EMX2,GATM,SALL1,HOXC10,IRX5,MAB21L1,STIM1,CAV1,SHOX2,HAPLN1,GJB5	up_VSAP_VSMC
GO:0070887	0.000751	1	68	775	cellular response to chemical stimulus	BP	0.133	ARHGEF2,VEGFA,P4HB,SULF1,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,SPARC,ERO1A,ENPP1,JCAD,SNX25,HYOU1,PGK1,PTPN11,FLNB,DPYSL3,TRIB3,ILK,PPP1R12A,PRCP,SMARCA4,SESN2,TGFBR1,PTGS2,MYO1C,MSN,KIF5B,HIF1A,CX3CL1,ZPR1,PTPN2,YES1,NEO1,MTDH,ADAM17,AGRN,CNOT7,GNAQ,CTNNB1,ENSCAFG00000002015,TFRC,ZC3H15,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,ATF3,CDC37,GBP5,REST,EIF2S1,PAK2,CREB3L2,NR4A1,ENSCAFG00000018360,HIF1AN,BTK,NRP1,YWHAH,KDM3A	down_VSAP_EC
GO:0120163	0.000754	1	2	17	negative regulation of cold-induced	BP	1	HOXC10,LNPEP	up_AORTRT_EC

GO:0023056	0.000758	1	57	462	positive regulation of signaling	BP	0.0814	TEK,HCLS1,IL7R,SELP,KIT,PRKCH,MAP3K11,PDGFB,RELN,FERMT1,ATF3,DLL4,TLR4,NLRC5,GPR4,GATA3,EDN1,PELI1,PPP3CA,GUCY1A1,CASP8,NECTIN2,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CAV2,BMP2K,ITPKB,MADD,PAK2,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,AKAP12,NCK1,JAG1,RAPGEF2,CREB1,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,LSM14A,SKIL,MCU,PDGFD,HIF1A,ENSCAFG00000002015,RGL2,JCAD,CDON	up_VCAV_EC
GO:0032501	0.00076	1	15	1782	multicellular organismal process	BP	1	NR1H4,TBX5,HOXA2,MAPK10,BPI,HTR7,HOXA3,PLCL1,PCSK1N,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:0006334	0.00076	1	11	45	nucleosome assembly	BP	0.0545	CENPA,OIP5,IPO4,HIST1H1A,HMGB2,HIST1H2BB,CENPP,GRWD1,HAT1,MIS18A,H3F3B	down_ACOR_VSMC
GO:0014706	0.000761	1	20	112	striated muscle tissue development	BP	0.0814	EPHB1,IFRD1,ADAMTS9,MEF2C,ATF3,CHD7,DLL4,EDN1,FOXN2,PPP3CA,MTOR,BMP2,CAV2,PROX1,ENSCAFG00000010596,FLNB,CREB1,NR1D2,P2RX2,CDON	up_VCAV_EC
GO:0003218	0.000765	1	1	1	cardiac left ventricle formation	BP	1	TBX5	up_APUL_VSMC
GO:0040012	0.000772	1	7	303	regulation of locomotion	BP	0.276	ACVRL1,LYN,IGF1R,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0048705	0.00078	1	4	95	skeletal system morphogenesis	BP	0.352	HOXA11,TBX15,IRX5,SHOX2	up_VSAP_VSMC
GO:0007275	0.000786	1	14	1370	multicellular organism development	BP	0.352	HOXA11,TBX15,HOXA9,PITX1,EMX2,GATM,SALL1,HOXC10,IRX5,MAB21L1,CAV1,SHOX2,HAPLN1,GJB5	up_VSAP_VSMC
GO:0003158	0.000791	1	10	38	endothelium development	BP	0.084	PDE4D,DLL4,RAPGEF1,STC1,SOX18,PROX1,HOXB5,JAG1,RAPGEF2,ZEB1	up_VCAV_EC
GO:0090102	0.000793	1	2	10	cochlea development	BP	0.194	EYA1,SIX1	up_VFEM_EC
GO:0008284	0.000795	1	6	238	positive regulation of cell proliferation	BP	0.276	ACVRL1,LYN,HOXA3,IGF1R,SULF1,STX4	down_ACOR_EC
GO:0071840	0.000797	0.999	207	2059	cellular component organization or biogenesis	BP	0.0569	ACSL3,FSCN1,HMGB1,MCM6,SREBF1,MCM4,FLNB,POLE3,IRAK1,MCM7,RPA1,NCAPD2,ANLN,STXBP6,USP4,FMNL3,ATAD2,HMGA1,HMGCR,EDC3,HNRNPD,SMC1A,UBE2S,NEDD4,RRM1,ZW10,ENSCAFG00000016482,CAPG,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,CENPN,TOP3A,TRIP13,COLGALT1,SLC25A5,TIMM44,SF1,SGO1,GINS4,C1QTNF6,NOP56,SDC1,ARFGAP1,CTDNEP1,FBXO5,HSPA9,RAN,B3GNT2,CFAP298,PRELID1,PSMD13,BIRC5,INSIG1,PRMT1,CAV1,CDK1,RAD51,LIMA1,NF2,AURKB,MMP14,TK1,CDKN2C,DSN1,EZH2,STMN1,CENPO,HAUS8,GREM1,NCAPD3,MAP3K20,NEK2,CHCHD3,FBL,FEN1,SMARCC1,MND1,GAS2L3,PLK3,HMGB3,RCC1,DHX33,KIF22,UHRF1,CKS2,DIS3,GMNN,CDCA8,CENPH,DHCR24,NCAPH,POC1A,BRCA1,NOC4L,WDR62,CENPI,FASTKD3,NOC2L,EIF5A,B4GALT1,SMC2,FARSA,PREB,ESPL1,SPC25,CDC6,NDC80,OIP5,IPO4,HIST1H1A,RAC1,NUP62,EMP2,DDX28,PDXP,FOSL1,PLK4,IQGAP1,SUV39H1,HASPIN,RSL1D1,TOMM34,IQGAP2,SAMM50,RRP1,REEP4,HMGB2,DMAP1,CDC42EP4,HIST1H2BB,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,RAB35,STAG1,ENSCAFG00000005299,EZR,SMC6,SF3A2,SASS6,BUB1,RBM14,CORO1A,NOLC1,CE	down_ACOR_VSMC
GO:0002886	0.000803	1	2	10	regulation of myeloid leukocyte mediated	BP	0.276	LYN,STX4	down_ACOR_EC
GO:0040011	0.000805	1	9	505	locomotion	BP	0.276	ACVRL1,LYN,IGF1R,PDPN,NRP2,HOXA7,SULF1,STX4,NEDD4	down_ACOR_EC
GO:0009653	0.000806	0.999	90	773	anatomical structure morphogenesis	BP	0.085	EPHB1,PLK2,HOXB7,TEK,IL7R,ADGRF5,KIT,PRCP,CXCL8,ARHGEF15,IFRD1,EMCN,CLEC14A,CALCRL,FLI1,TIE1,TNFAIP3,ADAMTS9,AMOT,PODXL,RELN,CD34,MEF2C,CHD7,TIPARP,DLL4,GPR4,STC1,GATA3,EDN1,HOXB8,RAB11A,APLNR,ARAP3,SMAD1,NTN4,NEDD9,SOX18,PIK3C2A,TMOD1,PPP3CA,PTPRB,MTSS1,EPHB4,NECTIN2,MTOR,MAP3K3,BMP2,HHEX,PREX2,PDZD8,ANGPT2,PROX1,ENSCAFG00000010224,MDFI,STMN1,FLNB,SNX2,TSPAN12,PRKD2,TLR3,BTBD7,EXOC5,TIMELESS,HOXB5,FES,JAG1,RAPGEF2,CREB1,BCL10,FMNL3,ADIPOR2,SPTBN4,ITGA6,SKIL,HIF1A,ALS2,ATRX,ALDH1A3,ENSCAFG00000002015,LUZP1,VASH1,JCAD,TMOD3,ZEB1,ARHGEF2,FSCN1,CDON,ELK3,ZMYM2	up_VCAV_EC

GO:0034123	0.00081	1	2	10	positive regulation of toll-like receptor signaling	BP	0.353	TLR2,CAV1	up_VSAP_VSMC
GO:0009887	0.000813	1	3	314	animal organ morphogenesis	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0032715	0.000814	1	2	11	negative regulation of interleukin-6 production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0050931	0.00082	1	5	10	pigment cell differentiation	BP	0.0858	EDNRB,KIT,ADAMTS9,MEF2C,RAB27A	up_VCAV_EC
GO:0030036	0.000823341	0.99973	15	223	actin cytoskeleton organization	BP	0.7009284	MYOZ2,TMOD1,ARHGAP6,AQP1,SYNPO2,DIXDC1,PDLIM3,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,NRP1,PRKCD	up_ACOR_EC
GO:2001224	0.000824	1	4	5	positive regulation of neuron migration	BP	0.0858	RELN,RAPGEF2,ARHGEF2,ZNF609	up_VCAV_EC
GO:0048856	0.000826	1	9	1533	anatomical structure development	BP	0.599	HOXA3,TBX5,GATA5,HOXA2,TMEM176A,TMEM176B,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0007389	0.000829	1	3	137	pattern specification process	BP	0.777	HOXC10,EYA1,HOXA9	up_AFEM_VSMC
GO:0007338	0.000837	1	2	16	single fertilization	BP	0.375	HOXA9,HOXA11	up_VFEM_VSMC
GO:0048646	0.000838	1	47	349	anatomical structure formation involved in morphogenesis	BP	0.0858	EPHB1,PLK2,TEK,PRCP,CXCL8,EMCN,CLEC14A,CALCRL,TIE1,TNFAIP3,ADAMTS9,AMOT,PODXL,RELN,CD34,MEF2C,DLL4,GPR4,GATA3,EDN1,APLNR,SMAD1,SOX18,PIK3C2A,TMOD1,PTPRB,EPHB4,NECTIN2,MAP3K3,HHEX,ANGPT2,PROX1,TSPAN12,PRKD2,TLR3,BCL10,ADIPOR2,ITGA6,SKIL,HIF1A,ALDH1A3,LUZP1,VASH1,JCAD,TMOD3,CDON,ELK3	up_VCAV_EC
GO:0003129	0.000839	1	1	3	heart induction	BP	0.702	GATA5	down_VFEM_VSMC
GO:0001816	0.00084	1	29	194	cytokine production	BP	0.0858	ACKR1,GBP5,KIT,TNFAIP3,TMEM173,CD34,PDE4D,FERMT1,TLR4,GATA3,HOMER3,IRF8,PELI1,ARG2,ABCA1,MAPK13,RIOK3,PRKD2,TLR3,APOD,CD200,PLCG2,BCL10,HMGB1,NOS2,RIPK1,LSM14A,HIF1A,ARHGEF2	up_VCAV_EC
GO:0048731	0.00084	1	13	1247	system development	BP	0.198	HOXC10,TBX15,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,CYP26B1,MTSS1	up_VFEM_EC
GO:0035480	0.00084	1	1	1	regulation of Notch signaling pathway involved in heart	BP	1	GATA5	down_VSAP_VSMC
GO:0035481	0.00084	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	1	GATA5	down_VSAP_VSMC
GO:0003137	0.00084	1	1	1	Notch signaling pathway involved in heart	BP	1	GATA5	down_VSAP_VSMC
GO:0061999	0.00084	1	1	1	regulation of cardiac endothelial to	BP	1	GATA5	down_VSAP_VSMC
GO:0062000	0.00084	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	1	GATA5	down_VSAP_VSMC
GO:0090381	0.00084	1	1	1	regulation of heart induction	BP	1	GATA5	down_VSAP_VSMC
GO:1901321	0.00084	1	1	1	positive regulation of heart induction	BP	1	GATA5	down_VSAP_VSMC
GO:0090190	0.000845	1	2	10	positive regulation of branching involved in ureteric bud	BP	0.198	HOXB7,SIX1	up_VFEM_EC
GO:0008283	0.000856	1	9	545	cell proliferation	BP	0.285	ACVRL1,LYN,HOXA3,IGF1R,PDPN,USP28,SULF1,WDR12,STX4	down_ACOR_EC
GO:0045446	0.00086	1	9	32	endothelial cell differentiation	BP	0.0873	PDE4D,RAPGEF1,STC1,SOX18,PROX1,HOXB5,JAG1,RAPGEF2,ZEB1	up_VCAV_EC
GO:0001763	0.00086	1	3	78	morphogenesis of a branching structure	BP	0.375	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0001823	0.000865	1	3	45	mesonephros development	BP	0.199	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0010543	0.000865	1	2	10	regulation of platelet activation	BP	0.285	LYN,PDPN	down_ACOR_EC
GO:1904888	0.000866	1	2	31	cranial skeletal system development	BP	0.777	TBX15,IRX5	up_AFEM_VSMC
GO:0061343	0.00087	1	1	3	cell adhesion involved in heart morphogenesis	BP	0.702	GATA5	down_VFEM_VSMC
GO:0003128	0.000876	1	1	6	heart field specification	BP	0.942	GATA5	down_AFEM_VSMC
GO:0060297	0.000886	1	3	3	regulation of sarcomere organization	BP	0.0891	MEF2C,EDN1,PROX1	up_VCAV_EC
GO:0019932	0.000889	1	16	82	second-messenger-mediated signaling	BP	0.0891	EDNRB,SELP,CXCR4,CALCRL,PDE4D,EDN1,APLNR,HOMER3,PPP3CA,GUCY1A1,MTOR,ABCA1,GUCY1B1,RAPGEF2,NOS2,MCU	up_VCAV_EC
GO:0071470	0.000893	1	2	13	cellular response to osmotic stress	BP	1	PTGER2,ARHGEF2	up_VPUL_EC

GO:0002520	0.0009	1	39	279	immune system development	BP	0.0896	HOXB7,HCLS1,IL7R,ADGRF5,KIT,IL6,FLI1,TNFAIP3,MEF2C,CHD7,TIPARP,DLL4,GATA3,HOXB8,ENSCAFG00000003530,IRF8,CASP8,MTOR,TENT2,HHEX,ITPKB,THOC1,SWAP70,MFNG,FES,JAG1,PLCG2,CREB1,HMGB1,RIPK1,CRIP2,ATP11C,CUL4A,BMX,HIF1A,TMOD3,ZEB1,TET2,TJP2	up_VCAV_EC
GO:0060411	0.000901	1	10	33	cardiac septum morphogenesis	BP	0.485	SMAD6,GATA4,BMP4,FGFR2,CITED2,EGLN1,NRP1,TBX20,TBX5,CHD7	up_ACOR_VSMC
GO:0009792	0.000903	1	6	231	embryo development ending in birth or egg	BP	0.289	ACVRL1,HOXA3,ACSL4,HOXA7,SULF1,HOXA1	down_ACOR_EC
GO:0009952	0.000905	1	2	66	anterior/posterior pattern specification	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0060914	0.000914	1	2	11	heart formation	BP	0.208	EYA1,SIX1	up_VFEM_EC
GO:0036344	0.000916	1	4	8	platelet morphogenesis	BP	0.154	MYH9,ACTN1,PTPN11,WDR1	down_VSAP_EC
GO:0071356	0.000918	1	3	57	cellular response to tumor necrosis factor	BP	1	NR1H4,CCL24,ARHGEF2	up_VPUL_EC
GO:0010596	0.000919	1	7	21	negative regulation of endothelial cell migration	BP	0.0902	ADAMTS9,MEF2C,DLL4,STC1,ANGPT2,HMGB1,VASH1	up_VCAV_EC
GO:0061448	0.000919	1	4	89	connective tissue development	BP	0.289	HOXA3,SULF1,CSGALNACT1,HOXC4	down_ACOR_EC
GO:0002371	0.000922	1	3	3	dendritic cell cytokine production	BP	0.0902	KIT,TLR4,TLR3	up_VCAV_EC
GO:0050851	0.000927	1	9	34	antigen receptor-mediated signaling	BP	0.0902	PRKCH,PDE4D,MEF2C,EIF2B2,GATA3,NECTIN2,PRKD2,PLCG2,BCL10	up_VCAV_EC
GO:0002520	0.000935	1	6	279	immune system development	BP	0.21	HOXA9,TOX,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0003006	0.000948	1	3	180	developmental process involved in reproduction	BP	0.434	HOXA9,WNT7A,ESR1	up_AORTRT_VSMC
GO:0043408	0.000953	1	35	211	regulation of MAPK cascade	BP	0.485	ADRA1B,LEP,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,NDRG2,F2RL1,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,FRS2,DAG1,APP,PSEN1,SYNJ2BP,CCL5,DUSP22,EDN1,DUSP26,NOD2,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0000910	0.000954	1	12	52	cytokinesis	BP	0.0663	ANLN,CENPA,BIRC5,AURKB,STMN1,PLK3,E2F8,CDC6,NUP62,PDXP,RAB35,ENSCAFG00000005299	down_ACOR_VSMC
GO:0035850	0.000961	1	8	25	epithelial cell differentiation involved in	BP	0.0926	PDGFB,PODXL,MEF2C,GPR4,GATA3,MTSS1,JAG1,BASP1	up_VCAV_EC
GO:0009790	0.000962	1	3	335	embryo development	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0048518	0.000964	0.999	169	1676	positive regulation of biological process	BP	0.0926	EPHB1,PLK2,HOXB7,TEK,HCLS1,IL7R,GBP5,ADGRF5,SELP,KIT,SELE,PPP2R5A,CXCL8,PRKCH,ARHGEF15,DOCK4,CALCRL,TNFAIP3,ADAMTS9,PPARG,MAP3K11,ATP8A1,TNIP1,AMOT,PDGFB,PODXL,STK10,BAIAP2L1,TMEM173,RELN,CD34,PDE4D,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,STC1,EIF2B2,GATA3,EDN1,RAB11A,RALB,APLNR,RAB27A,TCF4,SMAD1,FOXN2,TNFAIP8,ENSCAFG00000017103,NEDD9,IRF8,PIK3C2A,EGFL7,PELI1,PPP3CA,YES1,GUCY1A1,ODC1,SPTLC2,ARG2,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CREM,CAV2,SLK,BMP2K,CNOT6,CCAR1,ABCA1,MAPK13,ITPKB,NCKAP1,GDPD5,RIOK3,PROX1,UHRF2,IQGAP2,MADD,EPB41,ARID4B,STMN1,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,MFNG,AKAP12,NCK1,TIMELESS,OTUD4,LDB2,CD200,FES,JAG1,NSD1,HIST1H1A,PTGS2,MMD,RAPGEF2,PLCG2,CTDSPL2,CREB1,BCL10,PAN3,ZC4H2,TAOK1,CTNNA1,CNOT7,GCH1,ADIPOR2,HMGB1,AHR,NOS2,PMAIP1,ARPC5L,BLM,SPTBN4,RIPK1,CRIP2,NRAS,SMC5,LSM14A,ITGA6,RAD21,ATP11C,SKIL,GPBP1,MCU,PDGFD,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ALDH	up_VCAV_EC

GO:0022607	0.000969	0.999	107	969	cellular component assembly	BP	0.0671	ACSL3,FSCN1,HMGB1,IRAK1,ANLN,STXBP6,USP4,HMGA1,HMGCR,EDC3,SMC1A,UBE2S,RRM1,ZW10,CAPG,CENPA,SLC29A1,NDC1,CENPN,TRIP13,C1QTNF6,SDC1,FBXO5,HSPA9,CFAP298,PSMD13,BIRC5,INSIG1,PRMT1,CAV1,RAD51,LIMA1,NF2,AURKB,TK1,STMN1,CENPO,HAUS8,GREM1,NEK2,RCC1,DHX33,GMNN,CENPH,POC1A,WDR62,CENPI,FASTKD3,NOC2L,B4GALT1,FARSA,PREB,OIP5,IPO4,HIST1H1A,RAC1,NUP62,EMP2,DDX28,PDXP,FOSL1,PLK4,IQGAP2,SAMM50,HMGB2,CDC42EP4,HIST1H2BB,SMC3,CDK2,DDX39B,STAG1,ENSCAFG00000005299,EZR,SF3A2,SASS6,RBM14,CORO1A,CENPW,FOXRED1,CDC20,SIGMAR1,ASPM,ARPC1B,CENPP,GRWD1,ENSCAFG00000010224,PRMT5,PSMC1,CTH,TRAPPC6A,ENSCAFG00000015189,KIF11,HAT1,TINF2,GEMIN7,UBE2C,MIS18A,TBCC,SIX4,H3F3B,CEP83,PDSS1,TTLL1,TPBG,SF3A1,EIF3M,KIF24	down_ACOR_VSMC
GO:0032879	0.000969	1	32	767	regulation of localization	BP	0.919	CMKLR1,LEP,KCNC4,CRY2,RAB20,GAS1,ANGPT4,HOXA7,DLL1,CRYAB,KCND1,PLXNA4,GPAM,CHRM2,TWIST2,GREM1,CAMK2A,CYLD,FXYD1,LRRC15,RECK,TBXA2R,REEP2,BVES,LGR6,RAB7A,ACACB,CCL5,DMPK,ADAM17,CLIC4,KANK1	up_AFEM_EC
GO:0003006	0.000971	1	5	180	developmental process involved in reproduction	BP	0.387	HOXA11,HOXA9,SALL1,IRX5,GJB5	up_VSAP_VSMC
GO:0008584	0.000972	1	2	39	male gonad development	BP	0.434	HOXA9,ESR1	up_AORTRT_VSMC
GO:0046546	0.000972	1	2	39	development of primary male sexual	BP	0.434	HOXA9,ESR1	up_AORTRT_VSMC
GO:0003180	0.000975	1	1	7	aortic valve morphogenesis	BP	0.947	GATA5	down_AFEM_VSMC
GO:0046649	0.000986	1	26	162	lymphocyte activation	BP	0.0934	IL7R,KIT,IL6,TNFAIP3,MEF2C,CHD7,DLL4,TLR4,GATA3,RAB27A,PELI1,ARG2,MTOR,ELF4,HHEX,ITPKB,THOC1,SWAP70,MFNG,NCK1,PLCG2,BCL10,HMGB1,ATP11C,BMX,ZEB1	up_VCAV_EC
GO:0002064	0.00099	1	15	71	epithelial cell development	BP	0.0934	PDGFB,PODXL,PDE4D,RAPGEF1,GPR4,STC1,SOX18,TMOD1,PROX1,ARID4B,FLNB,JAG1,RAPGEF2,HIF1A,ATRX	up_VCAV_EC
GO:0001501	0.00099	1	3	178	skeletal system development	BP	0.434	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0009653	0.000993	1	10	773	anatomical structure morphogenesis	BP	0.387	HOXA11,TBX15,HOXA9,PITX1,SALL1,HOXC10,IRX5,CAV1,SHOX2,GJB5	up_VSAP_VSMC
GO:0070527	0.000998	1	2	10	platelet aggregation	BP	0.302	LYN,PDPN	down_ACOR_EC
GO:0021983	0.000998	1	2	11	pituitary gland development	BP	0.387	PITX1,SALL1	up_VSAP_VSMC
GO:1901213	0.000998	1	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	0.947	GATA5	down_AFEM_VSMC
GO:0060351	0.001	1	2	11	cartilage development involved in endochondral bone morphogenesis	BP	0.387	HOXA11,SHOX2	up_VSAP_VSMC

GO:0048522	0.00101	0.999	152	1484	positive regulation of cellular process	BP	0.0945	EPHB1,PLK2,TEK,HCLS1,IL7R,GBP5,ADGRF5,SELP,KIT,SELE,PPP2R5A,CXCL8,PRKCH,ARHGEF15,DOCK4,CALCRL,TNFAIP3,ADAMTS9,PPARG,MAP3K11,ATP8A1,TNIP1,PDGFB,PODXL,STK10,BAIAP2L1,TMEM173,RELN,CD34,MEF2C,FERMT1,ATF3,CHD7,DLL4,RAPGEF1,TLR4,NLRC5,GPR4,GATA3,EDN1,RAB11A,RALB,APLNR,RAB27A,TCF4,FOXN2,TNFAIP8,ENSCAFG00000017103,NEDD9,IRF8,PIK3C2A,EGFL7,PELI1,PPP3CA,YES1,GUCY1A1,ODC1,SPTLC2,ARG2,CASP8,NECTIN2,MTOR,ACPP,TSPAN14,MAP3K3,BMP2,HHEX,CREM,CAV2,SLK,BMP2K,CNOT6,CCAR1,ITPKB,NCKAP1,GDPD5,PROX1,UHRF2,IQGAP2,MADD,ARID4B,STMN1,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,MFNG,AKAP12,NCK1,TIMELESS,OTUD4,LDB2,CD200,FES,JAG1,NSD1,HIST1H1A,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BCL10,PAN3,ZC4H2,TAOK1,CTNNA1,CNOT7,HMGB1,AHR,NOS2,PMAIP1,ARPC5L,BLM,RIPK1,CRIP2,NRAS,SMC5,LSM14A,ITGA6,RAD21,ATP11C,SKIL,GPBP1,MCU,PDGFD,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ALDH1A3,ENSCAFG00000002015,PTP4A1,RGL2,JCAD,TMOD3,ZEB1,TET2,ARHGEF2,FSCN1,FBXO5,CDON,ZNF609	up_VCAV_EC
GO:0016239	0.00101	1	6	20	positive regulation of macroautophagy	BP	0.168	SESN2,HIF1A,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0048568	0.00101	1	3	148	embryonic organ development	BP	0.786	TBX15,EYA1,IRX5	up_AFEM_VSMC
GO:0032412	0.00101	1	3	46	regulation of ion transmembrane	BP	0.387	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0071606	0.00101	1	1	1	chemokine (C-C motif) ligand 4 production	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0071608	0.00101	1	1	1	macrophage inflammatory protein-1	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0071640	0.00101	1	1	1	regulation of macrophage inflammatory protein 1 alpha production	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0071641	0.00101	1	1	1	negative regulation of macrophage inflammatory protein 1	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0071643	0.00101	1	1	1	regulation of chemokine (C-C motif) ligand 4	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0071644	0.00101	1	1	1	negative regulation of chemokine (C-C motif)	BP	0.434	ARG2	up_AORTRT_VSMC
GO:1905076	0.00101	1	1	1	regulation of interleukin-17 secretion	BP	0.434	ARG2	up_AORTRT_VSMC
GO:1905077	0.00101	1	1	1	negative regulation of interleukin-17 secretion	BP	0.434	ARG2	up_AORTRT_VSMC
GO:1905403	0.00101	1	1	1	negative regulation of activated CD8-positive, alpha-beta T cell	BP	0.434	ARG2	up_AORTRT_VSMC
GO:2000666	0.00101	1	1	1	negative regulation of interleukin-13 secretion	BP	0.434	ARG2	up_AORTRT_VSMC
GO:0051704	0.00102	0.999	58	476	multi-organism process	BP	0.0952	GBP5,KIT,LYZ,CXCL8,PTCHD1,TNFAIP3,ADAMTS9,TNIP1,MX2,BAIAP2L1,TMEM173,TSPAN8,PDE4D,MEF2C,CHD7,TLR4,NLRC5,GATA3,PSME4,IRF8,FIGNL1,PELI1,SERINC5,GUCY1A1,ODC1,ARG2,NECTIN2,MTOR,CDYL,CREM,ABCA1,RIOK3,PROX1,ARID4B,STMN1,THOC1,SMARCA4,TLR3,OAS3,NCK1,HIST1H1A,PTGS2,PLCG2,BCL10,CNOT7,GCH1,NOS2,PMAIP1,SPTBN4,LSM14A,AFF4,ARHGDIB,KDM3A,ATRX,IVNS1ABP,SPATA6,FBXO5,USP6NL	up_VCAV_EC
GO:0000086	0.00102	1	12	52	G2/M transition of mitotic cell cycle	BP	0.0701	BIRC5,CDK1,FANCI,TOPBP1,CDK4,RNASEH2B,DTL,CDK2,CCNA2,ENSCAFG00000005299,CLSPN,CCNB3	down_ACOR_VSMC
GO:1901184	0.00102	1	6	20	regulation of ERBB signaling pathway	BP	0.168	SOCS5,ERRFI1,PTPN2,ADAM17,CBLC,RHBDF2	down_VSAP_EC
GO:1904467	0.001026912	0.99996	3	8	regulation of tumor necrosis factor secretion	BP	0.7009284	NR1H4,FZD5,MAVS	up_ACOR_EC

GO:0048513	0.00103	0.999	101	906	animal organ development	BP	0.0952	EPHB1,EDNRB,HOXB7,HCLS1,PCDH12,IL7R,ADGRF5,KIT,CXCL8,PTCHD1,PRKCH,ARHGEF15,IL6,CALCRL,FLI1,TNFAIP3,ADAMTS9,PDGFB,PODXL,RELN,CD34,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,GPR4,STC1,EIF2B2,GATA3,EDN1,HOXB8,APLNR,NTN4,FOXN2,IGSF3,ENSCAFG00000003530,IRF8,SOX18,TMOD1,PPP3CA,MTSS1,ODC1,ARG2,CASP8,MTOR,TENT2,HOOK3,BMP2,HHEX,CAV2,BMP2K,ITPKB,GDPD5,PROX1,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,ARID4B,STMN1,FLNB,TSPAN12,SMARCA4,MFNG,APOD,BTBD7,TIMELESS,HOXB5,LDB2,SLC25A25,FES,JAG1,PTGS2,RAPGEF2,PLCG2,CREB1,BASP1,HMGB1,NUP133,RIPK1,CRIP2,ITGA6,ATP11C,SKIL,CUL4A,BMX,NR1D2,HIF1A,ATRX,ALDH1A3,P2RX2,LUZP1,RBBP6,VASH1,TMOD3,ZEB1,TET2,FBXO5,CDON,TJP2	up_VCAV_EC
GO:2000107	0.00103	1	6	16	negative regulation of leukocyte apoptotic	BP	0.0952	HCLS1,IL7R,ARG2,ITPKB,BCL10,HIF1A	up_VCAV_EC
GO:0061213	0.00103	1	2	11	positive regulation of mesonephros	BP	0.228	HOXB7,SIX1	up_VFEM_EC
GO:0002040	0.00104	1	11	46	sprouting angiogenesis	BP	0.0954	PLK2,TEK,CLEC14A,ADAMTS9,DLL4,APLNR,SMAD1,PIK3C2A,EPHB4,MAP3K3,JCAD	up_VCAV_EC
GO:0071398	0.00104	1	2	14	cellular response to fatty acid	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0050900	0.00105	1	16	89	leukocyte migration	BP	0.0955	EDNRB,SELP,KIT,SELE,CXCL8,PDGFB,STK10,CD34,SELL,PDE4D,GATA3,MMP28,SWAP70,APOD,HMGB1,ITGA6	up_VCAV_EC
GO:0042474	0.00105	1	2	11	middle ear morphogenesis	BP	0.23	EYA1,SIX1	up_VFEM_EC
GO:0045167	0.00105	1	1	1	asymmetric protein localization involved in cell fate determination	BP	0.434	WNT7A	up_AORTRT_VSMC
GO:0061038	0.00105	1	1	1	uterus morphogenesis	BP	0.434	WNT7A	up_AORTRT_VSMC
GO:1904889	0.00105	1	1	1	regulation of excitatory synapse assembly	BP	0.434	WNT7A	up_AORTRT_VSMC
GO:1904891	0.00105	1	1	1	positive regulation of excitatory synapse	BP	0.434	WNT7A	up_AORTRT_VSMC
GO:0030099	0.00107	1	22	133	myeloid cell differentiation	BP	0.0967	HOXB7,HCLS1,ADGRF5,KIT,FLI1,MEF2C,GATA3,HOXB8,IRF8,CASP8,MTOR,HHEX,ITPKB,FES,JAG1,CREB1,RIPK1,CUL4A,HIF1A,TMOD3,TET2,TJP2	up_VCAV_EC
GO:0043300	0.00107	1	2	11	regulation of leukocyte degranulation	BP	0.315	LYN,STX4	down_ACOR_EC
GO:0065007	0.00109	0.999	375	3499	biological regulation	BP	0.515	SYNPO2L,EXPH5,TNNT2,SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,DNAJC6,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,CASP10,IFNGR1,LEP,PLCL1,LBH,DCBLD2,MAP3K8,MID1,SLC26A7,KCNE3,GATA5,BCL2,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,PCGF5,ENSCAFG00000016285,HTR2B,RASSF2,TCAF1,MEIS2,USP6NL,FNDC5,MBP,ZRANB1,FBXL20,C28H10orf71,PRDX4,RECK,LIPT2,FEZ1,SKP2,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,LCAT,ZNF331,TPC3,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,TM7SF3,NPPB,CNNM2,FGFR2,TP53BP1,MX1,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,SCARB2,ATRX,MED14,HRH1,CASTOR1,TRPS1,TLR3,SH3RF2,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,RERG,GLRB,PKP4,ARHGAP29,CCNG2,MAOA,ISG15,ZNRF3,ZNF782,CD274,ZNF365,PLPP2,MARCKSL1,AR,PTGIR,ZNF484,SARAF,SASH1,SLC2A5,STX11,GPR155,LMO4,GTF3C1,PTPN3,TMEM108,ZNF572,CLCN3,FGF18,FAM210B,ARHGEF26,NDRG2,ATRN,P4HTM,MICU2,TMX3,CHN2,CDKN2B,ADCY6,USP53,ZMYM2,ITPR1,GRK7,CST3,ZNF174,PLAC8B,KLHL20,LIMS2,BLNK,ANKRD1,PLEKHB2,F2RL1	up_ACOR_VSMC
GO:0007155	0.00109	0.999	29	324	cell adhesion	BP	0.928	GPAM,KIRREL1,CERCAM,FBLN2,ITGB5,PRNP,SDC4,FBN1,THBS3,TLN2,RHOD,ENSCAFG00000014978,TFE3,LAMA3,THY1,HAPLN3,VCAN,B4GALT1,GLI3,ZFP36L1,CDH2,EDIL3,LOXL3,CD164,SHC1,GREM1,RAC2,ZBTB16,ECM2	down_VCAV_EC
GO:0106106	0.00109	1	3	48	cold-induced thermogenesis	BP	0.396	GATM,HOXC10,CAV1	up_VSAP_VSMC

GO:0120161	0.00109	1	3	48	regulation of cold-induced thermogenesis	BP	0.396	GATM,HOXC10,CAV1	up_VSAP_VSMC
GO:0048731	0.0011	1	13	1247	system development	BP	0.396	HOXA11,TBX15,HOXA9,PITX1,EMX2,SALL1,HOXC10,IRX5,MAB21L1,CAV1,SHOX2,HAPLN1,GJB5	up_VSAP_VSMC
GO:0003170	0.0011	1	2	25	heart valve development	BP	0.599	TBX5,GATA5	up_VPUL_VSMC
GO:0098911	0.0011	1	1	4	regulation of ventricular cardiac muscle cell action	BP	0.773	JUP	down_VFEM_VSMC
GO:0007173	0.00111	1	7	27	epidermal growth factor receptor signaling	BP	0.18	SOCS5,ERRFI1,PTPN11,PTPN2,ADAM17,CBLC,RHBDF2	down_VSAP_EC
GO:0034097	0.00111	1	5	238	response to cytokine	BP	1	NR1H4,MRC1,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:1901228	0.00112	1	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	0.773	GATA5	down_VFEM_VSMC
GO:0031347	0.00113	1	23	144	regulation of defense response	BP	0.1	GBP5,TNFAIP3,TNIP1,BCL6B,TMEM173,MEF2C,TLR4,NLRC5,GATA3,PELI1,ARG2,NECTIN2,RIOK3,TLR3,APOD,OTUD4,PTGS2,CNOT7,HMGB1,NOS2,LSM14A,NR1D2,ENSCAFG00000025410	up_VCAV_EC
GO:0032970	0.00113	1	22	130	regulation of actin filament-based process	BP	0.1	TEK,HCLS1,ARHGEF15,BAIAP2L1,PDE4D,MEF2C,STC1,EDN1,ARHGAP28,TMOD1,MTOR,NCKAP1,PROX1,IQGAP2,STMN1,SWAP70,NCK1,FES,ARPC5L,ARHGDIB,TMOD3,FSCN1	up_VCAV_EC
GO:0007275	0.00114	0.999	109	1370	multicellular organism development	BP	0.18	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,SERPINH1,MYH9,NR1H4,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,SGK1,PRKACB,PTPN14,ERRFI1,ITGA2,SEC24D,JCAD,CASP3,PGK1,BCAR3,PTPN11,AARS,FLNB,ENSCAFG00000032470,DPYSL3,HOOK3,IFRD1,TMED2,ILK,FHL2,PRCP,SMARCA4,TGFBR1,PTGS2,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,HIF1A,SLC45A3,SLC20A1,THBS2,ACTG2,TNIK,NXN,UBA6,ZPR1,PTPN2,UCHL5,EIF2B1,EVI2B,NEO1,MTDH,ESM1,ACTA2,ADAMTS6,UST,CDH11,MAGED1,CTNNB1,ANLN,CRYAB,STARD13,TFRC,APOE,PLOD3,KLF5,LYN,STRAP,DDIT3,PDS5B,MMD,PLS3,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,HTT,REST,RBBP8,MAPK10,PRMT1,SH2B3,EXT1,GLO1,DISC1,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,COL12A1,RTCB,HOMER1	down_VSAP_EC
GO:0040011	0.00114	0.999	48	505	locomotion	BP	0.18	ARHGEF2,VEGFA,SULF1,MYH9,FMNL3,HSPA5,SERPINE1,SPARC,ITGA2,JCAD,PTPN11,FSCN1,DPYSL3,ILK,PRCP,WDR1,MYO1C,PIK3C2A,MSN,KIF5B,HIF1A,CX3CL1,PTPN2,NEO1,SDC3,ADAM17,PALLD,CTNNB1,ANLN,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,PDS5B,CCNYL1,NEXN,SDC4,ZMYND8,EXT1,DISC1,PAK2,SIX4,NRP1,USP14,ARF4,TNFAIP1	down_VSAP_EC
GO:0016525	0.00114	1	10	38	negative regulation of angiogenesis	BP	0.1	PLK2,TEK,TIE1,ADAMTS9,AMOT,DLL4,GPR4,HHEX,ANGPT2,VASH1	up_VCAV_EC
GO:2000181	0.00114	1	10	38	negative regulation of blood vessel	BP	0.1	PLK2,TEK,TIE1,ADAMTS9,AMOT,DLL4,GPR4,HHEX,ANGPT2,VASH1	up_VCAV_EC
GO:2001238	0.00114	1	7	23	positive regulation of extrinsic apoptotic	BP	0.1	ATF3,PAK2,BCL10,CTNNA1,PMAIP1,RIPK1,SKIL	up_VCAV_EC
GO:0010501	0.00114	1	6	15	RNA secondary structure unwinding	BP	0.0782	DDX39A,EIF4A3,DDX23,DDX51,DDX28,DDX39B	down_ACOR_VSMC
GO:0031032	0.001141497	0.9998	7	61	actomyosin structure organization	BP	0.7009284	MYOZ2,TMOD1,ARHGAP6,ACTN2,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0051246	0.00115	0.999	71	832	regulation of protein metabolic process	BP	0.18	ARHGEF2,PRICKLE1,VEGFA,MYH9,PLK3,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PUM3,PM20D2,ILK,PPP1R12A,SESN2,PTGS2,MSN,IWS1,DNAJC10,TNIK,NXN,PTPN2,UCHL5,SPOPL,YES1,PLCL1,ADAM17,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,APOE,LYN,STRAP,FAM162A,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,HTT,REST,EIF2S1,SPOP,CALM1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,MADD,KDM3A,MID1	down_VSAP_EC
GO:0048731	0.00115	1	8	1247	system development	BP	0.599	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0022898	0.00115	1	3	48	regulation of transmembrane	BP	0.404	NETO1,STIM1,CAV1	up_VSAP_VSMC

GO:0032720	0.00115	1	2	13	negative regulation of tumor necrosis factor	BP	1	NR1H4,BPI	up_APUL_EC
GO:0086069	0.00115	1	1	4	bundle of His cell to Purkinje myocyte	BP	0.773	JUP	down_VFEM_VSMC
GO:0048704	0.00116	1	3	46	embryonic skeletal system morphogenesis	BP	0.335	HOXA3,HOXA7,HOXA1	down_ACOR_EC
GO:0048706	0.00117	1	14	59	embryonic skeletal system development	BP	0.803	TBX15,HOXA11,HOXA7,HOXA9,WNT11,OSR2,IRX5,HOXD3,HOXA6,OSR1,ZEB1,SULF2,SHOX2,TGFBR2	up_VSAP_EC
GO:0002429	0.00117	1	9	35	immune response-activating cell surface receptor signaling	BP	0.101	PRKCH,PDE4D,MEF2C,EIF2B2,GATA3,NECTIN2,PRKD2,PLCG2,BCL10	up_VCAV_EC
GO:0010633	0.00117	1	8	28	negative regulation of epithelial cell migration	BP	0.101	ADAMTS9,MEF2C,DLL4,STC1,ANGPT2,MCC,HMGB1,VASH1	up_VCAV_EC
GO:0060828	0.00117	1	3	82	regulation of canonical Wnt signaling pathway	BP	1	NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0110053	0.001176249	0.99973	9	98	regulation of actin filament organization	BP	0.7009284	TMOD1,ARHGAP6,SYNPO2,ACTN2,ARHGAP28,PAK3,PTGER4,NRP1,PRKCD	up_ACOR_EC
GO:0080134	0.00118	0.999	50	386	regulation of response to stress	BP	0.101	EPHB1,PLK2,GBP5,SELP,TNFAIP3,MAP3K11,TNIP1,PDGFB,BCL6B,TMEM173,CD34,MEF2C,KLKB1,TLR4,NLRC5,GATA3,EDN1,TFPI,FIGNL1,PELI1,PPP3CA,ARG2,NECTIN2,MTOR,MAP3K3,BMP2,RIOK3,THOC1,TLR3,APOD,NCK1,TIMELESS,OTUD4,PTGS2,ETAA1,TAOK1,CNOT7,GCH1,HMGB1,NOS2,PMAIP1,RIPK1,LSM14A,SKIL,CUL4A,NR1D2,ENSCAFG00000025410,HIF1A,VASH1,ARHGEF2	up_VCAV_EC
GO:0071887	0.00118	1	9	34	leukocyte apoptotic process	BP	0.101	HCLS1,IL7R,MEF2C,ARG2,ITPKB,RAPGEF2,BCL10,RIPK1,HIF1A	up_VCAV_EC
GO:0043086	0.00119	1	5	170	negative regulation of catalytic activity	BP	0.336	LYN,IGF1R,PRKAR2A,MYO1D,ASPN	down_ACOR_EC
GO:0016477	0.0012	0.999	42	426	cell migration	BP	0.186	ARHGEF2,VEGFA,SULF1,MYH9,FMNL3,HSPA5,SERPINE1,SPARC,ITGA2,JCAD,PTPN11,FSCN1,DPYSL3,ILK,PRCP,WDR1,MYO1C,PIK3C2A,MSN,HIF1A,CX3CL1,SDC3,ADAM17,PALLD,CTNNB1,ANLN,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,PDS5B,NEXN,SDC4,ZMYND8,DISC1,PAK2,SIX4,NRP1,ARF4,TNFAIP1	down_VSAP_EC
GO:0006336	0.0012	1	5	11	DNA replication-independent nucleosome	BP	0.0819	OIP5,IPO4,CENPP,HAT1,MIS18A	down_ACOR_VSMC
GO:0044281	0.00121	0.999	83	622	small molecule metabolic process	BP	0.803	PEX7,NAPEPLD,HNF4A,ACSM3,DHDH,LIPC,INSIG2,ACAA1,ACACB,GDA,NADK,PEX2,GOT1,DLST,INPP5E,GLUL,ADHFE1,ENSCAFG00000013986,WARS2,C1QTNF2,COQ9,ALDH6A1,NDUFS1,ENSCAFG00000004260,HSD17B8,FAAH,LMF1,PPIP5K1,PDK2,GALK2,FXN,GALK1,RETSAT,ENTPD3,PTGES,SUOX,CTNS,HACD4,GCDH,ABAT,BCKDHB,ENSCAFG00000016140,CLYBL,NDUFS2,PASK,NT5C2,AZIN2,DAGLB,KHK,MARC1,EHHADH,FARS2,LCAT,PCBD1,LONP2,ACSS2,TKFC,PC,DHRS9,MVK,ABHD16A,LIPE,PNPO,DCAKD,ENSCAFG00000002977,HPGD,ENSCAFG00000013366,PNP,NCOA2,QARS,ENSCAFG00000023820,IDH1,IDH3A,CYB5R3,ENSCAFG00000006639,ASS1,NDUFV1,CHST7,LARS2,AHCYL1,DDIT4,SOAT1,IDO2	up_VSAP_EC
GO:0022610	0.00121	0.999	29	326	biological adhesion	BP	0.973	GPAM,KIRREL1,CERCAM,FBLN2,ITGB5,PRNP,SDC4,FBN1,THBS3,TLN2,RHOD,ENSCAFG00000014978,TFE3,LAMA3,THY1,HAPLN3,VCAN,B4GALT1,GLI3,ZFP36L1,CDH2,EDIL3,LOXL3,CD164,SHC1,GREM1,RAC2,ZBTB16,ECM2	down_VCAV_EC
GO:0072359	0.00121	1	4	368	circulatory system development	BP	0.69	SLITRK5,GATA5,C6,TGFBI	up_VCAV_VSMC
GO:0032330	0.00121	1	2	20	regulation of chondrocyte differentiation	BP	0.495	HOXA11,SHOX2	up_VFEM_VSMC
GO:0070542	0.00121	1	2	15	response to fatty acid	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0002934	0.00121	1	1	4	desmosome organization	BP	0.773	JUP	down_VFEM_VSMC
GO:0003008	0.00122	0.999	44	336	system process	BP	0.104	EPHB1,PLK2,EDNRB,ADGRF5,KIT,PRCP,PTCHD1,DOCK4,FLI1,ATP8A1,PDGFB,RELN,CD34,PDE4D,MEF2C,CHD7,TLR4,STC1,GATA3,EDN1,HOXB8,HOMER3,PTGS1,TMOD1,PPP3CA,GUCY1A1,TMEM150C,ARG2,MTOR,NAV2,ACPP,MMP24,KCNJ2,PTGS2,CREB1,GCH1,NOS2,SPTBN4,HIF1A,ALDH1A3,DOP1B,P2RX2,ATP2A1,TMOD3	up_VCAV_EC

GO:0034612	0.00122	1	3	63	response to tumor necrosis factor	BP	1	NR1H4,CCL24,ARHGEF2	up_VPUL_EC
GO:0042496	0.00122	1	1	1	detection of diacyl bacterial lipopeptide	BP	0.786	TLR2	up_AFEM_VSMC
GO:0071724	0.00122	1	1	1	response to diacyl bacterial lipopeptide	BP	0.786	TLR2	up_AFEM_VSMC
GO:0071726	0.00122	1	1	1	cellular response to diacyl bacterial lipopeptide	BP	0.786	TLR2	up_AFEM_VSMC
GO:1903971	0.00122	1	1	1	positive regulation of response to macrophage colony-stimulating factor	BP	0.786	TLR2	up_AFEM_VSMC
GO:1903974	0.00122	1	1	1	positive regulation of cellular response to macrophage colony-	BP	0.786	TLR2	up_AFEM_VSMC
GO:0030326	0.00123	1	3	51	embryonic limb morphogenesis	BP	0.26	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0035113	0.00123	1	3	51	embryonic appendage morphogenesis	BP	0.26	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0030177	0.00123	1	3	51	positive regulation of Wnt signaling pathway	BP	0.415	SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0003156	0.00123	1	2	20	regulation of animal organ formation	BP	0.495	EYA1,HOXA11	up_VFEM_VSMC
GO:0032787	0.00124	0.999	26	144	monocarboxylic acid metabolic process	BP	0.803	PEX7,ACSM3,LIPC,INSIG2,ACAA1,ACACB,PEX2,C1QTNF2,HSD17B8,FAAH,PDK2,GALK1,PTGES,HACD4,GCDH,ABAT,DAGLB,EHHADH,LONP2,ACSS2,PC,DHRS9,ABHD16A,HPGD,ENSCAFG00000023820,DDIT4	up_VSAP_EC
GO:0007519	0.00124	1	3	49	skeletal muscle tissue development	BP	0.415	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0090189	0.00125	1	2	12	regulation of branching involved in ureteric bud	BP	0.262	HOXB7,SIX1	up_VFEM_EC
GO:0070972	0.00126	1	6	23	protein localization to endoplasmic reticulum	BP	0.193	HSPA5,TRAM1,SRP54,SRPRA,SRP72,KDELR2	down_VSAP_EC
GO:0046661	0.00126	1	2	45	male sex differentiation	BP	0.504	HOXA9,ESR1	up_AORTRT_VSMC
GO:0003176	0.00126	1	1	9	aortic valve development	BP	1	GATA5	down_AFEM_VSMC
GO:1990845	0.00127	1	3	51	adaptive thermogenesis	BP	0.415	GATM,HOXC10,CAV1	up_VSAP_VSMC
GO:0030513	0.00128	1	2	11	positive regulation of BMP signaling pathway	BP	0.353	ACVRL1,SULF1	down_ACOR_EC
GO:0060575	0.00128	1	1	9	intestinal epithelial cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0043535	0.00129	1	9	45	regulation of blood vessel endothelial cell migration	BP	0.193	VEGFA,JCAD,PRCP,PIK3C2A,HIF1A,ADAM17,STARD13,APOE,NRP1	down_VSAP_EC
GO:0016477	0.00129	1	8	426	cell migration	BP	0.353	ACVRL1,LYN,IGF1R,PDPN,NRP2,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0010822	0.00129	1	7	31	positive regulation of mitochondrion	BP	0.193	HIF1A,BNIP3,FAM162A,GSK3B,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0050819	0.00129	1	5	12	negative regulation of coagulation	BP	0.109	PDGFB,CD34,KLKB1,TFPI,PROCR	up_VCAV_EC
GO:0009083	0.00129	1	3	5	branched-chain amino acid catabolic process	BP	0.993	ENSCAFG00000002977,BCKDHB,ACAT1	down_VCAV_EC
GO:1901379	0.00129	1	2	12	regulation of potassium ion transmembrane	BP	0.415	NETO1,CAV1	up_VSAP_VSMC
GO:1900122	0.00129	1	1	3	positive regulation of receptor binding	BP	1	PLCL1	down_VFEM_EC
GO:0071680	0.00129	1	1	4	response to indole-3-methanol	BP	0.773	JUP	down_VFEM_VSMC
GO:0071681	0.00129	1	1	4	cellular response to indole-3-methanol	BP	0.773	JUP	down_VFEM_VSMC
GO:0050715	0.0013	1	9	29	positive regulation of cytokine secretion	BP	0.546	TLR1,HTR2B,MBP,FERMT1,CD274,F2RL1,PTPN22,NOD2,SCAMP5	up_ACOR_VSMC
GO:0010458	0.0013	1	5	12	exit from mitosis	BP	0.0872	UBE2S,ZW10,BIRC5,ENSCAFG00000005299,UBE2C	down_ACOR_VSMC
GO:0009952	0.00131	1	15	66	anterior/posterior pattern specification	BP	0.815	HOXA11,EMX2,HOXA7,HOXA9,CDON,AXIN2,HOXD3,DLL1,HOXA6,OSR1,ZBTB16,RARG,HOXC4,HOXC10,KDM2B	up_VSAP_EC
GO:2000146	0.00132	1	17	92	negative regulation of cell motility	BP	0.11	TIE1,ADAMTS9,MEF2C,DLL4,STC1,GATA3,MMP28,ARAP3,ANGPT2,ENSCAFG00000010224,MCC,APOD,JAG1,CTNNA1,HMGB1,ARHGDIB,VASH1	up_VCAV_EC
GO:0032508	0.00132	1	5	11	DNA duplex unwinding	BP	0.0879	MCM6,MCM4,MCM7,GINS4,RAD51	down_ACOR_VSMC
GO:0008608	0.00132	1	4	7	attachment of spindle microtubules to	BP	0.0879	DSN1,NEK2,NDC80,KNL1	down_ACOR_VSMC

GO:1902680	0.00133	0.999	54	415	positive regulation of RNA biosynthetic process	BP	0.11	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:1903508	0.00133	0.999	54	415	positive regulation of nucleic acid-templated transcription	BP	0.11	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0016053	0.00134	1	14	97	organic acid biosynthetic process	BP	0.195	ASNS,PLOD2,NR1H4,PGK1,TPI1,TRIB3,PGAM1,PTGS2,HIF1A,SLC45A3,ALDH18A1,ALDOC,PLOD3,BCAT1	down_VSAP_EC
GO:0046394	0.00134	1	14	97	carboxylic acid biosynthetic process	BP	0.195	ASNS,PLOD2,NR1H4,PGK1,TPI1,TRIB3,PGAM1,PTGS2,HIF1A,SLC45A3,ALDH18A1,ALDOC,PLOD3,BCAT1	down_VSAP_EC
GO:1903556	0.00134	1	2	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4,BPI	up_APUL_EC
GO:0051050	0.001344794	0.99954	15	235	positive regulation of transport	BP	0.7009284	CDH3,NR1H4,CALY,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,NOD2,ACTN2,PTGER4,MAVS,RARRES2,AZIN2,PRKCD	up_ACOR_EC
GO:1902749	0.00136	1	10	39	regulation of cell cycle G2/M phase transition	BP	0.0893	CDK1,FANCI,TOPBP1,CDK4,RNASEH2B,DTL,CDK2,CLSPN,CDC25A,CCNB3	down_ACOR_VSMC
GO:0035909	0.00136	1	2	14	aorta morphogenesis	BP	0.281	EYA1,SIX1	up_VFEM_EC
GO:0048566	0.00136	1	2	13	embryonic digestive tract development	BP	0.429	SALL1,SHOX2	up_VSAP_VSMC
GO:0009888	0.00137	1	9	545	tissue development	BP	0.367	ACVRL1,HOXA3,PDPN,NRP2,HOXA7,SULF1,CSGALNACT1,HOXC4,ASPN	down_ACOR_EC
GO:0007267	0.00137	1	6	332	cell-cell signaling	BP	1	NR1H4,TBX5,HTR7,PLCL1,SLITRK5,NTRK2	up_APUL_EC
GO:0051239	0.00137	1	5	859	regulation of multicellular organismal process	BP	0.504	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORTRT_VSMC
GO:0086005	0.00137	1	1	5	ventricular cardiac muscle cell action potential	BP	0.773	JUP	down_VFEM_VSMC
GO:0048193	0.00138	1	16	116	Golgi vesicle transport	BP	0.198	SEC24D,HYOU1,EXOC5,SEC23A,RAB6A,LMAN1,YIPF5,USO1,COPB2,HTT,CREB3L2,STX6,ARF4,BLZF1,SEC13,RINT1	down_VSAP_EC
GO:0007186	0.001386572	0.99964	10	124	G protein-coupled receptor signaling	BP	0.7009284	PLCL1,CALY,PTH1R,RGS1,AGRN,GNAO1,PTGIR,ACTN2,PTGER4,GNAZ	up_ACOR_EC
GO:0048519	0.001389674	0.9992	59	1554	negative regulation of biological process	BP	0.7009284	CDH3,NR1H4,TMOD1,BRSK1,TRPS1,PLCL1,PKIB,SOX9,ARHGAP6,PTH1R,PCSK1N,FNDC4,NDRG2,AQP1,KCNB1,FZD5,CCDC3,IFI6,SEMA6D,DUSP26,DIXDC1,PTGIR,RGMA,SMAD6,ACTN2,ZMYND8,ARHGAP28,RNLS,MMP28,BCL2,TRIM8,PTGER4,ARHGDIB,CST3,PIAS1,DCLK2,ADAMTSL2,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,TBX5,LRP4,CLSTN1,LRRC4,CLU,SFMBT2,CHMP4B,TP53INP2,RIOX2,NRP1,AZIN2,PRKCD,PPP1R26,PM20D1,DBNDD2,EFEMP1,TUBB4A	up_ACOR_EC
GO:0001817	0.00139	0.999	27	182	regulation of cytokine production	BP	0.114	ACKR1,GBP5,TNFAIP3,TMEM173,CD34,PDE4D,FERMT1,TLR4,GATA3,HOMER3,IRF8,PELI1,ARG2,MAPK13,RIOK3,PRKD2,TLR3,APOD,CD200,PLCG2,BCL10,HMGB1,NOS2,RIPK1,LSM14A,HIF1A,ARHGEF2	up_VCAV_EC
GO:0003281	0.0014	1	9	30	ventricular septum development	BP	0.546	SMAD6,BMP4,FGFR2,CITED2,LMO4,EGLN1,TBX5,FRS2,AP2B1	up_ACOR_VSMC
GO:1905330	0.0014	1	2	48	regulation of morphogenesis of an	BP	0.504	WNT7A,ESR1	up_AORTRT_VSMC
GO:0001905	0.0014	1	1	1	activation of membrane attack complex	BP	0.69	C6	up_VCAV_VSMC
GO:0001970	0.0014	1	1	1	positive regulation of activation of membrane	BP	0.69	C6	up_VCAV_VSMC
GO:0002922	0.0014	1	1	1	positive regulation of humoral immune	BP	0.69	C6	up_VCAV_VSMC
GO:0001969	0.0014	1	1	1	regulation of activation of membrane attack	BP	0.69	C6	up_VCAV_VSMC

GO:2000259	0.0014	1	1	1	positive regulation of protein activation cascade	BP	0.69	C6	up_VCAV_VSMC
GO:0045917	0.0014	1	1	1	positive regulation of complement activation	BP	0.69	C6	up_VCAV_VSMC
GO:0006351	0.00141	1	6	1069	transcription, DNA-templated	BP	0.795	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0048732	0.00141	1	4	116	gland development	BP	0.429	HOXA9,PITX1,SALL1,CAV1	up_VSAP_VSMC
GO:0060538	0.00141	1	3	51	skeletal muscle organ development	BP	0.429	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0048871	0.001417327	0.99963	10	120	multicellular organismal homeostasis	BP	0.7009284	CDH3,PLCL1,SOX9,PTH1R,AQP1,NOD2,FOXC2,CHMP4B,TP53INP2,PM20D1	up_ACOR_EC
GO:0035150	0.00143	1	10	36	regulation of tube size	BP	0.546	ADRA1B,HTR2B,NPPB,HRH1,ADCY6,F2RL1,HRH2,PTGDR,EDN1,DOCK5	up_ACOR_VSMC
GO:0050880	0.00143	1	10	36	regulation of blood vessel size	BP	0.546	ADRA1B,HTR2B,NPPB,HRH1,ADCY6,F2RL1,HRH2,PTGDR,EDN1,DOCK5	up_ACOR_VSMC
GO:0097659	0.00143	1	6	1072	nucleic acid-templated transcription	BP	0.795	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0019538	0.00144	0.999	128	1713	protein metabolic process	BP	0.202	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,HM13,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,ENSCAFG00000032470,TRIB3,PUM3,PM20D2,ILK,PPP1R12A,PRCP,SESN2,PTGS2,PPIB,CHSY1,MSN,SEL1L,HIF1A,USP12,MRPL1,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,PTPN2,UCHL5,MORF4L2,SPOPL,YARS,TARS,YES1,PLCL1,TTLL7,NARS,ADAM17,EIF4EBP1,CNOT7,MAGED1,DNAJB9,CTNNB1,CRYAB,CDK8,APOE,PLOD3,USP48,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,SPOP,CALM1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,CAMK2D,HIF1AN,BTK,MSRB3,CDKN1A,TMTC3,RSL24D1,NRP1,SPINK2,SH3RF3,RHBDF2,USP14,ARF4,TNFAIP1,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:0050793	0.00144	0.999	64	731	regulation of developmental process	BP	0.202	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,MYH9,NR1H4,FMNL3,SERPINE1,SOCS5,SPARC,PRKACB,ENPP1,ERRFI1,JCAD,PGK1,AKAP2,NUAK1,PTPN11,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,TGFBR1,PTGS2,WDR1,PIK3C2A,MSN,HOXB7,HIF1A,SLC45A3,THBS2,TNIK,ZPR1,PTPN2,EVI2B,MTDH,UST,MAGED1,CTNNB1,STARD13,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,BNIP3,STRAP,DDIT3,MMD,VLDLR,REST,PRMT1,DISC1,LRRTM2,INHBA,HIF1AN,SIX4,NRP1,YWHAH,KDM3A	down_VSAP_EC
GO:0032774	0.00144	1	6	1073	RNA biosynthetic process	BP	0.795	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0010614	0.00144	1	1	5	negative regulation of cardiac muscle	BP	0.773	GATA5	down_VFEM_VSMC
GO:0014741	0.00144	1	1	5	negative regulation of muscle hypertrophy	BP	0.773	GATA5	down_VFEM_VSMC
GO:0006629	0.00145	0.999	55	382	lipid metabolic process	BP	0.868	PEX7,NAPEPLD,HNF4A,ACSM3,LIPC,INSIG2,ENPP2,PLBD1,ACAA1,ACACB,PEX2,SULT1A1,INPP5E,CERS4,HSD17B14,DHRS4,KDELC2,C1QTNF2,PAFAH2,ABHD15,HSD3B7,HSD17B8,PLPP3,ENSCAFG00000000071,FAAH,AMBRA1,RBL2,LMF1,LPL,PDK2,RETSAT,PIK3R1,PLA2G6,PIK3IP1,PTGES,HACD4,GCDH,GDPD5,DAGLB,EHHADH,LCAT,LONP2,DHRS9,MVK,ABHD16A,LIPE,FAXDC2,HPGD,ZFYVE21,ENSCAFG00000023820,IDH1,CYB5R3,PLPP5,B3GALT4,SOAT1	up_VSAP_EC
GO:0048731	0.00145	1	9	1247	system development	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0060562	0.00145	1	4	120	epithelial tube morphogenesis	BP	0.287	EYA1,HOXB7,SIX1,MTSS1	up_VFEM_EC
GO:0032409	0.00145	1	3	52	regulation of transporter activity	BP	0.434	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0002933	0.00145	1	1	1	lipid hydroxylation	BP	0.69	CYP1A1	up_VCAV_VSMC

GO:0001932	0.001452741	0.99939	22	416	regulation of protein phosphorylation	BP	0.7009284	PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,TNFRSF19,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,NRP1,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0007015	0.001452856	0.99959	11	144	actin filament organization	BP	0.7009284	TMOD1,ARHGAP6,SYNPO2,PDLIM3,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,NRP1,PRKCD	up_ACOR_EC
GO:1903827	0.001459915	0.99956	12	164	regulation of cellular protein localization	BP	0.7009284	SH3TC2,KCNB1,EDEM2,PLS1,ACTN2,TRIM8,DCLK2,MAVS,LRRC15,LRP4,TP53INP2,PRKCD	up_ACOR_EC
GO:0044839	0.00146	1	13	61	cell cycle G2/M phase transition	BP	0.0927	BIRC5,CDK1,FANCI,TOPBP1,CDK4,RNASEH2B,DTL,CDK2,CCNA2,ENSCAFG00000005299,CLSPN,CDC25A,CCNB3	down_ACOR_VSMC
GO:0043618	0.00146	1	6	22	regulation of transcription from RNA polymerase II promoter in response to	BP	0.202	SESN2,HIF1A,DDIT3,BACH1,ATF3,HIF1AN	down_VSAP_EC
GO:0006614	0.00146	1	4	10	SRP-dependent cotranslational protein	BP	0.202	TRAM1,SRP54,SRPRA,SRP72	down_VSAP_EC
GO:0007268	0.00146	1	4	130	chemical synaptic transmission	BP	1	HTR7,PLCL1,SLITRK5,NTRK2	up_APUL_EC
GO:0098916	0.00146	1	4	130	anterograde trans-synaptic signaling	BP	1	HTR7,PLCL1,SLITRK5,NTRK2	up_APUL_EC
GO:1903706	0.00146	1	4	119	regulation of hemopoiesis	BP	0.287	HOXA9,TOX,HOXA7,CYP26B1	up_VFEM_EC
GO:0031055	0.00146	1	3	4	chromatin remodeling at centromere	BP	0.0927	OIP5,CENPP,MIS18A	down_ACOR_VSMC
GO:0034080	0.00146	1	3	4	CENP-A containing nucleosome assembly	BP	0.0927	OIP5,CENPP,MIS18A	down_ACOR_VSMC
GO:0061641	0.00146	1	3	4	CENP-A containing chromatin organization	BP	0.0927	OIP5,CENPP,MIS18A	down_ACOR_VSMC
GO:0045087	0.00147	0.999	25	161	innate immune response	BP	0.12	GBP5,TNFAIP3,TNIP1,MX2,TMEM173,TLR4,NLRC5,RAB27A,IRF8,PELI1,SERINC5,NECTIN2,ELF4,RIOK3,FLNB,TLR3,OTUD4,FES,BCL10,CNOT7,GCH1,HMGB1,LSM14A,BMX,ARHGEF2	up_VCAV_EC
GO:0003018	0.00147	1	11	42	vascular process in circulatory system	BP	0.546	ADRA1B,HTR2B,NPPB,HRH1,ADCY6,F2RL1,HRH2,CLSTN1,PTGDR,EDN1,DOCK5	up_ACOR_VSMC
GO:0048562	0.00147	1	4	102	embryonic organ morphogenesis	BP	0.388	HOXA3,HOXA7,HOXA1,HOXC4	down_ACOR_EC
GO:0061217	0.00147	1	2	13	regulation of mesonephros	BP	0.287	HOXB7,SIX1	up_VFEM_EC
GO:0035480	0.00147	1	1	1	regulation of Notch signaling pathway involved in heart	BP	0.69	GATA5	up_VCAV_VSMC
GO:0035481	0.00147	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	0.69	GATA5	up_VCAV_VSMC
GO:0048539	0.00147	1	1	1	bone marrow development	BP	0.69	LRRC17	up_VCAV_VSMC
GO:0003137	0.00147	1	1	1	Notch signaling pathway involved in heart	BP	0.69	GATA5	up_VCAV_VSMC
GO:0061999	0.00147	1	1	1	regulation of cardiac endothelial to	BP	0.69	GATA5	up_VCAV_VSMC
GO:0062000	0.00147	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	0.69	GATA5	up_VCAV_VSMC
GO:0090381	0.00147	1	1	1	regulation of heart induction	BP	0.69	GATA5	up_VCAV_VSMC
GO:1901321	0.00147	1	1	1	positive regulation of heart induction	BP	0.69	GATA5	up_VCAV_VSMC
GO:0032847	0.00148	1	1	1	regulation of cellular pH reduction	BP	0.69	CA2	up_VCAV_VSMC
GO:0032849	0.00148	1	1	1	positive regulation of cellular pH reduction	BP	0.69	CA2	up_VCAV_VSMC
GO:0042938	0.00148	1	1	1	dipeptide transport	BP	0.69	CA2	up_VCAV_VSMC
GO:0090088	0.00148	1	1	1	regulation of oligopeptide transport	BP	0.69	CA2	up_VCAV_VSMC
GO:0090089	0.00148	1	1	1	regulation of dipeptide transport	BP	0.69	CA2	up_VCAV_VSMC
GO:2000878	0.00148	1	1	1	positive regulation of oligopeptide transport	BP	0.69	CA2	up_VCAV_VSMC
GO:0035442	0.00148	1	1	1	dipeptide transmembrane transport	BP	0.69	CA2	up_VCAV_VSMC
GO:2000880	0.00148	1	1	1	positive regulation of dipeptide transport	BP	0.69	CA2	up_VCAV_VSMC
GO:2001148	0.00148	1	1	1	regulation of dipeptide transmembrane transport	BP	0.69	CA2	up_VCAV_VSMC

GO:2001150	0.00148	1	1	1	positive regulation of dipeptide transmembrane	BP	0.69	CA2	up_VCAV_VSMC
GO:0051493	0.001484217	0.99953	13	188	regulation of cytoskeleton organization	BP	0.7009284	TMOD1,ARHGAP6,SYNPO2,DIXDC1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,CHMP4B,NRP1,PRKCD,TUBB4A	up_ACOR_EC
GO:0003179	0.001489276	0.99988	4	19	heart valve morphogenesis	BP	0.7009284	GATA4,SOX9,SMAD6,TBX5	up_ACOR_EC
GO:0099537	0.00149	1	4	131	trans-synaptic signaling	BP	1	HTR7,PLCL1,SLITRK5,NTRK2	up_APUL_EC
GO:0003002	0.00149	1	3	118	regionalization	BP	0.599	HOXA3,GATA5,HOXB5	up_VPUL_VSMC
GO:1990774	0.001494156	0.99994	3	9	tumor necrosis factor secretion	BP	0.7009284	NR1H4,FZD5,MAVS	up_ACOR_EC
GO:0051716	0.001497654	0.99911	72	2001	cellular response to stimulus	BP	0.7009284	SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,CALY,SOX9,RHOU,ARHGAP6,PTH1R,RGS1,NDRG2,AQP1,PORCN,ENSCAFG00000004331,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,RGMA,PDE4A,INSYN1,SMAD6,PLCE1,ACTN2,ARHGAP28,ESM1,PAK3,MMP28,GUCY1B1,GRK7,TNFRSF19,PTGER4,ARHGDIB,ELMO2,DCLK2,ADAMTSL2,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,RARRES2,PRKACA,STK32C,NRP1,HM13,ARHGEF26,PRKCD,GNAZ,RIN2,PYGO2,MFAP4,ADGRL1	up_ACOR_EC
GO:0051094	0.0015	1	4	388	positive regulation of developmental process	BP	0.69	SLITRK5,LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0048598	0.0015	1	3	207	embryonic morphogenesis	BP	0.504	HOXC10,HOXA9,WNT7A	up_AORTRT_VSMC
GO:0001659	0.0015	1	3	54	temperature homeostasis	BP	0.44	GATM,HOXC10,CAV1	up_VSAP_VSMC
GO:0032231	0.001503254	0.99982	5	32	regulation of actin filament bundle assembly	BP	0.7009284	ARHGAP6,SYNPO2,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0002460	0.00151	1	13	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	0.123	IL7R,IL6,TNFAIP3,MEF2C,GATA3,RAB27A,NECTIN2,MTOR,THOC1,SWAP70,JAG1,BCL10,HMGB1	up_VCAV_EC
GO:0048729	0.00151	1	5	209	tissue morphogenesis	BP	0.29	EYA1,HOXB7,SIX1,MTSS1,CA9	up_VFEM_EC
GO:0060350	0.00151	1	2	23	endochondral bone morphogenesis	BP	0.595	HOXA11,SHOX2	up_VFEM_VSMC
GO:0055074	0.00152	1	3	95	calcium ion homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:0032502	0.00153	1	9	1661	developmental process	BP	0.599	HOXA3,TBX5,GATA5,HOXA2,TMEM176A,TMEM176B,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0055081	0.00154	1	2	17	anion homeostasis	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:0003164	0.00154	1	1	2	His-Purkinje system development	BP	1	TBX5	up_APUL_VSMC
GO:0003166	0.00154	1	1	2	bundle of His development	BP	1	TBX5	up_APUL_VSMC
GO:0071702	0.00155	0.999	60	687	organic substance transport	BP	0.21	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SLC7A5,ENPP1,SEC24D,PTPN11,SEC23A,SLC38A1,TRIB3,SESN2,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,SLC2A1,OSBPL9,ZPR1,STAM2,YES1,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,TFRC,APOE,KPNA4,LYN,SLC2A3,OSBPL6,SLC7A11,GSK3B,GBP5,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,INHBA,STX6,ESYT3,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0009888	0.00155	1	6	545	tissue development	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0034453	0.00155	1	2	8	microtubule anchoring	BP	1	HOOK3,GCC2	up_VPOR_EC
GO:0010159	0.00155	1	1	2	specification of animal organ position	BP	1	HOXA3	up_APUL_VSMC
GO:1901699	0.001554842	0.99953	12	164	cellular response to nitrogen compound	BP	0.7009284	NR1H4,SOX9,AQP1,ENSCAFG00000004331,AGRN,NOD2,ACTN2,GUCY1B1,MAVS,FOXC2,RARRES2,PRKCD	up_ACOR_EC

GO:0015031	0.00156	0.999	47	510	protein transport	BP	0.21	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SEC24D,PTPN11,SEC23A,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,TFRC,APOE,KPNA4,LYN,GSK3B,GBP5,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,STX6,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0001508	0.00156	1	8	25	action potential	BP	0.546	FGF13,KCNE3,TPC3,SCARB2,PTPN3,USP53,JUP,GNAQ	up_ACOR_VSMC
GO:0003203	0.00156	1	1	11	endocardial cushion morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0055022	0.00156	1	1	2	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0060044	0.00156	1	1	2	negative regulation of cardiac muscle cell	BP	1	TBX5	up_APUL_VSMC
GO:0061117	0.00156	1	1	2	negative regulation of heart growth	BP	1	TBX5	up_APUL_VSMC
GO:0099536	0.00157	1	4	133	synaptic signaling	BP	1	HTR7,PLCL1,SLITRK5,NTRK2	up_APUL_EC
GO:0060040	0.00157	1	1	1	retinal bipolar neuron differentiation	BP	0.795	IRX5	up_AFEM_VSMC
GO:0002793	0.00158	1	13	54	positive regulation of peptide secretion	BP	0.546	EXPH5,TLR1,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,NOD2,SCAMP5	up_ACOR_VSMC
GO:0050714	0.00158	1	13	54	positive regulation of protein secretion	BP	0.546	EXPH5,TLR1,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,NOD2,SCAMP5	up_ACOR_VSMC
GO:2000826	0.00158	1	2	14	regulation of heart morphogenesis	BP	0.3	EYA1,SIX1	up_VFEM_EC
GO:0032502	0.00159	1	17	1661	developmental process	BP	0.415	ACVRL1,LYN,HOXA3,ACSL4,SPG11,PDPN,NRP2,HIVEP2,HOXA7,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,HOXC4,ASPN,NEDD4	down_ACOR_EC
GO:0030029	0.001596185	0.99944	15	239	actin filament-based process	BP	0.7009284	MYOZ2,TMOD1,ARHGAP6,AQP1,SYNPO2,DIXDC1,PDLIM3,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,NRP1,PRKCD	up_ACOR_EC
GO:0048856	0.0016	0.999	53	1533	anatomical structure development	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,LEP,LBH,XYLT1,ANGPT4,HOXA7,COL8A2,CD40,DLL1,CRYAB,F3,VXN,PLXNA4,NEFH,MAB21L1,THRB,LGI4,TMEM100,PLAGL2,GREM1,NFE2L1,OVOL1,CAMK2A,GREM2,HOXA6,CYLD,POSTN,LUZP1,RECK,PTHLH,TBXA2R,EVI2B,CNNM4,BVES,LGR6,PTPRB,AXIN2,ACACB,PPARGC1A,CDC42EP5,DMPK,ADAM17,CLIC4,LRRN2,HSPB2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC
GO:1903524	0.0016	1	5	11	positive regulation of blood circulation	BP	0.546	ADRA1B,HRH1,F2RL1,HRH2,EDN1	up_ACOR_VSMC
GO:0010611	0.0016	1	1	11	regulation of cardiac muscle hypertrophy	BP	1	GATA5	down_AFEM_VSMC
GO:0014743	0.0016	1	1	11	regulation of muscle hypertrophy	BP	1	GATA5	down_AFEM_VSMC
GO:0032879	0.001603155	0.99919	34	767	regulation of localization	BP	0.7009284	SH3TC2,CDH3,NR1H4,CALY,SOX9,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,SEMA6D,NOD2,PLS1,ACTN2,ZMYND8,MMP28,TRIM8,PTGER4,ARHGDIB,PREB,DCLK2,MAPK8IP2,MAVS,FOXC2,LRRC15,TBX5,LRP4,TP53INP2,RARRES2,VPS16,NRP1,AZIN2,PRKCD,PM20D1	up_ACOR_EC
GO:0021602	0.00161	1	2	16	cranial nerve morphogenesis	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0060914	0.00161	1	1	11	heart formation	BP	1	GATA5	down_AFEM_VSMC

GO:0051239	0.00162	0.999	107	859	regulation of multicellular organismal process	BP	0.934	HOXA11,FZD1,THRB,HOXA7,TWIST2,HOXA9,CDON,WNT11,HNF4A,CD274,AXIN2,C5AR2,WASF3,OSR2,AMIGO1,ENPP2,LRRN3,PPARGC1B,LIMS2,ACACB,IL6R,IRX5,SLIT2,ZHX3,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,KLKB1,EMP2,KCNE3,CHRM1,DLL1,EPN2,OSR1,IL17RC,SAV1,ANXA4,HPSE,PLXNA4,ANKRD54,ZBTB16,TOX,RARG,CCBE1,STAT5A,STAT6,F2RL1,DDR2,MFN2,ZFP36L1,FXN,PIK3R1,TIAM1,OMD,MYC,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,RTN4RL1,SASH1,AGTR1,HOXC10,MYD88,TFE3,LRP4,PASK,DPYSL2,GDPD5,PRKAB1,FBXO7,NTN4,LCAT,LIMD1,NLRX1,TKFC,CD83,KDM2B,RNF216,ZFP36L2,PNP,MAPKBP1,NFIB,ZNF580,CYBA,CYB5D2,PQBP1,TTL,ACVRL1,HTRA2,FLOT1,NCK1,MAVS,BGLAP,HMOX1,MAP2K2,TGFBR2,CITED2,TRADD,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0030001	0.00162	0.999	29	172	metal ion transport	BP	0.546	FGF13,ACTN2,PLCG2,KCNE3,HTR2B,TPC3,NIPAL3,SARAF,PTPN3,MICU2,ITPR1,CACNB3,AKAP6,DMPK,ATP7A,KCNJ4,PRKCE,PSEN1,CHD7,RAB11B,KCNC4,LMTK2,B2M,FXYD1,INPP5K,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0043266	0.00162	1	2	14	regulation of potassium ion transport	BP	0.467	NETO1,CAV1	up_VSAP_VSMC
GO:0044092	0.00163	1	6	270	negative regulation of molecular function	BP	0.416	LYN,IGF1R,PRKAR2A,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0008015	0.00165	0.999	20	120	blood circulation	BP	0.133	EDNRB,PRCP,DOCK4,FLI1,PDGFB,CD34,PDE4D,CHD7,STC1,EDN1,PTGS1,GUCY1A1,MTOR,NAV2,KCNJ2,PTGS2,GCH1,NOS2,SPTBN4,P2RX2	up_VCAV_EC
GO:0050818	0.00165	1	7	24	regulation of coagulation	BP	0.133	SELP,PDGFB,CD34,KLKB1,TLR4,TFPI,PROCR	up_VCAV_EC
GO:0045595	0.00165	1	5	469	regulation of cell differentiation	BP	0.599	TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0001658	0.00165	1	2	24	branching involved in ureteric bud	BP	0.628	EYA1,HOXA11	up_VFEM_VSMC
GO:0006616	0.00166	1	3	5	SRP-dependent cotranslational protein targeting to membrane,	BP	0.221	TRAM1,SRP54,SRP72	down_VSAP_EC
GO:0023051	0.00167	0.999	79	954	regulation of signaling	BP	0.221	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,HYOU1,PTPN11,TRIB3,FARP1,ILK,FHL2,PRCP,SMARCA4,SESN2,PTGS2,MYO1C,CHSY1,UACA,KIF5B,HIF1A,ENSCAFG00000000562,TNIK,NXN,RGS2,PTPN2,NEO1,PLCL1,MTDH,ESM1,ADAM17,CNOT7,CDH11,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,CBLC,ATF3,GSK3B,CDC37,SH3GLB1,TAX1BP3,HTT,REST,RDH11,ARFGEF3,CALM1,RAB11FIP1,DISC1,PAK2,LRRTM2,INHBA,HIF1AN,LMO7,NRP1,SH3RF3,RHBDF2,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:1901992	0.00168	1	7	23	positive regulation of mitotic cell cycle phase	BP	0.105	BIRC5,CDK1,CDK4,DTL,ENSCAFG00000005299,UBE2C,MTBP	down_ACOR_VSMC
GO:0009185	0.00169	1	6	23	ribonucleoside diphosphate metabolic	BP	0.221	PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:0060842	0.00169	1	2	3	arterial endothelial cell differentiation	BP	1	DLL1,TMEM100	up_AFEM_EC
GO:0086065	0.00169	1	1	6	cell communication involved in cardiac	BP	0.829	JUP	down_VFEM_VSMC
GO:0006811	0.0017	0.999	48	330	ion transport	BP	0.546	FGF13,ACTN2,PLCG2,LEP,SLC26A7,KCNE3,HTR2B,TCAF1,TPC3,ABCA1,GJA1,NIPAL3,SARAF,PTPN3,CLCN3,MICU2,ITPR1,DAPK1,SLC17A5,CACNB3,AKAP6,LRRC8C,DMPK,ATP7A,SCP2,KCNJ4,SLCO1A2,PRKCE,PSEN1,CHD7,CLN8,ATP6V0E1,RAB11B,SLC25A20,KCNC4,LMTK2,B2M,PLIN2,FXYD1,CFI,INPP5K,WFS1,ATP2C1,SLC25A12,NDUFA4L2,PARK7,SLC8A1,STC2	up_ACOR_VSMC
GO:0009887	0.0017	1	6	314	animal organ morphogenesis	BP	0.307	TBX15,EYA1,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0048754	0.0017	1	3	57	branching morphogenesis of an epithelial tube	BP	0.307	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0003274	0.0017	1	1	2	endocardial cushion fusion	BP	1	GATA5	down_VSAP_VSMC
GO:0001776	0.00171	1	7	23	leukocyte homeostasis	BP	0.137	TNFAIP3,MEF2C,ITPKB,BCL10,HMGB1,SKIL,HIF1A	up_VCAV_EC

GO:0090184	0.00171	1	2	14	positive regulation of kidney development	BP	0.307	HOXB7,SIX1	up_VFEM_EC
GO:1902106	0.00171	1	2	31	negative regulation of leukocyte differentiation	BP	0.599	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0033554	0.00172	0.999	82	708	cellular response to stress	BP	0.107	HMGB1,SREBF1,USP1,MCM7,RPA1,DDX39A,CBX5,HMGA1,SREBF2,SMC1A,HINFP,NEDD4,WDR76,INTS7,MNDA,POLA1,TRIP13,PPP1R15B,PARPBP,GINS4,RAD54L,POLE,HM13,UBE2T,RFC2,INSIG1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,FANCD2,TIMELESS,TOPBP1,EZH2,MAP3K20,RFC4,FEN1,MND1,RNASEH2B,PLK3,PCNA,TONSL,ARG2,MCM10,RNF152,BRCA1,PPARD,POLH,NEIL3,UBE2J2,DTL,SUV39H1,RSL1D1,DMAP1,SMARCB1,DDX39B,ENSCAFG00000030087,RBBP8,EZR,CLSPN,SMC6,RBM14,MIOS,RBM17,RAD23A,SIGMAR1,MELK,SMARCAL1,TXNDC12,PSMC1,AIFM1,ARHGEF2,H2AFX,CDC5L,ATRIP,NUDT1,HMGN1,APEX1,GEN1	down_ACOR_VSMC
GO:0007010	0.00172	0.999	43	441	cytoskeleton organization	BP	0.221	ARHGEF2,SIPA1L1,MYH9,FMNL3,PLK3,ACTN1,VASP,TPM4,CORO1C,FSCN1,FLNB,MZT1,DPYSL3,HOOK3,PPP1R12A,WDR1,TUBB,TNIK,ZPR1,TMSB10,ACTR3,PALLD,CTNNB1,KPNB1,TWF1,PLEKHG2,TLN1,PLS3,GSK3B,NEXN,DAAM1,CCSER2,HTT,ENSCAFG00000017326,DISC1,PAK2,CAPG,SIX4,NRP1,ENSCAFG00000030508,TNFAIP1,MYBPC2,MID1	down_VSAP_EC
GO:0003205	0.00172	0.999	15	67	cardiac chamber development	BP	0.546	TNNT2,SMAD6,GATA4,BMP4,FGFR2,CITED2,LMO4,EGLN1,NRP1,SMARCD3,TBX20,TBX5,FRS2,CHD7,AP2B1	up_ACOR_VSMC
GO:2000106	0.00172	1	8	29	regulation of leukocyte apoptotic process	BP	0.137	HCLS1,IL7R,MEF2C,ARG2,ITPKB,RAPGEF2,BCL10,HIF1A	up_VCAV_EC
GO:0051093	0.00172	1	4	273	negative regulation of developmental process	BP	0.599	TBX5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0007214	0.00172	1	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	down_VFEM_EC
GO:0018193	0.00173	0.999	37	368	peptidyl-amino acid modification	BP	0.221	ARHGEF2,VEGFA,P4HB,PLOD2,NR1H4,SOCS5,SGK1,ERRFI1,P4HA1,BCAR3,ILK,PTGS2,PPIB,IWS1,GALNT1,NAA10,PTPN2,MORF4L2,YES1,PLCL1,ADAM17,CNOT7,PLOD3,LYN,ASPH,STT3A,CBLC,GSK3B,PRMT1,P3H4,PAK2,CAMK2D,HIF1AN,BTK,NRP1,RPN1,KDM3A	down_VSAP_EC
GO:0002443	0.00173	0.999	14	71	leukocyte mediated immunity	BP	0.138	IL7R,KIT,TLR4,GATA3,RAB27A,NECTIN2,SNAP23,THOC1,SWAP70,TLR3,FES,JAG1,BCL10,HMGB1	up_VCAV_EC
GO:0050730	0.00173	1	11	66	regulation of peptidyl-tyrosine phosphorylation	BP	0.221	ARHGEF2,VEGFA,SOCS5,ERRFI1,PTPN2,YES1,ADAM17,CNOT7,LYN,CBLC,NRP1	down_VSAP_EC
GO:1905314	0.00173	1	1	12	semi-lunar valve development	BP	1	GATA5	down_AFEM_VSMC
GO:0140074	0.00173	1	1	2	cardiac endothelial to mesenchymal transition	BP	1	GATA5	down_VSAP_VSMC
GO:2000026	0.00174	1	8	560	regulation of multicellular organismal development	BP	0.308	EYA1,HOXA9,TOX,HOXB7,HOXA7,SIX1,TIAM1,CYP26B1	up_VFEM_EC
GO:0009566	0.00174	1	2	24	fertilization	BP	0.628	HOXA9,HOXA11	up_VFEM_VSMC
GO:0021953	0.00175	1	2	49	central nervous system neuron differentiation	BP	0.504	HOXC10,WNT7A	up_AORTRT_VSMC
GO:0050793	0.00176	0.999	93	731	regulation of developmental process	BP	0.98	HOXA11,FZD1,THRB,HOXA7,NAPEPLD,TWIST2,HOXA9,CDON,WNT11,HNF4A,CD274,AXIN2,WASF3,OSR2,AMIGO1,ENPP2,LRRN3,PPARGC1B,LIMS2,ACACB,DDHD1,SLIT2,ZHX3,HOXD3,SLC6A4,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,MAP3K5,CDC42EP5,SAV1,HPSE,PLXNA4,ANKRD54,CDC42EP2,ZBTB16,TOX,RARG,CCBE1,STAT6,DDR2,ZFP36L1,FXN,PIK3R1,TIAM1,OMD,MYC,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,RTN4RL1,SASH1,TFE3,LRP4,DPYSL2,GDPD5,ZADH2,FBXO7,NTN4,LIMD1,CDK9,CD83,KDM2B,FBLN1,ZFP36L2,PLEKHB2,YPEL3,PNP,TAF8,NFIB,CYB5D2,PQBP1,TTL,ACVRL1,HTRA2,FLOT1,NCK1,BGLAP,HMOX1,MAP2K2,TGFBR2,CITED2,TRADD,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0016125	0.00176	1	10	41	sterol metabolic process	BP	0.109	SQLE,LSS,SREBF1,HMGCR,INSIG1,ENSCAFG00000018572,DHCR24,MVD,FDFT1,LIPC	down_ACOR_VSMC
GO:0048870	0.00176	1	8	451	cell motility	BP	0.438	ACVRL1,LYN,IGF1R,PDPN,NRP2,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0051674	0.00176	1	8	451	localization of cell	BP	0.438	ACVRL1,LYN,IGF1R,PDPN,NRP2,HOXA7,SULF1,STX4	down_ACOR_EC

GO:0048513	0.00176	1	5	906	animal organ development	BP	0.504	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORTRT_VSMC
GO:0001707	0.00176	1	2	25	mesoderm formation	BP	0.628	EYA1,HOXA11	up_VFEM_VSMC
GO:0072001	0.00177	1	3	104	renal system development	BP	0.628	EYA1,EMX2,HOXA11	up_VFEM_VSMC
GO:0048762	0.00177	1	2	77	mesenchymal cell differentiation	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:1902903	0.001779217	0.99953	10	125	regulation of supramolecular fiber	BP	0.7009284	TMOD1,ARHGAP6,SYNPO2,ACTN2,ARHGAP28,PAK3,PTGER4,NRP1,PRKCD,TUBB4A	up_ACOR_EC
GO:0010811	0.00178	1	10	36	positive regulation of cell-substrate adhesion	BP	0.546	FERMT1,NRP1,NPNT,PRKCE,ECM2,JUP,NID1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0032502	0.00179	0.999	15	1661	developmental process	BP	0.499	HOXA11,TBX15,HOXA9,PITX1,EMX2,GATM,SALL1,HOXC10,IRX5,MAB21L1,STIM1,CAV1,SHOX2,HAPLN1,GJB5	up_VSAP_VSMC
GO:0010508	0.00179	1	8	38	positive regulation of autophagy	BP	0.223	PLK3,SESN2,HIF1A,MTDH,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0032835	0.00179	1	7	21	glomerulus development	BP	0.141	PDGFB,PODXL,MEF2C,GPR4,MTSS1,JAG1,BASP1	up_VCAV_EC
GO:0009653	0.00179	1	7	773	anatomical structure morphogenesis	BP	1	CHL1,HOXA3,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0019471	0.00179	1	4	7	4-hydroxyproline metabolic process	BP	0.546	PRDX4,ERO1B,EGLN1,P4HA1	up_ACOR_VSMC
GO:0003002	0.00179	1	4	118	regionalization	BP	0.499	HOXA11,HOXA9,EMX2,HOXC10	up_VSAP_VSMC
GO:0061035	0.00179	1	2	24	regulation of cartilage development	BP	0.628	HOXA11,SHOX2	up_VFEM_VSMC
GO:0007586	0.001797952	0.99985	4	20	digestion	BP	0.7009284	SOX9,AQP1,NOD2,PLS1	up_ACOR_EC
GO:0022600	0.001797952	0.99985	4	20	digestive system process	BP	0.7009284	SOX9,AQP1,NOD2,PLS1	up_ACOR_EC
GO:0016043	0.0018	0.999	197	1973	cellular component organization	BP	0.11	ACSL3,FSCN1,HMGB1,MCM6,SREBF1,MCM4,FLNB,POLE3,IRAK1,MCM7,RPA1,NCAPD2,ANLN,STXBP6,USP4,FMNL3,ATAD2,HMGA1,HMGCR,EDC3,HNRNPD,SMC1A,UBE2S,NEDD4,RRM1,ZW10,ENSCAFG00000016482,CAPG,SMC4,CENPA,SLC29A1,ENSCAFG00000017264,NDC1,CENPN,TOP3A,TRIP13,COLGALT1,SLC25A5,TIMM44,SF1,SGO1,GINS4,C1QTNF6,SDC1,ARFGAP1,CTDNEP1,FBXO5,HSPA9,RAN,B3GNT2,CFAP298,PRELID1,PSMD13,BIRC5,INSIG1,PRMT1,CAV1,CDK1,RAD51,LIMA1,NF2,AURKB,MMP14,TK1,CDKN2C,DSN1,EZH2,STMN1,CENPO,HAUS8,GREM1,NCAPD3,MAP3K20,NEK2,CHCHD3,FBL,FEN1,SMARCC1,MND1,GAS2L3,PLK3,HMGB3,RCC1,DHX33,KIF22,UHRF1,CKS2,GMNN,CDCA8,CENPH,DHCR24,NCAPH,POC1A,BRCA1,WDR62,CENPI,FASTKD3,NOC2L,EIF5A,B4GALT1,SMC2,FARSA,PREB,ESPL1,SPC25,CDC6,NDC80,OIP5,IPO4,HIST1H1A,RAC1,NUP62,EMP2,DDX28,PDXP,FOSL1,PLK4,IQGAP1,SUV39H1,HASPIN,TOMM34,IQGAP2,SAMM50,REEP4,HMGB2,DMAP1,CDC42EP4,HIST1H2BB,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,RAB35,STAG1,ENSCAFG00000005299,EZR,SMC6,SF3A2,SASS6,BUB1,RBM14,CORO1A,NOLC1,CENPW,FOXRED1,PHACTR4,CDC20,	down_ACOR_VSMC
GO:0010648	0.0018	0.999	40	407	negative regulation of cell communication	BP	0.223	ARHGEF2,PRICKLE1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,SNX25,HYOU1,PTPN11,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,NXN,RGS2,PTPN2,ADAM17,CNOT7,CTNNB1,APOE,WWC3,LYN,STRAP,DDIT3,CBLC,ATF3,GSK3B,TAX1BP3,HTT,REST,CALM1,RAB11FIP1,HIF1AN,NRP1,TNFAIP1	down_VSAP_EC
GO:0048534	0.0018	0.999	36	262	hematopoietic or lymphoid organ development	BP	0.141	HOXB7,HCLS1,IL7R,ADGRF5,KIT,IL6,FLI1,MEF2C,CHD7,TIPARP,DLL4,GATA3,HOXB8,ENSCAFG00000003530,IRF8,CASP8,MTOR,TENT2,HHEX,ITPKB,MFNG,FES,JAG1,PLCG2,CREB1,HMGB1,RIPK1,CRIP2,ATP11C,CUL4A,BMX,HIF1A,TMOD3,ZEB1,TET2,TJP2	up_VCAV_EC
GO:0045197	0.0018	1	4	10	establishment or maintenance of epithelial cell apical/basal polarity	BP	0.223	ILK,WDR1,MSN,ARF4	down_VSAP_EC
GO:0048705	0.0018	1	2	95	skeletal system morphogenesis	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0003128	0.0018	1	1	6	heart field specification	BP	0.829	GATA5	down_VFEM_VSMC
GO:0019359	0.00181	1	6	23	nicotinamide nucleotide biosynthetic process	BP	0.223	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC

GO:0019363	0.00181	1	6	23	pyridine nucleotide biosynthetic process	BP	0.223	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0001775	0.00181	1	3	219	cell activation	BP	0.504	HOXA9,WNT7A,ARG2	up_AORTRT_VSMC
GO:0061437	0.001812027	0.99992	3	10	renal system vasculature development	BP	0.7009284	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0061440	0.001812027	0.99992	3	10	kidney vasculature development	BP	0.7009284	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0003013	0.00182	0.999	20	121	circulatory system process	BP	0.142	EDNRB,PRCP,DOCK4,FLI1,PDGFB,CD34,PDE4D,CHD7,STC1,EDN1,PTGS1,GUCY1A1,MTOR,NAV2,KCNJ2,PTGS2,GCH1,NOS2,SPTBN4,P2RX2	up_VCAV_EC
GO:0046642	0.00182	1	1	2	negative regulation of alpha-beta T cell	BP	0.504	ARG2	up_AORTRT_VSMC
GO:1905397	0.00182	1	1	2	activated CD8-positive, alpha-beta T cell	BP	0.504	ARG2	up_AORTRT_VSMC
GO:1905402	0.00182	1	1	2	regulation of activated CD8-positive, alpha-beta T cell apoptotic process	BP	0.504	ARG2	up_AORTRT_VSMC
GO:2000562	0.00182	1	1	2	negative regulation of CD4-positive, alpha-beta T cell proliferation	BP	0.504	ARG2	up_AORTRT_VSMC
GO:0051017	0.001821495	0.99971	6	49	actin filament bundle assembly	BP	0.7009284	ARHGAP6,SYNPO2,PLS1,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0045595	0.00183	0.999	57	469	regulation of cell differentiation	BP	0.142	EPHB1,EDNRB,HCLS1,IL7R,KIT,PRKCH,IFRD1,ADAMTS9,PPARG,PDGFB,BCL6B,RELN,CD34,MEF2C,CHD7,DLL4,RAPGEF1,GATA3,EDN1,HOXB8,RAB11A,TCF4,NEDD9,PPP3CA,CASP8,MTOR,HOOK3,BMP2,HMG20A,ITPKB,GDPD5,PROX1,ENSCAFG00000010596,NCK1,FES,JAG1,PTGS2,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,HMGB1,RIPK1,ATP11C,SKIL,CUL4A,NR1D2,HIF1A,KDM3A,ENSCAFG00000002015,ZEB1,ARHGEF2,FBXO5,CDON,TJP2,ZNF609	up_VCAV_EC
GO:0032956	0.00183	0.999	20	116	regulation of actin cytoskeleton organization	BP	0.142	TEK,HCLS1,ARHGEF15,BAIAP2L1,MEF2C,EDN1,ARHGAP28,TMOD1,MTOR,NCKAP1,PROX1,IQGAP2,STMN1,SWAP70,NCK1,FES,ARPC5L,ARHGDIB,TMOD3,FSCN1	up_VCAV_EC
GO:0002683	0.00183	1	3	126	negative regulation of immune system process	BP	0.599	TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0000165	0.00184	0.999	37	236	MAPK cascade	BP	0.551	FGF13,ADRA1B,LEP,MID1,HTR2B,RASSF2,MBP,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,NDRG2,F2RL1,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,FRS2,DAG1,APP,PSEN1,SYNJ2BP,CCL5,DUSP22,EDN1,DUSP26,NOD2,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0048332	0.00184	1	2	26	mesoderm morphogenesis	BP	0.63	EYA1,HOXA11	up_VFEM_VSMC
GO:0001759	0.00185	1	1	13	organ induction	BP	1	GATA5	down_AFEM_VSMC
GO:0032880	0.001851663	0.99932	16	266	regulation of protein localization	BP	0.7009284	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PLS1,ACTN2,TRIM8,PTGER4,DCLK2,MAVS,LRRC15,LRP4,TP53INP2,PRKCD	up_ACOR_EC
GO:0055081	0.00187	1	2	17	anion homeostasis	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0043062	0.00188	1	4	99	extracellular structure organization	BP	0.446	PDPN,SULF1,CSGALNACT1,ACSL3	down_ACOR_EC
GO:0045668	0.00188	1	3	11	negative regulation of osteoblast differentiation	BP	1	TWIST2,GREM1,AXIN2	up_AFEM_EC
GO:0001953	0.00188	1	2	14	negative regulation of cell-matrix adhesion	BP	0.446	ACVRL1,HOXA7	down_ACOR_EC

GO:0050896	0.00189	0.999	261	2346	response to stimulus	BP	0.555	TNNT2,SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,SEMA5A,TLR1,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,IFNGR1,LEP,PLCL1,LBH,DCBLD2,AFF3,MAP3K8,MID1,GATA5,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,ENSCAFG00000016285,HTR2B,RASSF2,FNDC5,MBP,TMEM255A,ZRANB1,FBXL20,C28H10orf71,RECK,FEZ1,SKP2,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,LNPK,TM7SF3,FGFR2,TP53BP1,MX1,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TLR3,LRRN4,SH3RF2,PPARGC1A,LATS2,LPL,PDE5A,CITED2,TP53INP1,RERG,GLRB,ARHGAP29,ZBTB40,ISG15,ZNRF3,CD274,ZNF365,PLPP2,AR,PTGIR,SASH1,CTSS,SLC2A5,GPR155,TMEM108,FGF18,FAM210B,ARHGEF26,NDRG2,TMX3,CHN2,CDKN2B,ADCY6,ZBTB4,USP53,POLK,TINAGL1,ITPR1,GRK7,PLAC8B,KLHL20,LIMS2,BLNK,ANKRD1,F2RL1,MXRA5,HRH2,ADGRL1,FAM129A,CAMK2D,PSEN2,ENPP4,PPP2R5E,GABARAPL1,DAPK1,CTSB,ARHGAP5,RBM4B,BNIP3,EGLN1,SLC17A5,NCEH1,AKAP6,CDKN1A,JMY,C1S,GNA14,P2RX7,CRLF3,EDA,TNFSF10,CLSTN1,LRRC8C,CREBRF,NRP1,UBR1,PDE1A,PTPN22,GPM6A,CHD2,ULK2,DMPK,TCN2,NPNT,OS9,UNC5B,STT3B,EVL,SMPD1,RCAN2,APL	up_ACOR_VSMC
GO:0001894	0.001897603	0.99969	6	49	tissue homeostasis	BP	0.7009284	CDH3,SOX9,PTH1R,NOD2,CHMP4B,TP53INP2	up_ACOR_EC
GO:0009719	0.0019	1	6	395	response to endogenous stimulus	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2,NEO1,MXRA5	up_VPUL_EC
GO:0035107	0.0019	1	3	60	appendage morphogenesis	BP	0.33	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0035108	0.0019	1	3	60	limb morphogenesis	BP	0.33	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0098901	0.0019	1	1	7	regulation of cardiac muscle cell action	BP	0.829	JUP	down_VFEM_VSMC
GO:2000026	0.00191	0.999	74	560	regulation of multicellular organismal development	BP	1	HOXA11,FZD1,THRB,HOXA7,HOXA9,CDON,WNT11,HNF4A,CD274,AXIN2,WASF3,OSR2,AMIGO1,ENPP2,LRRN3,PPARGC1B,LIMS2,ACACB,SLIT2,HOXD3,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,SAV1,HPSE,PLXNA4,ANKRD54,ZBTB16,TOX,RARG,CCBE1,STAT6,DDR2,ZFP36L1,PIK3R1,TIAM1,OMD,MYC,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,RTN4RL1,SASH1,TFE3,LRP4,DPYSL2,GDPD5,FBXO7,NTN4,CD83,ZFP36L2,PNP,NFIB,CYB5D2,PQBP1,TTL,ACVRL1,FLOT1,NCK1,BGLAP,HMOX1,MAP2K2,TGFBR2,CITED2,TRADD,LBH,KEAP1	up_VSAP_EC
GO:0042059	0.00191	1	4	10	negative regulation of epidermal growth factor receptor signaling	BP	0.23	SOCS5,ERRFI1,PTPN2,CBLC	down_VSAP_EC
GO:0048870	0.00192	0.999	43	451	cell motility	BP	0.23	ARHGEF2,VEGFA,SULF1,MYH9,FMNL3,HSPA5,SERPINE1,SPARC,ITGA2,JCAD,PTPN11,FSCN1,DPYSL3,ILK,PRCP,WDR1,MYO1C,PIK3C2A,MSN,HIF1A,CX3CL1,SDC3,ADAM17,PALLD,CTNNB1,ANLN,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,PDS5B,CCNYL1,NEXN,SDC4,ZMYND8,DISC1,PAK2,SIX4,NRP1,ARF4,TNFAIP1	down_VSAP_EC
GO:0051674	0.00192	0.999	43	451	localization of cell	BP	0.23	ARHGEF2,VEGFA,SULF1,MYH9,FMNL3,HSPA5,SERPINE1,SPARC,ITGA2,JCAD,PTPN11,FSCN1,DPYSL3,ILK,PRCP,WDR1,MYO1C,PIK3C2A,MSN,HIF1A,CX3CL1,SDC3,ADAM17,PALLD,CTNNB1,ANLN,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,PDS5B,CCNYL1,NEXN,SDC4,ZMYND8,DISC1,PAK2,SIX4,NRP1,ARF4,TNFAIP1	down_VSAP_EC
GO:0006694	0.00192	1	10	42	steroid biosynthetic process	BP	0.117	SQLE,LSS,SREBF1,HMGCR,SF1,INSIG1,ENSCAFG00000018572,DHCR24,MVD,FDFT1	down_ACOR_VSMC
GO:0072507	0.00192	1	3	103	divalent inorganic cation homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:0007155	0.00193	0.999	34	324	cell adhesion	BP	0.23	COL15A1,VEGFA,SULF1,MYH9,SERPINE1,ACTN1,SOCS5,ITGA2,FAM49B,NUAK1,PTPN11,FBLIM1,ILK,PPP1R12A,MSN,THBS2,PTPN2,PVR,ADAM17,CDH11,CTNNB1,ENSCAFG00000002015,TFRC,IGFBP7,LYN,CD44,TLN1,SLC7A11,GSK3B,ITGB3,SDC4,ICAM5,LMO7,NRP1	down_VSAP_EC

GO:0051960	0.00193	0.999	32	216	regulation of nervous system development	BP	0.147	EPHB1,EDNRB,PRKCH,ARHGEF15,IFRD1,RELN,MEF2C,CHD7,DLL4,RAPGEF1,GATA3,RAB11A,TCF4,PPP3CA,MTOR,HOOK3,BMP2,HMG20A,GDPD5,PROX1,NCK1,FES,JAG1,MMD,RAPGEF2,ZC4H2,CTNNA1,HIF1A,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0022603	0.00193	1	2	301	regulation of anatomical structure morphogenesis	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0003180	0.00193	1	1	7	aortic valve morphogenesis	BP	0.829	GATA5	down_VFEM_VSMC
GO:0086002	0.00193	1	1	7	cardiac muscle cell action potential involved in	BP	0.829	JUP	down_VFEM_VSMC
GO:0010646	0.00194	0.999	78	945	regulation of cell communication	BP	0.23	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,HYOU1,PTPN11,TRIB3,FARP1,ILK,FHL2,PRCP,SMARCA4,SESN2,PTGS2,MYO1C,CHSY1,UACA,KIF5B,HIF1A,ENSCAFG00000000562,TNIK,NXN,RGS2,PTPN2,NEO1,PLCL1,MTDH,ESM1,ADAM17,CNOT7,CDH11,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,CBLC,ATF3,GSK3B,CDC37,SH3GLB1,TAX1BP3,HTT,REST,RDH11,ARFGEF3,CALM1,RAB11FIP1,DISC1,PAK2,LRRTM2,INHBA,HIF1AN,NRP1,SH3RF3,RHBDF2,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:0003002	0.00194	1	9	118	regionalization	BP	1	HOXA9,IRX3,HOXC10,HOXA7,DLL1,GREM1,GREM2,HOXA6,AXIN2	up_AFEM_EC
GO:0048066	0.00194	1	5	12	developmental pigmentation	BP	0.148	EDNRB,KIT,ADAMTS9,MEF2C,RAB27A	up_VCAV_EC
GO:0051965	0.00194	1	2	17	positive regulation of synapse assembly	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0071650	0.00194	1	1	2	negative regulation of chemokine (C-C motif)	BP	0.504	ARG2	up_AORTRT_VSMC
GO:0032102	0.001945554	0.99962	7	67	negative regulation of response to external	BP	0.7009284	NR1H4,FNDC4,RGMA,MMP28,PTGER4,NRP1,PRKCD	up_ACOR_EC
GO:0050793	0.00195	1	5	731	regulation of developmental process	BP	0.874	SLITRK5,LIMK1,GATA5,LRRC17,C6	up_VCAV_VSMC
GO:0032528	0.00196	1	4	9	microvillus organization	BP	0.231	PTPN11,FSCN1,TNIK,KLF5	down_VSAP_EC
GO:0072001	0.001967691	0.99951	9	104	renal system development	BP	0.7009284	TBX18,SOX9,AQP1,SMAD6,FOXC2,LRP4,CLSTN1,NRP1,PYGO2	up_ACOR_EC
GO:0009062	0.00197	1	9	31	fatty acid catabolic process	BP	1	PEX7,ACAA1,ACACB,PEX2,FAAH,GCDH,EHHADH,LONP2,ABHD16A	up_VSAP_EC
GO:0035480	0.00197	1	1	1	regulation of Notch signaling pathway involved in heart	BP	0.599	GATA5	up_VPUL_VSMC
GO:0035481	0.00197	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	0.599	GATA5	up_VPUL_VSMC
GO:0003137	0.00197	1	1	1	Notch signaling pathway involved in heart	BP	0.599	GATA5	up_VPUL_VSMC
GO:0061999	0.00197	1	1	1	regulation of cardiac endothelial to	BP	0.599	GATA5	up_VPUL_VSMC
GO:0062000	0.00197	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	0.599	GATA5	up_VPUL_VSMC
GO:0090381	0.00197	1	1	1	regulation of heart induction	BP	0.599	GATA5	up_VPUL_VSMC
GO:1901321	0.00197	1	1	1	positive regulation of heart induction	BP	0.599	GATA5	up_VPUL_VSMC
GO:0023057	0.00198	0.999	40	409	negative regulation of signaling	BP	0.231	ARHGEF2,PRICKLE1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,SNX25,HYOU1,PTPN11,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,NXN,RGS2,PTPN2,ADAM17,CNOT7,CTNNB1,APOE,WWC3,LYN,STRAP,DDIT3,CBLC,ATF3,GSK3B,TAX1BP3,HTT,REST,CALM1,RAB11FIP1,HIF1AN,NRP1,TNFAIP1	down_VSAP_EC
GO:0008406	0.00198	1	2	57	gonad development	BP	0.504	HOXA9,ESR1	up_AORTRT_VSMC
GO:0045137	0.00198	1	2	57	development of primary sexual characteristics	BP	0.504	HOXA9,ESR1	up_AORTRT_VSMC
GO:0048641	0.00198	1	2	16	regulation of skeletal muscle tissue	BP	0.34	SIX1,CYP26B1	up_VFEM_EC
GO:0000050	0.00198	1	1	2	urea cycle	BP	0.504	ARG2	up_AORTRT_VSMC
GO:0032696	0.00198	1	1	2	negative regulation of interleukin-13 production	BP	0.504	ARG2	up_AORTRT_VSMC

GO:0046777	0.00199	0.999	17	86	protein autophosphorylation	BP	0.151	EPHB1,TEK,KIT,MAP3K11,PDGFB,STK10,EPHB4,MTOR,MAP3K3,SLK,PAK2,PRKD2,FES,RIPK1,PDGFD,BMX,LMTK2	up_VCAV_EC
GO:0009887	0.00199	1	6	314	animal organ morphogenesis	BP	0.544	HOXA11,TBX15,SALL1,IRX5,CAV1,SHOX2	up_VSAP_VSMC
GO:0061572	0.001998061	0.99967	6	50	actin filament bundle organization	BP	0.7009284	ARHGAP6,SYNPO2,PLS1,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:2000826	0.00201	1	1	14	regulation of heart morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:1901213	0.00201	1	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	0.829	GATA5	down_VFEM_VSMC
GO:0003218	0.00201	1	1	1	cardiac left ventricle formation	BP	0.599	TBX5	up_VPUL_VSMC
GO:0045893	0.00204	0.999	53	413	positive regulation of transcription, DNA-templated	BP	0.154	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0043534	0.00205	0.999	10	57	blood vessel endothelial cell migration	BP	0.235	VEGFA,MYH9,JCAD,PRCP,PIK3C2A,HIF1A,ADAM17,STARD13,APOE,NRP1	down_VSAP_EC
GO:0072615	0.00205	1	1	2	interleukin-17 secretion	BP	0.504	ARG2	up_AORTRT_VSMC
GO:0045087	0.00206	1	4	161	innate immune response	BP	1	NR1H4,MRC1,CCL24,ARHGEF2	up_VPUL_EC
GO:0048562	0.00206	1	2	102	embryonic organ morphogenesis	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0030155	0.00208	1	5	180	regulation of cell adhesion	BP	0.473	ACVRL1,LYN,PDPN,HOXA7,STX4	down_ACOR_EC
GO:0060054	0.00208	1	1	2	positive regulation of epithelial cell proliferation involved in wound healing	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0021615	0.00208	1	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	up_APUL_VSMC
GO:0031133	0.00209	1	1	2	regulation of axon diameter	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0060068	0.00209	1	1	2	vagina development	BP	0.504	ESR1	up_AORTRT_VSMC
GO:0007275	0.0021	0.999	13	1370	multicellular organism development	BP	0.353	HOXC10,TBX15,EYA1,HOXA9,TOX,MME,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,CYP26B1,MTSS1	up_VFEM_EC
GO:0006928	0.0021	1	9	557	movement of cell or subcellular component	BP	0.473	ACVRL1,LYN,IGF1R,SPG11,PDPN,NRP2,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0003002	0.0021	1	4	118	regionalization	BP	0.473	HOXA3,NRP2,HOXA7,HOXC4	down_ACOR_EC
GO:1900122	0.0021	1	1	3	positive regulation of receptor binding	BP	1	HOXA3	up_APUL_VSMC
GO:0042060	0.00211	1	4	103	wound healing	BP	0.473	ACVRL1,LYN,PDPN,ELK3	down_ACOR_EC
GO:0009952	0.00211	1	2	66	anterior/posterior pattern specification	BP	0.504	HOXC10,HOXA9	up_AORTRT_VSMC
GO:0001554	0.00211	1	1	1	luteolysis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0010593	0.00211	1	1	1	negative regulation of lamellipodium assembly	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0021823	0.00211	1	1	1	cerebral cortex tangential migration using cell-cell interactions	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0021827	0.00211	1	1	1	postnatal olfactory bulb interneuron migration	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0021836	0.00211	1	1	1	chemorepulsion involved in postnatal olfactory bulb interneuron migration	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0021966	0.00211	1	1	1	corticospinal neuron axon guidance	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0021972	0.00211	1	1	1	corticospinal neuron axon guidance through spinal	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0035385	0.00211	1	1	1	Roundabout signaling pathway	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0050924	0.00211	1	1	1	positive regulation of negative chemotaxis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0050929	0.00211	1	1	1	induction of negative chemotaxis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0051414	0.00211	1	1	1	response to cortisol	BP	0.599	SLIT2	up_VPUL_VSMC

GO:0061364	0.00211	1	1	1	apoptotic process involved in luteolysis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0070099	0.00211	1	1	1	regulation of chemokine-mediated signaling	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0070100	0.00211	1	1	1	negative regulation of chemokine-mediated	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0071670	0.00211	1	1	1	smooth muscle cell chemotaxis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0071671	0.00211	1	1	1	regulation of smooth muscle cell chemotaxis	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0071672	0.00211	1	1	1	negative regulation of smooth muscle cell	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0090260	0.00211	1	1	1	negative regulation of retinal ganglion cell axon	BP	0.599	SLIT2	up_VPUL_VSMC
GO:0050896	0.002112158	0.99871	81	2346	response to stimulus	BP	0.72518906	C7,SH3TC2,CDH3,NR1H4,GATA4,BRSK1,PLCL1,CALY,SOX9,HMCN1,RHOU,ARHGAP6,PTH1R,RGS1,PCSK1N,FNDC4,NDRG2,AQP1,PORCN,ENSCAFG00000004331,KCNB1,ADAMTS13,EDEM2,FZD5,CCDC3,AGRN,PDE1A,IFI6,GNAO1,DUSP26,DIXDC1,RASL11A,PTGIR,NOD2,IL33,RGMA,PDE4A,INSYN1,SMAD6,PLCE1,ACTN2,ARHGAP28,ESM1,PAK3,MMP28,GUCY1B1,GRK7,TRIM8,TNFRSF19,PTGER4,ARHGDIB,ELMO2,DCLK2,ADAMTSL2,USP53,MAPK8IP2,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,RARRES2,AGBL5,PRKACA,STK32C,NRP1,HM13,ARHGEF26,PRKCD,GNAZ,RIN2,PYGO2,MFAP4,ADGRL1	up_ACOR_EC
GO:1901655	0.00212	1	7	20	cellular response to ketone	BP	0.612	PRKAA2,ADCY6,PTGDR,PRKCE,NR3C1,DDIT4,PARK7	up_ACOR_VSMC
GO:0000082	0.00213	0.999	12	57	G1/S transition of mitotic cell cycle	BP	0.129	HINFP,POLE,CASP2,CDKN2C,EZH2,CDK4,PLK3,RCC1,CDK2,RBBP8,CDKN3,MTBP	down_ACOR_VSMC
GO:0031128	0.00214	1	1	15	developmental induction	BP	1	GATA5	down_AFEM_VSMC
GO:0022610	0.00215	0.999	34	326	biological adhesion	BP	0.243	COL15A1,VEGFA,SULF1,MYH9,SERPINE1,ACTN1,SOCS5,ITGA2,FAM49B,NUAK1,PTPN11,FBLIM1,ILK,PPP1R12A,MSN,THBS2,PTPN2,PVR,ADAM17,CDH11,CTNNB1,ENSCAFG00000002015,TFRC,IGFBP7,LYN,CD44,TLN1,SLC7A11,GSK3B,ITGB3,SDC4,ICAM5,LMO7,NRP1	down_VSAP_EC
GO:0036003	0.00215	1	4	10	positive regulation of transcription from RNA polymerase II promoter in response to stress	BP	0.243	SESN2,HIF1A,DDIT3,ATF3	down_VSAP_EC
GO:1902117	0.00215	1	2	32	positive regulation of organelle assembly	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0097190	0.00218	0.999	24	217	apoptotic signaling pathway	BP	0.243	ARHGEF2,P4HB,SERPINE1,ERO1A,CASP3,HYOU1,PTGS2,UACA,HIF1A,DNAJC10,PTPN2,MAGED1,CTNNB1,BNIP3,DDIT3,FAM162A,ATF3,SH3GLB1,HTT,PAK2,INHBA,CDKN1A,NRP1,MADD	down_VSAP_EC
GO:0072525	0.00218	1	6	24	pyridine-containing compound biosynthetic	BP	0.243	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0048643	0.0022	1	4	7	positive regulation of skeletal muscle tissue	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0050919	0.0022	1	2	10	negative chemotaxis	BP	1	SEMA3A,SEMA3D	up_VPOR_EC
GO:0010563	0.00221	1	5	203	negative regulation of phosphorus metabolic	BP	0.483	LYN,IGF1R,PRKAR2A,MYO1D,ASPN	down_ACOR_EC
GO:0045936	0.00221	1	5	203	negative regulation of phosphate metabolic	BP	0.483	LYN,IGF1R,PRKAR2A,MYO1D,ASPN	down_ACOR_EC
GO:1903670	0.00223	1	8	30	regulation of sprouting angiogenesis	BP	0.166	PLK2,ADAMTS9,DLL4,APLNR,SMAD1,PIK3C2A,MAP3K3,JCAD	up_VCAV_EC
GO:0060523	0.00223	1	1	2	prostate epithelial cord elongation	BP	0.504	ESR1	up_AORTRT_VSMC
GO:0003214	0.00223	1	1	3	cardiac left ventricle morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0072513	0.00223	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0086091	0.00224	1	1	8	regulation of heart rate by cardiac conduction	BP	0.829	JUP	down_VFEM_VSMC
GO:0021684	0.00224	1	1	2	cerebellar granular layer formation	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0021707	0.00224	1	1	2	cerebellar granule cell differentiation	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0009653	0.00225	1	5	773	anatomical structure morphogenesis	BP	0.851	HOXC10,TBX15,EYA1,HOXA9,IRX5	up_AFEM_VSMC

GO:0030326	0.00225	1	2	51	embryonic limb morphogenesis	BP	0.851	HOXC10,HOXA9	up_AFEM_VSMC
GO:0035113	0.00225	1	2	51	embryonic appendage morphogenesis	BP	0.851	HOXC10,HOXA9	up_AFEM_VSMC
GO:0006104	0.00225	1	1	1	succinyl-CoA metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0006422	0.00226	1	1	1	aspartyl-tRNA aminoacylation	BP	1	DARS	down_AFEM_EC
GO:0051093	0.00227	0.999	29	273	negative regulation of developmental process	BP	0.251	PRICKLE1,SULF1,SERPINE1,SOCS5,SPARC,PRKACB,ENPP1,PGK1,DPYSL3,HOOK3,TRIB3,IFRD1,HIF1A,THBS2,PTPN2,CTNNB1,STARD13,APOE,WWC3,LYN,BNIP3,STRAP,DDIT3,REST,PRMT1,INHBA,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0030154	0.00227	0.999	11	1040	cell differentiation	BP	0.373	HOXC10,EYA1,HOXA9,TOX,HOXB7,HOXA7,SIX1,TIAM1,RADIL,CYP26B1,MTSS1	up_VFEM_EC
GO:0003197	0.00227	1	1	16	endocardial cushion development	BP	1	GATA5	down_AFEM_VSMC
GO:0035801	0.00227	1	1	1	adrenal cortex development	BP	1	CITED2	down_VPOR_EC
GO:0035802	0.00227	1	1	1	adrenal cortex formation	BP	1	CITED2	down_VPOR_EC
GO:0014719	0.00227	1	1	2	skeletal muscle satellite cell activation	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0071310	0.0023	0.999	56	634	cellular response to organic substance	BP	0.253	ARHGEF2,VEGFA,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,SPARC,ERO1A,ENPP1,JCAD,SNX25,PTPN11,FLNB,DPYSL3,TRIB3,ILK,PRCP,SMARCA4,SESN2,TGFBR1,MYO1C,MSN,KIF5B,HIF1A,CX3CL1,ZPR1,PTPN2,YES1,NEO1,MTDH,ADAM17,AGRN,CNOT7,GNAQ,CTNNB1,ENSCAFG00000002015,TFRC,ZC3H15,KLF5,UBA5,LYN,STRAP,DDIT3,ATF3,CDC37,GBP5,REST,PAK2,CREB3L2,NR4A1,ENSCAFG00000018360,BTK,NRP1,YWHAH,KDM3A	down_VSAP_EC
GO:0001974	0.0023	1	2	13	blood vessel remodeling	BP	0.488	ACVRL1,HOXA3	down_ACOR_EC
GO:0007155	0.0023	1	2	324	cell adhesion	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0014834	0.0023	1	1	2	skeletal muscle satellite cell maintenance involved in skeletal muscle	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0048729	0.00232	0.999	24	209	tissue morphogenesis	BP	0.253	PRICKLE1,SULF1,PRKACB,PTK7,ITGA2,EXOC5,ENSCAFG00000032470,TMED2,ILK,WDR1,MSN,HOXB7,HIF1A,ACTG2,ADAM17,ACTA2,MAGED1,CTNNB1,STARD13,PLOD3,SDC4,INHBA,SIX4,NRP1	down_VSAP_EC
GO:0051153	0.00232	1	2	28	regulation of striated muscle cell differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0009968	0.00233	1	5	392	negative regulation of signal transduction	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0001570	0.00233	1	2	37	vasculogenesis	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0022610	0.00233	1	2	326	biological adhesion	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0060675	0.00233	1	2	29	ureteric bud morphogenesis	BP	0.785	EYA1,HOXA11	up_VFEM_VSMC
GO:0043502	0.00233	1	1	16	regulation of muscle adaptation	BP	1	GATA5	down_AFEM_VSMC
GO:0051891	0.00233	1	1	3	positive regulation of cardioblast differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0085020	0.00234	1	3	4	protein K6-linked ubiquitination	BP	0.141	UBE2S,UBE2T,BRCA1	down_ACOR_VSMC
GO:0070235	0.00234	1	2	2	regulation of activation-induced cell death of T	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0070236	0.00234	1	2	2	negative regulation of activation-induced cell	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0003197	0.00236	1	6	16	endocardial cushion development	BP	0.656	GATA5,GATA4,BMP4,CITED2,TBX20,TBX5	up_ACOR_VSMC
GO:0001937	0.00236	1	2	15	negative regulation of endothelial cell	BP	0.488	ACVRL1,SULF1	down_ACOR_EC
GO:0060017	0.00236	1	1	3	parathyroid gland development	BP	1	HOXA3	up_APUL_VSMC
GO:0060351	0.00237	1	5	11	cartilage development involved in endochondral bone morphogenesis	BP	1	HOXA11,AXIN2,RARG,SHOX2,TGFBR2	up_VSAP_EC
GO:0003008	0.00237	1	2	336	system process	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0051241	0.00239	1	2	336	negative regulation of multicellular organismal	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0120163	0.00239	1	2	17	negative regulation of cold-induced	BP	0.389	HOXC10,MAP2K6	up_VFEM_EC

GO:0030282	0.00239	1	2	37	bone mineralization	BP	0.666	HOXA3,PHEX	up_VPUL_VSMC
GO:0001503	0.002399262	0.99939	9	109	ossification	BP	0.7913958	SOX9,PTH1R,SMAD6,PTGER4,FOXC2,FIGNL1,LRP4,CLSTN1,TP53INP2	up_ACOR_EC
GO:0035296	0.0024	0.999	9	32	regulation of tube diameter	BP	0.656	ADRA1B,HTR2B,HRH1,ADCY6,F2RL1,HRH2,PTGDR,EDN1,DOCK5	up_ACOR_VSMC
GO:0097746	0.0024	0.999	9	32	regulation of blood vessel diameter	BP	0.656	ADRA1B,HTR2B,HRH1,ADCY6,F2RL1,HRH2,PTGDR,EDN1,DOCK5	up_ACOR_VSMC
GO:0042221	0.00241	0.998	107	1012	response to chemical	BP	0.178	ACKR1,EPHB1,EDNRB,HCLS1,GBP5,KIT,SELE,PRCP,CXCL8,LAPTM5,CXCR4,DOCK4,CALCRL,TIE1,TNFAIP3,PPARG,TNIP1,MX2,AMOT,PDGFB,P2RX7,BAIAP2L1,TMEM173,RELN,CD34,SELL,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,MMP28,EDN1,RALB,SMAD1,TFPI,IRF8,PELI1,PPP3CA,YES1,CASP8,MTOR,BMP2,TJP1,HHEX,RALBP1,ST3GAL6,ABCA1,MAPK13,ITPKB,IFNGR1,RIOK3,ANGPT2,ENSCAFG00000010596,FLNB,PAK2,PRKD2,SWAP70,SMARCA4,TLR3,APOD,NCK1,TIMELESS,OTUD4,SLC25A25,FES,JAG1,GUCY1B1,PTGS2,TOP1,RAPGEF2,PLCG2,CTDSPL2,CREB1,BCL10,CTNNA1,CNOT7,GCH1,ADIPOR2,HMGB1,AHR,PMAIP1,BLM,RIPK1,LSM14A,USP13,SKIL,PDGFD,UFSP2,HIF1A,KDM3A,ATRX,NR4A1,HP1BP3,ARID5A,ENSCAFG00000002015,P2RX2,JCAD,ZEB1,ARHGEF2,TJP2	up_VCAV_EC
GO:0061418	0.00241	1	3	5	regulation of transcription from RNA polymerase II promoter in response to	BP	0.26	HIF1A,BACH1,HIF1AN	down_VSAP_EC
GO:0034109	0.00241	1	2	14	homotypic cell-cell adhesion	BP	0.488	LYN,PDPN	down_ACOR_EC
GO:0050793	0.00242	0.999	9	731	regulation of developmental process	BP	0.39	EYA1,HOXA9,TOX,HOXB7,HOXA7,SIX1,TIAM1,CYP26B1,CDC42EP5	up_VFEM_EC
GO:0060070	0.00242	1	3	105	canonical Wnt signaling pathway	BP	1	NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0007338	0.00242	1	2	16	single fertilization	BP	0.652	HOXA11,HOXA9	up_VSAP_VSMC
GO:0007167	0.00243	0.999	29	274	enzyme linked receptor protein signaling pathway	BP	0.26	VEGFA,SIPA1L1,SULF1,NR1H4,HSPA5,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,PTPN11,ILK,TGFBR1,MYO1C,HIF1A,PTPN2,NEO1,ESM1,ADAM17,CTNNB1,LYN,STRAP,CBLC,MYO1E,INHBA,ENSCAFG00000018360,BTK,NRP1,RHBDF2	down_VSAP_EC
GO:0032493	0.00243	1	1	2	response to bacterial lipoprotein	BP	0.851	TLR2	up_AFEM_VSMC
GO:0042494	0.00243	1	1	2	detection of bacterial lipoprotein	BP	0.851	TLR2	up_AFEM_VSMC
GO:0042495	0.00243	1	1	2	detection of triacyl bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0070339	0.00243	1	1	2	response to bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0070340	0.00243	1	1	2	detection of bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0071220	0.00243	1	1	2	cellular response to bacterial lipoprotein	BP	0.851	TLR2	up_AFEM_VSMC
GO:0071221	0.00243	1	1	2	cellular response to bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0071725	0.00243	1	1	2	response to triacyl bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0071727	0.00243	1	1	2	cellular response to triacyl bacterial lipopeptide	BP	0.851	TLR2	up_AFEM_VSMC
GO:0045165	0.00244	1	2	65	cell fate commitment	BP	0.504	HOXC10,WNT7A	up_AORTRT_VSMC
GO:0006468	0.002452682	0.99884	26	544	protein phosphorylation	BP	0.7913958	BRSK1,PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,GRK7,TNFRSF19,DCLK2,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,STK32C,NRP1,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0086001	0.00246	1	1	9	cardiac muscle cell action potential	BP	0.829	JUP	down_VFEM_VSMC
GO:0048736	0.00247	1	3	66	appendage development	BP	0.391	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:0060173	0.00247	1	3	66	limb development	BP	0.391	HOXC10,HOXA9,CYP26B1	up_VFEM_EC
GO:2001222	0.00248	1	2	11	regulation of neuron migration	BP	1	ARHGEF2,SEMA3A	up_VPOR_EC
GO:0061005	0.00249	0.999	8	28	cell differentiation involved in kidney	BP	0.182	PDGFB,PODXL,MEF2C,GPR4,GATA3,MTSS1,JAG1,BASP1	up_VCAV_EC

GO:0043620	0.00249	1	6	24	regulation of DNA-templated transcription in	BP	0.262	SESN2,HIF1A,DDIT3,BACH1,ATF3,HIF1AN	down_VSAP_EC
GO:0060272	0.00249	1	4	7	embryonic skeletal joint morphogenesis	BP	1	HOXA11,OSR2,OSR1,SHOX2	up_VSAP_EC
GO:0001655	0.00249	1	3	116	urogenital system development	BP	0.82	EYA1,EMX2,HOXA11	up_VFEM_VSMC
GO:0023014	0.0025	0.999	38	248	signal transduction by protein phosphorylation	BP	0.673	FGF13,ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,MBP,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,NDRG2,F2RL1,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,FRS2,DAG1,APP,PSEN1,SYNJ2BP,CCL5,DUSP22,EDN1,DUSP26,NOD2,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0044267	0.00251	0.998	118	1583	cellular protein metabolic process	BP	0.262	ARHGEF2,PRICKLE1,VEGFA,P4HB,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,HM13,SGK1,ERO1A,HSP90B1,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,SARS,WSB1,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PUM3,PM20D2,ILK,PPP1R12A,SESN2,PTGS2,PPIB,MSN,SEL1L,USP12,MRPL1,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,PTPN2,UCHL5,MORF4L2,SPOPL,YARS,TARS,YES1,PLCL1,TTLL7,NARS,ADAM17,EIF4EBP1,CNOT7,MAGED1,DNAJB9,CTNNB1,CRYAB,CDK8,APOE,PLOD3,USP48,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,SPOP,CALM1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,CAMK2D,HIF1AN,BTK,MSRB3,CDKN1A,TMTC3,RSL24D1,NRP1,SPINK2,SH3RF3,USP14,ARF4,TNFAIP1,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:0014045	0.00251	1	1	2	establishment of endothelial blood-brain	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0022009	0.00251	1	1	2	central nervous system vasculogenesis	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0060066	0.00251	1	1	2	oviduct development	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0060856	0.00251	1	1	2	establishment of blood-brain barrier	BP	0.504	WNT7A	up_AORTRT_VSMC
GO:0009617	0.002512916	0.9993	10	133	response to bacterium	BP	0.7913958	NR1H4,HMCN1,RGS1,FZD5,PTGIR,NOD2,PTGER4,MAVS,RARRES2,PRKCD	up_ACOR_EC
GO:0009081	0.00252	1	3	6	branched-chain amino acid metabolic process	BP	1	ENSCAFG00000002977,BCKDHB,ACAT1	down_VCAV_EC
GO:0003176	0.00252	1	1	9	aortic valve development	BP	0.829	GATA5	down_VFEM_VSMC
GO:0015833	0.00253	0.999	47	521	peptide transport	BP	0.262	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SEC24D,PTPN11,SEC23A,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,TFRC,APOE,KPNA4,LYN,GSK3B,GBP5,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,STX6,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0007176	0.00253	1	4	10	regulation of epidermal growth factor-activated	BP	0.262	SOCS5,ERRFI1,ADAM17,CBLC	down_VSAP_EC
GO:1904062	0.00253	1	3	62	regulation of cation transmembrane transport	BP	0.668	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0072171	0.00254	1	2	30	mesonephric tubule morphogenesis	BP	0.82	EYA1,HOXA11	up_VFEM_VSMC
GO:0003129	0.00254	1	1	3	heart induction	BP	1	GATA5	down_VSAP_VSMC
GO:0009132	0.00256	1	6	25	nucleoside diphosphate metabolic process	BP	0.263	PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:0007417	0.00257	1	5	235	central nervous system development	BP	0.668	PITX1,EMX2,SALL1,HOXC10,HAPLN1	up_VSAP_VSMC
GO:0060485	0.00257	1	2	93	mesenchyme development	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0060575	0.00257	1	1	9	intestinal epithelial cell differentiation	BP	0.829	GATA5	down_VFEM_VSMC
GO:0003162	0.00257	1	1	1	atrioventricular node development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003165	0.00257	1	1	1	Purkinje myocyte development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003168	0.00257	1	1	1	Purkinje myocyte differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003292	0.00257	1	1	1	cardiac septum cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC

GO:0060922	0.00257	1	1	1	atrioventricular node cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060927	0.00257	1	1	1	cardiac pacemaker cell fate commitment	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060928	0.00257	1	1	1	atrioventricular node cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060929	0.00257	1	1	1	atrioventricular node cell fate commitment	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060932	0.00257	1	1	1	His-Purkinje system cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0021545	0.00258	1	2	21	cranial nerve development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0061343	0.00258	1	1	3	cell adhesion involved in heart morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0090130	0.00259	0.999	16	121	tissue migration	BP	0.265	VEGFA,MYH9,SPARC,JCAD,PTPN11,PRCP,PIK3C2A,HIF1A,ACTG2,ADAM17,ACTA2,ANLN,STARD13,APOE,STRAP,NRP1	down_VSAP_EC
GO:0045747	0.00259	1	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	down_AFEM_VSMC
GO:0070887	0.0026	0.998	85	775	cellular response to chemical stimulus	BP	0.19	ACKR1,EPHB1,EDNRB,HCLS1,GBP5,KIT,PRCP,CXCL8,LAPTM5,CXCR4,DOCK4,CALCRL,TNFAIP3,PPARG,TNIP1,PDGFB,BAIAP2L1,TMEM173,CD34,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,MMP28,RALB,SMAD1,TFPI,IRF8,PPP3CA,YES1,MTOR,BMP2,TJP1,HHEX,ST3GAL6,ABCA1,MAPK13,ITPKB,IFNGR1,RIOK3,ENSCAFG00000010596,FLNB,PAK2,PRKD2,SWAP70,SMARCA4,NCK1,TIMELESS,OTUD4,GUCY1B1,PTGS2,RAPGEF2,CTDSPL2,CREB1,CTNNA1,CNOT7,GCH1,ADIPOR2,HMGB1,AHR,PMAIP1,BLM,RIPK1,LSM14A,SKIL,PDGFD,UFSP2,HIF1A,KDM3A,ATRX,NR4A1,HP1BP3,ARID5A,ENSCAFG00000002015,P2RX2,JCAD,ZEB1,ARHGEF2,TJP2	up_VCAV_EC
GO:0002762	0.0026	1	2	15	negative regulation of myeloid leukocyte	BP	0.488	LYN,HOXA7	down_ACOR_EC
GO:0044319	0.0026	1	2	12	wound healing, spreading of cells	BP	0.488	ACVRL1,PDPN	down_ACOR_EC
GO:0090504	0.0026	1	2	12	epiboly	BP	0.488	ACVRL1,PDPN	down_ACOR_EC
GO:0090505	0.0026	1	2	12	epiboly involved in wound healing	BP	0.488	ACVRL1,PDPN	down_ACOR_EC
GO:0021563	0.0026	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_APUL_VSMC
GO:0001654	0.002602942	0.99933	9	110	eye development	BP	0.7913958	CPAMD8,TMOD1,SOX9,AQP1,FZD5,FOXC2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0048880	0.002602942	0.99933	9	110	sensory system development	BP	0.7913958	CPAMD8,TMOD1,SOX9,AQP1,FZD5,FOXC2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0150063	0.002602942	0.99933	9	110	visual system development	BP	0.7913958	CPAMD8,TMOD1,SOX9,AQP1,FZD5,FOXC2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0045165	0.00261	1	3	65	cell fate commitment	BP	0.669	HOXA11,PITX1,HOXC10	up_VSAP_VSMC
GO:0048646	0.00261	1	2	349	anatomical structure formation involved in	BP	0.829	JUP,GATA5	down_VFEM_VSMC

GO:0051179	0.00263	0.998	172	1747	localization	BP	0.191	EPHB1,PLK2,EDNRB,TEK,HCLS1,GBP5,SELP,KIT,SELE,PRCP,PPP2R5A,CXCL8,CP,OSBPL9,DOCK4,CLEC14A,CALCRL,TIE1,TNFAIP3,ADAMTS9,ATP8A1,LRRC8D,MX2,AMOT,PDGFB,MALL,PODXL,STK10,TMEM173,ATP2B1,EXOC3L2,RELN,CD34,SELL,PDE4D,IWS1,MEF2C,FERMT1,CHD7,DLL4,SLC35A3,TLR4,QKI,TSPAN15,STC1,GATA3,MMP28,EDN1,RAB11A,KIF3C,APLNR,ARAP3,RAB27A,SLC39A8,EXOC6,CTTNBP2NL,SNCAIP,SLC49A3,ZDHHC22,NEDD9,IRF8,SLCO2A1,SOX18,PIK3C2A,PPP3CA,YES1,SLC38A1,ARG2,EPHB4,NECTIN2,MTOR,HOOK3,SNAP23,LRRC8C,TSPAN14,MAP3K3,BMP2,HHEX,RAB6A,SPNS3,CAV2,SLK,CEP68,BMP2K,RALBP1,SCAMP1,RSC1A1,PDZD8,ANKRD50,CCAR1,ABCA1,KCNJ3,MZT1,ANGPT2,PROX1,ENSCAFG00000010224,OSBPL6,EPB41,ELMO1,STMN1,SNX2,SLCO3A1,PAK2,MCC,PRKD2,THOC1,SH3GLB1,SWAP70,AKAP12,APOD,CENPC,SLC2A3,NCK1,KCNJ2,EXOC5,LDB2,CD200,SLC25A25,FES,JAG1,HIST1H1A,MMD,EHD4,RAPGEF2,PLCG2,CTDSPL2,CREB1,PAN3,GCC2,CTNNA1,FMNL3,STX11,SMG7,VPS54,PRAG1,HMGB1,TBC1D1,NOS2,PMAIP1,ARPC5L,NUP133,SPTBN4,RIPK1,CHIC2,ITGA6,RAD21,MCU,DNAJC13,PDGFD,ARHGDIB,ZW10,HIF1A,IPO11,ALS2,L	up_VCAV_EC
GO:0048382	0.00263	1	2	2	mesendoderm development	BP	1	BMPR1A,ZFP36L1	down_VCAV_EC
GO:0014896	0.00263	1	1	18	muscle hypertrophy	BP	1	GATA5	down_AFEM_VSMC
GO:0014897	0.00263	1	1	18	striated muscle hypertrophy	BP	1	GATA5	down_AFEM_VSMC
GO:0003300	0.00263	1	1	18	cardiac muscle hypertrophy	BP	1	GATA5	down_AFEM_VSMC
GO:0051271	0.00264	0.999	17	98	negative regulation of cellular component movement	BP	0.191	TIE1,ADAMTS9,MEF2C,DLL4,STC1,GATA3,MMP28,ARAP3,ANGPT2,ENSCAFG00000010224,MCC,APOD,JAG1,CTNNA1,HMGB1,ARHGDIB,VASH1	up_VCAV_EC
GO:0072359	0.00264	1	3	368	circulatory system development	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0008300	0.00264	1	1	1	isoprenoid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0016103	0.00264	1	1	1	diterpenoid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0016115	0.00264	1	1	1	terpenoid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0035981	0.00264	1	1	1	tongue muscle cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0042363	0.00264	1	1	1	fat-soluble vitamin catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0070268	0.00264	1	1	1	cornification	BP	1	CYP26B1	up_VPOR_VSMC
GO:1902809	0.00264	1	1	1	regulation of skeletal muscle fiber	BP	1	CYP26B1	up_VPOR_VSMC
GO:1902811	0.00264	1	1	1	positive regulation of skeletal muscle fiber	BP	1	CYP26B1	up_VPOR_VSMC
GO:2001035	0.00264	1	1	1	regulation of tongue muscle cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:2001037	0.00264	1	1	1	positive regulation of tongue muscle cell	BP	1	CYP26B1	up_VPOR_VSMC
GO:0034653	0.00264	1	1	1	retinoic acid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0030857	0.00266	1	2	15	negative regulation of epithelial cell	BP	0.488	ACVRL1,HOXA7	down_ACOR_EC
GO:0110111	0.00266	1	2	17	negative regulation of animal organ	BP	0.488	SULF1,ASPN	down_ACOR_EC
GO:0050982	0.00266	1	1	9	detection of mechanical stimulus	BP	0.829	JUP	down_VFEM_VSMC
GO:0014068	0.00267	1	7	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	0.192	TEK,HCLS1,SELP,PDGFB,RELN,PDGFD,RGL2	up_VCAV_EC
GO:0003007	0.00267	1	2	94	heart morphogenesis	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0048706	0.00268	1	6	59	embryonic skeletal system development	BP	1	TBX15,HOXA9,IRX5,XYLT1,HOXA7,HOXA6	up_AFEM_EC
GO:0006983	0.00268	1	3	5	ER overload response	BP	0.27	HSPA5,DDIT3,GSK3B	down_VSAP_EC
GO:0002444	0.00268	1	2	18	myeloid leukocyte mediated immunity	BP	0.488	LYN,STX4	down_ACOR_EC

GO:0050771	0.00268	1	2	11	negative regulation of axonogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0060745	0.00268	1	1	2	mammary gland branching involved in	BP	0.504	ESR1	up_AORTRT_VSMC
GO:0035295	0.00269	1	2	356	tube development	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:2001275	0.002697327	0.99986	3	11	positive regulation of glucose import in response to insulin	BP	0.7913958	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:1902533	0.00271	0.999	36	271	positive regulation of intracellular signal transduction	BP	0.195	TEK,HCLS1,IL7R,SELP,KIT,MAP3K11,PDGFB,RELN,TLR4,GPR4,GATA3,EDN1,PELI1,PPP3CA,GUCY1A1,CASP8,MAP3K3,BMP2,ITPKB,MADD,PRKD2,TLR3,AKAP12,NCK1,RAPGEF2,BCL10,TAOK1,HMGB1,PMAIP1,RIPK1,SKIL,PDGFD,ENSCAFG00000002015,RGL2,JCAD,CDON	up_VCAV_EC
GO:0008406	0.00271	1	2	57	gonad development	BP	0.874	HOXA9,IRX5	up_AFEM_VSMC
GO:0045137	0.00271	1	2	57	development of primary sexual characteristics	BP	0.874	HOXA9,IRX5	up_AFEM_VSMC
GO:0032501	0.00273	0.999	15	1782	multicellular organismal process	BP	0.427	HOXC10,TBX15,EYA1,HOXA9,TOX,MAP2K6,MME,AVPR1A,HOXB7,HOXA7,SIX1,MAB21L1,TIAM1,CYP26B1,MTSS1	up_VFEM_EC
GO:0043299	0.00273	1	2	18	leukocyte degranulation	BP	0.488	LYN,STX4	down_ACOR_EC
GO:0086004	0.00274	1	1	10	regulation of cardiac muscle cell contraction	BP	0.829	JUP	down_VFEM_VSMC
GO:0030258	0.00275	0.999	15	71	lipid modification	BP	1	PEX7,ACAA1,ACACB,PEX2,INPP5E,C1QTNF2,PLPP3,PIK3R1,GCDH,EHHADH,LCAT,LONP2,ZFYVE21,PLPP5,SOAT1	up_VSAP_EC
GO:0034112	0.00275	1	1	1	positive regulation of homotypic cell-cell	BP	0.488	PDPN	down_ACOR_EC
GO:1901731	0.00275	1	1	1	positive regulation of platelet aggregation	BP	0.488	PDPN	down_ACOR_EC
GO:1904328	0.00275	1	1	1	regulation of myofibroblast contraction	BP	0.488	PDPN	down_ACOR_EC
GO:1905863	0.00275	1	1	1	invadopodium organization	BP	0.488	PDPN	down_ACOR_EC
GO:1990764	0.00275	1	1	1	myofibroblast contraction	BP	0.488	PDPN	down_ACOR_EC
GO:0010092	0.00275	1	1	19	specification of animal organ identity	BP	1	GATA5	down_AFEM_VSMC
GO:0044283	0.00276	0.999	22	201	small molecule biosynthetic process	BP	0.273	ASNS,PLOD2,NR1H4,ENPP1,PGK1,TPI1,TRIB3,PGAM1,SESN2,PTGS2,HIF1A,SLC45A3,PTPN2,ALDH18A1,ENTPD4,ALDOC,APOE,PLOD3,ATF3,REST,BCAT1,KDM3A	down_VSAP_EC
GO:0010648	0.00276	1	5	407	negative regulation of cell communication	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0008627	0.00276	1	3	5	intrinsic apoptotic signaling pathway in response to osmotic	BP	0.273	ARHGEF2,CASP3,PTGS2	down_VSAP_EC
GO:0003263	0.00276	1	1	4	cardioblast proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0009966	0.00277	0.998	72	868	regulation of signal transduction	BP	0.273	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,HYOU1,PTPN11,TRIB3,FARP1,ILK,FHL2,PRCP,SMARCA4,SESN2,PTGS2,MYO1C,CHSY1,UACA,HIF1A,ENSCAFG00000000562,TNIK,NXN,RGS2,PTPN2,NEO1,MTDH,ESM1,ADAM17,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,CBLC,ATF3,GSK3B,CDC37,SH3GLB1,TAX1BP3,HTT,RDH11,ARFGEF3,CALM1,DISC1,PAK2,INHBA,HIF1AN,NRP1,SH3RF3,RHBDF2,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:0010595	0.00277	0.999	11	52	positive regulation of endothelial cell migration	BP	0.197	PLK2,TEK,PDGFB,GATA3,PIK3C2A,MAP3K3,PROX1,PRKD2,HMGB1,HIF1A,JCAD	up_VCAV_EC
GO:0003179	0.00277	1	1	19	heart valve morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0086003	0.00277	1	1	10	cardiac muscle cell contraction	BP	0.829	JUP	down_VFEM_VSMC
GO:0003211	0.00278	1	1	4	cardiac ventricle formation	BP	1	TBX5	up_APUL_VSMC
GO:0042670	0.00279	1	2	2	retinal cone cell differentiation	BP	1	THY1,THRB	down_VCAV_EC
GO:0046549	0.00279	1	2	2	retinal cone cell development	BP	1	THY1,THRB	down_VCAV_EC

GO:0048863	0.00279	1	2	70	stem cell differentiation	BP	0.504	WNT7A,ESR1	up_AORTRT_VSMC
GO:0003002	0.0028	1	3	118	regionalization	BP	1	HOXC10,HOXA9,HOXC6	up_AORT_EC
GO:2000027	0.0028	1	2	72	regulation of animal organ morphogenesis	BP	0.504	WNT7A,ESR1	up_AORT_VSMC
GO:0003002	0.0028	1	2	118	regionalization	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0030154	0.00281	0.999	11	1040	cell differentiation	BP	0.707	HOXA11,HOXA9,PITX1,EMX2,SALL1,HOXC10,IRX5,STIM1,CAV1,SHOX2,GJB5	up_VSAP_VSMC
GO:1990009	0.00281	1	2	2	retinal cell apoptotic process	BP	1	AKT2,THRB	down_VCAV_EC
GO:2001233	0.00282	0.999	18	149	regulation of apoptotic signaling pathway	BP	0.275	ARHGEF2,P4HB,SERPINE1,HYOU1,PTGS2,HIF1A,PTPN2,MAGED1,CTNNB1,BNIP3,FAM162A,ATF3,SH3GLB1,HTT,PAK2,INHBA,NRP1,MADD	down_VSAP_EC
GO:0023057	0.00283	1	5	409	negative regulation of signaling	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0060216	0.00283	1	1	3	definitive hemopoiesis	BP	0.504	HOXA9	up_AORT_VSMC
GO:0007275	0.00284	0.999	9	1370	multicellular organism development	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0045595	0.00284	0.999	7	469	regulation of cell differentiation	BP	0.44	EYA1,HOXA9,TOX,HOXA7,SIX1,TIAM1,CYP26B1	up_VFEM_EC
GO:0003008	0.00285	1	6	336	system process	BP	0.707	NETO1,GATM,HOXC10,IRX5,CAV1,F5	up_VSAP_VSMC
GO:0006970	0.00285	1	2	23	response to osmotic stress	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0003156	0.00285	1	1	20	regulation of animal organ formation	BP	1	GATA5	down_AFEM_VSMC
GO:0022616	0.00286	1	4	8	DNA strand elongation	BP	0.17	POLA1,POLE,FEN1,PCNA	down_ACOR_VSMC
GO:0072359	0.00286	1	2	368	circulatory system development	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:0009887	0.00287	1	4	314	animal organ morphogenesis	BP	0.771	HOXA3,TBX5,GATA5,HOXB5	up_VPUL_VSMC
GO:0071495	0.00287	1	2	365	cellular response to endogenous stimulus	BP	0.829	JUP,GATA5	down_VFEM_VSMC
GO:1901185	0.00288	1	4	11	negative regulation of ERBB signaling pathway	BP	0.279	SOCS5,ERRFI1,PTPN2,CBLC	down_VSAP_EC
GO:0034113	0.00288	1	1	10	heterotypic cell-cell adhesion	BP	0.829	JUP	down_VFEM_VSMC
GO:0010033	0.00289	0.998	65	772	response to organic substance	BP	0.279	ARHGEF2,VEGFA,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,HM13,SPARC,ERO1A,HSP90B1,ENPP1,JCAD,SNX25,PTPN11,FLNB,DPYSL3,TRIB3,ILK,FHL2,PRCP,SMARCA4,SESN2,TGFBR1,MYO1C,MSN,SEL1L,KIF5B,HIF1A,CX3CL1,DNAJC10,ZPR1,PTPN2,YES1,NEO1,MTDH,ADAM17,AGRN,CNOT7,DNAJB9,GNAQ,CTNNB1,ENSCAFG00000002015,TFRC,APOE,ZC3H15,KLF5,UBA5,LYN,STRAP,DDIT3,ATF3,CDC37,GBP5,REST,PAK2,CREB3L2,NR4A1,ENSCAFG00000018360,BTK,NRP1,USP14,YWHAH,KDM3A,HOMER1	down_VSAP_EC
GO:0043331	0.00289	1	6	20	response to dsRNA	BP	0.205	TMEM173,RALB,PELI1,RIOK3,TLR3,PMAIP1	up_VCAV_EC
GO:0140074	0.00289	1	1	2	cardiac endothelial to mesenchymal transition	BP	1	GATA5	up_VCAV_VSMC
GO:0007169	0.0029	0.999	21	178	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.279	VEGFA,SIPA1L1,SULF1,NR1H4,SOCS5,ENPP1,ERRFI1,JCAD,PTPN11,MYO1C,HIF1A,PTPN2,ESM1,ADAM17,CTNNB1,LYN,CBLC,MYO1E,BTK,NRP1,RHBDF2	down_VSAP_EC
GO:0035739	0.0029	1	1	3	CD4-positive, alpha-beta T cell proliferation	BP	0.504	ARG2	up_AORT_VSMC
GO:2000561	0.0029	1	1	3	regulation of CD4-positive, alpha-beta T cell	BP	0.504	ARG2	up_AORT_VSMC
GO:0051890	0.0029	1	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0051254	0.00291	0.998	54	431	positive regulation of RNA metabolic process	BP	0.206	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0018158	0.00291	1	3	4	protein oxidation	BP	0.71	TMX3,SUMF1,PARK7	up_ACOR_VSMC

GO:0007548	0.00291	1	2	68	sex differentiation	BP	0.504	HOXA9,ESR1	up_AORT_VSMC
GO:0016576	0.00291	1	1	2	histone dephosphorylation	BP	0.917	EYA1	up_AFEM_VSMC
GO:0002275	0.00292	1	2	18	myeloid cell activation involved in immune	BP	0.507	LYN,STX4	down_ACOR_EC
GO:0003274	0.00292	1	1	2	endocardial cushion fusion	BP	1	GATA5	up_VCAV_VSMC
GO:0032989	0.00294	1	5	292	cellular component morphogenesis	BP	1	MYBPC2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0032501	0.00296	0.999	10	1782	multicellular organismal process	BP	1	HOXC10,DKK2,HOXA9,HOXC6,LNPEP,SGCD,TAOK1,DUSP2,BPI,GPR155	up_AORT_EC
GO:0015669	0.00297	1	1	2	gas transport	BP	1	CA2	up_VCAV_VSMC
GO:0015670	0.00297	1	1	2	carbon dioxide transport	BP	1	CA2	up_VCAV_VSMC
GO:0008593	0.00299	0.999	8	33	regulation of Notch signaling pathway	BP	0.21	DLL4,EGFL7,TSPAN14,BMP2K,GDPD5,MFNG,JAG1,PEAR1	up_VCAV_EC
GO:1900120	0.00299	1	1	7	regulation of receptor binding	BP	1	PLCL1	down_VFEM_EC
GO:0006600	0.00299	1	1	1	creatine metabolic process	BP	0.83	GATM	up_VFEM_VSMC
GO:0006601	0.00299	1	1	1	creatine biosynthetic process	BP	0.83	GATM	up_VFEM_VSMC
GO:0014889	0.00299	1	1	1	muscle atrophy	BP	0.83	GATM	up_VFEM_VSMC
GO:0008203	0.003	0.999	9	37	cholesterol metabolic process	BP	0.177	SQLE,LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1,LIPC	down_ACOR_VSMC
GO:1905332	0.003	1	2	20	positive regulation of morphogenesis of an	BP	0.462	HOXB7,SIX1	up_VFEM_EC
GO:1900425	0.003	1	1	2	negative regulation of defense response to	BP	0.504	ARG2	up_AORT_VSMC
GO:0042692	0.00301	0.999	18	105	muscle cell differentiation	BP	0.21	EDNRB,KIT,IFRD1,PDGFB,MEF2C,EDN1,TMOD1,PPP3CA,MTOR,BMP2,CAV2,PROX1,ENSCAFG00000010596,ASF1A,P2RX2,TMOD3,ZEB1,CDON	up_VCAV_EC
GO:0018108	0.00301	0.999	12	79	peptidyl-tyrosine phosphorylation	BP	0.285	ARHGEF2,VEGFA,SOCS5,ERRFI1,PTPN2,YES1,ADAM17,CNOT7,LYN,CBLC,BTK,NRP1	down_VSAP_EC
GO:0006909	0.00301	1	5	42	phagocytosis	BP	1	LEP,RAB20,ICAM5,RAB7A,ANXA11	up_AFEM_EC
GO:0097009	0.00301	1	3	13	energy homeostasis	BP	1	DLL1,ACACB,PPARGC1A	up_AFEM_EC
GO:0071609	0.00301	1	1	3	chemokine (C-C motif) ligand 5 production	BP	0.504	ARG2	up_AORT_VSMC
GO:0071649	0.00301	1	1	3	regulation of chemokine (C-C motif) ligand 5	BP	0.504	ARG2	up_AORT_VSMC
GO:0071286	0.00301	1	1	1	cellular response to magnesium ion	BP	0.83	FBP1	up_VFEM_VSMC
GO:0019752	0.00302	0.998	29	283	carboxylic acid metabolic process	BP	0.285	P4HB,ASNS,CARS,PLOD2,NR1H4,ENSCAFG00000009211,ERO1A,P4HA1,SARS,PGK1,AARS,TPI1,TRIB3,PGAM1,ALDH1L2,SESN2,PTGS2,CEMIP2,HIF1A,SLC45A3,NMNAT2,ALDH18A1,YARS,TARS,NARS,ALDOC,PLOD3,RAB11FIP1,BCAT1	down_VSAP_EC
GO:0030168	0.00302	0.999	7	23	platelet activation	BP	0.21	SELP,F8,PDGFB,VWF,TLR4,ITGB3,PEAR1	up_VCAV_EC
GO:0035107	0.00302	1	2	60	appendage morphogenesis	BP	0.917	HOXC10,HOXA9	up_AFEM_VSMC
GO:0035108	0.00302	1	2	60	limb morphogenesis	BP	0.917	HOXC10,HOXA9	up_AFEM_VSMC
GO:0019627	0.00302	1	1	3	urea metabolic process	BP	0.504	ARG2	up_AORT_VSMC
GO:0007267	0.003022562	0.99876	18	332	cell-cell signaling	BP	0.8655851	CNTNAP4,CDH3,NR1H4,BRSK1,PLCL1,SOX9,AQP1,PORCN,KCNB1,FZD5,DIXDC1,INSYN1,MAPK8IP2,TBX5,LRP4,CLSTN1,LRRC4,PYGO2	up_ACOR_EC
GO:0014051	0.00303	1	1	1	gamma-aminobutyric acid secretion	BP	1	TRPC4	up_VPOR_VSMC
GO:0015812	0.00303	1	1	1	gamma-aminobutyric acid transport	BP	1	TRPC4	up_VPOR_VSMC
GO:1901292	0.00304	0.999	7	34	nucleoside phosphate catabolic process	BP	0.285	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:0030199	0.00305	1	5	21	collagen fibril organization	BP	1	ADAMTS2,LUM,LOX,DDR2,GREM1	down_VCAV_EC
GO:0007389	0.00305	1	4	137	pattern specification process	BP	0.708	HOXA11,HOXA9,EMX2,HOXC10	up_VSAP_VSMC
GO:0072078	0.00306	1	2	33	nephron tubule morphogenesis	BP	0.83	EYA1,HOXA11	up_VFEM_VSMC
GO:0043500	0.00306	1	1	21	muscle adaptation	BP	1	GATA5	down_AFEM_VSMC

GO:0050852	0.00308	0.999	7	26	T cell receptor signaling pathway	BP	0.214	PDE4D,EIF2B2,GATA3,NECTIN2,PRKD2,PLCG2,BCL10	up_VCAV_EC
GO:0048731	0.00308	1	6	1247	system development	BP	0.917	HOXC10,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:0051094	0.00308	0.999	6	388	positive regulation of developmental process	BP	1	NR1H4,TBX5,SLITRK5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0042886	0.00309	0.998	47	527	amide transport	BP	0.286	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SEC24D,PTPN11,SEC23A,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,TFRC,APOE,KPNA4,LYN,GSK3B,GBP5,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,STX6,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0042273	0.00309	1	3	35	ribosomal large subunit biogenesis	BP	1	RSL24D1,RPL10L,RRP15	up_VPOR_EC
GO:0048731	0.0031	0.998	44	1247	system development	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,LEP,LBH,XYLT1,ANGPT4,HOXA7,COL8A2,DLL1,CRYAB,F3,VXN,PLXNA4,NEFH,MAB21L1,THRB,LGI4,TMEM100,GREM1,NFE2L1,OVOL1,CAMK2A,HOXA6,CYLD,LUZP1,RECK,PTHLH,TBXA2R,EVI2B,CNNM4,BVES,PTPRB,AXIN2,ACACB,PPARGC1A,CLIC4,LRRN2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0009952	0.0031	1	3	66	anterior/posterior pattern specification	BP	0.526	HOXA3,HOXA7,HOXC4	down_ACOR_EC
GO:0048743	0.0031	1	1	1	positive regulation of skeletal muscle fiber	BP	0.83	SHOX2	up_VFEM_VSMC
GO:0038127	0.00311	0.999	7	32	ERBB signaling pathway	BP	0.286	SOCS5,ERRFI1,PTPN11,PTPN2,ADAM17,CBLC,RHBDF2	down_VSAP_EC
GO:0001708	0.00311	1	2	20	cell fate specification	BP	0.708	HOXA11,HOXC10	up_VSAP_VSMC
GO:0048872	0.00312	0.999	15	85	homeostasis of number of cells	BP	0.215	HCLS1,IL7R,ADGRF5,KIT,TNFAIP3,MEF2C,GATA3,ITPKB,EXOC5,BCL10,VPS54,HMGB1,SKIL,HIF1A,TMOD3	up_VCAV_EC
GO:0034654	0.00312	1	6	1236	nucleobase-containing compound biosynthetic	BP	0.917	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0060341	0.003126791	0.99883	15	255	regulation of cellular localization	BP	0.8655851	SH3TC2,CDH3,NR1H4,KCNB1,EDEM2,PLS1,ACTN2,TRIM8,PREB,DCLK2,MAVS,LRRC15,LRP4,TP53INP2,PRKCD	up_ACOR_EC
GO:0031175	0.00313	0.999	25	224	neuron projection development	BP	0.286	SIPA1L1,SGK1,PTPN11,DPYSL3,IFRD1,KIF5B,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,APOE,LYN,GSK3B,VLDLR,SDC4,PRMT1,EXT1,DISC1,PAK2,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0001782	0.00313	1	4	8	B cell homeostasis	BP	0.215	TNFAIP3,MEF2C,BCL10,HIF1A	up_VCAV_EC
GO:0003203	0.00314	1	1	11	endocardial cushion morphogenesis	BP	0.859	GATA5	down_VFEM_VSMC
GO:0042742	0.003149619	0.99955	5	39	defense response to bacterium	BP	0.8655851	NR1H4,NOD2,MAVS,RARRES2,PRKCD	up_ACOR_EC
GO:2000418	0.00315	1	1	1	positive regulation of eosinophil migration	BP	1	CCL24	up_VPUL_EC
GO:0006812	0.00316	0.998	34	222	cation transport	BP	0.71	FGF13,ACTN2,PLCG2,KCNE3,HTR2B,TPC3,NIPAL3,SARAF,PTPN3,MICU2,ITPR1,DAPK1,CACNB3,AKAP6,DMPK,ATP7A,KCNJ4,PRKCE,PSEN1,CHD7,ATP6V0E1,RAB11B,SLC25A20,KCNC4,LMTK2,B2M,FXYD1,INPP5K,WFS1,ATP2C1,NDUFA4L2,PARK7,SLC8A1,STC2	up_ACOR_VSMC
GO:0048640	0.00316	0.999	7	21	negative regulation of developmental growth	BP	0.71	BMP4,PLAC8B,NRP1,ULK2,TBX5,WWC2,STC2	up_ACOR_VSMC
GO:0014850	0.00316	1	3	4	response to muscle activity	BP	0.71	FNDC5,PRKAA2,PPARGC1A	up_ACOR_VSMC
GO:0051094	0.00316	1	2	388	positive regulation of developmental process	BP	0.859	JUP,GATA5	down_VFEM_VSMC
GO:0033002	0.003164747	0.99943	6	55	muscle cell proliferation	BP	0.8655851	NDRG2,PTGIR,FOXC2,TBX5,CLSTN1,C23H3orf58	up_ACOR_EC
GO:0072358	0.00317	0.998	28	268	cardiovascular system development	BP	0.287	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,LTBP1,PTPN14,ERRFI1,JCAD,PGK1,TMED2,PRCP,PIK3C2A,HIF1A,THBS2,NXN,MTDH,ESM1,ACTA2,ADAMTS6,CTNNB1,STARD13,APOE,KLF5,DDIT3,MYO1E,NRP1	down_VSAP_EC
GO:2001135	0.00317	1	3	4	regulation of endocytic recycling	BP	0.71	ACTN2,RAB11B,BVES	up_ACOR_VSMC
GO:1904468	0.00317	1	1	3	negative regulation of tumor necrosis factor	BP	0.504	ARG2	up_AORT_VSMC
GO:0035270	0.00318	1	2	35	endocrine system development	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0061034	0.00318	1	1	1	olfactory bulb mitral cell layer development	BP	0.708	SALL1	up_VSAP_VSMC

GO:0032874	0.00319	0.999	13	57	positive regulation of stress-activated MAPK cascade	BP	0.71	LEP,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:1905114	0.00319	1	4	150	cell surface receptor signaling pathway involved in cell-cell	BP	0.708	NETO1,SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0038083	0.00319	1	2	16	peptidyl-tyrosine autophosphorylation	BP	0.528	LYN,IGF1R	down_ACOR_EC
GO:0021796	0.00319	1	1	1	cerebral cortex regionalization	BP	0.83	EMX2	up_VFEM_VSMC
GO:0048645	0.0032	1	2	33	animal organ formation	BP	0.83	EYA1,HOXA11	up_VFEM_VSMC
GO:0030097	0.00321	1	5	244	hemopoiesis	BP	0.488	HOXA9,TOX,HOXB7,HOXA7,CYP26B1	up_VFEM_EC
GO:0090385	0.00322	1	2	4	phagosome-lysosome fusion	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:1903115	0.00322	1	1	12	regulation of actin filament-based movement	BP	0.859	JUP	down_VFEM_VSMC
GO:1902904	0.003221181	0.99954	5	38	negative regulation of supramolecular fiber	BP	0.86633664	TMOD1,ARHGAP6,ARHGAP28,PRKCD,TUBB4A	up_ACOR_EC
GO:0040013	0.00323	0.999	17	100	negative regulation of locomotion	BP	0.22	TIE1,ADAMTS9,MEF2C,DLL4,STC1,GATA3,MMP28,ARAP3,ANGPT2,ENSCAFG00000010224,MCC,APOD,JAG1,CTNNA1,HMGB1,ARHGDIB,VASH1	up_VCAV_EC
GO:0001547	0.00323	1	1	3	antral ovarian follicle growth	BP	0.504	ESR1	up_AORT_VSMC
GO:0071391	0.00323	1	1	3	cellular response to estrogen stimulus	BP	0.504	ESR1	up_AORT_VSMC
GO:0072132	0.00324	1	1	23	mesenchyme morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0072611	0.00324	1	1	3	interleukin-13 secretion	BP	0.504	ARG2	up_AORT_VSMC
GO:2000665	0.00324	1	1	3	regulation of interleukin-13 secretion	BP	0.504	ARG2	up_AORT_VSMC
GO:0061737	0.00324	1	1	1	leukotriene signaling pathway	BP	1	RGS1	up_VPUL_EC
GO:0003206	0.00325	0.999	12	51	cardiac chamber morphogenesis	BP	0.71	TNNT2,SMAD6,GATA4,BMP4,FGFR2,CITED2,EGLN1,NRP1,SMARCD3,TBX20,TBX5,CHD7	up_ACOR_VSMC
GO:0016054	0.00325	0.999	9	61	organic acid catabolic process	BP	1	AKT2,ACAA1,THNSL2,PEX5,ENSCAFG00000002977,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0046395	0.00325	0.999	9	61	carboxylic acid catabolic process	BP	1	AKT2,ACAA1,THNSL2,PEX5,ENSCAFG00000002977,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0002064	0.00325	1	2	71	epithelial cell development	BP	0.504	WNT7A,ESR1	up_AORT_VSMC
GO:0010033	0.00326	0.999	8	772	response to organic substance	BP	1	NR1H4,MRC1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1,MXRA5	up_VPUL_EC
GO:0032735	0.00326	1	4	9	positive regulation of interleukin-12 production	BP	0.221	TLR4,IRF8,TLR3,HMGB1	up_VCAV_EC
GO:0051239	0.00327	0.999	7	859	regulation of multicellular organismal process	BP	0.83	HOXC10,EYA1,GATM,HOXA9,NETO1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0010611	0.00327	1	1	11	regulation of cardiac muscle hypertrophy	BP	0.859	GATA5	down_VFEM_VSMC
GO:0014743	0.00327	1	1	11	regulation of muscle hypertrophy	BP	0.859	GATA5	down_VFEM_VSMC
GO:0010819	0.00328	1	2	4	regulation of T cell chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0010820	0.00328	1	2	4	positive regulation of T cell chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0021533	0.00328	1	1	3	cell differentiation in hindbrain	BP	0.504	WNT7A	up_AORT_VSMC
GO:0060737	0.00328	1	1	3	prostate gland morphogenetic growth	BP	0.504	ESR1	up_AORT_VSMC
GO:0060525	0.00329	1	1	3	prostate glandular acinus development	BP	0.504	ESR1	up_AORT_VSMC
GO:0060526	0.00329	1	1	3	prostate glandular acinus morphogenesis	BP	0.504	ESR1	up_AORT_VSMC
GO:0060527	0.00329	1	1	3	prostate epithelial cord arborization involved in prostate glandular acinus	BP	0.504	ESR1	up_AORT_VSMC
GO:0010810	0.00331	1	3	60	regulation of cell-substrate adhesion	BP	0.528	ACVRL1,PDPN,HOXA7	down_ACOR_EC
GO:0060837	0.00331	1	2	4	blood vessel endothelial cell differentiation	BP	1	DLL1,TMEM100	up_AFEM_EC
GO:0060914	0.00331	1	1	11	heart formation	BP	0.859	GATA5	down_VFEM_VSMC
GO:1904861	0.00331	1	1	3	excitatory synapse assembly	BP	0.504	WNT7A	up_AORT_VSMC
GO:0034969	0.00333	1	2	2	histone arginine methylation	BP	0.294	NR1H4,PRMT1	down_VSAP_EC

GO:0048263	0.00333	1	2	4	determination of dorsal identity	BP	1	GREM1,GREM2	up_AFEM_EC
GO:0009888	0.00334	0.998	49	545	tissue development	BP	0.294	PRICKLE1,SULF1,SERPINH1,TAGLN2,NR1H4,SERPINE1,ACTN1,PRKACB,PTK7,ERRFI1,ITGA2,CASP3,PGK1,EXOC5,FLNB,ENSCAFG00000032470,IFRD1,TMED2,ILK,FHL2,TGFBR1,PTGS2,WDR1,CHSY1,MSN,HOXB7,HIF1A,SLC20A1,ACTG2,ADAM17,ACTA2,MAGED1,CTNNB1,STARD13,PLOD3,KLF5,STRAP,ATF3,GSK3B,NEXN,MYO1E,SDC4,EXT1,CREB3L2,INHBA,SIX4,NRP1,COL12A1,HOMER1	down_VSAP_EC
GO:0075525	0.00334	1	3	4	viral translational termination-reinitiation	BP	1	EIF3G,EIF3L,EIF3D	up_VSAP_EC
GO:0001656	0.00334	1	2	35	metanephros development	BP	0.83	EYA1,HOXA11	up_VFEM_VSMC
GO:0061333	0.00334	1	2	35	renal tubule morphogenesis	BP	0.83	EYA1,HOXA11	up_VFEM_VSMC
GO:0009719	0.00335	1	2	395	response to endogenous stimulus	BP	0.859	JUP,GATA5	down_VFEM_VSMC
GO:0003156	0.00335	1	2	20	regulation of animal organ formation	BP	0.505	EYA1,SIX1	up_VFEM_EC
GO:0021683	0.00335	1	1	3	cerebellar granular layer morphogenesis	BP	0.505	WNT7A	up_AORT_VSMC
GO:0055062	0.00335	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0072505	0.00335	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0072506	0.00335	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0002366	0.00336	0.999	13	65	leukocyte activation involved in immune response	BP	0.226	KIT,IL6,TLR4,GATA3,RAB27A,MTOR,SNAP23,THOC1,SWAP70,MFNG,FES,PLCG2,HMGB1	up_VCAV_EC
GO:0014902	0.00336	1	2	34	myotube differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0051024	0.00336	1	1	1	positive regulation of immunoglobulin secretion	BP	0.528	STX4	down_ACOR_EC
GO:0032501	0.00337	0.998	133	1782	multicellular organismal process	BP	0.295	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,NR1H4,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,SGK1,PRKACB,PTPN14,ERRFI1,SLC1A4,ITGA2,SEC24D,JCAD,TPM4,CASP3,FAM49B,PGK1,BCAR3,PTPN11,EXOC5,AARS,FLNB,ENSCAFG00000032470,DPYSL3,HOOK3,IFRD1,TMED2,ILK,FHL2,BHLHE40,PRCP,SMARCA4,TGFBR1,PTGS2,WDR1,PIK3C2A,CHSY1,MSN,HOXB7,RPGR,KIF5B,HIF1A,HTR7,SLC45A3,SLC20A1,THBS2,ACTG2,TNIK,NXN,UBA6,ZPR1,PTPN2,UCHL5,PHC2,EIF2B1,EVI2B,NEO1,PLCL1,MTDH,ESM1,ADAM17,ACTA2,ADAMTS6,UST,CDH11,MAGED1,CTNNB1,ANLN,CRYAB,STARD13,TFRC,APOE,WWC3,PLOD3,KLF5,UBA5,LYN,STRAP,DDIT3,PDS5B,CCNYL1,MMD,PLS3,SLC7A11,ATF3,GSK3B,VLDLR,NEXN,ITGB3,GBP5,MYO1E,SDC4,HTT,REST,RBBP8,MAPK10,PRMT1,SH2B3,P3H4,EXT1,CALM1,RAB11FIP1,GLO1,DISC1,CDYL,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,BTK,SIX4,NRP1,SPINK2,ARF4,YWHAH,COL12A1,RTCB,SNRPA1,KDM3A,MYBPC2,HOMER1	down_VSAP_EC
GO:0044087	0.00338	0.998	43	339	regulation of cellular component biogenesis	BP	0.226	EPHB1,PLK2,TEK,HCLS1,GBP5,SELP,PRKCH,ARHGEF15,PODXL,BAIAP2L1,MEF2C,RAPGEF1,TLR4,EDN1,RALB,SNCAIP,IRF8,ARHGAP28,TMOD1,MTOR,SAMD8,SLK,CNOT6,NCKAP1,RIOK3,PROX1,IQGAP2,STMN1,SH3GLB1,SWAP70,APOD,NCK1,LDB2,FES,RAPGEF2,SENP6,PAN3,HMGB1,PMAIP1,ARPC5L,ENSCAFG00000002015,TMOD3,FSCN1	up_VCAV_EC
GO:0051216	0.00339	1	3	70	cartilage development	BP	0.708	HOXA11,PITX1,SHOX2	up_VSAP_VSMC
GO:1901228	0.00339	1	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GATA5	down_VSAP_VSMC
GO:0006808	0.0034	1	1	1	regulation of nitrogen utilization	BP	1	NR1H4	up_VPUL_EC
GO:0019676	0.0034	1	1	1	ammonia assimilation cycle	BP	1	NR1H4	up_VPUL_EC
GO:0019740	0.0034	1	1	1	nitrogen utilization	BP	1	NR1H4	up_VPUL_EC

GO:0034255	0.0034	1	1	1	regulation of urea metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0034971	0.0034	1	1	1	histone H3-R17 methylation	BP	1	NR1H4	up_VPUL_EC
GO:0038183	0.0034	1	1	1	bile acid signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0038185	0.0034	1	1	1	intracellular bile acid receptor signaling	BP	1	NR1H4	up_VPUL_EC
GO:0045848	0.0034	1	1	1	positive regulation of nitrogen utilization	BP	1	NR1H4	up_VPUL_EC
GO:1903314	0.0034	1	1	1	regulation of nitrogen cycle metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:1905693	0.0034	1	1	1	regulation of phosphatidic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:1905695	0.0034	1	1	1	positive regulation of phosphatidic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:2000211	0.0034	1	1	1	regulation of glutamate metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:2000213	0.0034	1	1	1	positive regulation of glutamate metabolic	BP	1	NR1H4	up_VPUL_EC
GO:2001248	0.0034	1	1	1	regulation of ammonia assimilation cycle	BP	1	NR1H4	up_VPUL_EC
GO:2001250	0.0034	1	1	1	positive regulation of ammonia assimilation	BP	1	NR1H4	up_VPUL_EC
GO:0071380	0.00341	1	4	7	cellular response to prostaglandin E stimulus	BP	0.731	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0071294	0.00342	1	2	4	cellular response to zinc ion	BP	1	MT2A,ENSCAFG00000009113	up_AFEM_EC
GO:0003218	0.00342	1	1	1	cardiac left ventricle formation	BP	1	TBX5	up_VPUL_EC
GO:0048562	0.00343	0.999	19	102	embryonic organ morphogenesis	BP	1	TBX15,HOXA11,HOXA7,WNT11,OSR2,INSIG2,LRIG3,IRX5,HOXD3,DLL1,HOXA6,OSR1,RARG,HOXC4,ZEB1,SHOX2,KDM2B,TGFBR2,CITED2	up_VSAP_EC
GO:0042118	0.00343	1	1	4	endothelial cell activation	BP	1	TGFBR1	down_VSAP_VSMC
GO:2000377	0.00344	0.999	9	41	regulation of reactive oxygen species metabolic	BP	0.228	PRCP,PDGFB,CD34,TLR4,RAB27A,ARG2,GCH1,RIPK1,HIF1A	up_VCAV_EC
GO:0019438	0.00344	1	6	1258	aromatic compound biosynthetic process	BP	0.926	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0061138	0.00344	1	3	73	morphogenesis of a branching epithelium	BP	0.507	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0021536	0.00344	1	2	21	diencephalon development	BP	0.708	PITX1,SALL1	up_VSAP_VSMC
GO:0032228	0.00344	1	1	8	regulation of synaptic transmission, GABAergic	BP	1	PLCL1	down_VFEM_EC
GO:1905314	0.00344	1	1	12	semi-lunar valve development	BP	0.867	GATA5	down_VFEM_VSMC
GO:2000027	0.00345	1	3	72	regulation of animal organ morphogenesis	BP	0.507	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:0051704	0.003452041	0.9984	23	476	multi-organism process	BP	0.91320638	NR1H4,SOX9,HMCN1,RGS1,ATG16L2,AQP1,FZD5,PTGIR,NOD2,TRIM8,PTGER4,ARHGDIB,MAPK8IP2,MAVS,FIGNL1,LRRC15,IFIT2,CHMP4B,RARRES2,AGBL5,PRKCD,PYGO2,CCNYL1	up_ACOR_EC
GO:0019229	0.00346	1	5	12	regulation of vasoconstriction	BP	0.731	ADRA1B,HRH1,HRH2,EDN1,DOCK5	up_ACOR_VSMC
GO:0060749	0.00346	1	1	3	mammary gland alveolus development	BP	0.513	ESR1	up_AORT_VSMC
GO:0061377	0.00346	1	1	3	mammary gland lobule development	BP	0.513	ESR1	up_AORT_VSMC
GO:0032501	0.00347	1	7	1782	multicellular organismal process	BP	0.926	HOXC10,TLR2,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:0009617	0.00348	0.998	20	133	response to bacterium	BP	0.228	GBP5,LYZ,CXCL8,TNFAIP3,ADAMTS9,TNIP1,BAIAP2L1,PDE4D,MEF2C,CHD7,TLR4,NLRC5,IRF8,PELI1,ARG2,ABCA1,PLCG2,BCL10,GCH1,NOS2	up_VCAV_EC
GO:0030282	0.00348	1	3	37	bone mineralization	BP	1	HOXA3,ASPN,ACVR2A	up_VPOR_EC
GO:0030010	0.00348	1	2	41	establishment of cell polarity	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0051240	0.00349	1	4	489	positive regulation of multicellular organismal	BP	1	SLITRK5,LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0007634	0.00349	1	1	1	optokinetic behavior	BP	0.528	HOXA1	down_ACOR_EC
GO:0021560	0.00349	1	1	1	abducens nerve development	BP	0.528	HOXA1	down_ACOR_EC
GO:0021598	0.00349	1	1	1	abducens nerve morphogenesis	BP	0.528	HOXA1	down_ACOR_EC

GO:0021599	0.00349	1	1	1	abducens nerve formation	BP	0.528	HOXA1	down_ACOR_EC
GO:0099537	0.0035	0.998	23	131	trans-synaptic signaling	BP	0.731	PLCL1,FBXL20,HRH1,GLRB,STX11,TMEM108,EGLN1,CACNB3,SLC12A7,DMPK,SLITRK5,PRKCE,RNF19A,DAG1,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,INSYN1,PREPL,PARK7	up_ACOR_VSMC
GO:0018130	0.0035	1	6	1261	heterocycle biosynthetic process	BP	0.926	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0003264	0.0035	1	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0003266	0.0035	1	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_APUL_VSMC
GO:0071724	0.0035	1	1	1	response to diacyl bacterial lipopeptide	BP	0.708	TLR2	up_VSAP_VSMC
GO:0071726	0.0035	1	1	1	cellular response to diacyl bacterial lipopeptide	BP	0.708	TLR2	up_VSAP_VSMC
GO:1903971	0.0035	1	1	1	positive regulation of response to macrophage colony-stimulating factor	BP	0.708	TLR2	up_VSAP_VSMC
GO:1903974	0.0035	1	1	1	positive regulation of cellular response to macrophage colony-	BP	0.708	TLR2	up_VSAP_VSMC
GO:0042496	0.0035	1	1	1	detection of diacyl bacterial lipopeptide	BP	0.708	TLR2	up_VSAP_VSMC
GO:0044255	0.00351	0.998	43	293	cellular lipid metabolic process	BP	1	PEX7,NAPEPLD,ACSM3,LIPC,INSIG2,ENPP2,ACAA1,ACACB,PEX2,INPP5E,CERS4,DHRS4,KDELC2,C1QTNF2,ABHD15,HSD17B8,PLPP3,ENSCAFG00000000071,FAAH,AMBRA1,LMF1,PDK2,RETSAT,PIK3R1,PLA2G6,PIK3IP1,PTGES,HACD4,GCDH,DAGLB,EHHADH,LCAT,LONP2,DHRS9,MVK,ABHD16A,HPGD,ZFYVE21,ENSCAFG00000023820,IDH1,PLPP5,B3GALT4,SOAT1	up_VSAP_EC
GO:0090075	0.00351	1	4	8	relaxation of muscle	BP	0.23	PDE4D,GUCY1A1,KCNJ2,ATP2A1	up_VCAV_EC
GO:0072088	0.00352	1	2	36	nephron epithelium morphogenesis	BP	0.861	EYA1,HOXA11	up_VFEM_VSMC
GO:0003345	0.00352	1	1	1	proepicardium cell migration involved in pericardium	BP	1	FLRT3	up_VPUL_EC
GO:0006096	0.00353	1	5	18	glycolytic process	BP	0.302	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0006165	0.00353	1	5	18	nucleoside diphosphate phosphorylation	BP	0.302	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0006757	0.00353	1	5	18	ATP generation from ADP	BP	0.302	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0042866	0.00353	1	5	18	pyruvate biosynthetic process	BP	0.302	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0031214	0.00354	1	2	45	biomineral tissue development	BP	0.798	HOXA3,PHEX	up_VPUL_VSMC
GO:0002027	0.00354	1	2	20	regulation of heart rate	BP	0.708	IRX5,CAV1	up_VSAP_VSMC
GO:2001273	0.003547365	0.99979	3	12	regulation of glucose import in response to	BP	0.92328747	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0048705	0.00355	0.999	18	95	skeletal system morphogenesis	BP	1	TBX15,HOXA11,HOXA7,PEX7,AXIN2,OSR2,INSIG2,PPARGC1B,IRX5,HOXD3,HOXA6,OSR1,RARG,ZEB1,SHOX2,ZFAND5,TGFBR2,CITED2	up_VSAP_EC
GO:0034755	0.00355	1	3	4	iron ion transmembrane transport	BP	1	SLC25A28,SCARA5,STEAP3	up_VSAP_EC
GO:0003207	0.00355	1	1	5	cardiac chamber formation	BP	1	TBX5	up_APUL_VSMC
GO:0090183	0.00356	1	2	21	regulation of kidney development	BP	0.517	HOXB7,SIX1	up_VFEM_EC
GO:0045165	0.00357	1	2	65	cell fate commitment	BP	0.926	HOXC10,EYA1	up_AFEM_VSMC
GO:0048704	0.00359	0.999	11	46	embryonic skeletal system morphogenesis	BP	1	TBX15,HOXA11,HOXA7,OSR2,IRX5,HOXD3,HOXA6,OSR1,ZEB1,SHOX2,TGFBR2	up_VSAP_EC
GO:0061061	0.0036	0.998	26	179	muscle structure development	BP	0.234	EPHB1,EDNRB,KIT,IFRD1,PDGFB,MEF2C,ATF3,CHD7,DLL4,EDN1,FOXN2,TMOD1,PPP3CA,MTOR,BMP2,CAV2,PROX1,ENSCAFG00000010596,FLNB,CREB1,ASF1A,NR1D2,P2RX2,TMOD3,ZEB1,CDON	up_VCAV_EC
GO:0006351	0.0036	0.999	11	1069	transcription, DNA-templated	BP	0.708	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0048736	0.0036	1	2	66	appendage development	BP	0.926	HOXC10,HOXA9	up_AFEM_VSMC
GO:0060173	0.0036	1	2	66	limb development	BP	0.926	HOXC10,HOXA9	up_AFEM_VSMC

GO:0032330	0.0036	1	2	20	regulation of chondrocyte differentiation	BP	0.708	HOXA11,SHOX2	up_VSAP_VSMC
GO:0010812	0.00361	1	2	19	negative regulation of cell-substrate adhesion	BP	0.528	ACVRL1,HOXA7	down_ACOR_EC
GO:0003170	0.00362	1	1	25	heart valve development	BP	1	GATA5	down_AFEM_VSMC
GO:0008380	0.00363	1	3	149	RNA splicing	BP	1	IVNS1ABP,SRSF6,TSEN15	down_AFEM_EC
GO:1903715	0.00363	1	2	2	regulation of aerobic respiration	BP	0.309	HIF1A,BNIP3	down_VSAP_EC
GO:0048598	0.00364	0.999	12	207	embryonic morphogenesis	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,HOXA7,DLL1,GREM1,GREM2,HOXA6,LUZP1,RECK	up_AFEM_EC
GO:0043536	0.00364	0.999	8	32	positive regulation of blood vessel endothelial	BP	0.236	PLK2,PDGFB,PIK3C2A,MAP3K3,PRKD2,HMGB1,HIF1A,JCAD	up_VCAV_EC
GO:0007389	0.00364	1	4	137	pattern specification process	BP	0.528	HOXA3,NRP2,HOXA7,HOXC4	down_ACOR_EC
GO:0048704	0.00364	1	2	46	embryonic skeletal system morphogenesis	BP	0.798	HOXA3,HOXB5	up_VPUL_VSMC
GO:0050793	0.00365	0.998	29	731	regulation of developmental process	BP	1	HOXA9,CMKLR1,IRX3,LEP,LBH,ANGPT4,HOXA7,DLL1,F3,PLXNA4,GPAM,TWIST2,THRB,LGI4,TMEM100,GREM1,CAMK2A,CYLD,PTHLH,TBXA2R,EVI2B,BVES,AXIN2,ACACB,NAPEPLD,PPARGC1A,CDC42EP5,DMPK,KANK1	up_AFEM_EC
GO:2000026	0.00365	1	5	560	regulation of multicellular organismal development	BP	0.798	TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0048534	0.00365	1	4	262	hematopoietic or lymphoid organ	BP	1	HOXA3,BARX1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0061156	0.00365	1	3	4	pulmonary artery morphogenesis	BP	0.735	BMP4,SEC24B,CITED2	up_ACOR_VSMC
GO:0010634	0.00366	0.999	13	68	positive regulation of epithelial cell migration	BP	0.236	PLK2,TEK,PDGFB,GATA3,RAB11A,PIK3C2A,MTOR,MAP3K3,PROX1,PRKD2,HMGB1,HIF1A,JCAD	up_VCAV_EC
GO:0006641	0.00367	0.999	7	25	triglyceride metabolic process	BP	0.212	SREBF1,CTDNEP1,INSIG1,CAV1,ABHD5,LIPC,GK5	down_ACOR_VSMC
GO:0051382	0.00367	1	4	9	kinetochore assembly	BP	0.212	CENPA,CENPN,CENPH,CENPW	down_ACOR_VSMC
GO:0055059	0.00367	1	1	1	asymmetric neuroblast division	BP	1	ARHGEF2	up_VPUL_EC
GO:0018212	0.00368	0.999	12	81	peptidyl-tyrosine modification	BP	0.311	ARHGEF2,VEGFA,SOCS5,ERRFI1,PTPN2,YES1,ADAM17,CNOT7,LYN,CBLC,BTK,NRP1	down_VSAP_EC
GO:0097659	0.00369	0.999	11	1072	nucleic acid-templated transcription	BP	0.714	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:1902652	0.00369	0.999	9	38	secondary alcohol metabolic process	BP	0.213	SQLE,LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1,LIPC	down_ACOR_VSMC
GO:0070304	0.00371	0.999	13	58	positive regulation of stress-activated protein kinase signaling cascade	BP	0.735	LEP,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0021520	0.00371	1	1	3	spinal cord motor neuron cell fate specification	BP	0.53	HOXC10	up_AORT_VSMC
GO:0019220	0.00372	0.998	61	525	regulation of phosphate metabolic process	BP	0.238	EPHB1,TEK,HCLS1,ADGRF5,KIT,PPP2R5A,CDA,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,NLRC5,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,PPP1R2,ITPKB,PROX1,MADD,PAK2,PRKD2,SH3GLB1,SWAP70,TLR3,NCK1,LDB2,NSD1,PTGS2,MMD,RAPGEF2,TAOK1,CNOT7,HMGB1,NOS2,BLM,SPTBN4,RIPK1,ITGA6,RAD17,PDGFD,HIF1A,FKBP15,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0051174	0.00372	0.998	61	525	regulation of phosphorus metabolic process	BP	0.238	EPHB1,TEK,HCLS1,ADGRF5,KIT,PPP2R5A,CDA,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,NLRC5,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,PPP1R2,ITPKB,PROX1,MADD,PAK2,PRKD2,SH3GLB1,SWAP70,TLR3,NCK1,LDB2,NSD1,PTGS2,MMD,RAPGEF2,TAOK1,CNOT7,HMGB1,NOS2,BLM,SPTBN4,RIPK1,ITGA6,RAD17,PDGFD,HIF1A,FKBP15,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0032774	0.00372	0.999	11	1073	RNA biosynthetic process	BP	0.714	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0010463	0.00372	0.999	8	28	mesenchymal cell proliferation	BP	1	WNT11,FGF7,OSR1,ZEB1,FBXW4,SHOX2,NFIB,TGFBR2	up_VSAP_EC
GO:1903727	0.00372	1	2	16	positive regulation of phospholipid metabolic	BP	0.528	LYN,ACSL3	down_ACOR_EC
GO:0060750	0.00372	1	1	3	epithelial cell proliferation involved in mammary gland duct elongation	BP	0.53	ESR1	up_AORT_VSMC
GO:0060751	0.00372	1	1	3	branch elongation involved in mammary	BP	0.53	ESR1	up_AORT_VSMC

GO:0008299	0.00373	1	5	14	isoprenoid biosynthetic process	BP	0.214	HMGCR,ENSCAFG00000018572,MVD,NUS1,PDSS1	down_ACOR_VSMC
GO:1905314	0.00373	1	5	12	semi-lunar valve development	BP	0.735	SMAD6,GATA5,GATA4,BMP4,TBX20	up_ACOR_VSMC
GO:0032092	0.00373	1	2	38	positive regulation of protein binding	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0035914	0.00373	1	2	22	skeletal muscle cell differentiation	BP	0.523	SIX1,CYP26B1	up_VFEM_EC
GO:0001759	0.00373	1	1	13	organ induction	BP	0.926	GATA5	down_VFEM_VSMC
GO:0051491	0.00375	1	3	6	positive regulation of filopodium assembly	BP	0.312	FSCN1,DPYSL3,NRP1	down_VSAP_EC
GO:0072028	0.00375	1	2	37	nephron morphogenesis	BP	0.903	EYA1,HOXA11	up_VFEM_VSMC
GO:0055026	0.00376	1	1	5	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0051973	0.00378	0.999	6	19	positive regulation of telomerase activity	BP	0.216	HNRNPD,SLC29A1,AURKB,GREM1,NEK2,CCT4	down_ACOR_VSMC
GO:0032501	0.00379	1	7	1782	multicellular organismal process	BP	1	HOXC6,SLITRK5,LIMK1,GATA5,LRRC17,C6,TGFBI	up_VCAV_VSMC
GO:0055090	0.00379	1	3	6	acylglycerol homeostasis	BP	0.312	NR1H4,SESN2,APOE	down_VSAP_EC
GO:0070328	0.00379	1	3	6	triglyceride homeostasis	BP	0.312	NR1H4,SESN2,APOE	down_VSAP_EC
GO:0051239	0.0038	1	5	859	regulation of multicellular organismal process	BP	0.926	HOXC10,TLR2,EYA1,HOXA9,IRX5	up_AFEM_VSMC
GO:0007423	0.00381	1	4	155	sensory organ development	BP	0.523	EYA1,SIX1,MAB21L1,CYP26B1	up_VFEM_EC
GO:0007548	0.00381	1	2	68	sex differentiation	BP	0.926	HOXA9,IRX5	up_AFEM_VSMC
GO:0007275	0.00382	0.998	47	1370	multicellular organism development	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,LEP,LBH,XYLT1,ANGPT4,HOXA7,COL8A2,CD40,DLL1,CRYAB,F3,VXN,PLXNA4,NEFH,MAB21L1,THRB,LGI4,TMEM100,PLAGL2,GREM1,NFE2L1,OVOL1,CAMK2A,GREM2,HOXA6,CYLD,LUZP1,RECK,PTHLH,TBXA2R,EVI2B,CNNM4,BVES,PTPRB,AXIN2,ACACB,PPARGC1A,CLIC4,LRRN2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0071384	0.00382	1	5	12	cellular response to corticosteroid stimulus	BP	1	FAM107A,ZFP36L1,CREBRF,ZFP36L2,DDIT4	up_VSAP_EC
GO:0071385	0.00382	1	5	12	cellular response to glucocorticoid stimulus	BP	1	FAM107A,ZFP36L1,CREBRF,ZFP36L2,DDIT4	up_VSAP_EC
GO:0045766	0.00384	0.999	12	63	positive regulation of angiogenesis	BP	0.244	PLK2,TEK,CXCL8,CD34,APLNR,SMAD1,PIK3C2A,MAP3K3,PRKD2,TLR3,HIF1A,JCAD	up_VCAV_EC
GO:0022008	0.00385	0.998	39	406	neurogenesis	BP	0.316	ARHGEF2,VEGFA,SIPA1L1,ETV6,SGK1,CASP3,PTPN11,DPYSL3,HOOK3,IFRD1,ILK,KIF5B,HIF1A,SLC45A3,TNIK,UBA6,ZPR1,EIF2B1,NEO1,UST,CDH11,CTNNB1,APOE,LYN,MMD,GSK3B,VLDLR,SDC4,REST,MAPK10,PRMT1,EXT1,DISC1,PAK2,INHBA,SIX4,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0051781	0.00385	0.999	6	18	positive regulation of cell division	BP	0.741	LBH,HTR2B,FGFR2,PKP4,PRKCE,CAT	up_ACOR_VSMC
GO:0030855	0.00387	0.998	26	183	epithelial cell differentiation	BP	0.244	PRKCH,PDGFB,PODXL,PDE4D,MEF2C,RAPGEF1,GPR4,STC1,GATA3,SOX18,TMOD1,MTSS1,BMP2,HHEX,PROX1,ARID4B,FLNB,HOXB5,JAG1,RAPGEF2,CREB1,BASP1,SKIL,HIF1A,ATRX,ZEB1	up_VCAV_EC
GO:0051932	0.00387	1	1	9	synaptic transmission, GABAergic	BP	1	PLCL1	down_VFEM_EC
GO:0045089	0.00388	0.999	13	70	positive regulation of innate immune response	BP	0.244	GBP5,TNFAIP3,TNIP1,TMEM173,TLR4,NLRC5,PELI1,NECTIN2,RIOK3,TLR3,OTUD4,HMGB1,LSM14A	up_VCAV_EC
GO:0034329	0.00389	0.999	10	60	cell junction assembly	BP	0.316	VEGFA,NR1H4,ACTN1,FSCN1,WDR1,MYO1C,CTNNB1,ENSCAFG00000002015,TLN1,NRP1	down_VSAP_EC
GO:0009611	0.00389	1	4	122	response to wounding	BP	0.528	ACVRL1,LYN,PDPN,ELK3	down_ACOR_EC
GO:0060429	0.00389	1	4	341	epithelium development	BP	0.798	TBX5,GATA5,HOXB5,SLIT2	up_VPUL_VSMC
GO:0030155	0.0039	0.998	26	180	regulation of cell adhesion	BP	0.244	TEK,IL7R,CXCL8,EMCN,PODXL,FERMT1,GATA3,NEDD9,PELI1,PPP3CA,ARG2,BMP2,SLK,ITPKB,ANGPT2,PRKD2,SWAP70,APOD,NCK1,FES,JAG1,BCL10,PPP1CB,HMGB1,ITGA6,ENSCAFG00000002015	up_VCAV_EC
GO:0032879	0.0039	0.999	10	767	regulation of localization	BP	0.528	ACVRL1,LYN,HOXA3,IGF1R,PDPN,HOXA7,SULF1,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0060042	0.00391	1	3	14	retina morphogenesis in camera-type eye	BP	1	IRX5,DLL1,THRB	up_AFEM_EC

GO:0070170	0.00391	1	1	1	regulation of tooth mineralization	BP	0.528	ASPN	down_ACOR_EC
GO:0070171	0.00391	1	1	1	negative regulation of tooth mineralization	BP	0.528	ASPN	down_ACOR_EC
GO:0050901	0.00392	1	3	5	leukocyte tethering or rolling	BP	0.244	SELP,SELE,SELL	up_VCAV_EC
GO:0061756	0.00392	1	3	5	leukocyte adhesion to vascular endothelial cell	BP	0.244	SELP,SELE,SELL	up_VCAV_EC
GO:0071695	0.00393	0.999	5	45	anatomical structure maturation	BP	1	IRX5,XYLT1,LGI4,GREM1,RECK	up_AFEM_EC
GO:0002765	0.00393	1	1	1	immune response-inhibiting signal	BP	0.528	LYN	down_ACOR_EC
GO:0002767	0.00393	1	1	1	immune response-inhibiting cell surface receptor signaling	BP	0.528	LYN	down_ACOR_EC
GO:0002774	0.00393	1	1	1	Fc receptor mediated inhibitory signaling	BP	0.528	LYN	down_ACOR_EC
GO:0034136	0.00393	1	1	1	negative regulation of toll-like receptor 2 signaling	BP	0.528	LYN	down_ACOR_EC
GO:0070667	0.00393	1	1	1	negative regulation of mast cell proliferation	BP	0.528	LYN	down_ACOR_EC
GO:0043269	0.00395	0.998	23	135	regulation of ion transport	BP	0.746	ACTN2,PLCG2,KCNE3,TCAF1,GJA1,SARAF,PTPN3,DAPK1,CACNB3,AKAP6,DMPK,KCNJ4,PRKCE,PSEN1,CHD7,RAB11B,KCNC4,B2M,FXYD1,INPP5K,WFS1,PARK7,STC2	up_ACOR_VSMC
GO:0009952	0.00396	1	2	66	anterior/posterior pattern specification	BP	0.926	HOXC10,HOXA9	up_AFEM_VSMC
GO:0002376	0.00397	0.999	7	622	immune system process	BP	1	HOXA3,NR1H4,EVI2B,IL18BP,MRC1,CCL24,ARHGEF2	up_VPUL_EC
GO:0055022	0.00397	1	1	2	negative regulation of cardiac muscle tissue	BP	0.798	TBX5	up_VPUL_VSMC
GO:0060044	0.00397	1	1	2	negative regulation of cardiac muscle cell	BP	0.798	TBX5	up_VPUL_VSMC
GO:0061117	0.00397	1	1	2	negative regulation of heart growth	BP	0.798	TBX5	up_VPUL_VSMC
GO:0043010	0.003971675	0.999	8	96	camera-type eye development	BP	0.96436359	TMOD1,SOX9,AQP1,FZD5,FOXC2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0022414	0.00398	1	3	294	reproductive process	BP	0.53	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0034121	0.00398	1	2	22	regulation of toll-like receptor signaling	BP	0.739	TLR2,CAV1	up_VSAP_VSMC
GO:0003218	0.00398	1	1	1	cardiac left ventricle formation	BP	1	TBX5	up_APUL_EC
GO:0097195	0.00398	1	1	1	pilomotor reflex	BP	1	NPNT	up_APUL_EC
GO:0099551	0.00398	1	1	1	trans-synaptic signaling by neuropeptide, modulating synaptic transmission	BP	1	NTRK2	up_APUL_EC
GO:0006808	0.00398	1	1	1	regulation of nitrogen utilization	BP	1	NR1H4	up_APUL_EC
GO:0007634	0.00398	1	1	1	optokinetic behavior	BP	1	HOXA1	up_APUL_EC
GO:0019676	0.00398	1	1	1	ammonia assimilation cycle	BP	1	NR1H4	up_APUL_EC
GO:0019740	0.00398	1	1	1	nitrogen utilization	BP	1	NR1H4	up_APUL_EC
GO:0021560	0.00398	1	1	1	abducens nerve development	BP	1	HOXA1	up_APUL_EC
GO:0021598	0.00398	1	1	1	abducens nerve morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0021599	0.00398	1	1	1	abducens nerve formation	BP	1	HOXA1	up_APUL_EC
GO:0034255	0.00398	1	1	1	regulation of urea metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0034971	0.00398	1	1	1	histone H3-R17 methylation	BP	1	NR1H4	up_APUL_EC
GO:0038183	0.00398	1	1	1	bile acid signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0038185	0.00398	1	1	1	intracellular bile acid receptor signaling	BP	1	NR1H4	up_APUL_EC
GO:0045848	0.00398	1	1	1	positive regulation of nitrogen utilization	BP	1	NR1H4	up_APUL_EC
GO:1903314	0.00398	1	1	1	regulation of nitrogen cycle metabolic process	BP	1	NR1H4	up_APUL_EC
GO:1905693	0.00398	1	1	1	regulation of phosphatidic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:1905695	0.00398	1	1	1	positive regulation of phosphatidic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC

GO:2000211	0.00398	1	1	1	regulation of glutamate metabolic process	BP	1	NR1H4	up_APUL_EC
GO:2000213	0.00398	1	1	1	positive regulation of glutamate metabolic	BP	1	NR1H4	up_APUL_EC
GO:2001248	0.00398	1	1	1	regulation of ammonia assimilation cycle	BP	1	NR1H4	up_APUL_EC
GO:2001250	0.00398	1	1	1	positive regulation of ammonia assimilation	BP	1	NR1H4	up_APUL_EC
GO:0009888	0.00399	1	3	545	tissue development	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0010159	0.00399	1	1	2	specification of animal organ position	BP	0.798	HOXA3	up_VPUL_VSMC
GO:0003274	0.00399	1	1	2	endocardial cushion fusion	BP	0.798	GATA5	up_VPUL_VSMC
GO:0072329	0.004	0.999	9	34	monocarboxylic acid catabolic process	BP	1	PEX7,ACAA1,ACACB,PEX2,FAAH,GCDH,EHHADH,LONP2,ABHD16A	up_VSAP_EC
GO:0048598	0.004	0.999	5	207	embryonic morphogenesis	BP	0.529	HOXA3,HOXA7,SULF1,HOXA1,HOXC4	down_ACOR_EC
GO:0014821	0.004	1	3	5	phasic smooth muscle contraction	BP	0.248	EDNRB,EDN1,P2RX2	up_VCAV_EC
GO:0055114	0.00401	1	3	157	oxidation-reduction process	BP	1	ETFA,SUCLG2,NDUFA10	down_AFEM_EC
GO:0000003	0.00401	1	3	295	reproduction	BP	0.53	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0003164	0.00401	1	1	2	His-Purkinje system development	BP	0.798	TBX5	up_VPUL_VSMC
GO:0003166	0.00401	1	1	2	bundle of His development	BP	0.798	TBX5	up_VPUL_VSMC
GO:0007507	0.00402	0.998	31	194	heart development	BP	0.746	TNNT2,PDLIM3,SMAD6,ACTN2,GATA5,GATA4,HTR2B,BMP4,FGFR2,GJA1,SEC24B,XIRP1,CITED2,LMO4,NEBL,ANKRD1,EGLN1,NRP1,SMARCD3,TBX20,TBX5,FRS2,PSEN1,TGFBR1,CHD7,PSKH1,EDN1,AP2B1,GAA,BVES,CRKL	up_ACOR_VSMC
GO:1901362	0.00402	1	6	1293	organic cyclic compound biosynthetic process	BP	0.928	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0003179	0.00402	0.999	6	19	heart valve morphogenesis	BP	0.249	ADAMTS9,MEF2C,GATA3,MTOR,BMP2,JAG1	up_VCAV_EC
GO:0051239	0.00402	1	5	859	regulation of multicellular organismal process	BP	1	SLITRK5,LIMK1,GATA5,LRRC17,C6	up_VCAV_VSMC
GO:0046184	0.00402	1	3	6	aldehyde biosynthetic process	BP	0.323	TPI1,REST,KDM3A	down_VSAP_EC
GO:0008584	0.00403	1	2	39	male gonad development	BP	0.929	HOXA9,HOXA11	up_VFEM_VSMC
GO:0046546	0.00403	1	2	39	development of primary male sexual	BP	0.929	HOXA9,HOXA11	up_VFEM_VSMC
GO:1903707	0.00403	1	2	48	negative regulation of hemopoiesis	BP	0.798	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0046449	0.00403	1	1	1	creatinine metabolic process	BP	0.523	MME	up_VFEM_EC
GO:0071492	0.00403	1	1	1	cellular response to UV-A	BP	0.523	MME	up_VFEM_EC
GO:0072338	0.00403	1	1	1	cellular lactam metabolic process	BP	0.523	MME	up_VFEM_EC
GO:0032700	0.00404	1	1	4	negative regulation of interleukin-17 production	BP	0.53	ARG2	up_AORT_VSMC
GO:0050665	0.00404	1	1	3	hydrogen peroxide biosynthetic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0035544	0.00404	1	1	1	negative regulation of SNARE complex assembly	BP	0.523	TRIM9	up_VFEM_EC
GO:0140074	0.00405	1	1	2	cardiac endothelial to mesenchymal transition	BP	0.798	GATA5	up_VPUL_VSMC
GO:0060971	0.00406	1	1	2	embryonic heart tube left/right pattern	BP	1	NKX2-5	up_VPOR_VSMC
GO:1903364	0.00407	0.999	10	61	positive regulation of cellular protein catabolic	BP	0.325	PRICKLE1,PLK3,SOCS5,TRIB3,MSN,APOE,GSK3B,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:0007099	0.00407	0.999	6	19	centriole replication	BP	0.23	WDR62,NUP62,PLK4,CDK2,SASS6,RBM14	down_ACOR_VSMC
GO:0098534	0.00407	0.999	6	19	centriole assembly	BP	0.23	WDR62,NUP62,PLK4,CDK2,SASS6,RBM14	down_ACOR_VSMC
GO:0030193	0.00407	1	2	21	regulation of blood coagulation	BP	0.529	LYN,PDPN	down_ACOR_EC
GO:1900046	0.00407	1	2	21	regulation of hemostasis	BP	0.529	LYN,PDPN	down_ACOR_EC
GO:0071623	0.00407	1	1	2	negative regulation of granulocyte chemotaxis	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0090024	0.00407	1	1	2	negative regulation of neutrophil chemotaxis	BP	0.798	SLIT2	up_VPUL_VSMC
GO:1902623	0.00407	1	1	2	negative regulation of neutrophil migration	BP	0.798	SLIT2	up_VPUL_VSMC

GO:0048583	0.004071257	0.99768	43	1095	regulation of response to stimulus	BP	0.96436359	C7,SH3TC2,CDH3,NR1H4,SOX9,RGS1,FNDC4,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,CCDC3,IFI6,DUSP26,DIXDC1,PTGIR,NOD2,IL33,RGMA,PDE4A,SMAD6,ESM1,PAK3,MMP28,TNFRSF19,PTGER4,ARHGDIB,ADAMTSL2,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,RARRES2,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0008284	0.00408	0.998	31	238	positive regulation of cell proliferation	BP	0.25	HCLS1,IL7R,KIT,PRKCH,CALCRL,TNFAIP3,PDGFB,MEF2C,DLL4,TLR4,EDN1,APLNR,EGFL7,PELI1,ODC1,MAP3K3,BMP2,CNOT6,CCAR1,PROX1,PRKD2,NCK1,CNOT7,HMGB1,CRIP2,NRAS,PDGFD,CUL4A,HIF1A,JCAD,CDON	up_VCAV_EC
GO:0045944	0.00409	1	3	287	positive regulation of transcription by RNA polymerase II	BP	0.53	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:2001247	0.0041	1	1	1	positive regulation of phosphatidylcholine biosynthetic process	BP	0.53	ACSL3	down_ACOR_EC
GO:0030449	0.0041	1	1	3	regulation of complement activation	BP	1	C6	up_VCAV_VSMC
GO:2000257	0.0041	1	1	3	regulation of protein activation cascade	BP	1	C6	up_VCAV_VSMC
GO:0001655	0.004100579	0.99886	9	116	urogenital system development	BP	0.96436359	TBX18,SOX9,AQP1,SMAD6,FOXC2,LRP4,CLSTN1,NRP1,PYGO2	up_ACOR_EC
GO:0051303	0.00411	0.999	7	26	establishment of chromosome localization	BP	0.23	ZW10,BIRC5,KIF22,CDCA8,NDC80,NUP62,ENSCAFG00000005299	down_ACOR_VSMC
GO:0071941	0.00411	1	1	4	nitrogen cycle metabolic process	BP	0.53	ARG2	up_AORT_VSMC
GO:0043116	0.00411	1	1	2	negative regulation of vascular permeability	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0071676	0.00411	1	1	2	negative regulation of mononuclear cell	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0001763	0.00412	1	3	78	morphogenesis of a branching structure	BP	0.523	EYA1,HOXB7,SIX1	up_VFEM_EC
GO:2000826	0.00412	1	1	14	regulation of heart morphogenesis	BP	0.984	GATA5	down_VFEM_VSMC
GO:0061476	0.00412	1	1	2	response to anticoagulant	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0071503	0.00412	1	1	2	response to heparin	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0071504	0.00412	1	1	2	cellular response to heparin	BP	0.798	SLIT2	up_VPUL_VSMC
GO:1903672	0.00413	0.999	6	20	positive regulation of sprouting angiogenesis	BP	0.252	PLK2,APLNR,SMAD1,PIK3C2A,MAP3K3,JCAD	up_VCAV_EC
GO:0055083	0.00413	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0006857	0.00413	1	1	3	oligopeptide transport	BP	1	CA2	up_VCAV_VSMC
GO:0035672	0.00413	1	1	3	oligopeptide transmembrane transport	BP	1	CA2	up_VCAV_VSMC
GO:0060429	0.004130529	0.99825	18	341	epithelium development	BP	0.96436359	CDH3,TMOD1,GATA4,BRSK1,SOX9,AQP1,FZD5,SMAD6,DLX3,TNFRSF19,ADAMTSL2,FOXC2,TBX5,LRP4,CLSTN1,NRP1,ARHGEF26,PYGO2	up_ACOR_EC
GO:0019835	0.00414	1	2	2	cytolysis	BP	0.252	LYZ,MMD	up_VCAV_EC
GO:0020027	0.00415	1	2	2	hemoglobin metabolic process	BP	0.328	HIF1A,INHBA	down_VSAP_EC
GO:0042541	0.00415	1	2	2	hemoglobin biosynthetic process	BP	0.328	HIF1A,INHBA	down_VSAP_EC
GO:0021520	0.00415	1	1	3	spinal cord motor neuron cell fate specification	BP	0.944	HOXC10	up_AFEM_VSMC
GO:0048537	0.00416	1	1	1	mucosal-associated lymphoid tissue	BP	0.523	TOX	up_VFEM_EC
GO:0048541	0.00416	1	1	1	Peyer's patch development	BP	0.523	TOX	up_VFEM_EC
GO:0045899	0.00419	1	1	4	positive regulation of RNA polymerase II transcriptional	BP	0.53	ESR1	up_AORT_VSMC
GO:0003170	0.004195057	0.99953	4	25	heart valve development	BP	0.96436359	GATA4,SOX9,SMAD6,TBX5	up_ACOR_EC
GO:0001933	0.0042	1	4	146	negative regulation of protein phosphorylation	BP	0.538	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0007498	0.0042	1	2	38	mesoderm development	BP	0.929	EYA1,HOXA11	up_VFEM_VSMC
GO:0007624	0.0042	1	1	1	ultradian rhythm	BP	0.523	ENOX1	up_VFEM_EC
GO:0034109	0.00421	1	1	14	homotypic cell-cell adhesion	BP	0.984	JUP	down_VFEM_VSMC

GO:0032616	0.00421	1	1	4	interleukin-13 production	BP	0.53	ARG2	up_AORT_VSMC
GO:0032656	0.00421	1	1	4	regulation of interleukin-13 production	BP	0.53	ARG2	up_AORT_VSMC
GO:1902744	0.00421	1	1	2	negative regulation of lamellipodium	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0060349	0.00422	1	2	38	bone morphogenesis	BP	0.929	HOXA11,SHOX2	up_VFEM_VSMC
GO:0090259	0.00422	1	1	2	regulation of retinal ganglion cell axon	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0034622	0.00423	0.997	50	421	cellular protein-containing complex assembly	BP	0.236	HMGB1,STXBP6,USP4,EDC3,UBE2S,CAPG,CENPA,SLC29A1,NDC1,CENPN,FBXO5,PSMD13,INSIG1,RAD51,STMN1,CENPO,DHX33,GMNN,CENPH,CENPI,FASTKD3,OIP5,IPO4,HIST1H1A,RAC1,DDX28,IQGAP2,SAMM50,HMGB2,CDC42EP4,HIST1H2BB,DDX39B,SF3A2,CORO1A,CENPW,FOXRED1,ARPC1B,CENPP,GRWD1,PRMT5,PSMC1,ENSCAFG00000015189,HAT1,GEMIN7,UBE2C,MIS18A,TBCC,H3F3B,SF3A1,EIF3M	down_ACOR_VSMC
GO:0050923	0.00423	1	1	2	regulation of negative chemotaxis	BP	0.798	SLIT2	up_VPUL_VSMC
GO:0019220	0.00424	0.997	47	525	regulation of phosphate metabolic process	BP	0.332	ARHGEF2,VEGFA,NR1H4,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,TRIB3,PGAM1,ILK,PPP1R12A,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,VLDLR,SH3GLB1,HTT,ARFGEF3,CALM1,PAK2,INHBA,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0051174	0.00424	0.997	47	525	regulation of phosphorus metabolic process	BP	0.332	ARHGEF2,VEGFA,NR1H4,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,TRIB3,PGAM1,ILK,PPP1R12A,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,VLDLR,SH3GLB1,HTT,ARFGEF3,CALM1,PAK2,INHBA,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0007389	0.00424	1	3	137	pattern specification process	BP	1	HOXC10,HOXA9,HOXC6	up_AORT_EC
GO:0099536	0.00425	0.998	23	133	synaptic signaling	BP	0.776	PLCL1,FBXL20,HRH1,GLRB,STX11,TMEM108,EGLN1,CACNB3,SLC12A7,DMPK,SLITRK5,PRKCE,RNF19A,DAG1,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,INSYN1,PREPL,PARK7	up_ACOR_VSMC
GO:0050678	0.00425	0.998	18	117	regulation of epithelial cell proliferation	BP	0.258	TNFAIP3,PDGFB,MEF2C,DLL4,GATA3,APLNR,EGFL7,MTSS1,BMP2,CAV2,PROX1,MCC,PRKD2,HMGB1,NRAS,NR4A1,VASH1,JCAD	up_VCAV_EC
GO:0051290	0.00425	1	4	9	protein heterotetramerization	BP	0.236	RRM1,RCC1,FARSA,PDSS1	down_ACOR_VSMC
GO:0048646	0.00425	1	4	349	anatomical structure formation involved in	BP	0.798	HOXA3,TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:0098900	0.00425	1	1	15	regulation of action potential	BP	0.984	JUP	down_VFEM_VSMC
GO:0060687	0.00425	1	1	4	regulation of branching involved in prostate gland	BP	0.53	ESR1	up_AORT_VSMC
GO:0090343	0.00425	1	1	4	positive regulation of cell aging	BP	0.53	ARG2	up_AORT_VSMC
GO:2000774	0.00425	1	1	4	positive regulation of cellular senescence	BP	0.53	ARG2	up_AORT_VSMC
GO:0032007	0.00428	0.999	8	27	negative regulation of TOR signaling	BP	0.776	PRKAA2,CASTOR1,UBR1,SESN3,SESN1,DDIT4,BMT2,SH3BP4	up_ACOR_VSMC
GO:0048878	0.00428	1	4	283	chemical homeostasis	BP	1	HOXA3,TRPC4,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0010960	0.00428	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0048568	0.00429	1	2	148	embryonic organ development	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0042118	0.00429	1	1	4	endothelial cell activation	BP	0.53	HOXA9	up_AORT_VSMC
GO:0010614	0.0043	1	1	5	negative regulation of cardiac muscle	BP	1	GATA5	down_VSAP_VSMC
GO:0014741	0.0043	1	1	5	negative regulation of muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC
GO:0031128	0.00431	1	1	15	developmental induction	BP	0.984	GATA5	down_VFEM_VSMC

GO:0060429	0.00432	0.997	43	341	epithelium development	BP	0.261	HOXB7,PRKCH,PDGFB,PODXL,PDE4D,MEF2C,FERMT1,CHD7,DLL4,RAPGEF1,GPR4,STC1,GATA3,EDN1,NTN4,SOX18,TMOD1,MTSS1,ARG2,MTOR,BMP2,HHEX,PROX1,ARID4B,FLNB,BTBD7,EXOC5,TIMELESS,HOXB5,LDB2,JAG1,RAPGEF2,CREB1,BCL10,BASP1,NUP133,SKIL,HIF1A,ATRX,ALDH1A3,LUZP1,RBBP6,ZEB1	up_VCAV_EC
GO:0046398	0.00432	1	1	1	UDP-glucuronate metabolic process	BP	0.541	CSGALNACT1	down_ACOR_EC
GO:0050653	0.00432	1	1	1	chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	BP	0.541	CSGALNACT1	down_ACOR_EC
GO:0051716	0.00433	0.997	146	2001	cellular response to stimulus	BP	0.333	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,ASNS,NR1H4,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,SOCS5,HM13,SPARC,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CBX5,CASP3,ENSCAFG00000003477,HYOU1,PGK1,WSB1,BCAR3,NUAK1,PTPN11,FLNB,DPYSL3,LRRC8A,TRIB3,FARP1,ILK,FHL2,PPP1R12A,PRCP,SMARCA4,SESN2,TGFBR1,PTGS2,REM1,MYO1C,PIK3C2A,CHSY1,MSN,UACA,SEL1L,KIF5B,HIF1A,CX3CL1,ENSCAFG00000000562,DNAJC10,TNIK,NXN,UBA6,RGS2,ZPR1,PTPN2,EIF2B1,YES1,NEO1,PLCL1,MTDH,ESM1,DDX39B,ADAM17,AGRN,EIF4EBP1,SKAP2,PDIA4,CNOT7,ADGRE5,MAGED1,DNAJB9,GNAQ,CTNNB1,KPNB1,CRYAB,STARD13,ENSCAFG00000002015,TFRC,APOE,WWC3,PDE1A,ZC3H15,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,PLEKHG2,TLN1,CBLC,ATF3,GSK3B,CDC37,GTF2H1,ITGB3,GBP5,SH3GLB1,TAX1BP3,MYO1E,KPNA1,HTT,REST,RBBP8,MAPK10,EIF2S1,SH2B3,RDH11,ARFGEF3,CALM1,DISC1,RAD23A,PAK2,CREB3L2,INHBA,CAMK2D,NR4A1,ENSCAFG00000018360,HIF1AN,BTK,CDKN1A,TMTC3,NRP1,SH3RF3,RHBDF2,USP14,YWHAH,TNFAIP1,MADD,SEC13,KDM3A,MID1	down_VSAP_EC
GO:0003044	0.00433	1	4	8	regulation of systemic arterial blood pressure mediated by a chemical	BP	0.777	ADRA1B,SLC2A5,F2RL1,EDN1	up_ACOR_VSMC
GO:0001704	0.00433	1	2	43	formation of primary germ layer	BP	0.929	EYA1,HOXA11	up_VFEM_VSMC
GO:0043537	0.00433	1	1	15	negative regulation of blood vessel endothelial	BP	0.984	JUP	down_VFEM_VSMC
GO:0002829	0.00433	1	1	4	negative regulation of type 2 immune response	BP	0.53	ARG2	up_AORT_VSMC
GO:0045054	0.00434	1	1	2	constitutive secretory pathway	BP	1	RAB11B	down_VPOR_EC
GO:0061343	0.00435	1	1	3	cell adhesion involved in heart morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0008150	0.004356435	0.99775	162	5646	biological_process	BP	0.96436359	C7,CNTNAP4,SH3TC2,MYOZ2,CA4,FMOD,CPAMD8,CDH3,NR1H4,TMOD1,CLIC3,GATA4,BRSK1,TRPS1,KCTD12,TBX18,PLCL1,PKIB,CALY,THNSL2,SOX9,HMCN1,NMNAT2,RHOU,PKNOX2,ARHGAP6,PTH1R,GALNT5,RGS1,PCSK1N,ENSCAFG00000002230,FNDC4,PHF20,ATG16L2,NDRG2,AQP1,PORCN,ENSCAFG00000004331,SYNPO2,KCNB1,ADAMTS13,SARDH,EDEM2,PI3,FZD5,CCDC3,AGRN,PDE1A,IFI6,SEMA6D,GNAO1,HSF4,DUSP26,DIXDC1,RASL11A,PTGIR,PDLIM3,NOD2,IL33,RGMA,CASP10,BTD,LHX9,ENSCAFG00000028814,PDE4A,INSYN1,SMAD6,B3GNT7,DYNC1I1,KLHL25,PLCE1,PLS1,ACTN2,ZMYND8,ARHGAP28,RNLS,ESM1,NIT2,PTGDS,PAK3,CFI,MMP28,IL11RA,DLX3,GUCY1B1,FMO3,GRK7,BCL2,TRIM8,TNFRSF19,PTGER4,ARHGDIB,ELMO2,PREB,CST3,PIAS1,SLC25A42,DCLK2,ADAMTSL2,USP53,CHPT1,MAPK8IP2,PDRG1,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,KLHDC8B,ARSK,TBX5,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,PRELP,RBM38,TAPBP,CLU,SLC9A9,SFMBT2,ALDOC,C23H3orf58,ZNF229,CHMP4B,TP53INP2,TMTC2,RARRES2,VPS16,GMEB2,AGBL5,RIOX2,ABCB9,PRKACA,RNF114,VCAM1,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,FKBP11,ARHGEF26,PRKCD	up_ACOR_EC

GO:0017185	0.00436	1	3	6	peptidyl-lysine hydroxylation	BP	0.333	PLOD2,PLOD3,P3H4	down_VSAP_EC
GO:0060350	0.00436	1	2	23	endochondral bone morphogenesis	BP	0.739	HOXA11,SHOX2	up_VSAP_VSMC
GO:0019276	0.00436	1	1	2	UDP-N-acetylgalactosamine	BP	1	EXTL2	down_AFEM_EC
GO:0048513	0.00437	0.999	11	906	animal organ development	BP	0.542	ACVRL1,LYN,HOXA3,PDPN,NRP2,HOXA7,SULF1,HOXA1,CSGALNACT1,HOXC4,ASPN	down_ACOR_EC
GO:1902105	0.00437	1	3	80	regulation of leukocyte differentiation	BP	0.523	TOX,HOXA7,CYP26B1	up_VFEM_EC
GO:0002250	0.00439	0.998	13	68	adaptive immune response	BP	0.263	IL7R,IL6,TNFAIP3,MEF2C,GATA3,RAB27A,NECTIN2,MTOR,THOC1,SWAP70,JAG1,BCL10,HMGB1	up_VCAV_EC
GO:0060971	0.00439	1	1	2	embryonic heart tube left/right pattern	BP	1	CITED2	down_VPOR_EC
GO:0021681	0.00439	1	1	4	cerebellar granular layer development	BP	0.53	WNT7A	up_AORT_VSMC
GO:0003129	0.00439	1	1	3	heart induction	BP	1	GATA5	up_VCAV_VSMC
GO:0048513	0.0044	0.999	7	906	animal organ development	BP	0.929	HOXC10,EYA1,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:1903969	0.0044	1	1	3	regulation of response to macrophage colony-stimulating factor	BP	0.972	TLR2	up_AFEM_VSMC
GO:1903972	0.0044	1	1	3	regulation of cellular response to macrophage colony-stimulating factor	BP	0.972	TLR2	up_AFEM_VSMC
GO:0032536	0.0044	1	1	4	regulation of cell projection size	BP	0.53	WNT7A	up_AORT_VSMC
GO:0003342	0.0044	1	1	2	proepicardium development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003343	0.0044	1	1	2	septum transversum development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0030193	0.00441	0.999	6	21	regulation of blood coagulation	BP	0.263	SELP,PDGFB,CD34,KLKB1,TLR4,TFPI	up_VCAV_EC
GO:1900046	0.00441	0.999	6	21	regulation of hemostasis	BP	0.263	SELP,PDGFB,CD34,KLKB1,TLR4,TFPI	up_VCAV_EC
GO:0038107	0.00441	1	1	2	nodal signaling pathway involved in determination of left/right asymmetry	BP	1	CITED2	down_VPOR_EC
GO:1900094	0.00441	1	1	2	regulation of transcription from RNA polymerase II promoter involved in determination of	BP	1	CITED2	down_VPOR_EC
GO:1900164	0.00441	1	1	2	nodal signaling pathway involved in determination of lateral mesoderm	BP	1	CITED2	down_VPOR_EC
GO:0008300	0.00441	1	1	1	isoprenoid catabolic process	BP	0.523	CYP26B1	up_VFEM_EC
GO:0016103	0.00441	1	1	1	diterpenoid catabolic process	BP	0.523	CYP26B1	up_VFEM_EC
GO:0016115	0.00441	1	1	1	terpenoid catabolic process	BP	0.523	CYP26B1	up_VFEM_EC
GO:0035981	0.00441	1	1	1	tongue muscle cell differentiation	BP	0.523	CYP26B1	up_VFEM_EC
GO:0042363	0.00441	1	1	1	fat-soluble vitamin catabolic process	BP	0.523	CYP26B1	up_VFEM_EC
GO:0070268	0.00441	1	1	1	cornification	BP	0.523	CYP26B1	up_VFEM_EC
GO:1902809	0.00441	1	1	1	regulation of skeletal muscle fiber	BP	0.523	CYP26B1	up_VFEM_EC
GO:1902811	0.00441	1	1	1	positive regulation of skeletal muscle fiber	BP	0.523	CYP26B1	up_VFEM_EC
GO:2001035	0.00441	1	1	1	regulation of tongue muscle cell differentiation	BP	0.523	CYP26B1	up_VFEM_EC
GO:2001037	0.00441	1	1	1	positive regulation of tongue muscle cell	BP	0.523	CYP26B1	up_VFEM_EC
GO:0034653	0.00441	1	1	1	retinoic acid catabolic process	BP	0.523	CYP26B1	up_VFEM_EC
GO:0016202	0.00442	1	2	39	regulation of striated muscle tissue	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0033555	0.00443	0.999	5	13	multicellular organismal response to stress	BP	0.263	RELN,MEF2C,PPP3CA,ALS2,P2RX2	up_VCAV_EC
GO:0060149	0.00443	1	1	4	negative regulation of posttranscriptional gene	BP	0.53	ESR1	up_AORT_VSMC
GO:0060965	0.00443	1	1	4	negative regulation of gene silencing by miRNA	BP	0.53	ESR1	up_AORT_VSMC
GO:0060967	0.00443	1	1	4	negative regulation of gene silencing by RNA	BP	0.53	ESR1	up_AORT_VSMC

GO:1903799	0.00443	1	1	4	negative regulation of production of miRNAs involved in gene silencing	BP	0.53	ESR1	up_AORT_VSMC
GO:0034097	0.00444	0.998	31	238	response to cytokine	BP	0.263	ACKR1,HCLS1,GBP5,KIT,SELE,CXCL8,LAPTM5,CXCR4,MX2,PDGFB,TMEM173,NLRC5,GATA3,IRF8,CASP8,ST3GAL6,MAPK13,IFNGR1,FLNB,OTUD4,CREB1,CNOT7,GCH1,ADIPOR2,RIPK1,LSM14A,HIF1A,KDM3A,ENSCAFG00000002015,ARHGEF2,TJP2	up_VCAV_EC
GO:0006040	0.00444	1	2	12	amino sugar metabolic process	BP	1	OGA,GNPNAT1	up_VPOR_EC
GO:2000729	0.00444	1	1	1	positive regulation of mesenchymal cell proliferation involved in	BP	0.523	SIX1	up_VFEM_EC
GO:2000015	0.00445	1	2	2	regulation of determination of dorsal	BP	0.337	CTNNB1,DDIT3	down_VSAP_EC
GO:0019755	0.00445	1	1	3	one-carbon compound transport	BP	1	CA2	up_VCAV_VSMC
GO:1903078	0.00448	1	2	19	positive regulation of protein localization to	BP	0.548	ACSL3,STX4	down_ACOR_EC
GO:0071310	0.00449	0.999	7	634	cellular response to organic substance	BP	1	NR1H4,MRC1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0061326	0.00449	1	2	41	renal tubule development	BP	0.929	EYA1,HOXA11	up_VFEM_VSMC
GO:0072080	0.00449	1	2	41	nephron tubule development	BP	0.929	EYA1,HOXA11	up_VFEM_VSMC
GO:0030336	0.0045	0.998	15	86	negative regulation of cell migration	BP	0.266	TIE1,ADAMTS9,MEF2C,DLL4,STC1,MMP28,ARAP3,ANGPT2,ENSCAFG00000010224,MCC,APOD,JAG1,HMGB1,ARHGDIB,VASH1	up_VCAV_EC
GO:0043044	0.0045	0.999	5	14	ATP-dependent chromatin remodeling	BP	0.248	SMARCC1,OIP5,SMARCB1,CENPP,MIS18A	down_ACOR_VSMC
GO:0060920	0.0045	1	1	2	cardiac pacemaker cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060926	0.0045	1	1	2	cardiac pacemaker cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035904	0.00451	1	2	25	aorta development	BP	0.523	EYA1,SIX1	up_VFEM_EC
GO:0023052	0.00452	0.997	120	1602	signaling	BP	0.339	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,NR1H4,HSPA5,SERPINE1,SOCS5,SGK1,ERO1A,PRKACB,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CASP3,HYOU1,WSB1,BCAR3,NUAK1,PTPN11,LRRC8A,TRIB3,FARP1,ILK,FHL2,PPP1R12A,PRCP,SMARCA4,SESN2,TGFBR1,PTGS2,REM1,MYO1C,PIK3C2A,CHSY1,UACA,KIF5B,HIF1A,HTR7,CX3CL1,ENSCAFG00000000562,DNAJC10,TNIK,NXN,RGS2,PTPN2,EIF2B1,NEO1,PLCL1,MTDH,ESM1,ADAM17,AGRN,EIF4EBP1,SKAP2,CNOT7,CDH11,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,STARD13,ENSCAFG00000002015,APOE,WWC3,PDE1A,ZC3H15,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,TLN1,CBLC,ATF3,GSK3B,CDC37,ITGB3,SH3GLB1,TAX1BP3,MYO1E,KPNA1,HTT,REST,MAPK10,SH2B3,RDH11,ARFGEF3,CALM1,RAB11FIP1,DISC1,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,ENSCAFG00000018360,HIF1AN,BTK,CDKN1A,LMO7,NRP1,SH3RF3,RHBDF2,USP14,YWHAH,TNFAIP1,MADD,SEC13,KDM3A,MID1	down_VSAP_EC
GO:0006955	0.00452	0.999	5	327	immune response	BP	1	NR1H4,IL18BP,MRC1,CCL24,ARHGEF2	up_VPUL_EC
GO:1905832	0.00452	1	1	2	positive regulation of spindle assembly	BP	1	GPSM2	down_AFEM_EC
GO:1904776	0.00452	1	1	2	regulation of protein localization to cell cortex	BP	1	GPSM2	down_AFEM_EC
GO:1904778	0.00452	1	1	2	positive regulation of protein localization to cell	BP	1	GPSM2	down_AFEM_EC
GO:0072513	0.00452	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	0.983	EYA1	up_AFEM_VSMC
GO:0044381	0.004526718	0.9997	3	13	glucose import in response to insulin	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0048699	0.00453	0.997	36	371	generation of neurons	BP	0.339	ARHGEF2,VEGFA,SIPA1L1,SGK1,CASP3,PTPN11,DPYSL3,HOOK3,IFRD1,KIF5B,HIF1A,SLC45A3,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,APOE,LYN,MMD,GSK3B,VLDLR,SDC4,REST,MAPK10,PRMT1,EXT1,DISC1,PAK2,INHBA,SIX4,NRP1,ARF4,YWHAH	down_VSAP_EC

GO:0120034	0.00454	0.999	6	28	positive regulation of plasma membrane bounded cell projection	BP	0.339	FSCN1,DPYSL3,DYNLL1,ANLN,HTT,NRP1	down_VSAP_EC
GO:0051445	0.00454	0.999	5	14	regulation of meiotic cell cycle	BP	0.25	FBXO5,CDK1,CDC20,TTK,ASPM	down_ACOR_VSMC
GO:0035295	0.00454	1	4	356	tube development	BP	0.842	HOXA3,TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:0051963	0.00455	1	2	26	regulation of synapse assembly	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0046939	0.00456	0.999	5	19	nucleotide phosphorylation	BP	0.339	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0002520	0.00456	1	4	279	immune system development	BP	1	HOXA3,BARX1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0061337	0.00456	1	1	16	cardiac conduction	BP	1	JUP	down_VFEM_VSMC
GO:0003197	0.00457	1	1	16	endocardial cushion development	BP	1	GATA5	down_VFEM_VSMC
GO:0032026	0.00457	1	1	2	response to magnesium ion	BP	0.933	FBP1	up_VFEM_VSMC
GO:1900078	0.004578934	0.99969	3	13	positive regulation of cellular response to	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0001992	0.00458	1	1	1	regulation of systemic arterial blood pressure by	BP	0.528	AVPR1A	up_VFEM_EC
GO:0032502	0.00459	0.999	13	1661	developmental process	BP	1	NR1H4,TBX5,HOXA2,MAPK10,HOXA3,ARHGEF26,ZDHHC16,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:0003208	0.00459	0.999	7	24	cardiac ventricle morphogenesis	BP	0.27	MEF2C,CHD7,DLL4,GATA3,PROX1,JAG1,HIF1A	up_VCAV_EC
GO:0060040	0.0046	1	1	1	retinal bipolar neuron differentiation	BP	0.739	IRX5	up_VSAP_VSMC
GO:0042221	0.00461	0.997	121	1012	response to chemical	BP	0.799	TNNT2,VEGFD,SEMA5A,TLR1,SMAD6,ACTN2,PLCG2,IFNGR1,LEP,LBH,AFF3,GATA5,GATA4,CD83,HTR2B,MBP,FEZ1,SKP2,PRKAA2,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,EIF4A2,ATRX,MED14,HRH1,CASTOR1,TLR3,PPARGC1A,LATS2,LPL,CITED2,TP53INP1,RERG,GLRB,ISG15,CD274,AR,PTGIR,SASH1,SLC2A5,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,KLHL20,ANKRD1,F2RL1,MXRA5,DAPK1,CTSB,BNIP3,EGLN1,NCEH1,AKAP6,P2RX7,CREBRF,NRP1,UBR1,PTPN22,TCN2,NPNT,OS9,UNC5B,STT3B,EVL,APLP1,SLITRK5,PTGDR,SESN3,CCDC3,PRKCE,FZD3,FRS2,AGRN,DAG1,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,JUP,CCL5,CLN8,NR3C1,DUSP22,RAB11B,EDN1,SESN1,OXR1,HPGD,NOD2,LRRC4,ARID5B,FAM107A,DDIT4,JAM3,B2M,ENSCAFG00000018360,JKAMP,TNFRSF11B,HERPUD1,FEZ2,GNAQ,INPP5K,FAF2,PFKL,WFS1,SLC25A12,CAT,DZIP3,SH3BP4,ENSCAFG00000029553,PARK7,STC2,CRKL	up_ACOR_VSMC
GO:0045596	0.00461	0.998	11	186	negative regulation of cell differentiation	BP	1	HOXA9,IRX3,LBH,HOXA7,DLL1,TWIST2,THRB,GREM1,CYLD,AXIN2,KANK1	up_AFEM_EC
GO:0072498	0.00461	1	4	8	embryonic skeletal joint development	BP	1	HOXA11,OSR2,OSR1,SHOX2	up_VSAP_EC
GO:0003161	0.00461	1	1	6	cardiac conduction system development	BP	1	TBX5	up_APUL_VSMC
GO:0007188	0.004621907	0.99927	5	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	0.96436359	PTH1R,GNAO1,PTGIR,PTGER4,GNAZ	up_ACOR_EC
GO:0007189	0.00463	0.999	7	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	0.799	ADRA1B,ADGRD1,ABCA1,PTGIR,ADCY6,APLP1,GNAQ	up_ACOR_VSMC
GO:0098543	0.00463	1	1	4	detection of other organism	BP	0.983	TLR2	up_AFEM_VSMC
GO:0016045	0.00463	1	1	4	detection of bacterium	BP	0.983	TLR2	up_AFEM_VSMC
GO:0070252	0.00464	1	1	17	actin-mediated cell contraction	BP	1	JUP	down_VFEM_VSMC

GO:0007165	0.00466	0.996	172	1496	signal transduction	BP	0.799	SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TLR1,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,IFNGR1,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,ADGRD1,CD83,EFNB2,ANGPT1,ENSCAFG00000016285,HTR2B,RASSF2,MBP,ZRANB1,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,ABCA1,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,RERG,GLRB,ARHGAP29,ZNRF3,CD274,PLPP2,AR,PTGIR,SASH1,GPR155,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ADCY6,ITPR1,GRK7,LIMS2,BLNK,ANKRD1,F2RL1,ADGRL1,CAMK2D,PSEN2,PPP2R5E,DAPK1,ARHGAP5,BNIP3,NCEH1,AKAP6,CDKN1A,JMY,GNA14,CRLF3,CLSTN1,LRRC8C,CREBRF,NRP1,UBR1,PDE1A,PTPN22,DMPK,NPNT,UNC5B,SMPD1,RCAN2,APLP1,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,FZD3,FRS2,AGRN,RND1,SCG5,RGS2,DAG1,FUT8,PARP9,APP,PSEN1,TGFBR1,SYNJ2BP,TESK2,PIK3C3,SIPA1L1,SENP7,CCL5,WWC2,PERP,PSKH1,RTKN2,DUSP22,SIAH1,TIRAP,EDN1,SESN1,HPGD,DUSP26,NOD2,LRRC4,ARID5B,INSYN1,DDIT4,ENSCAFG00000018360,DISC1,DEPDC7,RASGRP2,SH3RF3,SERINC3,TNFRSF11B,NCALD,PPP1R12B,USP20,HERPUD1,GNAQ,	up_ACOR_VSMC
GO:0001944	0.00466	0.998	27	263	vasculature development	BP	0.342	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,LTBP1,PTPN14,ERRFI1,JCAD,PGK1,TMED2,PRCP,PIK3C2A,HIF1A,THBS2,MTDH,ESM1,ACTA2,ADAMTS6,CTNNB1,STARD13,APOE,KLF5,DDIT3,MYO1E,NRP1	down_VSAP_EC
GO:0018208	0.00466	1	3	7	peptidyl-proline modification	BP	0.342	P4HB,P4HA1,PPIB	down_VSAP_EC
GO:0046947	0.00469	1	2	2	hydroxylysine biosynthetic process	BP	0.342	PLOD2,PLOD3	down_VSAP_EC
GO:0046946	0.00469	1	2	2	hydroxylysine metabolic process	BP	0.342	PLOD2,PLOD3	down_VSAP_EC
GO:0048634	0.00469	1	2	40	regulation of muscle organ development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0008593	0.0047	1	1	33	regulation of Notch signaling pathway	BP	1	GATA5	down_AFEM_VSMC
GO:0043502	0.00472	1	1	16	regulation of muscle adaptation	BP	1	GATA5	down_VFEM_VSMC
GO:0090066	0.00473	0.998	24	162	regulation of anatomical structure size	BP	0.276	EDNRB,HCLS1,IL7R,IFRD1,DOCK4,LRRC8D,BAIAP2L1,EDN1,RAB11A,TMOD1,GUCY1A1,MTOR,LRRC8C,SLC12A7,NCKAP1,IQGAP2,SWAP70,NCK1,CREB1,NOS2,ARPC5L,ALS2,HP1BP3,TMOD3	up_VCAV_EC
GO:0009952	0.00473	0.999	6	66	anterior/posterior pattern specification	BP	1	HOXA9,HOXC10,HOXA7,DLL1,HOXA6,AXIN2	up_AFEM_EC
GO:0048645	0.00473	1	1	33	animal organ formation	BP	1	GATA5	down_AFEM_VSMC
GO:0006525	0.00473	1	1	4	arginine metabolic process	BP	0.561	ARG2	up_AORT_VSMC
GO:0006182	0.00474	1	3	4	cGMP biosynthetic process	BP	0.276	NPR1,GUCY1A1,GUCY1B1	up_VCAV_EC
GO:0060216	0.00474	1	1	3	definitive hemopoiesis	BP	0.994	HOXA9	up_AFEM_VSMC
GO:0050778	0.00476	0.998	21	141	positive regulation of immune response	BP	0.277	GBP5,PRKCH,TNFAIP3,TNIP1,TMEM173,PDE4D,MEF2C,TLR4,NLRC5,EIF2B2,GATA3,PELI1,NECTIN2,RIOK3,PRKD2,TLR3,OTUD4,PLCG2,BCL10,HMGB1,LSM14A	up_VCAV_EC
GO:0048869	0.00477	1	5	1119	cellular developmental process	BP	0.562	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0060993	0.00478	1	2	42	kidney morphogenesis	BP	0.943	EYA1,HOXA11	up_VFEM_VSMC
GO:0034629	0.0048	0.999	5	14	cellular protein-containing complex localization	BP	0.26	STXBP6,NDC1,HASPIN,EZR,MIOS	down_ACOR_VSMC
GO:1904262	0.00484	1	4	8	negative regulation of TORC1 signaling	BP	0.822	CASTOR1,SESN3,SESN1,BMT2	up_ACOR_VSMC
GO:0110110	0.00484	1	1	34	positive regulation of animal organ	BP	1	GATA5	down_AFEM_VSMC
GO:0051764	0.00485	1	3	6	actin crosslink formation	BP	0.349	ACTN1,DPYSL3,PLS3	down_VSAP_EC
GO:0010825	0.00486	1	3	5	positive regulation of centrosome duplication	BP	0.261	POC1A,NUP62,PLK4	down_ACOR_VSMC

GO:0007154	0.00487	0.997	121	1622	cell communication	BP	0.349	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,ASNS,NR1H4,HSPA5,SERPINE1,SOCS5,SGK1,ERO1A,PRKACB,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CASP3,HYOU1,WSB1,BCAR3,NUAK1,PTPN11,LRRC8A,TRIB3,FARP1,ILK,FHL2,PPP1R12A,PRCP,SMARCA4,SESN2,TGFBR1,PTGS2,REM1,MYO1C,PIK3C2A,CHSY1,UACA,KIF5B,HIF1A,HTR7,CX3CL1,ENSCAFG00000000562,DNAJC10,TNIK,NXN,RGS2,PTPN2,EIF2B1,NEO1,PLCL1,MTDH,ESM1,ADAM17,AGRN,EIF4EBP1,SKAP2,CNOT7,CDH11,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,STARD13,ENSCAFG00000002015,APOE,WWC3,PDE1A,ZC3H15,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,TLN1,CBLC,ATF3,GSK3B,CDC37,ITGB3,SH3GLB1,TAX1BP3,MYO1E,KPNA1,HTT,REST,MAPK10,EIF2S1,SH2B3,RDH11,ARFGEF3,CALM1,RAB11FIP1,DISC1,PAK2,CREB3L2,LRRTM2,INHBA,CAMK2D,ENSCAFG00000018360,HIF1AN,BTK,CDKN1A,NRP1,SH3RF3,RHBDF2,USP14,YWHAH,TNFAIP1,MADD,SEC13,KDM3A,MID1	down_VSAP_EC
GO:0006284	0.00487	0.999	6	20	base-excision repair	BP	0.261	RPA1,HMGA1,POLE,FEN1,NEIL3,APEX1	down_ACOR_VSMC
GO:0044092	0.004871375	0.99808	15	270	negative regulation of molecular function	BP	0.96436359	NR1H4,PKIB,PCSK1N,IFI6,DUSP26,ACTN2,ARHGAP28,CST3,LRRC15,IFIT2,CLSTN1,LRRC4,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0019471	0.00488	1	3	7	4-hydroxyproline metabolic process	BP	0.349	P4HB,ERO1A,P4HA1	down_VSAP_EC
GO:0019221	0.00488	1	3	102	cytokine-mediated signaling pathway	BP	1	NR1H4,CCL24,FLRT3	up_VPUL_EC
GO:0001657	0.00488	1	2	42	ureteric bud development	BP	0.943	EYA1,HOXA11	up_VFEM_VSMC
GO:0072163	0.00488	1	2	42	mesonephric epithelium development	BP	0.943	EYA1,HOXA11	up_VFEM_VSMC
GO:0072164	0.00488	1	2	42	mesonephric tubule development	BP	0.943	EYA1,HOXA11	up_VFEM_VSMC
GO:0055065	0.00489	1	3	145	metal ion homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:0042127	0.00491	0.999	7	452	regulation of cell proliferation	BP	0.595	ACVRL1,LYN,HOXA3,IGF1R,PDPN,SULF1,STX4	down_ACOR_EC
GO:1902532	0.00491	0.999	4	204	negative regulation of intracellular signal	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0042482	0.00491	1	2	2	positive regulation of odontogenesis	BP	0.284	CD34,BMP2	up_VCAV_EC
GO:0001954	0.00491	1	1	17	positive regulation of cell-matrix adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0016576	0.00491	1	1	2	histone dephosphorylation	BP	0.943	EYA1	up_VFEM_VSMC
GO:0071705	0.00492	0.997	50	582	nitrogen compound transport	BP	0.349	PRICKLE1,MYH9,NR1H4,PLK3,HM13,TRAM1,PTPN14,SLC7A5,SEC24D,PTPN11,SEC23A,SLC38A1,SRP54,MYO1C,ENSCAFG00000031588,SEL1L,HIF1A,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,TFRC,APOE,KPNA4,LYN,SLC7A11,GSK3B,GBP5,KPNA1,REST,SCAMP1,RAB11FIP1,KDELR2,AP3S1,CLTC,STX6,CDKN1A,RHBDF2,YWHAH,BLZF1,SEC13	down_VSAP_EC
GO:0048012	0.00493	1	3	7	hepatocyte growth factor receptor signaling	BP	0.349	PTPN2,ESM1,NRP1	down_VSAP_EC
GO:0090092	0.00494	1	3	72	regulation of transmembrane receptor protein serine/threonine	BP	0.595	ACVRL1,SULF1,ASPN	down_ACOR_EC
GO:0040013	0.004945831	0.99871	8	100	negative regulation of locomotion	BP	0.96436359	SEMA6D,ZMYND8,MMP28,TRIM8,PTGER4,ARHGDIB,TBX5,NRP1	up_ACOR_EC
GO:0090596	0.00496	1	3	84	sensory organ morphogenesis	BP	0.568	EYA1,SIX1,CYP26B1	up_VFEM_EC
GO:1901861	0.00496	1	2	41	regulation of muscle tissue development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0006600	0.00496	1	1	1	creatine metabolic process	BP	0.739	GATM	up_VSAP_VSMC
GO:0006601	0.00496	1	1	1	creatine biosynthetic process	BP	0.739	GATM	up_VSAP_VSMC
GO:0014889	0.00496	1	1	1	muscle atrophy	BP	0.739	GATM	up_VSAP_VSMC
GO:0021675	0.00498	1	2	29	nerve development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:2000136	0.00499	1	1	7	regulation of cell proliferation involved in	BP	1	TBX5	up_APUL_VSMC

GO:0001822	0.004993389	0.9987	8	98	kidney development	BP	0.96436359	SOX9,AQP1,SMAD6,FOXC2,LRP4,CLSTN1,NRP1,PYGO2	up_ACOR_EC
GO:1900120	0.00501	1	1	7	regulation of receptor binding	BP	1	HOXA3	up_APUL_VSMC
GO:0050684	0.00502	0.999	10	46	regulation of mRNA processing	BP	0.266	RNPS1,SRSF2,U2AF2,THRAP3,HNRNPL,SF3B4,RBM14,WTAP,JMJD6,SF3A1	down_ACOR_VSMC
GO:0006886	0.00503	0.997	32	332	intracellular protein transport	BP	0.354	PRICKLE1,PLK3,HM13,TRAM1,PTPN14,SEC24D,PTPN11,SEC23A,SRP54,MYO1C,SEL1L,SSR1,IWS1,ZPR1,STAM2,SMG7,XPOT,USO1,SRPRA,DDX39B,COPG1,KPNB1,COPB2,SRP72,KPNA4,GSK3B,KPNA1,AP3S1,CLTC,STX6,CDKN1A,YWHAH	down_VSAP_EC
GO:0010159	0.00503	1	1	2	specification of animal organ position	BP	1	HOXA3	up_VPOR_VSMC
GO:0051972	0.00504	0.999	6	20	regulation of telomerase activity	BP	0.266	HNRNPD,SLC29A1,AURKB,GREM1,NEK2,CCT4	down_ACOR_VSMC
GO:0051240	0.00504	1	2	489	positive regulation of multicellular organismal	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0009566	0.00504	1	2	24	fertilization	BP	0.739	HOXA11,HOXA9	up_VSAP_VSMC
GO:0043537	0.00505	0.999	5	15	negative regulation of blood vessel endothelial	BP	0.29	MEF2C,DLL4,ANGPT2,HMGB1,VASH1	up_VCAV_EC
GO:0050818	0.00505	1	2	24	regulation of coagulation	BP	0.604	LYN,PDPN	down_ACOR_EC
GO:0061323	0.00505	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0048869	0.00506	0.999	11	1119	cellular developmental process	BP	0.739	HOXA11,HOXA9,PITX1,EMX2,SALL1,HOXC10,IRX5,STIM1,CAV1,SHOX2,GJB5	up_VSAP_VSMC
GO:0007519	0.00508	0.998	10	49	skeletal muscle tissue development	BP	0.291	EPHB1,MEF2C,ATF3,FOXN2,PPP3CA,CAV2,FLNB,NR1D2,P2RX2,CDON	up_VCAV_EC
GO:0048513	0.00508	0.999	9	906	animal organ development	BP	1	NR1H4,TBX5,HOXA3,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:0007275	0.00508	0.999	6	1370	multicellular organism development	BP	1	HOXC10,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:2000112	0.00509	0.999	11	1119	regulation of cellular macromolecule biosynthetic process	BP	0.739	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0010959	0.00509	1	3	79	regulation of metal ion transport	BP	0.739	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0072359	0.00511	0.999	4	368	circulatory system development	BP	0.936	HOXA3,TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:0032490	0.00512	1	1	4	detection of molecule of bacterial origin	BP	1	TLR2	up_AFEM_VSMC
GO:0003285	0.00513	1	1	2	septum secundum development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0009968	0.00514	0.997	37	392	negative regulation of signal transduction	BP	0.359	ARHGEF2,PRICKLE1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,SNX25,HYOU1,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,NXN,RGS2,PTPN2,ADAM17,CNOT7,CTNNB1,APOE,WWC3,LYN,STRAP,DDIT3,CBLC,ATF3,GSK3B,TAX1BP3,HTT,CALM1,HIF1AN,NRP1,TNFAIP1	down_VSAP_EC
GO:0071711	0.00514	1	4	8	basement membrane organization	BP	0.849	FERMT1,CTSS,SPINT2,DAG1	up_ACOR_VSMC
GO:0071696	0.00514	1	3	6	ectodermal placode development	BP	0.359	CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0010460	0.00514	1	2	2	positive regulation of heart rate	BP	0.293	EDN1,GCH1	up_VCAV_EC
GO:0048701	0.00514	1	2	25	embryonic cranial skeleton morphogenesis	BP	0.584	TBX15,SIX1	up_VFEM_EC
GO:0045898	0.00516	1	1	5	regulation of RNA polymerase II transcriptional	BP	0.604	ESR1	up_AORT_VSMC
GO:0010735	0.00518	1	1	2	positive regulation of transcription via serum response element binding	BP	1	NKX2-5	up_VPOR_VSMC
GO:0061035	0.0052	1	2	24	regulation of cartilage development	BP	0.739	HOXA11,SHOX2	up_VSAP_VSMC
GO:0045747	0.0052	1	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	down_VFEM_VSMC
GO:0008643	0.00521	0.999	8	45	carbohydrate transport	BP	0.361	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,SLC2A1,YES1,SLC2A3	down_VSAP_EC
GO:0009111	0.00521	1	1	2	vitamin catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048743	0.00521	1	1	1	positive regulation of skeletal muscle fiber	BP	0.739	SHOX2	up_VSAP_VSMC
GO:0043009	0.00522	0.999	5	227	chordate embryonic development	BP	0.619	ACVRL1,HOXA3,HOXA7,SULF1,HOXA1	down_ACOR_EC
GO:0003128	0.00523	1	1	6	heart field specification	BP	1	GATA5	down_VSAP_VSMC

GO:0003164	0.00523	1	1	2	His-Purkinje system development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003166	0.00523	1	1	2	bundle of His development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0050000	0.00524	0.999	7	27	chromosome localization	BP	0.273	ZW10,BIRC5,KIF22,CDCA8,NDC80,NUP62,ENSCAFG00000005299	down_ACOR_VSMC
GO:0010992	0.00524	1	2	2	ubiquitin recycling	BP	0.273	UBE2S,UBE2C	down_ACOR_VSMC
GO:0010994	0.00524	1	2	2	free ubiquitin chain polymerization	BP	0.273	UBE2S,UBE2C	down_ACOR_VSMC
GO:0009581	0.00524	1	1	18	detection of external stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0009582	0.00524	1	1	18	detection of abiotic stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0051130	0.00526	0.997	42	342	positive regulation of cellular component organization	BP	0.299	EPHB1,TEK,GBP5,SELE,ARHGEF15,ATP8A1,PDGFB,BAIAP2L1,RELN,RAPGEF1,TLR4,GATA3,EDN1,RAB11A,RALB,RAB27A,NEDD9,IRF8,PPP3CA,MTOR,CNOT6,NCKAP1,PROX1,IQGAP2,HMBOX1,PRKD2,SH3GLB1,SWAP70,NCK1,FES,HIST1H1A,RAPGEF2,PLCG2,PAN3,PMAIP1,ARPC5L,SMC5,RAD21,HIF1A,ATRX,ENSCAFG00000002015,FSCN1	up_VCAV_EC
GO:0007389	0.00529	0.998	9	137	pattern specification process	BP	1	HOXA9,IRX3,HOXC10,HOXA7,DLL1,GREM1,GREM2,HOXA6,AXIN2	up_AFEM_EC
GO:0048625	0.00529	1	1	1	myoblast fate commitment	BP	0.739	PITX1	up_VSAP_VSMC
GO:0001845	0.00531	1	2	5	phagolysosome assembly	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0046330	0.00532	0.998	11	47	positive regulation of JNK cascade	BP	0.849	RASSF2,TLR3,SH3RF2,SASH1,F2RL1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0140131	0.00532	1	2	5	positive regulation of lymphocyte chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0017000	0.00532	1	1	4	antibiotic biosynthetic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0043393	0.00533	0.998	15	77	regulation of protein binding	BP	0.849	PLCL1,BMP4,XIRP1,CLSTN1,LRPAP1,SMARCD3,CCPG1,APP,PSEN1,MITD1,AKTIP,B2M,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0072070	0.00534	1	2	5	loop of Henle development	BP	1	IRX3,DLL1	up_AFEM_EC
GO:0003181	0.00534	1	1	7	atrioventricular valve morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0065009	0.00535	0.996	91	735	regulation of molecular function	BP	0.849	TNNT2,ARHGAP28,ACTN2,PLCG2,LEP,PLCL1,MAP3K8,KCNE3,HTR2B,RASSF2,TCAF1,USP6NL,MBP,RECK,BMP4,EVI5L,FGFR2,EIF4A2,SCARB2,TLR3,SH3RF2,XIRP1,PPARGC1A,LATS2,PDE5A,PKP4,AR,SASH1,LMO4,PTPN3,FGF18,CHN2,CDKN2B,CST3,F2RL1,DAPK1,CTSB,EGLN1,CACNB3,AKAP6,CDKN1A,JMY,CLSTN1,LRPAP1,NPNT,ATP7A,SMARCD3,SMPD1,SH3RF1,CCNT1,MARF1,FRS2,CCPG1,PPP1R26,PARP9,APP,PSEN1,SGSM2,JUP,SPINK2,CCL5,DDR2,MITD1,PERP,DUSP22,EDN1,DYNC1I2,AKTIP,DUSP26,NOD2,LRRC4,ARID5B,PRKAG3,B2M,DISC1,FXYD1,DCUN1D4,HERPUD1,SBF2,MAP3K7,INPP5K,WFS1,SH3BP4,DYNC1I1,PARK7,GPATCH2,ZFYVE1,IL18R1,HMBOX1,BVES,LMF1	up_ACOR_VSMC
GO:0002065	0.00535	1	1	37	columnar/cuboidal epithelial cell	BP	1	GATA5	down_AFEM_VSMC
GO:0031399	0.00536	0.997	49	559	regulation of protein modification process	BP	0.366	ARHGEF2,PRICKLE1,VEGFA,HSPA5,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,TRIB3,PUM3,ILK,PPP1R12A,SESN2,PTGS2,IWS1,DNAJC10,TNIK,NXN,PTPN2,SPOPL,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,VLDLR,HTT,CALM1,CDYL,PAK2,INHBA,CDKN1A,NRP1,SH3RF3,MADD,KDM3A,MID1	down_VSAP_EC
GO:0014896	0.00536	1	1	18	muscle hypertrophy	BP	1	GATA5	down_VFEM_VSMC
GO:0014897	0.00536	1	1	18	striated muscle hypertrophy	BP	1	GATA5	down_VFEM_VSMC
GO:0003300	0.00536	1	1	18	cardiac muscle hypertrophy	BP	1	GATA5	down_VFEM_VSMC
GO:0007188	0.00537	0.998	10	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	0.849	ADRA1B,ADGRD1,ABCA1,PTGIR,ADCY6,GNA14,APLP1,SENP7,EDN1,GNAQ	up_ACOR_VSMC
GO:0045814	0.00537	0.999	7	27	negative regulation of gene expression,	BP	0.278	ATAD2,EZH2,UHRF1,SUV39H1,HAT1,HIST2H2AC,H2AFX	down_ACOR_VSMC

GO:0061099	0.00537	0.999	4	13	negative regulation of protein tyrosine kinase	BP	0.366	SOCS5,ERRFI1,PTPN2,CBLC	down_VSAP_EC
GO:0045047	0.00537	0.999	4	14	protein targeting to ER	BP	0.366	TRAM1,SRP54,SRPRA,SRP72	down_VSAP_EC
GO:0072599	0.00537	0.999	4	14	establishment of protein localization to endoplasmic reticulum	BP	0.366	TRAM1,SRP54,SRPRA,SRP72	down_VSAP_EC
GO:0040012	0.00538	0.998	15	303	regulation of locomotion	BP	1	CMKLR1,ANGPT4,HOXA7,PLXNA4,TWIST2,HTR1D,CAMK2A,LRRC15,RECK,TBXA2R,BVES,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0042472	0.00538	1	2	27	inner ear morphogenesis	BP	0.607	EYA1,SIX1	up_VFEM_EC
GO:0046661	0.00538	1	2	45	male sex differentiation	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:1900182	0.00539	0.999	6	33	positive regulation of protein localization to	BP	1	ENSCAFG00000014978,TRIM8,GLI3,PARK7,MAVS,GLIS2	down_VCAV_EC
GO:0045605	0.00539	1	2	5	negative regulation of epidermal cell	BP	1	HOXA7,DLL1	up_AFEM_EC
GO:0051240	0.0054	0.999	6	489	positive regulation of multicellular organismal	BP	1	TBX5,NR1H4,EVI2B,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0008016	0.0054	0.999	5	48	regulation of heart contraction	BP	1	IRX5,CHRM2,THRB,BVES,DMPK	up_AFEM_EC
GO:0048585	0.0054	0.999	5	475	negative regulation of response to stimulus	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0007399	0.00542	0.997	50	564	nervous system development	BP	0.367	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,HSPA5,ETV6,SGK1,PRKACB,CASP3,PTPN11,AARS,DPYSL3,HOOK3,IFRD1,TMED2,ILK,KIF5B,HIF1A,SLC45A3,TNIK,UBA6,ZPR1,UCHL5,EIF2B1,NEO1,UST,CDH11,CTNNB1,APOE,PLOD3,LYN,PDS5B,MMD,GSK3B,VLDLR,SDC4,REST,MAPK10,PRMT1,EXT1,DISC1,PAK2,LRRTM2,INHBA,CAMK2D,SIX4,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0010818	0.00542	1	2	5	T cell chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0043010	0.00543	0.998	16	96	camera-type eye development	BP	0.307	EPHB1,ARHGEF15,CHD7,DLL4,GATA3,TMOD1,PROX1,TSPAN12,SMARCA4,SLC25A25,JAG1,SKIL,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0060736	0.00543	1	1	5	prostate gland growth	BP	0.629	ESR1	up_AORT_VSMC
GO:0046621	0.00543	1	1	8	negative regulation of organ growth	BP	1	TBX5	up_APUL_VSMC
GO:0045088	0.00546	0.998	14	81	regulation of innate immune response	BP	0.307	GBP5,TNFAIP3,TNIP1,TMEM173,TLR4,NLRC5,PELI1,NECTIN2,RIOK3,TLR3,OTUD4,CNOT7,HMGB1,LSM14A	up_VCAV_EC
GO:0003008	0.00546	1	3	336	system process	BP	0.629	HOXC10,WNT7A,ARG2	up_AORT_VSMC
GO:1904377	0.00546	1	2	21	positive regulation of protein localization to cell	BP	0.64	ACSL3,STX4	down_ACOR_EC
GO:0048701	0.00546	1	2	25	embryonic cranial skeleton morphogenesis	BP	0.739	TBX15,IRX5	up_VSAP_VSMC
GO:1904659	0.00547	0.999	7	36	glucose transmembrane transport	BP	0.368	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,YES1,SLC2A3	down_VSAP_EC
GO:0072358	0.00548	1	3	268	cardiovascular system development	BP	1	SLITRK5,C6,TGFBI	up_VCAV_VSMC
GO:0048262	0.00549	1	2	5	determination of dorsal/ventral asymmetry	BP	1	GREM1,GREM2	up_AFEM_EC
GO:0060911	0.00549	1	1	2	cardiac cell fate commitment	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060923	0.00549	1	1	2	cardiac muscle cell fate commitment	BP	1	NKX2-5	up_VPOR_VSMC
GO:0042325	0.005495518	0.99739	22	463	regulation of phosphorylation	BP	0.96436359	PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,TNFRSF19,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,NRP1,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0060056	0.00551	1	2	2	mammary gland involution	BP	0.284	CAV1,B4GALT1	down_ACOR_VSMC
GO:0044062	0.00551	1	2	2	regulation of excretion	BP	0.309	STC1,EDN1	up_VCAV_EC
GO:0021796	0.00552	1	1	1	cerebral cortex regionalization	BP	0.739	EMX2	up_VSAP_VSMC
GO:0045596	0.00553	1	3	186	negative regulation of cell differentiation	BP	0.961	TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0003179	0.00554	1	1	19	heart valve morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:0002920	0.00554	1	1	4	regulation of humoral immune response	BP	1	C6	up_VCAV_VSMC

GO:0006874	0.00555	0.998	17	91	cellular calcium ion homeostasis	BP	0.849	ADRA1B,PLCG2,HTR2B,MICU2,ITPR1,F2RL1,DMPK,PRKCE,APP,PSEN1,CHD7,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,STC2	up_ACOR_VSMC
GO:0048565	0.00555	1	1	38	digestive tract development	BP	1	GATA5	down_AFEM_VSMC
GO:0042325	0.00557	0.997	42	463	regulation of phosphorylation	BP	0.373	ARHGEF2,VEGFA,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,PTPN11,TRIB3,PGAM1,ILK,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,VLDLR,SH3GLB1,HTT,PAK2,INHBA,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0006936	0.00557	0.998	13	74	muscle contraction	BP	0.309	EDNRB,DOCK4,PDE4D,STC1,EDN1,TMOD1,GUCY1A1,ARG2,MTOR,KCNJ2,P2RX2,ATP2A1,TMOD3	up_VCAV_EC
GO:1903708	0.00557	0.998	12	65	positive regulation of hemopoiesis	BP	0.309	HCLS1,IL7R,GATA3,CASP8,ITPKB,FES,JAG1,CREB1,HMGB1,RIPK1,ATP11C,HIF1A	up_VCAV_EC
GO:0048568	0.00557	0.999	4	148	embryonic organ development	BP	0.646	HOXA3,HOXA7,HOXA1,HOXC4	down_ACOR_EC
GO:2000484	0.00557	1	1	4	positive regulation of interleukin-8 secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0055005	0.00557	1	1	2	ventricular cardiac myofibril assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071379	0.00558	1	4	8	cellular response to prostaglandin stimulus	BP	0.849	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0002682	0.00558	1	3	343	regulation of immune system process	BP	0.636	HOXA9,ARG2,ESR1	up_AORT_VSMC
GO:0106106	0.00558	1	2	48	cold-induced thermogenesis	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0120161	0.00558	1	2	48	regulation of cold-induced thermogenesis	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0003263	0.00558	1	1	4	cardioblast proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0000154	0.00559	0.999	5	15	rRNA modification	BP	0.288	NOP56,FBL,ENSCAFG00000019620,NOP58,EMG1	down_ACOR_VSMC
GO:0032649	0.0056	0.999	6	23	regulation of interferon-gamma production	BP	0.309	PDE4D,TLR4,GATA3,IRF8,TLR3,HMGB1	up_VCAV_EC
GO:0051147	0.0056	1	2	44	regulation of muscle cell differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0048645	0.00561	1	2	33	animal organ formation	BP	1	TBX5,HOXA3	up_VPUL_EC
GO:0010092	0.00561	1	1	19	specification of animal organ identity	BP	1	GATA5	down_VFEM_VSMC
GO:0006817	0.00561	1	1	5	phosphate ion transport	BP	0.636	SLC20A2	up_AORT_VSMC
GO:0030195	0.00562	0.999	4	10	negative regulation of blood coagulation	BP	0.309	PDGFB,CD34,KLKB1,TFPI	up_VCAV_EC
GO:1900047	0.00562	0.999	4	10	negative regulation of hemostasis	BP	0.309	PDGFB,CD34,KLKB1,TFPI	up_VCAV_EC
GO:0002831	0.00564	0.998	10	42	regulation of response to biotic stimulus	BP	1	CD274,F2RL1,SASH1,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,PQBP1,MAVS	up_VSAP_EC
GO:0090596	0.00564	1	2	84	sensory organ morphogenesis	BP	1	EYA1,IRX5	up_AFEM_VSMC
GO:0032469	0.00565	0.999	5	13	endoplasmic reticulum calcium ion homeostasis	BP	0.852	ITPR1,APP,PSEN1,HERPUD1,WFS1	up_ACOR_VSMC
GO:2000312	0.00565	1	1	2	regulation of kainate selective glutamate	BP	1	NETO1	up_VFEM_VSMC
GO:0007187	0.00565341	0.99906	5	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	0.96436359	PTH1R,GNAO1,PTGIR,PTGER4,GNAZ	up_ACOR_EC
GO:0001767	0.00567	1	1	2	establishment of lymphocyte polarity	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001768	0.00567	1	1	2	establishment of T cell polarity	BP	1	CYP26B1	up_VPOR_VSMC
GO:0098528	0.00567	1	1	2	skeletal muscle fiber differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:2001016	0.00567	1	1	2	positive regulation of skeletal muscle cell	BP	1	CYP26B1	up_VPOR_VSMC
GO:0002027	0.00568	1	1	20	regulation of heart rate	BP	1	JUP	down_VFEM_VSMC
GO:2000172	0.00568	1	1	2	regulation of branching morphogenesis of a nerve	BP	1	SHOX2	up_VFEM_VSMC
GO:0031349	0.00569	0.998	15	90	positive regulation of defense response	BP	0.312	GBP5,TNFAIP3,TNIP1,TMEM173,MEF2C,TLR4,NLRC5,PELI1,NECTIN2,RIOK3,TLR3,OTUD4,PTGS2,HMGB1,LSM14A	up_VCAV_EC
GO:2001225	0.00569	1	1	4	regulation of chloride transport	BP	1	CA2	up_VCAV_VSMC
GO:0010644	0.00569	1	1	1	cell communication by electrical coupling	BP	0.739	CAV1	up_VSAP_VSMC

GO:0019065	0.00569	1	1	1	receptor-mediated endocytosis of virus by	BP	0.739	CAV1	up_VSAP_VSMC
GO:0033484	0.00569	1	1	1	nitric oxide homeostasis	BP	0.739	CAV1	up_VSAP_VSMC
GO:0044860	0.00569	1	1	1	protein localization to plasma membrane raft	BP	0.739	CAV1	up_VSAP_VSMC
GO:0048550	0.00569	1	1	1	negative regulation of pinocytosis	BP	0.739	CAV1	up_VSAP_VSMC
GO:0072584	0.00569	1	1	1	caveolin-mediated endocytosis	BP	0.739	CAV1	up_VSAP_VSMC
GO:0075509	0.00569	1	1	1	endocytosis involved in viral entry into host cell	BP	0.739	CAV1	up_VSAP_VSMC
GO:0086064	0.00569	1	1	1	cell communication by electrical coupling involved in cardiac	BP	0.739	CAV1	up_VSAP_VSMC
GO:0086098	0.00569	1	1	1	angiotensin-activated signaling pathway	BP	0.739	CAV1	up_VSAP_VSMC
GO:1900085	0.00569	1	1	1	negative regulation of peptidyl-tyrosine	BP	0.739	CAV1	up_VSAP_VSMC
GO:1901844	0.00569	1	1	1	regulation of cell communication by electrical coupling	BP	0.739	CAV1	up_VSAP_VSMC
GO:1901979	0.00569	1	1	1	regulation of inward rectifier potassium	BP	0.739	CAV1	up_VSAP_VSMC
GO:1903596	0.00569	1	1	1	regulation of gap junction assembly	BP	0.739	CAV1	up_VSAP_VSMC
GO:1903598	0.00569	1	1	1	positive regulation of gap junction assembly	BP	0.739	CAV1	up_VSAP_VSMC
GO:1903609	0.00569	1	1	1	negative regulation of inward rectifier potassium channel activity	BP	0.739	CAV1	up_VSAP_VSMC
GO:0010649	0.00569	1	1	1	regulation of cell communication by	BP	0.739	CAV1	up_VSAP_VSMC
GO:0072330	0.0057	0.998	10	68	monocarboxylic acid biosynthetic process	BP	0.378	ASNS,NR1H4,PGK1,TPI1,TRIB3,PGAM1,PTGS2,HIF1A,SLC45A3,ALDOC	down_VSAP_EC
GO:0001823	0.00571	1	2	45	mesonephros development	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0007275	0.00572	1	4	1370	multicellular organism development	BP	1	HOXA3,TBX5,HOXA2,HOXB5	up_APUL_VSMC
GO:0060374	0.00572	1	2	2	mast cell differentiation	BP	0.313	KIT,GATA3	up_VCAV_EC
GO:0003012	0.00574	0.998	15	90	muscle system process	BP	0.313	EDNRB,DOCK4,PDE4D,MEF2C,STC1,EDN1,TMOD1,PPP3CA,GUCY1A1,ARG2,MTOR,KCNJ2,P2RX2,ATP2A1,TMOD3	up_VCAV_EC
GO:2001243	0.00574	1	2	33	negative regulation of intrinsic apoptotic	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0003156	0.00574	1	1	20	regulation of animal organ formation	BP	1	GATA5	down_VFEM_VSMC
GO:0070372	0.00575	0.998	16	85	regulation of ERK1 and ERK2 cascade	BP	0.859	HTR2B,BMP4,FGFR2,FGF18,NDRG2,F2RL1,NRP1,PTPN22,NPNT,FRS2,APP,SYNJ2BP,CCL5,DUSP26,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0061550	0.00575	1	3	6	cranial ganglion development	BP	0.38	CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0051129	0.005750515	0.99786	13	221	negative regulation of cellular component organization	BP	0.96436359	TMOD1,ARHGAP6,RGMA,SMAD6,ARHGAP28,PTGER4,LRP4,CLSTN1,CLU,CHMP4B,NRP1,PRKCD,TUBB4A	up_ACOR_EC
GO:0009615	0.00577	0.998	14	83	response to virus	BP	0.314	MX2,TMEM173,NLRC5,GATA3,SERINC5,ODC1,RIOK3,STMN1,TLR3,OAS3,CNOT7,PMAIP1,LSM14A,IVNS1ABP	up_VCAV_EC
GO:0022027	0.00579	1	2	2	interkinetic nuclear migration	BP	0.314	HOOK3,HHEX	up_VCAV_EC
GO:0010556	0.00581	0.998	11	1137	regulation of macromolecule	BP	0.739	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0006355	0.00581	0.998	10	974	regulation of transcription, DNA-	BP	0.739	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0038166	0.00581	1	1	4	angiotensin-activated signaling pathway	BP	1	CA2	up_VCAV_VSMC
GO:0009790	0.00583	1	3	335	embryo development	BP	0.653	HOXC10,HOXA9,WNT7A	up_AORT_VSMC
GO:0055123	0.00583	1	1	40	digestive system development	BP	1	GATA5	down_AFEM_VSMC
GO:1901228	0.00583	1	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GATA5	up_VCAV_VSMC
GO:0060413	0.00585	1	1	8	atrial septum morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0003283	0.00585	1	1	8	atrial septum development	BP	1	TBX5	up_APUL_VSMC

GO:0002683	0.00586	0.997	19	126	negative regulation of immune system process	BP	0.315	IL7R,ADGRF5,TNFAIP3,NLRC5,MMP28,HOXB8,PELI1,ARG2,ITPKB,RIOK3,THOC1,APOD,OTUD4,CD200,BCL10,CNOT7,HMGB1,CUL4A,TJP2	up_VCAV_EC
GO:0010628	0.00586	0.999	7	527	positive regulation of gene expression	BP	0.739	HOXA11,HOXA9,SALL1,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0072009	0.00586	1	2	48	nephron epithelium development	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0055117	0.00586	1	1	21	regulation of cardiac muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0042325	0.00587	0.996	54	463	regulation of phosphorylation	BP	0.315	EPHB1,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,ATF3,RAPGEF1,TLR4,NLRC5,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,ITPKB,PROX1,MADD,PAK2,PRKD2,SH3GLB1,TLR3,NCK1,LDB2,NSD1,PTGS2,MMD,RAPGEF2,TAOK1,CNOT7,HMGB1,BLM,SPTBN4,RIPK1,ITGA6,RAD17,PDGFD,HIF1A,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0045664	0.00587	0.997	22	144	regulation of neuron differentiation	BP	0.315	EDNRB,IFRD1,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,TCF4,PPP3CA,BMP2,HMG20A,GDPD5,PROX1,NCK1,FES,JAG1,MMD,RAPGEF2,ZC4H2,ZEB1,ARHGEF2,CDON	up_VCAV_EC
GO:0042118	0.00587	1	1	4	endothelial cell activation	BP	1	HOXA9	up_AFEM_VSMC
GO:0030099	0.00588	0.998	16	133	myeloid cell differentiation	BP	0.385	VEGFA,MYH9,ACTN1,CASP3,PTPN11,WDR1,HOXB7,HIF1A,PTPN2,EVI2B,CTNNB1,TFRC,LYN,PRMT1,GLO1,INHBA	down_VSAP_EC
GO:0051216	0.00589	0.998	14	70	cartilage development	BP	1	HOXA11,AXIN2,OSR2,HOXD3,OSR1,ZBTB16,RARG,HOXC4,ZEB1,FBXW4,SULF2,SHOX2,NFIB,TGFBR2	up_VSAP_EC
GO:0032101	0.005891594	0.99801	11	173	regulation of response to external stimulus	BP	0.96436359	NR1H4,FNDC4,NOD2,IL33,RGMA,MMP28,PTGER4,MAVS,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0003180	0.0059	1	1	7	aortic valve morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:1905606	0.00591	1	1	5	regulation of presynapse assembly	BP	0.655	WNT7A	up_AORT_VSMC
GO:0060017	0.00591	1	1	3	parathyroid gland development	BP	0.961	HOXA3	up_VPUL_VSMC
GO:0090090	0.00593	1	2	44	negative regulation of canonical Wnt signaling	BP	1	NKX2-5,ANKRD6	up_VPOR_VSMC
GO:1900424	0.00593	1	1	5	regulation of defense response to bacterium	BP	0.655	ARG2	up_AORT_VSMC
GO:0048706	0.00594	1	2	59	embryonic skeletal system development	BP	0.961	HOXA3,HOXB5	up_VPUL_VSMC
GO:0045637	0.00595	0.998	13	73	regulation of myeloid cell differentiation	BP	0.318	HCLS1,MEF2C,HOXB8,CASP8,MTOR,ITPKB,FES,JAG1,CREB1,RIPK1,CUL4A,HIF1A,TJP2	up_VCAV_EC
GO:0060047	0.00595	0.998	12	57	heart contraction	BP	0.881	TNNT2,ADRA1B,KCNE3,GJA1,PDE5A,DMPK,RNLS,JUP,EDN1,GAA,SLC8A1,BVES	up_ACOR_VSMC
GO:1903506	0.00595	0.998	10	977	regulation of nucleic acid-templated transcription	BP	0.742	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0036005	0.00595	1	1	4	response to macrophage colony-stimulating factor	BP	1	TLR2	up_AFEM_VSMC
GO:0036006	0.00595	1	1	4	cellular response to macrophage colony-	BP	1	TLR2	up_AFEM_VSMC
GO:0051241	0.00596	0.998	16	336	negative regulation of multicellular organismal process	BP	1	HOXA9,CMKLR1,IRX3,HOXC10,CRY2,ANGPT4,HOXA7,DLL1,BPI,TWIST2,THRB,GREM1,CYLD,TBXA2R,AXIN2,KANK1	up_AFEM_EC
GO:0005985	0.00596	1	1	2	sucrose metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0005986	0.00596	1	1	2	sucrose biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0003129	0.00596	1	1	3	heart induction	BP	0.961	GATA5	up_VPUL_VSMC
GO:0042733	0.00598	1	2	27	embryonic digit morphogenesis	BP	0.742	HOXA11,SALL1	up_VSAP_VSMC
GO:0051891	0.00598	1	1	3	positive regulation of cardioblast differentiation	BP	0.961	TBX5	up_VPUL_VSMC
GO:0019220	0.005989672	0.99705	24	525	regulation of phosphate metabolic process	BP	0.96436359	NR1H4,PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,TNFRSF19,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,NRP1,PRKCD,PPP1R26,DBNDD2,CCNYL1	up_ACOR_EC
GO:0051174	0.005989672	0.99705	24	525	regulation of phosphorus metabolic process	BP	0.96436359	NR1H4,PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,TNFRSF19,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,NRP1,PRKCD,PPP1R26,DBNDD2,CCNYL1	up_ACOR_EC

GO:1901213	0.00599	1	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GATA5	down_VSAP_VSMC
GO:0065009	0.006	0.996	79	735	regulation of molecular function	BP	0.318	TEK,HCLS1,KIT,SELE,PPP2R5A,PRKCH,ARHGEF15,TNFAIP3,MAP3K11,AMOT,PDGFB,STK10,TMEM173,RELN,FGD6,PDE4D,MEF2C,RAPGEF1,TLR4,NLRC5,GATA3,EDN1,RALB,CTTNBP2NL,HOMER3,NEDD9,ARHGAP28,PELI1,PPP3CA,CASP8,MTOR,MAP3K3,BMP2,HHEX,CHN2,PREX2,SLK,SH3BP5,CNOT6,PPP1R2,PROX1,IQGAP2,ENSCAFG00000010596,MADD,STMN1,HMBOX1,PAK2,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,LDB2,CD200,NSD1,PTGS2,MMD,RAPGEF2,PLCG2,BCL10,GCH1,HMGB1,TBC1D1,NOS2,PMAIP1,BLM,RIPK1,ITGA6,PDGFD,KDM5A,HIF1A,ALS2,ENSCAFG00000002015,FKBP15,PSMB9,RABGAP1,ARHGEF2,CDON,USP6NL	up_VCAV_EC
GO:0003008	0.006	0.998	16	336	system process	BP	1	IRX5,HOXC10,LEP,CRY2,F5,DLL1,LMCD1,CHRM2,THRB,TMEM100,HTR1D,AVPR1A,TBXA2R,REEP2,BVES,DMPK	up_AFEM_EC
GO:1900122	0.00601	1	1	3	positive regulation of receptor binding	BP	0.961	HOXA3	up_VPUL_VSMC
GO:0002263	0.00602	0.998	13	68	cell activation involved in immune response	BP	0.318	KIT,IL6,TLR4,GATA3,RAB27A,MTOR,SNAP23,THOC1,SWAP70,MFNG,FES,PLCG2,HMGB1	up_VCAV_EC
GO:0031214	0.00602	1	3	45	biomineral tissue development	BP	1	HOXA3,ASPN,ACVR2A	up_VPOR_EC
GO:0090091	0.00602	1	1	3	positive regulation of extracellular matrix	BP	1	FSCN1	down_AFEM_EC
GO:0035637	0.00602	1	1	21	multicellular organismal signaling	BP	1	JUP	down_VFEM_VSMC
GO:0042326	0.00603	0.999	4	163	negative regulation of phosphorylation	BP	0.69	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0001501	0.00603	1	2	178	skeletal system development	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0032675	0.00603	1	2	34	regulation of interleukin-6 production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0061343	0.00603	1	1	3	cell adhesion involved in heart morphogenesis	BP	0.961	GATA5	up_VPUL_VSMC
GO:1901605	0.00604	0.998	10	67	alpha-amino acid metabolic process	BP	0.39	P4HB,ASNS,PLOD2,NR1H4,ERO1A,P4HA1,NMNAT2,ALDH18A1,PLOD3,BCAT1	down_VSAP_EC
GO:0010596	0.00604	1	1	21	negative regulation of endothelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:2001141	0.00605	0.998	10	979	regulation of RNA biosynthetic process	BP	0.746	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0072513	0.00605	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	0.961	TBX5	up_VPUL_VSMC
GO:0038084	0.00606	0.999	4	13	vascular endothelial growth factor signaling	BP	0.39	VEGFA,JCAD,MYO1C,NRP1	down_VSAP_EC
GO:0030516	0.00606	1	2	15	regulation of axon extension	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0003214	0.00606	1	1	3	cardiac left ventricle morphogenesis	BP	0.961	TBX5	up_VPUL_VSMC
GO:0021615	0.00609	1	1	3	glossopharyngeal nerve morphogenesis	BP	0.961	HOXA3	up_VPUL_VSMC
GO:0045617	0.00611	1	1	3	negative regulation of keratinocyte	BP	1	SRSF6	down_AFEM_EC
GO:0021889	0.00611	1	1	3	olfactory bulb interneuron	BP	0.961	SLIT2	up_VPUL_VSMC
GO:0021891	0.00611	1	1	3	olfactory bulb interneuron development	BP	0.961	SLIT2	up_VPUL_VSMC
GO:0051093	0.00612	0.997	35	273	negative regulation of developmental process	BP	0.322	EPHB1,PLK2,EDNRB,TEK,ARHGEF15,IFRD1,TIE1,ADAMTS9,AMOT,PDGFB,FERMT1,DLL4,GPR4,GATA3,HOXB8,PPP3CA,HOOK3,MAP3K3,BMP2,HMG20A,HHEX,ITPKB,ANGPT2,THOC1,JAG1,RAPGEF2,CTNNA1,HMGB1,SKIL,ARHGDIB,CUL4A,HIF1A,VASH1,ZEB1,TJP2	up_VCAV_EC
GO:0009887	0.00612	0.999	5	314	animal organ morphogenesis	BP	1	TBX5,HOXA3,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0021957	0.00612	1	1	3	corticospinal tract morphogenesis	BP	0.961	SLIT2	up_VPUL_VSMC
GO:0022028	0.00613	1	1	3	tangential migration from the subventricular zone to the olfactory bulb	BP	0.961	SLIT2	up_VPUL_VSMC
GO:0050707	0.006138209	0.99896	5	44	regulation of cytokine secretion	BP	0.96436359	NR1H4,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0032612	0.00614	0.999	6	22	interleukin-1 production	BP	0.322	GBP5,TNFAIP3,TLR4,ARG2,ABCA1,HMGB1	up_VCAV_EC

GO:0050923	0.00614	1	2	2	regulation of negative chemotaxis	BP	1	SLIT2,PLXNA4	up_VSAP_EC
GO:0048742	0.00615	1	1	2	regulation of skeletal muscle fiber development	BP	1	SHOX2	up_VFEM_VSMC
GO:1990845	0.00616	1	2	51	adaptive thermogenesis	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0045931	0.00617	0.998	10	49	positive regulation of mitotic cell cycle	BP	0.313	BIRC5,CDK1,CDK4,NDC80,NUP62,DTL,ENSCAFG00000005299,UBE2C,MTBP,GEN1	down_ACOR_VSMC
GO:0046640	0.00617	1	1	6	regulation of alpha-beta T cell proliferation	BP	0.674	ARG2	up_AORT_VSMC
GO:0051494	0.006182931	0.99895	5	44	negative regulation of cytoskeleton organization	BP	0.96436359	TMOD1,ARHGAP6,ARHGAP28,PRKCD,TUBB4A	up_ACOR_EC
GO:0106106	0.00619	1	2	48	cold-induced thermogenesis	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0120161	0.00619	1	2	48	regulation of cold-induced thermogenesis	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0098581	0.00619	1	1	5	detection of external biotic stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0060444	0.00619	1	1	5	branching involved in mammary gland duct	BP	0.674	ESR1	up_AORT_VSMC
GO:0043500	0.0062	1	1	21	muscle adaptation	BP	1	GATA5	down_VFEM_VSMC
GO:0048856	0.00622	0.999	9	1533	anatomical structure development	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0002260	0.00622	0.999	5	15	lymphocyte homeostasis	BP	0.326	TNFAIP3,MEF2C,BCL10,SKIL,HIF1A	up_VCAV_EC
GO:0060429	0.00622	1	3	341	epithelium development	BP	0.674	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0051492	0.006238924	0.99921	4	28	regulation of stress fiber assembly	BP	0.96436359	ARHGAP6,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0007517	0.00624	0.997	16	100	muscle organ development	BP	0.326	EPHB1,MEF2C,ATF3,CHD7,DLL4,EDN1,FOXN2,PPP3CA,BMP2,CAV2,PROX1,FLNB,CREB1,NR1D2,P2RX2,CDON	up_VCAV_EC
GO:0034695	0.00624	0.999	4	8	response to prostaglandin E	BP	0.896	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0001942	0.00625738	0.99921	4	28	hair follicle development	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0022404	0.00625738	0.99921	4	28	molting cycle process	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0022405	0.00625738	0.99921	4	28	hair cycle process	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0051222	0.006271917	0.9983	8	103	positive regulation of protein transport	BP	0.96436359	NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,MAVS,PRKCD	up_ACOR_EC
GO:0007015	0.00628	0.997	17	144	actin filament organization	BP	0.4	ARHGEF2,ACTN1,VASP,TPM4,FSCN1,DPYSL3,WDR1,TMSB10,ACTR3,TWF1,PLEKHG2,PLS3,CAPG,NRP1,ENSCAFG00000030508,TNFAIP1,MYBPC2	down_VSAP_EC
GO:0002062	0.00628	1	2	48	chondrocyte differentiation	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0010002	0.00628	1	1	9	cardioblast differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0003140	0.00629	1	1	3	determination of left/right asymmetry in	BP	1	CITED2	down_VPOR_EC
GO:0030182	0.0063	0.997	32	327	neuron differentiation	BP	0.4	ARHGEF2,SIPA1L1,SGK1,CASP3,PTPN11,DPYSL3,IFRD1,KIF5B,HIF1A,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,APOE,LYN,MMD,GSK3B,VLDLR,SDC4,REST,MAPK10,PRMT1,EXT1,DISC1,PAK2,INHBA,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0051480	0.0063	1	2	50	regulation of cytosolic calcium ion concentration	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0031291	0.00632	1	1	3	Ran protein signal transduction	BP	1	GPSM2	down_AFEM_EC
GO:0044089	0.00634	0.997	24	170	positive regulation of cellular component biogenesis	BP	0.329	EPHB1,TEK,GBP5,ARHGEF15,BAIAP2L1,TLR4,EDN1,RALB,IRF8,MTOR,CNOT6,NCKAP1,PROX1,IQGAP2,SH3GLB1,SWAP70,NCK1,LDB2,FES,PAN3,PMAIP1,ARPC5L,ENSCAFG00000002015,FSCN1	up_VCAV_EC
GO:0030326	0.00637	1	2	51	embryonic limb morphogenesis	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:0035113	0.00637	1	2	51	embryonic appendage morphogenesis	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:0008645	0.00638	0.999	7	37	hexose transmembrane transport	BP	0.401	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,YES1,SLC2A3	down_VSAP_EC
GO:0015749	0.00638	0.999	7	37	monosaccharide transmembrane transport	BP	0.401	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,YES1,SLC2A3	down_VSAP_EC
GO:0034219	0.00638	0.999	7	37	carbohydrate transmembrane transport	BP	0.401	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,YES1,SLC2A3	down_VSAP_EC
GO:0045653	0.00638	1	1	3	negative regulation of megakaryocyte	BP	1	GABPA	down_AFEM_EC

GO:0009617	0.0064	0.997	22	133	response to bacterium	BP	0.896	VEGFD,TLR1,PLCG2,TMEM255A,COCH,ABCA1,ISG15,PTGIR,SASH1,PLAC8B,ANKRD1,F2RL1,BNIP3,SLC17A5,GPM6A,PRKCE,CHD7,NOD2,NAALADL2,B2M,TNFRSF11B,WASL	up_ACOR_VSMC
GO:0032535	0.0064	0.997	20	128	regulation of cellular component size	BP	0.331	HCLS1,IL7R,IFRD1,LRRC8D,BAIAP2L1,EDN1,RAB11A,TMOD1,MTOR,LRRC8C,SLC12A7,NCKAP1,IQGAP2,SWAP70,NCK1,CREB1,ARPC5L,ALS2,HP1BP3,TMOD3	up_VCAV_EC
GO:0035519	0.0064	1	2	2	protein K29-linked ubiquitination	BP	0.323	UBE2S,UBE2T	down_ACOR_VSMC
GO:0031589	0.00641	0.999	3	93	cell-substrate adhesion	BP	0.713	HOXA7,TIAM1,RADIL	up_VFEM_EC
GO:0032388	0.006414809	0.99865	6	62	positive regulation of intracellular transport	BP	0.96436359	CDH3,KCNB1,EDEM2,ACTN2,MAVS,PRKCD	up_ACOR_EC
GO:0048856	0.00643	0.999	9	1533	anatomical structure development	BP	1	HOXC10,EYA1,GATM,HOXA9,SPINK5,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0043271	0.00643	1	2	28	negative regulation of ion transport	BP	0.718	HOXA3,NEDD4	down_ACOR_EC
GO:0060442	0.00645	1	1	6	branching involved in prostate gland	BP	0.681	ESR1	up_AORT_VSMC
GO:0071392	0.00645	1	1	6	cellular response to estradiol stimulus	BP	0.681	ESR1	up_AORT_VSMC
GO:0048245	0.00645	1	1	2	eosinophil chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0060675	0.00646	0.999	6	29	ureteric bud morphogenesis	BP	0.403	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0048752	0.00646	1	1	5	semicircular canal morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0070920	0.00646	1	1	6	regulation of production of small RNA involved in gene silencing by RNA	BP	0.681	ESR1	up_AORT_VSMC
GO:1903798	0.00646	1	1	6	regulation of production of miRNAs involved in gene silencing by miRNA	BP	0.681	ESR1	up_AORT_VSMC
GO:0030216	0.00647	1	2	29	keratinocyte differentiation	BP	0.715	HOXA7,CYP26B1	up_VFEM_EC
GO:0051865	0.00648	0.998	8	31	protein autoubiquitination	BP	0.896	SH3RF2,SASH1,MARCH5,SH3RF1,RNF141,SH3RF3,RNF181,CNOT4	up_ACOR_VSMC
GO:0072132	0.00648	1	1	23	mesenchyme morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:0007268	0.00649	0.997	22	130	chemical synaptic transmission	BP	0.896	PLCL1,FBXL20,HRH1,GLRB,STX11,TMEM108,EGLN1,CACNB3,SLC12A7,DMPK,SLITRK5,PRKCE,RNF19A,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,INSYN1,PREPL,PARK7	up_ACOR_VSMC
GO:0098916	0.00649	0.997	22	130	anterograde trans-synaptic signaling	BP	0.896	PLCL1,FBXL20,HRH1,GLRB,STX11,TMEM108,EGLN1,CACNB3,SLC12A7,DMPK,SLITRK5,PRKCE,RNF19A,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,INSYN1,PREPL,PARK7	up_ACOR_VSMC
GO:0007175	0.0065	1	3	7	negative regulation of epidermal growth factor-activated receptor activity	BP	0.403	SOCS5,ERRFI1,CBLC	down_VSAP_EC
GO:2000272	0.0065	1	3	7	negative regulation of signaling receptor activity	BP	0.403	SOCS5,ERRFI1,CBLC	down_VSAP_EC
GO:0030048	0.00651	1	1	23	actin filament-based movement	BP	1	JUP	down_VFEM_VSMC
GO:0046326	0.006517214	0.99949	3	15	positive regulation of glucose import	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0031334	0.00653	0.997	14	84	positive regulation of protein complex assembly	BP	0.335	GBP5,BAIAP2L1,TLR4,IRF8,MTOR,CNOT6,NCKAP1,IQGAP2,NCK1,FES,PAN3,PMAIP1,ARPC5L,FSCN1	up_VCAV_EC
GO:1903587	0.00654	1	3	5	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	0.335	DLL4,APLNR,JCAD	up_VCAV_EC
GO:1902202	0.00655	1	2	3	regulation of hepatocyte growth factor receptor	BP	0.404	PTPN2,ESM1	down_VSAP_EC
GO:0035295	0.00656	1	3	356	tube development	BP	0.688	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0098742	0.00656	1	1	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5	down_AFEM_VSMC
GO:0019722	0.00658	0.998	9	45	calcium-mediated signaling	BP	0.335	EDNRB,SELP,CXCR4,PDE4D,EDN1,HOMER3,PPP3CA,MTOR,MCU	up_VCAV_EC

GO:0048513	0.00659	0.996	73	906	animal organ development	BP	0.404	PRICKLE1,VEGFA,SULF1,SERPINH1,MYH9,NR1H4,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,LTBP1,ERRFI1,CASP3,BCAR3,PTPN11,AARS,FLNB,ENSCAFG00000032470,HOOK3,TMED2,ILK,FHL2,SMARCA4,TGFBR1,PTGS2,WDR1,CHSY1,MSN,HOXB7,HIF1A,SLC20A1,ACTG2,UBA6,ZPR1,PTPN2,UCHL5,EVI2B,ACTA2,ADAMTS6,MAGED1,CTNNB1,ANLN,CRYAB,TFRC,PLOD3,KLF5,LYN,STRAP,PDS5B,PLS3,ATF3,GSK3B,VLDLR,NEXN,MYO1E,SDC4,HTT,REST,PRMT1,SH2B3,EXT1,GLO1,DISC1,CREB3L2,INHBA,BTK,SIX4,NRP1,SPINK2,RTCB,HOMER1	down_VSAP_EC
GO:0002009	0.00659	0.997	20	177	morphogenesis of an epithelium	BP	0.404	PRICKLE1,SULF1,PRKACB,PTK7,EXOC5,ENSCAFG00000032470,TMED2,ILK,WDR1,MSN,HOXB7,HIF1A,ADAM17,MAGED1,CTNNB1,STARD13,PLOD3,SDC4,SIX4,NRP1	down_VSAP_EC
GO:0061448	0.00659	0.999	3	89	connective tissue development	BP	0.781	HOXA11,PITX1,SHOX2	up_VSAP_VSMC
GO:0034654	0.0066	0.999	8	1236	nucleobase-containing compound biosynthetic	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0021697	0.00661	1	1	6	cerebellar cortex formation	BP	0.688	WNT7A	up_AORT_VSMC
GO:0060017	0.00661	1	1	3	parathyroid gland development	BP	1	HOXA3	up_VPOR_VSMC
GO:0060538	0.00662	0.998	10	51	skeletal muscle organ development	BP	0.335	EPHB1,MEF2C,ATF3,FOXN2,PPP3CA,CAV2,FLNB,NR1D2,P2RX2,CDON	up_VCAV_EC
GO:0003148	0.00662	0.999	5	13	outflow tract septum morphogenesis	BP	0.898	SMAD6,BMP4,FGFR2,NRP1,TBX20	up_ACOR_VSMC
GO:0030201	0.00662	0.999	4	12	heparan sulfate proteoglycan metabolic	BP	0.405	SULF1,ENSCAFG00000032470,CTNNB1,EXT1	down_VSAP_EC
GO:2000026	0.00663	1	2	560	regulation of multicellular organismal development	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0006939	0.00663	1	2	32	smooth muscle contraction	BP	1	HTR7,NPNT	up_APUL_EC
GO:0048844	0.00663	1	2	30	artery morphogenesis	BP	0.727	EYA1,SIX1	up_VFEM_EC
GO:0045651	0.00664	1	3	6	positive regulation of macrophage	BP	0.335	HCLS1,CASP8,RIPK1	up_VCAV_EC
GO:0009888	0.00665	0.996	62	545	tissue development	BP	0.335	EPHB1,EDNRB,HOXB7,PRKCH,IFRD1,ADAMTS9,PDGFB,PODXL,PDE4D,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,GPR4,STC1,GATA3,EDN1,NTN4,FOXN2,SOX18,TMOD1,PPP3CA,MTSS1,ARG2,MTOR,BMP2,HHEX,CAV2,BMP2K,PROX1,ENSCAFG00000010596,ARID4B,FLNB,APOD,BTBD7,EXOC5,TIMELESS,HOXB5,LDB2,SLC25A25,JAG1,PTGS2,RAPGEF2,CREB1,BCL10,BASP1,NUP133,ITGA6,SKIL,NR1D2,HIF1A,ATRX,ALDH1A3,P2RX2,LUZP1,RBBP6,ZEB1,FBXO5,CDON	up_VCAV_EC
GO:0072593	0.00665	0.998	12	68	reactive oxygen species metabolic process	BP	0.335	PRCP,PDGFB,CD34,TLR4,NOS3,RAB27A,ARG2,GCH1,NOS2,PMAIP1,RIPK1,HIF1A	up_VCAV_EC
GO:0007098	0.00665	0.998	11	56	centrosome cycle	BP	0.333	HAUS8,NEK2,POC1A,WDR62,NUP62,PLK4,CDK2,SASS6,RBM14,KIF11,GEN1	down_ACOR_VSMC
GO:0010768	0.00665	1	1	1	negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage	BP	0.718	NEDD4	down_ACOR_EC
GO:0019089	0.00665	1	1	1	transmission of virus	BP	0.718	NEDD4	down_ACOR_EC
GO:0044007	0.00665	1	1	1	dissemination or transmission of symbiont	BP	0.718	NEDD4	down_ACOR_EC
GO:0044111	0.00665	1	1	1	development involved in symbiotic interaction	BP	0.718	NEDD4	down_ACOR_EC
GO:0051821	0.00665	1	1	1	dissemination or transmission of organism from other organism	BP	0.718	NEDD4	down_ACOR_EC
GO:0006355	0.00666	0.999	5	974	regulation of transcription, DNA-	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0010959	0.00666	0.999	3	79	regulation of metal ion transport	BP	0.718	LYN,HOXA3,NEDD4	down_ACOR_EC
GO:0045764	0.00666	1	1	2	positive regulation of cellular amino acid	BP	1	NR1H4	up_VPUL_EC

GO:0033043	0.00667	0.996	53	446	regulation of organelle organization	BP	0.333	FSCN1,SREBF1,STXBP6,ATAD2,HNRNPD,SMC1A,ZW10,CAPG,TRIP13,SLC25A5,SDC1,FBXO5,PRELID1,BIRC5,INSIG1,LIMA1,NF2,AURKB,STMN1,NEK2,FEN1,RCC1,UHRF1,POC1A,BRCA1,NOC2L,PREB,CDC6,NDC80,RAC1,NUP62,PDXP,PLK4,IQGAP2,CDC42EP4,SMC3,STAG1,ENSCAFG00000005299,EZR,BUB1,RBM14,CORO1A,CDC20,TTK,ARPC1B,ARHGEF2,KIF11,TADA2A,TINF2,UBE2C,CCT4,MTBP,GEN1	down_ACOR_VSMC
GO:0009887	0.00668	0.999	4	314	animal organ morphogenesis	BP	1	HOXA3,NKX2-5,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0007064	0.00669	0.999	5	15	mitotic sister chromatid cohesion	BP	0.333	SMC1A,ENSCAFG00000017264,SGO1,HASPIN,CDC20	down_ACOR_VSMC
GO:0044093	0.0067	0.996	51	437	positive regulation of molecular function	BP	0.336	TEK,HCLS1,KIT,SELE,PRKCH,MAP3K11,PDGFB,STK10,TMEM173,RELN,MEF2C,RAPGEF1,TLR4,GATA3,EDN1,RALB,NEDD9,PPP3CA,CASP8,MAP3K3,BMP2,SLK,CNOT6,PROX1,MADD,STMN1,HMBOX1,PAK2,PRKD2,SH3GLB1,SMARCA4,TLR3,MFNG,CD200,MMD,RAPGEF2,PLCG2,BCL10,GCH1,HMGB1,TBC1D1,NOS2,PMAIP1,RIPK1,ITGA6,PDGFD,ALS2,ENSCAFG00000002015,RABGAP1,ARHGEF2,USP6NL	up_VCAV_EC
GO:0051928	0.0067	1	2	28	positive regulation of calcium ion transport	BP	0.781	STIM1,CAV1	up_VSAP_VSMC
GO:0008643	0.006709349	0.99883	5	45	carbohydrate transport	BP	0.96436359	NR1H4,AQP1,ENSCAFG00000004331,PLS1,RARRES2	up_ACOR_EC
GO:0001767	0.00672	1	1	2	establishment of lymphocyte polarity	BP	0.727	CYP26B1	up_VFEM_EC
GO:0001768	0.00672	1	1	2	establishment of T cell polarity	BP	0.727	CYP26B1	up_VFEM_EC
GO:0034969	0.00672	1	1	2	histone arginine methylation	BP	1	NR1H4	up_VPUL_EC
GO:0050793	0.00673	0.999	4	731	regulation of developmental process	BP	0.697	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0021602	0.00673	1	2	16	cranial nerve morphogenesis	BP	1	HOXA3,SEMA3A	up_VPOR_EC
GO:0097306	0.00673	1	1	22	cellular response to alcohol	BP	1	JUP	down_VFEM_VSMC
GO:0010959	0.00674	0.997	15	79	regulation of metal ion transport	BP	0.898	ACTN2,PLCG2,KCNE3,SARAF,PTPN3,CACNB3,AKAP6,DMPK,PRKCE,CHD7,B2M,FXYD1,INPP5K,WFS1,STC2	up_ACOR_VSMC
GO:0055022	0.00674	1	1	2	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0060044	0.00674	1	1	2	negative regulation of cardiac muscle cell	BP	1	TBX5	up_VPUL_EC
GO:0061117	0.00674	1	1	2	negative regulation of heart growth	BP	1	TBX5	up_VPUL_EC
GO:0035909	0.00675	0.999	5	14	aorta morphogenesis	BP	0.337	ADAMTS9,CHD7,DLL4,PROX1,JAG1	up_VCAV_EC
GO:0042473	0.00675	1	1	5	outer ear morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:1903506	0.00676	0.999	5	977	regulation of nucleic acid-templated transcription	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC

GO:1901564	0.00677	0.995	144	2053	organonitrogen compound metabolic process	BP	0.411	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,HM13,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,ENSCAFG00000028814,TRIB3,PGAM1,PUM3,UGCG,PM20D2,ILK,ALDH1L2,PPP1R12A,PRCP,SESN2,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,HIF1A,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,YARS,TARS,YES1,PLCL1,TTLL7,NARS,ADAM17,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,CDK8,APOE,PLOD3,USP48,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,AK5,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,SPOP,CALM1,RAB11FIP1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,CAMK2D,HIF1AN,BTK,MSRB3,CDKN1A,TMTC3,RSL24D1,NRP1,SPINK2,SH3RF3,RHBDF2,USP14,ARF4,BCAT1,TNFAIP1,MADD,RPN1,KDM3A,MID1,CMPK1	down_VSAP_EC
GO:0072615	0.00677	1	1	2	interleukin-17 secretion	BP	1	NR1H4	up_VPUL_EC
GO:0032682	0.00678	1	1	7	negative regulation of chemokine production	BP	0.697	ARG2	up_AORT_VSMC
GO:0010159	0.00678	1	1	2	specification of animal organ position	BP	1	HOXA3	up_VPUL_EC
GO:0035556	0.00679	0.995	103	845	intracellular signal transduction	BP	0.898	FGF13,ADRA1B,PLCG2,LEP,PLCL1,MAP3K8,MID1,ADGRD1,ENSCAFG00000016285,HTR2B,RASSF2,MBP,C28H10orf71,NACC2,PRKAA2,BMP4,FGFR2,ABCA1,DOCK3,ATRX,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,ARHGAP29,PTGIR,SASH1,GPR155,FGF18,ARHGEF26,NDRG2,CHN2,ADCY6,ITPR1,BLNK,ANKRD1,F2RL1,CAMK2D,PSEN2,DAPK1,BNIP3,AKAP6,CDKN1A,JMY,CRLF3,NRP1,UBR1,PTPN22,DMPK,NPNT,UNC5B,SMPD1,RCAN2,APLP1,SESN3,SH3RF1,PRKCE,FRS2,RND1,DAG1,PARP9,APP,PSEN1,TGFBR1,SYNJ2BP,TESK2,PIK3C3,SIPA1L1,CCL5,WWC2,PERP,PSKH1,DUSP22,SIAH1,EDN1,SESN1,DUSP26,NOD2,LRRC4,DDIT4,DISC1,DEPDC7,RASGRP2,SH3RF3,SERINC3,NCALD,HERPUD1,GNAQ,MAP3K7,INPP5K,BMT2,WFS1,DOCK5,SH3BP4,ENSCAFG00000029553,PARK7,TEAD1,IL18R1,PAG1,CRKL,PIK3C2A,ZMAT3	up_ACOR_VSMC
GO:2000738	0.00679	1	1	9	positive regulation of stem cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:1990845	0.0068	1	2	51	adaptive thermogenesis	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0010988	0.0068	1	1	2	regulation of low-density lipoprotein particle	BP	1	NR1H4	up_VPUL_EC
GO:0003164	0.00681	1	1	2	His-Purkinje system development	BP	1	TBX5	up_VPUL_EC
GO:0003166	0.00681	1	1	2	bundle of His development	BP	1	TBX5	up_VPUL_EC
GO:0002456	0.00682	0.999	6	23	T cell mediated immunity	BP	0.34	IL7R,GATA3,RAB27A,NECTIN2,JAG1,HMGB1	up_VCAV_EC
GO:0009887	0.00682	0.999	4	314	animal organ morphogenesis	BP	1	EYA1,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:2000416	0.00682	1	1	2	regulation of eosinophil migration	BP	1	CCL24	up_VPUL_EC
GO:2001141	0.00683	0.999	5	979	regulation of RNA biosynthetic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0030540	0.00684	1	1	5	female genitalia development	BP	0.699	ESR1	up_AORT_VSMC
GO:0009790	0.00685	0.999	4	335	embryo development	BP	1	HOXC10,HOXA9,HOXC6,DUSP2	up_AORT_EC
GO:1902959	0.00685	1	1	2	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein	BP	0.718	LYN	down_ACOR_EC

GO:1902961	0.00685	1	1	2	positive regulation of aspartic-type endopeptidase activity involved in amyloid	BP	0.718	LYN	down_ACOR_EC
GO:1905245	0.00685	1	1	2	regulation of aspartic-type peptidase activity	BP	0.718	LYN	down_ACOR_EC
GO:1905247	0.00685	1	1	2	positive regulation of aspartic-type peptidase	BP	0.718	LYN	down_ACOR_EC
GO:1902714	0.00685	1	1	2	negative regulation of interferon-gamma	BP	1	NR1H4	up_VPUL_EC
GO:0060688	0.00686	1	2	29	regulation of morphogenesis of a	BP	0.738	HOXB7,SIX1	up_VFEM_EC
GO:0007010	0.006870002	0.99673	21	441	cytoskeleton organization	BP	0.96436359	MYOZ2,TMOD1,BRSK1,RHOU,ARHGAP6,AQP1,SYNPO2,DIXDC1,PDLIM3,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,ELMO2,DCLK2,CHMP4B,NRP1,PRKCD,TUBB4A	up_ACOR_EC
GO:1905114	0.006879945	0.99777	10	150	cell surface receptor signaling pathway involved in cell-cell	BP	0.96436359	CDH3,SOX9,PORCN,FZD5,DIXDC1,INSYN1,MAPK8IP2,LRP4,CLSTN1,PYGO2	up_ACOR_EC
GO:0060214	0.00688	1	2	2	endocardium formation	BP	0.341	SOX18,PROX1	up_VCAV_EC
GO:0032680	0.00688	1	2	36	regulation of tumor necrosis factor production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0003015	0.00689	0.998	12	58	heart process	BP	0.898	TNNT2,ADRA1B,KCNE3,GJA1,PDE5A,DMPK,RNLS,JUP,EDN1,GAA,SLC8A1,BVES	up_ACOR_VSMC
GO:0042307	0.00689	1	1	23	positive regulation of protein import into	BP	1	JUP	down_VFEM_VSMC
GO:0070858	0.00691	1	1	2	negative regulation of bile acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:1904252	0.00691	1	1	2	negative regulation of bile acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0006888	0.00692	0.998	8	49	ER to Golgi vesicle-mediated transport	BP	0.418	SEC24D,HYOU1,SEC23A,LMAN1,YIPF5,COPB2,CREB3L2,SEC13	down_VSAP_EC
GO:0014066	0.00693	0.998	7	26	regulation of phosphatidylinositol 3-	BP	0.343	TEK,HCLS1,SELP,PDGFB,RELN,PDGFD,RGL2	up_VCAV_EC
GO:0071447	0.00693	1	3	5	cellular response to hydroperoxide	BP	0.898	TP53INP1,DAPK1,OXR1	up_ACOR_VSMC
GO:0006972	0.00693	1	1	2	hyperosmotic response	BP	1	ARHGEF2	up_VPUL_EC
GO:0071474	0.00693	1	1	2	cellular hyperosmotic response	BP	1	ARHGEF2	up_VPUL_EC
GO:0065003	0.00694	0.995	68	616	protein-containing complex assembly	BP	0.342	ACSL3,FSCN1,HMGB1,IRAK1,STXBP6,USP4,HMGCR,EDC3,UBE2S,RRM1,ZW10,CAPG,CENPA,SLC29A1,NDC1,CENPN,C1QTNF6,FBXO5,PSMD13,INSIG1,PRMT1,CAV1,RAD51,TK1,STMN1,CENPO,RCC1,DHX33,GMNN,CENPH,CENPI,FASTKD3,B4GALT1,FARSA,PREB,OIP5,IPO4,HIST1H1A,RAC1,DDX28,FOSL1,IQGAP2,SAMM50,HMGB2,CDC42EP4,HIST1H2BB,DDX39B,SF3A2,CORO1A,CENPW,FOXRED1,SIGMAR1,ARPC1B,CENPP,GRWD1,PRMT5,PSMC1,CTH,ENSCAFG00000015189,HAT1,GEMIN7,UBE2C,MIS18A,TBCC,H3F3B,PDSS1,SF3A1,EIF3M	down_ACOR_VSMC
GO:0042743	0.00694	1	1	5	hydrogen peroxide metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0043112	0.00695	0.998	12	57	receptor metabolic process	BP	0.898	PLCG2,HTR2B,ATXN2,ZNRF3,LRPAP1,FUT8,PSEN1,RAB11B,EDN1,LMTK2,AP2B1,BVES	up_ACOR_VSMC
GO:0070374	0.00695	0.998	12	57	positive regulation of ERK1 and ERK2 cascade	BP	0.898	HTR2B,BMP4,FGFR2,FGF18,F2RL1,NRP1,PTPN22,NPNT,APP,CCL5,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0030182	0.00695	0.999	4	327	neuron differentiation	BP	1	HOXC10,EYA1,EMX2,SHOX2	up_VFEM_VSMC
GO:0001659	0.00695	1	2	54	temperature homeostasis	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0035356	0.00695	1	1	2	cellular triglyceride homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:1904177	0.00695	1	1	2	regulation of adipose tissue development	BP	1	NR1H4	up_VPUL_EC
GO:1904179	0.00695	1	1	2	positive regulation of adipose tissue	BP	1	NR1H4	up_VPUL_EC
GO:0070391	0.00696	1	1	5	response to lipoteichoic acid	BP	1	TLR2	up_AFEM_VSMC
GO:0071223	0.00696	1	1	5	cellular response to lipoteichoic acid	BP	1	TLR2	up_AFEM_VSMC
GO:0031034	0.00696	1	1	2	myosin filament assembly	BP	1	MYBPC2	up_VPUL_EC
GO:0071688	0.00696	1	1	2	striated muscle myosin thick filament assembly	BP	1	MYBPC2	up_VPUL_EC

GO:0021520	0.00698	1	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	up_AORT_EC
GO:0032493	0.00698	1	1	2	response to bacterial lipoprotein	BP	0.781	TLR2	up_VSAP_VSMC
GO:0042494	0.00698	1	1	2	detection of bacterial lipoprotein	BP	0.781	TLR2	up_VSAP_VSMC
GO:0042495	0.00698	1	1	2	detection of triacyl bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0070339	0.00698	1	1	2	response to bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0070340	0.00698	1	1	2	detection of bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0071220	0.00698	1	1	2	cellular response to bacterial lipoprotein	BP	0.781	TLR2	up_VSAP_VSMC
GO:0071221	0.00698	1	1	2	cellular response to bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0071725	0.00698	1	1	2	response to triacyl bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0071727	0.00698	1	1	2	cellular response to triacyl bacterial lipopeptide	BP	0.781	TLR2	up_VSAP_VSMC
GO:0098722	0.00701	1	1	2	asymmetric stem cell division	BP	1	ARHGEF2	up_VPUL_EC
GO:0002474	0.00702	0.999	4	9	antigen processing and presentation of peptide antigen via MHC class I	BP	0.899	DLA88,B2M,ERAP1,TAPBPL	up_ACOR_VSMC
GO:0061061	0.00702	0.999	4	179	muscle structure development	BP	0.781	PITX1,STIM1,CAV1,SHOX2	up_VSAP_VSMC
GO:0050718	0.007027832	0.99981	2	5	positive regulation of interleukin-1 beta	BP	0.96436359	FZD5,NOD2	up_ACOR_EC
GO:0007144	0.00703	1	2	2	female meiosis I	BP	0.345	TRIP13,FBXO5	down_ACOR_VSMC
GO:0014826	0.00704	1	2	2	vein smooth muscle contraction	BP	0.347	EDNRB,EDN1	up_VCAV_EC
GO:0001932	0.00706	0.996	38	416	regulation of protein phosphorylation	BP	0.425	ARHGEF2,VEGFA,SOCS5,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,PTPN11,TRIB3,ILK,SESN2,PTGS2,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,VLDLR,HTT,PAK2,INHBA,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:2000482	0.00706	0.999	4	9	regulation of interleukin-8 secretion	BP	1	C5AR2,ANXA4,F2RL1,MAPKBP1	up_VSAP_EC
GO:0048856	0.00707	0.998	12	1533	anatomical structure development	BP	1	NR1H4,TBX5,HOXA2,MAPK10,HOXA3,ARHGEF26,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:0043309	0.00707	1	1	2	regulation of eosinophil degranulation	BP	0.722	STX4	down_ACOR_EC
GO:0043311	0.00707	1	1	2	positive regulation of eosinophil degranulation	BP	0.722	STX4	down_ACOR_EC
GO:1902566	0.00707	1	1	2	regulation of eosinophil activation	BP	0.722	STX4	down_ACOR_EC
GO:1902568	0.00707	1	1	2	positive regulation of eosinophil activation	BP	0.722	STX4	down_ACOR_EC
GO:0051241	0.00708	0.999	4	336	negative regulation of multicellular organismal	BP	1	HOXC10,HOXA9,LNPEP,BPI	up_AORT_EC
GO:0019433	0.00708	1	2	2	triglyceride catabolic process	BP	0.346	ABHD5,LIPC	down_ACOR_VSMC
GO:0003264	0.00708	1	1	5	regulation of cardioblast proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0003266	0.00708	1	1	5	regulation of secondary heart field cardioblast	BP	1	EYA1	up_AFEM_VSMC
GO:0048665	0.0071	1	1	6	neuron fate specification	BP	0.721	HOXC10	up_AORT_VSMC
GO:0032230	0.0071	1	1	5	positive regulation of synaptic transmission,	BP	1	CA2	up_VCAV_VSMC
GO:1900122	0.0071	1	1	3	positive regulation of receptor binding	BP	1	HOXA3	up_VPOR_VSMC
GO:0055059	0.00711	1	1	1	asymmetric neuroblast division	BP	1	ARHGEF2	up_VPOR_EC
GO:0050715	0.007112369	0.99906	4	29	positive regulation of cytokine secretion	BP	0.96436359	FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0030855	0.00712	0.999	4	183	epithelial cell differentiation	BP	0.761	HOXA7,SIX1,CYP26B1,MTSS1	up_VFEM_EC
GO:1901653	0.007120284	0.99823	7	84	cellular response to peptide	BP	0.96436359	NR1H4,ENSCAFG00000004331,NOD2,ACTN2,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0098773	0.007133535	0.99906	4	29	skin epidermis development	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0071772	0.00715	1	1	50	response to BMP	BP	1	GATA5	down_AFEM_VSMC

GO:0071773	0.00715	1	1	50	cellular response to BMP stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0007501	0.00715	1	1	5	mesodermal cell fate specification	BP	1	EYA1	up_AFEM_VSMC
GO:0010614	0.00715	1	1	5	negative regulation of cardiac muscle	BP	1	GATA5	up_VCAV_VSMC
GO:0014741	0.00715	1	1	5	negative regulation of muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC
GO:0032635	0.00716	1	2	37	interleukin-6 production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:2001245	0.00716	1	1	2	regulation of phosphatidylcholine	BP	0.725	ACSL3	down_ACOR_EC
GO:0003278	0.00718	1	1	3	apoptotic process involved in heart	BP	1	NKX2-5	up_VPOR_VSMC
GO:1904469	0.007188837	0.9998	2	5	positive regulation of tumor necrosis factor	BP	0.96436359	FZD5,MAVS	up_ACOR_EC
GO:0007252	0.00719	1	1	6	I-kappaB phosphorylation	BP	1	TLR2	up_AFEM_VSMC
GO:0006464	0.007194768	0.99574	44	1162	cellular protein modification process	BP	0.96436359	NR1H4,BRSK1,PLCL1,PKIB,SOX9,GALNT5,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,DUSP26,NOD2,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0036211	0.007194768	0.99574	44	1162	protein modification process	BP	0.96436359	NR1H4,BRSK1,PLCL1,PKIB,SOX9,GALNT5,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,DUSP26,NOD2,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0006775	0.0072	1	1	3	fat-soluble vitamin metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:1900076	0.007204173	0.99905	4	29	regulation of cellular response to insulin	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2,PRKCD	up_ACOR_EC
GO:0001508	0.00722	1	1	25	action potential	BP	1	JUP	down_VFEM_VSMC
GO:1903555	0.00723	1	2	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0003170	0.00723	1	1	25	heart valve development	BP	1	GATA5	down_VFEM_VSMC
GO:0044242	0.00724	0.997	12	57	cellular lipid catabolic process	BP	1	PEX7,LIPC,ENPP2,ACAA1,ACACB,PEX2,FAAH,GCDH,EHHADH,LONP2,ABHD16A,IDH1	up_VSAP_EC
GO:0003008	0.00724	0.999	4	336	system process	BP	1	HOXC10,LNPEP,SGCD,GPR155	up_AORT_EC
GO:0007289	0.00725	1	3	5	spermatid nucleus differentiation	BP	0.354	PSME4,NECTIN2,KDM3A	up_VCAV_EC
GO:0099174	0.00726	1	1	6	regulation of presynapse organization	BP	0.727	WNT7A	up_AORT_VSMC
GO:0006924	0.00727	1	2	3	activation-induced cell death of T cells	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0014823	0.00728	1	3	5	response to activity	BP	0.907	FNDC5,PRKAA2,PPARGC1A	up_ACOR_VSMC
GO:0032660	0.00728	1	1	7	regulation of interleukin-17 production	BP	0.727	ARG2	up_AORT_VSMC
GO:0043666	0.00729	0.999	4	14	regulation of phosphoprotein	BP	0.436	NUAK1,PPP1R12A,HTT,CALM1	down_VSAP_EC
GO:0007166	0.007290762	0.99611	29	686	cell surface receptor signaling pathway	BP	0.96436359	SH3TC2,CDH3,NR1H4,SOX9,PTH1R,PORCN,ENSCAFG00000004331,ADAMTS13,FZD5,CCDC3,IFI6,DIXDC1,PTGIR,RGMA,INSYN1,SMAD6,ESM1,ADAMTSL2,MAPK8IP2,MAVS,FOXC2,LRRC15,LRP4,CLSTN1,LRRC4,NRP1,PRKCD,PYGO2,ADGRL1	up_ACOR_EC

GO:0010033	0.0073	0.995	82	772	response to organic substance	BP	0.355	ACKR1,HCLS1,GBP5,KIT,SELE,PRCP,CXCL8,LAPTM5,CXCR4,CALCRL,TIE1,TNFAIP3,PPARG,TNIP1,MX2,PDGFB,P2RX7,BAIAP2L1,TMEM173,SELL,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,RALB,SMAD1,TFPI,IRF8,PELI1,YES1,CASP8,MTOR,BMP2,HHEX,ST3GAL6,ABCA1,MAPK13,IFNGR1,RIOK3,ENSCAFG00000010596,FLNB,PAK2,PRKD2,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,JAG1,RAPGEF2,PLCG2,CTDSPL2,CREB1,BCL10,CTNNA1,CNOT7,GCH1,ADIPOR2,PMAIP1,BLM,RIPK1,LSM14A,USP13,SKIL,PDGFD,UFSP2,HIF1A,KDM3A,ATRX,NR4A1,ENSCAFG00000002015,P2RX2,JCAD,ZEB1,ARHGEF2,TJP2	up_VCAV_EC
GO:0048645	0.0073	1	2	33	animal organ formation	BP	1	TBX5,HOXA3	up_APUL_EC
GO:0006942	0.0073	1	1	26	regulation of striated muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0120163	0.00732	1	1	17	negative regulation of cold-induced	BP	1	PLCL1	down_VFEM_EC
GO:0060045	0.00733	1	1	11	positive regulation of cardiac muscle cell	BP	1	TBX5	up_APUL_VSMC
GO:1900424	0.00734	1	3	5	regulation of defense response to bacterium	BP	1	F2RL1,MAPKBP1,CYBA	up_VSAP_EC
GO:0034765	0.00734	0.999	3	91	regulation of ion transmembrane transport	BP	0.811	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0030308	0.00735	0.999	3	49	negative regulation of cell growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC
GO:0046633	0.00735	1	1	7	alpha-beta T cell proliferation	BP	0.727	ARG2	up_AORT_VSMC
GO:0021603	0.00735	1	1	2	cranial nerve formation	BP	1	HOXA1	up_APUL_EC
GO:0030326	0.00736	0.998	11	51	embryonic limb morphogenesis	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4	up_VSAP_EC
GO:0035113	0.00736	0.998	11	51	embryonic appendage morphogenesis	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4	up_VSAP_EC
GO:0007163	0.00736	1	2	60	establishment or maintenance of cell	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0048387	0.00736	1	1	3	negative regulation of retinoic acid receptor	BP	1	CYP26B1	up_VPOR_VSMC
GO:0090049	0.00737	0.999	5	21	regulation of cell migration involved in sprouting angiogenesis	BP	0.438	VEGFA,JCAD,PIK3C2A,STARD13,NRP1	down_VSAP_EC
GO:0009952	0.00737	1	2	66	anterior/posterior pattern specification	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0070662	0.00737	1	1	2	mast cell proliferation	BP	0.725	LYN	down_ACOR_EC
GO:0070666	0.00737	1	1	2	regulation of mast cell proliferation	BP	0.725	LYN	down_ACOR_EC
GO:0070668	0.00737	1	1	2	positive regulation of mast cell proliferation	BP	0.725	LYN	down_ACOR_EC
GO:0003350	0.00737	1	1	3	pulmonary myocardium development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0097327	0.00738	1	1	25	response to antineoplastic agent	BP	1	JUP	down_VFEM_VSMC
GO:0072171	0.00739	0.998	6	30	mesonephric tubule morphogenesis	BP	0.438	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0003416	0.00739	0.999	3	9	endochondral bone growth	BP	1	THBS3,EVC,DDR2	down_VCAV_EC
GO:0006796	0.00739384	0.99578	37	938	phosphate-containing compound metabolic process	BP	0.96436359	NR1H4,BRSK1,PLCL1,PKIB,THNSL2,SOX9,NMNAT2,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,CFI,GUCY1B1,GRK7,TNFRSF19,DCLK2,CHPT1,MAPK8IP2,MAVS,LRRC15,PIGS,LRP4,SH3RF3,AK7,LRRC4,ALDOC,RARRES2,STK32C,NRP1,AGPAT2,PRKCD,PPP1R26,DBNDD2,CCNYL1	up_ACOR_EC
GO:0061156	0.0074	1	1	4	pulmonary artery morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0006635	0.00741	0.999	5	25	fatty acid beta-oxidation	BP	1	AKT2,ACAA1,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:0060670	0.00741	1	3	5	branching involved in labyrinthine layer	BP	0.907	FGFR2,SPINT1,SPINT2	up_ACOR_VSMC
GO:0000027	0.00741	1	2	16	ribosomal large subunit assembly	BP	1	RSL24D1,RPL10L	up_VPOR_EC
GO:0048702	0.00741	1	1	2	embryonic neurocranium morphogenesis	BP	0.725	HOXA1	down_ACOR_EC
GO:0021520	0.00741	1	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	up_VFEM_VSMC

GO:0071345	0.00742	0.996	22	210	cellular response to cytokine stimulus	BP	0.438	ARHGEF2,NR1H4,HSPA5,SOCS5,FLNB,DPYSL3,ILK,MYO1C,KIF5B,HIF1A,CX3CL1,PTPN2,ADAM17,CNOT7,ENSCAFG00000002015,TFRC,ZC3H15,KLF5,CDC37,GBP5,BTK,KDM3A	down_VSAP_EC
GO:0045595	0.00742	0.997	20	469	regulation of cell differentiation	BP	1	HOXA9,CMKLR1,IRX3,LEP,LBH,HOXA7,DLL1,PLXNA4,TWIST2,THRB,TMEM100,GREM1,CAMK2A,CYLD,PTHLH,EVI2B,AXIN2,NAPEPLD,DMPK,KANK1	up_AFEM_EC
GO:0019438	0.00743	0.998	8	1258	aromatic compound biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0050701	0.00743	0.999	5	16	interleukin-1 secretion	BP	0.36	GBP5,TLR4,ARG2,ABCA1,HMGB1	up_VCAV_EC
GO:0007187	0.00744	0.998	10	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	0.907	ADRA1B,ADGRD1,ABCA1,PTGIR,ADCY6,GNA14,APLP1,SENP7,EDN1,GNAQ	up_ACOR_VSMC
GO:0030705	0.00744	0.998	9	56	cytoskeleton-dependent intracellular transport	BP	0.438	HOOK3,MYO1C,RPGR,KIF5B,HIF1A,DYNLL1,TRAK1,HTT,AP3S1	down_VSAP_EC
GO:0042110	0.00745	0.997	17	109	T cell activation	BP	0.36	IL7R,KIT,IL6,CHD7,DLL4,GATA3,RAB27A,PELI1,ARG2,MTOR,ELF4,ITPKB,NCK1,BCL10,HMGB1,BMX,ZEB1	up_VCAV_EC
GO:0045619	0.00745	0.998	10	44	regulation of lymphocyte differentiation	BP	1	ABL1,ZBTB16,TOX,ZFP36L1,ZEB1,FBXO7,CD83,ZFP36L2,PNP,TGFBR2	up_VSAP_EC
GO:1904591	0.00745	1	1	25	positive regulation of protein import	BP	1	JUP	down_VFEM_VSMC
GO:0060872	0.00745	1	1	6	semicircular canal development	BP	1	EYA1	up_AFEM_VSMC
GO:0001732	0.00746	0.999	4	9	formation of cytoplasmic translation initiation	BP	1	EIF3G,EIF3K,EIF3L,EIF3D	up_VSAP_EC
GO:0050877	0.00746	0.999	3	164	nervous system process	BP	1	HOXC10,GATM,NETO1	up_VFEM_VSMC
GO:0048598	0.00746	0.999	3	207	embryonic morphogenesis	BP	1	HOXA3,TBX5,HOXB5	up_VPUL_VSMC
GO:0022603	0.00747	0.999	3	301	regulation of anatomical structure morphogenesis	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0090257	0.00747	1	1	52	regulation of muscle system process	BP	1	GATA5	down_AFEM_VSMC
GO:0071495	0.00748	0.999	5	365	cellular response to endogenous stimulus	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0051891	0.00748	1	1	3	positive regulation of cardioblast differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032886	0.00749	0.997	14	81	regulation of microtubule-based process	BP	0.363	SMC1A,CFAP298,STMN1,NEK2,POC1A,RAC1,NUP62,PLK4,SMC3,STAG1,RBM14,ARHGEF2,KIF11,GEN1	down_ACOR_VSMC
GO:0045926	0.00749	0.997	14	72	negative regulation of growth	BP	0.907	DCBLD2,BMP4,GJA1,RERG,PLAC8B,CDKN1A,CRLF3,NRP1,ULK2,TBX5,WWC2,NAIF1,SH3BP4,STC2	up_ACOR_VSMC
GO:0071600	0.00749	1	1	5	otic vesicle morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0030177	0.00751	1	2	51	positive regulation of Wnt signaling pathway	BP	1	BAMBI,ANKRD6	up_VPOR_VSMC
GO:0120162	0.00751	1	2	31	positive regulation of cold-induced thermogenesis	BP	0.824	GATM,CAV1	up_VSAP_VSMC
GO:0060914	0.00752	1	1	11	heart formation	BP	1	TBX5	up_APUL_VSMC
GO:0048732	0.00754	1	2	116	gland development	BP	0.739	HOXA9,ESR1	up_AORT_VSMC
GO:0009595	0.00754	1	1	6	detection of biotic stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0002521	0.00755	0.996	22	149	leukocyte differentiation	BP	0.362	HCLS1,IL7R,KIT,IL6,MEF2C,CHD7,DLL4,GATA3,CASP8,MTOR,HHEX,ITPKB,MFNG,PLCG2,CREB1,HMGB1,RIPK1,ATP11C,CUL4A,BMX,ZEB1,TJP2	up_VCAV_EC
GO:0070507	0.00756	0.997	13	73	regulation of microtubule cytoskeleton organization	BP	0.364	SMC1A,STMN1,NEK2,POC1A,RAC1,NUP62,PLK4,SMC3,STAG1,RBM14,ARHGEF2,KIF11,GEN1	down_ACOR_VSMC
GO:0034308	0.00756	0.999	4	16	primary alcohol metabolic process	BP	1	CYP1B1,RETSAT,PARK7,NAPEPLD	down_VCAV_EC
GO:0070050	0.00756	1	1	3	neuron cellular homeostasis	BP	1	TAOK1	up_AORT_EC
GO:2000463	0.00756	1	1	5	positive regulation of excitatory postsynaptic	BP	0.739	WNT7A	up_AORT_VSMC

GO:0051240	0.00758	0.995	63	489	positive regulation of multicellular organismal process	BP	1	HOXA11,CDON,WNT11,CD274,AXIN2,WASF3,OSR2,AMIGO1,ENPP2,LRRN3,PPARGC1B,ACACB,IL6R,ZHX3,HOXD3,FGF7,ABL1,EBF2,BTG1,HDAC7,DLL1,OSR1,IL17RC,HPSE,ANKRD54,ZBTB16,TOX,CCBE1,STAT5A,STAT6,F2RL1,DDR2,MFN2,ZFP36L1,PIK3R1,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,SASH1,MYD88,GDPD5,PRKAB1,NLRX1,TKFC,CD83,KDM2B,PNP,ZNF580,CYBA,CYB5D2,PQBP1,ACVRL1,FLOT1,NCK1,MAVS,HMOX1,MAP2K2,TGFBR2,CITED2,TRADD,LBH	up_VSAP_EC
GO:0060876	0.00758	1	1	2	semicircular canal formation	BP	0.725	HOXA1	down_ACOR_EC
GO:0032924	0.00758	1	1	9	activin receptor signaling pathway	BP	1	TGFBR1	down_VSAP_VSMC
GO:0051049	0.00759	0.995	62	479	regulation of transport	BP	0.907	EXPH5,SH3TC2,TLR1,DNAJC6,ACTN2,PLCG2,LEP,KCNE3,HTR2B,TCAF1,USP6NL,MBP,FBXL20,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,GJA1,SEC24B,ATXN2,CD274,SARAF,PTPN3,ANKRD1,F2RL1,DAPK1,CACNB3,AKAP6,CDKN1A,PTPN22,LRPAP1,DMPK,OS9,SCP2,KCNJ4,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,CHD7,JUP,CCL5,RAB11B,EDN1,GTF2A1L,KCNC4,NOD2,B2M,FXYD1,SCAMP5,INPP5K,RAB5C,PREPL,PFKL,WFS1,AZIN2,PARK7,STC2,BVES,PTPN14	up_ACOR_VSMC
GO:0018130	0.00759	0.998	8	1261	heterocycle biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0009063	0.00759	0.999	5	25	cellular amino acid catabolic process	BP	1	THNSL2,ENSCAFG00000002977,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0002576	0.00761	1	1	2	platelet degranulation	BP	0.725	LYN	down_ACOR_EC
GO:0031326	0.00762	0.998	11	1176	regulation of cellular biosynthetic process	BP	0.825	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0001659	0.00762	1	2	54	temperature homeostasis	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0003176	0.00762	1	1	9	aortic valve development	BP	1	GATA5	down_VSAP_VSMC
GO:0031572	0.00764	0.999	5	15	G2 DNA damage checkpoint	BP	0.366	CDK1,FANCI,TOPBP1,DTL,CLSPN	down_ACOR_VSMC
GO:0035239	0.00764	0.999	5	299	tube morphogenesis	BP	0.795	EYA1,HOXB7,HOXA7,SIX1,MTSS1	up_VFEM_EC
GO:0060158	0.00764	1	2	2	phospholipase C-activating dopamine receptor signaling	BP	0.907	GNA14,GNAQ	up_ACOR_VSMC
GO:0042483	0.00764	1	1	2	negative regulation of odontogenesis	BP	0.725	ASPN	down_ACOR_EC
GO:0030888	0.00765	0.999	4	13	regulation of B cell proliferation	BP	0.446	TFRC,LYN,BTK,CDKN1A	down_VSAP_EC
GO:0070925	0.00766	0.996	37	293	organelle assembly	BP	0.366	FSCN1,EDC3,SMC1A,CENPA,CENPN,SDC1,FBXO5,CFAP298,BIRC5,AURKB,HAUS8,NEK2,RCC1,CENPH,POC1A,WDR62,NUP62,DDX28,PLK4,SMC3,CDK2,STAG1,ENSCAFG00000005299,EZR,SASS6,RBM14,CORO1A,CENPW,CDC20,ASPM,TRAPPC6A,ENSCAFG00000015189,KIF11,SIX4,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0050865	0.00766	0.996	20	135	regulation of cell activation	BP	0.366	IL7R,ADGRF5,SELP,TNFAIP3,PDGFB,MEF2C,TLR4,GATA3,PELI1,ARG2,NECTIN2,ITPKB,THOC1,NCK1,CD200,FES,BCL10,HMGB1,ATP11C,ZEB1	up_VCAV_EC
GO:1902105	0.00766	0.997	15	80	regulation of leukocyte differentiation	BP	1	HOXA7,PPARGC1B,ABL1,ZBTB16,TOX,ZFP36L1,PIK3R1,MYC,ZEB1,TFE3,FBXO7,CD83,ZFP36L2,PNP,TGFBR2	up_VSAP_EC
GO:0006635	0.00766	0.998	7	25	fatty acid beta-oxidation	BP	1	PEX7,ACAA1,ACACB,PEX2,GCDH,EHHADH,LONP2	up_VSAP_EC
GO:0048585	0.007670502	0.99625	22	475	negative regulation of response to stimulus	BP	0.96436359	NR1H4,SOX9,FNDC4,NDRG2,CCDC3,IFI6,DUSP26,PTGIR,RGMA,SMAD6,MMP28,PTGER4,ADAMTSL2,MAPK8IP2,FIGNL1,LRRC15,LRP4,CLSTN1,LRRC4,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0009135	0.00769	0.999	5	22	purine nucleoside diphosphate metabolic	BP	0.446	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0009179	0.00769	0.999	5	22	purine ribonucleoside diphosphate metabolic	BP	0.446	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0046031	0.00769	0.999	5	22	ADP metabolic process	BP	0.446	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0060575	0.00769	1	1	9	intestinal epithelial cell differentiation	BP	1	GATA5	down_VSAP_VSMC

GO:0002790	0.0077	0.996	22	133	peptide secretion	BP	0.907	EXPH5,TLR1,LEP,HTR2B,MBP,FERMT1,TM7SF3,ABCA1,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,CHD7,CCL5,RAB11B,EDN1,NOD2,SCAMP5,PFKL,PARK7,LMF1	up_ACOR_VSMC
GO:0003171	0.0077	1	1	10	atrioventricular valve development	BP	1	TBX5	up_APUL_VSMC
GO:0032675	0.00771	1	2	34	regulation of interleukin-6 production	BP	1	NR1H4,BPI	up_APUL_EC
GO:1903045	0.00771	1	1	1	neural crest cell migration involved in sympathetic nervous system	BP	1	SEMA3A	up_VPOR_EC
GO:0003197	0.007713142	0.99935	3	16	endocardial cushion development	BP	0.96436359	GATA4,SOX9,TBX5	up_ACOR_EC
GO:2000117	0.00773	1	1	27	negative regulation of cysteine-type	BP	1	CST3	down_AORT_EC
GO:2000406	0.00774	1	2	6	positive regulation of T cell migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:1904888	0.00774	1	2	31	cranial skeletal system development	BP	0.795	TBX15,SIX1	up_VFEM_EC
GO:0060969	0.00775	1	1	6	negative regulation of gene silencing	BP	0.744	ESR1	up_AORT_VSMC
GO:0050794	0.00776	0.997	23	3075	regulation of cellular process	BP	0.725	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,PDPN,NRP2,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,IPO7,ATRIP,SULF1,ELK3,HOXA1,ACSL3,WDR12,STX4,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0048729	0.00776	0.999	3	209	tissue morphogenesis	BP	1	TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:1905941	0.00776	1	1	4	positive regulation of gonad development	BP	1	CITED2	down_VPOR_EC
GO:2000018	0.00776	1	1	4	regulation of male gonad development	BP	1	CITED2	down_VPOR_EC
GO:2000020	0.00776	1	1	4	positive regulation of male gonad development	BP	1	CITED2	down_VPOR_EC
GO:0071468	0.00777	1	1	4	cellular response to acidic pH	BP	1	RAB11B	down_VPOR_EC
GO:0019276	0.00779	1	1	2	UDP-N-acetylgalactosamine	BP	0.725	CSGALNACT1	down_ACOR_EC
GO:0016310	0.0078	0.995	54	641	phosphorylation	BP	0.446	ARHGEF2,VEGFA,SOCS5,SGK1,ENPP1,ERRFI1,JCAD,SNX25,PGK1,BCAR3,NUAK1,PTPN11,TPI1,TRIB3,PGAM1,ILK,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,ALDOC,CTNNB1,CDK8,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,SH3GLB1,HTT,MAPK10,EIF2S1,PAK2,INHBA,CAMK2D,BTK,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0048147	0.0078	1	3	5	negative regulation of fibroblast proliferation	BP	1	PEX2,MORC3,FBXO4	up_VSAP_EC
GO:0030168	0.0078	1	2	23	platelet activation	BP	0.725	LYN,PDPN	down_ACOR_EC
GO:0060039	0.0078	1	1	11	pericardium development	BP	1	TBX5	up_APUL_VSMC
GO:0032872	0.00781	0.997	15	77	regulation of stress-activated MAPK cascade	BP	0.907	LEP,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,PTPN22,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0030199	0.00781	0.999	5	21	collagen fibril organization	BP	0.446	SERPINH1,P4HA1,PLOD3,P3H4,COL12A1	down_VSAP_EC
GO:0048731	0.00782	0.999	5	1247	system development	BP	0.746	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0030510	0.00782	1	2	27	regulation of BMP signaling pathway	BP	0.725	ACVRL1,SULF1	down_ACOR_EC
GO:0018197	0.00783	1	2	3	peptidyl-aspartic acid modification	BP	0.446	ASPH,HIF1AN	down_VSAP_EC
GO:0042264	0.00783	1	2	3	peptidyl-aspartic acid hydroxylation	BP	0.446	ASPH,HIF1AN	down_VSAP_EC
GO:0072513	0.00783	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:0021615	0.00784	1	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	up_VPOR_VSMC
GO:0032757	0.00785	0.999	5	14	positive regulation of interleukin-8 production	BP	0.907	TLR1,TLR3,F2RL1,NOD2,PARK7	up_ACOR_VSMC
GO:2001013	0.00785	1	1	2	epithelial cell proliferation involved in renal tubule morphogenesis	BP	0.795	MTSS1	up_VFEM_EC

GO:0032989	0.00786	0.996	29	292	cellular component morphogenesis	BP	0.446	ARHGEF2,VEGFA,SIPA1L1,MYH9,FMNL3,ACTN1,SPARC,SGK1,AKAP2,PTPN11,FLNB,IFRD1,ILK,WDR1,MSN,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,ENSCAFG00000002015,PLOD3,VLDLR,EXT1,SIX4,NRP1,YWHAH,MYBPC2	down_VSAP_EC
GO:0048665	0.00786	1	2	6	neuron fate specification	BP	1	HOXC10,DLL1	up_AFEM_EC
GO:0006044	0.00787	1	3	5	N-acetylglucosamine metabolic process	BP	1	RENBP,CHST7,GNPDA1	up_VSAP_EC
GO:0019098	0.00787	1	2	6	reproductive behavior	BP	1	THRB,AVPR1A	up_AFEM_EC
GO:1901623	0.00787	1	2	6	regulation of lymphocyte chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0051090	0.00788	0.996	20	134	regulation of DNA-binding transcription factor activity	BP	0.375	HCLS1,KIT,PRKCH,TNFAIP3,TMEM173,RELN,NLRC5,EDN1,PELI1,PPP3CA,PROX1,ENSCAFG00000010596,PRKD2,SMARCA4,TLR3,CD200,BCL10,RIPK1,KDM5A,ARHGEF2	up_VCAV_EC
GO:1901215	0.00788	0.998	9	57	negative regulation of neuron death	BP	0.446	HYOU1,AARS,HIF1A,ZPR1,CTNNB1,APOE,GSK3B,SIX4,NRP1	down_VSAP_EC
GO:0016070	0.00788	0.999	6	1479	RNA metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:2000721	0.00788	1	1	2	positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation	BP	1	NPNT	up_APUL_EC
GO:0010828	0.007908453	0.99933	3	16	positive regulation of glucose transmembrane	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0007143	0.00791	0.999	4	10	female meiotic nuclear division	BP	0.369	TRIP13,FBXO5,NCAPH,TTK	down_ACOR_VSMC
GO:0001835	0.00792	1	2	2	blastocyst hatching	BP	0.369	SMARCB1,RBBP8	down_ACOR_VSMC
GO:0035188	0.00792	1	2	2	hatching	BP	0.369	SMARCB1,RBBP8	down_ACOR_VSMC
GO:0071684	0.00792	1	2	2	organism emergence from protective structure	BP	0.369	SMARCB1,RBBP8	down_ACOR_VSMC
GO:0010606	0.00792	1	2	2	positive regulation of cytoplasmic mRNA	BP	0.375	CNOT6,PAN3	up_VCAV_EC
GO:0035356	0.00792	1	1	2	cellular triglyceride homeostasis	BP	1	NR1H4	up_APUL_EC
GO:1904177	0.00792	1	1	2	regulation of adipose tissue development	BP	1	NR1H4	up_APUL_EC
GO:1904179	0.00792	1	1	2	positive regulation of adipose tissue	BP	1	NR1H4	up_APUL_EC
GO:1901228	0.00793	1	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GATA5	up_VPUL_VSMC
GO:0007166	0.00794	0.995	57	686	cell surface receptor signaling pathway	BP	0.446	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,PTPN11,ILK,SMARCA4,TGFBR1,MYO1C,CHSY1,HIF1A,CX3CL1,NXN,PTPN2,EIF2B1,NEO1,MTDH,ESM1,ADAM17,CNOT7,ADGRE5,GNAQ,CTNNB1,ENSCAFG00000002015,APOE,ZC3H15,LYN,STRAP,DDIT3,TLN1,CBLC,ATF3,CDC37,ITGB3,TAX1BP3,MYO1E,HTT,DISC1,PAK2,INHBA,ENSCAFG00000018360,HIF1AN,BTK,NRP1,RHBDF2,MADD	down_VSAP_EC
GO:0030900	0.00794	0.999	3	101	forebrain development	BP	0.842	PITX1,EMX2,SALL1	up_VSAP_VSMC
GO:0007603	0.00794	1	2	3	phototransduction, visible light	BP	0.446	GNAQ,RDH11	down_VSAP_EC
GO:0070858	0.00794	1	1	2	negative regulation of bile acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:1904252	0.00794	1	1	2	negative regulation of bile acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0048738	0.00795	0.997	13	64	cardiac muscle tissue development	BP	0.907	TNNT2,ACTN2,BMP4,FGFR2,NEBL,ANKRD1,EGLN1,TBX20,TBX5,FRS2,CHD7,EDN1,BVES	up_ACOR_VSMC
GO:0001501	0.00795	0.999	3	178	skeletal system development	BP	1	HOXC10,HOXA9,HOXC6	up_AORT_EC
GO:0003164	0.00795	1	1	2	His-Purkinje system development	BP	1	TBX5	up_APUL_EC
GO:0003166	0.00795	1	1	2	bundle of His development	BP	1	TBX5	up_APUL_EC
GO:0099183	0.00795	1	1	2	trans-synaptic signaling by BDNF, modulating	BP	1	NTRK2	up_APUL_EC
GO:0099191	0.00795	1	1	2	trans-synaptic signaling by BDNF	BP	1	NTRK2	up_APUL_EC

GO:0099538	0.00795	1	1	2	synaptic signaling via neuropeptide	BP	1	NTRK2	up_APUL_EC
GO:0099540	0.00795	1	1	2	trans-synaptic signaling by neuropeptide	BP	1	NTRK2	up_APUL_EC
GO:0010159	0.00795	1	1	2	specification of animal organ position	BP	1	HOXA3	up_APUL_EC
GO:0010988	0.00795	1	1	2	regulation of low-density lipoprotein particle	BP	1	NR1H4	up_APUL_EC
GO:0034969	0.00795	1	1	2	histone arginine methylation	BP	1	NR1H4	up_APUL_EC
GO:0045764	0.00795	1	1	2	positive regulation of cellular amino acid	BP	1	NR1H4	up_APUL_EC
GO:0048702	0.00795	1	1	2	embryonic neurocranium morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0048934	0.00795	1	1	2	peripheral nervous system neuron	BP	1	NTRK2	up_APUL_EC
GO:0048935	0.00795	1	1	2	peripheral nervous system neuron	BP	1	NTRK2	up_APUL_EC
GO:0055022	0.00795	1	1	2	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0060044	0.00795	1	1	2	negative regulation of cardiac muscle cell	BP	1	TBX5	up_APUL_EC
GO:0060876	0.00795	1	1	2	semicircular canal formation	BP	1	HOXA1	up_APUL_EC
GO:0061117	0.00795	1	1	2	negative regulation of heart growth	BP	1	TBX5	up_APUL_EC
GO:0072615	0.00795	1	1	2	interleukin-17 secretion	BP	1	NR1H4	up_APUL_EC
GO:1902714	0.00795	1	1	2	negative regulation of interferon-gamma	BP	1	NR1H4	up_APUL_EC
GO:0051241	0.00796	0.996	32	336	negative regulation of multicellular organismal process	BP	0.446	PRICKLE1,SULF1,NR1H4,SERPINE1,SOCS5,SPARC,PRKACB,PGK1,PTPN11,DPYSL3,HOOK3,IFRD1,CHSY1,HIF1A,THBS2,PTPN2,PLCL1,CTNNB1,STARD13,APOE,WWC3,LYN,STRAP,DDIT3,REST,PRMT1,RAB11FIP1,INHBA,BTK,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0044281	0.00796	0.999	5	622	small molecule metabolic process	BP	1	ETFA,EXTL2,DARS,SUCLG2,NDUFA10	down_AFEM_EC
GO:0030001	0.00796	0.999	3	172	metal ion transport	BP	1	HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0030098	0.00798	0.997	15	87	lymphocyte differentiation	BP	0.376	IL7R,KIT,IL6,CHD7,DLL4,GATA3,MTOR,HHEX,ITPKB,MFNG,PLCG2,HMGB1,ATP11C,BMX,ZEB1	up_VCAV_EC
GO:0007379	0.00798	1	2	6	segment specification	BP	1	IRX3,DLL1	up_AFEM_EC
GO:0007267	0.00799	0.995	46	332	cell-cell signaling	BP	0.907	ADRA1B,LGR6,LEP,PLCL1,ZRANB1,FBXL20,RECK,MLLT3,FERMT1,BMP4,TM7SF3,FGFR2,GJA1,HRH1,LATS2,GLRB,ZNRF3,STX11,TMEM108,EGLN1,CACNB3,SLC12A7,CLSTN1,DMPK,SLITRK5,TBX5,PRKCE,FZD3,RNF19A,SCG5,DAG1,APP,PSEN1,CHD7,CCL5,RAB11B,EDN1,KCNC4,LRRC4,FAM107A,INSYN1,DISC1,PREPL,PFKL,ERAP1,PARK7	up_ACOR_VSMC
GO:0045214	0.00799	0.999	4	13	sarcomere organization	BP	0.446	ACTN1,WDR1,SIX4,MYBPC2	down_VSAP_EC
GO:0060838	0.00799	1	1	2	lymphatic endothelial cell fate commitment	BP	0.728	PDPN	down_ACOR_EC
GO:0022414	0.008	0.999	5	294	reproductive process	BP	0.842	HOXA11,HOXA9,SALL1,IRX5,GJB5	up_VSAP_VSMC
GO:0018171	0.00801	1	2	2	peptidyl-cysteine oxidation	BP	0.907	TMX3,PARK7	up_ACOR_VSMC
GO:0055023	0.00801	1	1	12	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0002526	0.00802	0.999	4	17	acute inflammatory response	BP	1	CLSTN1,B4GALT1,PARK7,A2M	down_VCAV_EC
GO:0042983	0.00802	1	2	3	amyloid precursor protein biosynthetic process	BP	1	NECAB3,SOAT1	down_VCAV_EC
GO:0042984	0.00802	1	2	3	regulation of amyloid precursor protein	BP	1	NECAB3,SOAT1	down_VCAV_EC
GO:0032640	0.00802	1	2	39	tumor necrosis factor production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0051235	0.00803	0.997	12	90	maintenance of location	BP	0.447	HSPA5,ERO1A,ENPP1,PTPN2,APOE,LYN,DDIT3,TLN1,HTT,ABHD5,CALM1,KDELR2	down_VSAP_EC
GO:0001525	0.00803	0.997	10	173	angiogenesis	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0003207	0.00803	1	3	5	cardiac chamber formation	BP	0.907	SMARCD3,TBX20,TBX5	up_ACOR_VSMC
GO:0007611	0.00803	1	2	54	learning or memory	BP	1	GATM,NETO1	up_VFEM_VSMC

GO:0051389	0.00803	1	1	1	inactivation of MAPKK activity	BP	0.728	IGF1R	down_ACOR_EC
GO:0061077	0.00804	0.999	5	25	chaperone-mediated protein folding	BP	1	HSPB6,FKBP10,FKBP5,FKBP11,CRTAP	down_VCAV_EC
GO:0010633	0.00804	1	1	28	negative regulation of epithelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0048169	0.00804	1	1	3	regulation of long-term neuronal synaptic	BP	1	NETO1	up_VFEM_VSMC
GO:0010646	0.008060643	0.99537	37	945	regulation of cell communication	BP	0.96436359	CNTNAP4,SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,SOX9,RGS1,NDRG2,KCNB1,FZD5,CCDC3,IFI6,DUSP26,DIXDC1,PTGIR,NOD2,PDE4A,SMAD6,ESM1,PAK3,TNFRSF19,ARHGDIB,ADAMTSL2,MAPK8IP2,MAVS,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0051890	0.00807	1	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0000724	0.00809	0.997	11	57	double-strand break repair via homologous	BP	0.375	RPA1,PARPBP,GINS4,RAD54L,RAD51,TONSL,BRCA1,RBBP8,SMC6,H2AFX,GEN1	down_ACOR_VSMC
GO:0007399	0.00809	0.998	7	564	nervous system development	BP	0.842	PITX1,EMX2,SALL1,HOXC10,IRX5,SHOX2,HAPLN1	up_VSAP_VSMC
GO:0010159	0.00809	1	1	2	specification of animal organ position	BP	0.728	HOXA3	down_ACOR_EC
GO:0070571	0.0081	1	2	3	negative regulation of neuron projection	BP	1	THY1,RGMA	down_VCAV_EC
GO:0051241	0.008103949	0.99641	17	336	negative regulation of multicellular organismal process	BP	0.96436359	CDH3,NR1H4,PLCL1,SOX9,NDRG2,DIXDC1,RGMA,SMAD6,RNLS,PTGER4,ARHGDIB,FOXC2,TBX5,LRP4,NRP1,PRKCD,EFEMP1	up_ACOR_EC
GO:0009416	0.00812	0.999	3	88	response to light stimulus	BP	0.728	USP28,HOXA1,NEDD4	down_ACOR_EC
GO:0009083	0.00812	1	3	5	branched-chain amino acid catabolic process	BP	1	ALDH6A1,BCKDHB,ENSCAFG00000002977	up_VSAP_EC
GO:0060216	0.00812	1	1	3	definitive hemopoiesis	BP	1	HOXA9	up_AORT_EC
GO:0000003	0.00813	0.999	5	295	reproduction	BP	0.842	HOXA11,HOXA9,SALL1,IRX5,GJB5	up_VSAP_VSMC
GO:0090076	0.00813	1	2	2	relaxation of skeletal muscle	BP	0.381	KCNJ2,ATP2A1	up_VCAV_EC
GO:0042303	0.008132091	0.99888	4	30	molting cycle	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0042633	0.008132091	0.99888	4	30	hair cycle	BP	0.96436359	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0060298	0.00814	1	2	2	positive regulation of sarcomere organization	BP	0.381	EDN1,PROX1	up_VCAV_EC
GO:2001135	0.00814	1	1	4	regulation of endocytic recycling	BP	1	RAB11B	down_VPOR_EC
GO:0003211	0.00814	1	1	4	cardiac ventricle formation	BP	1	TBX5	up_VPUL_VSMC
GO:0002755	0.00815	1	1	6	MyD88-dependent toll-like receptor signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0010832	0.00815	1	1	3	negative regulation of myotube differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003263	0.00815	1	1	4	cardioblast proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0045907	0.00816	1	2	6	positive regulation of vasoconstriction	BP	1	AVPR1A,TBXA2R	up_AFEM_EC
GO:0003179	0.00817	0.998	6	19	heart valve morphogenesis	BP	0.916	SMAD6,GATA5,GATA4,BMP4,TBX20,TBX5	up_ACOR_VSMC
GO:0071804	0.00817	1	2	31	cellular potassium ion transport	BP	0.842	NETO1,CAV1	up_VSAP_VSMC
GO:0071805	0.00817	1	2	31	potassium ion transmembrane transport	BP	0.842	NETO1,CAV1	up_VSAP_VSMC
GO:0016310	0.00818	0.994	70	641	phosphorylation	BP	0.381	EPHB1,PLK2,TEK,HCLS1,KIT,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,NLRC5,EDN1,RALB,APLNR,NEDD9,YES1,EPHB4,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,BMP2K,SH3BP5,ERC1,MAPK13,ITPKB,PROX1,ENSCAFG00000010596,MADD,PAK2,PRKD2,SH3GLB1,TLR3,ENSCAFG00000024323,NCK1,LDB2,FES,NSD1,PTGS2,MMD,TOP1,RAPGEF2,CREB1,TAOK1,CNOT7,HMGB1,BLM,SPTBN4,RIPK1,ITGA6,RAD17,IMPA1,PDGFD,BMX,HIF1A,LMTK2,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0006103	0.00818	1	3	5	2-oxoglutarate metabolic process	BP	1	GOT1,ADHFE1,IDH1	up_VSAP_EC
GO:1902415	0.00819	1	3	5	regulation of mRNA binding	BP	1	LARP6,CDK9,EIF3D	up_VSAP_EC

GO:1902416	0.00819	1	3	5	positive regulation of mRNA binding	BP	1	LARP6,CDK9,EIF3D	up_VSAP_EC
GO:1904888	0.00819	1	2	31	cranial skeletal system development	BP	0.842	TBX15,IRX5	up_VSAP_VSMC
GO:0060136	0.00819	1	1	4	embryonic process involved in female	BP	1	CITED2	down_VPOR_EC
GO:0042713	0.00819	1	1	1	sperm ejaculation	BP	1	ACVR2A	up_VPOR_EC
GO:0043084	0.00819	1	1	1	penile erection	BP	1	ACVR2A	up_VPOR_EC
GO:2001016	0.00819	1	1	2	positive regulation of skeletal muscle cell	BP	0.795	CYP26B1	up_VFEM_EC
GO:0021563	0.00819	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_VPUL_VSMC
GO:0051259	0.0082	0.996	20	140	protein complex oligomerization	BP	0.381	TEK,GBP5,CDA,VWF,ACPP,LRRC8C,LNX2,RIOK3,SNX2,KCNJ2,EHD4,BCL10,GCH1,PMAIP1,BLM,RIPK1,MCU,ALDH1A3,P2RX2,TNFAIP1	up_VCAV_EC
GO:0000902	0.00821	0.996	27	266	cell morphogenesis	BP	0.454	ARHGEF2,VEGFA,SIPA1L1,MYH9,FMNL3,ACTN1,SPARC,SGK1,AKAP2,PTPN11,FLNB,IFRD1,ILK,WDR1,MSN,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,ENSCAFG00000002015,PLOD3,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:1904951	0.008212854	0.99766	8	108	positive regulation of establishment of protein localization	BP	0.96436359	NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,MAVS,PRKCD	up_ACOR_EC
GO:0042462	0.00822	0.999	3	9	eye photoreceptor cell development	BP	1	NAGLU,THY1,THRB	down_VCAV_EC
GO:0051298	0.00823	0.998	8	35	centrosome duplication	BP	0.378	POC1A,WDR62,NUP62,PLK4,CDK2,SASS6,RBM14,GEN1	down_ACOR_VSMC
GO:0000731	0.00823	0.999	4	10	DNA synthesis involved in DNA repair	BP	0.378	POLE,PCNA,POLH,DTL	down_ACOR_VSMC
GO:0009887	0.00823	0.999	3	314	animal organ morphogenesis	BP	1	TBX15,EYA1,IRX5	up_AFEM_VSMC
GO:0071623	0.00823	1	2	2	negative regulation of granulocyte chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0090024	0.00823	1	2	2	negative regulation of neutrophil chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:1902623	0.00823	1	2	2	negative regulation of neutrophil migration	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0035754	0.00823	1	1	4	B cell chemotaxis	BP	1	HSD3B7	down_VPOR_EC
GO:0060261	0.00825	1	1	8	positive regulation of transcription initiation from RNA polymerase II	BP	0.775	ESR1	up_AORT_VSMC
GO:0002513	0.00827	1	1	2	tolerance induction to self antigen	BP	0.733	LYN	down_ACOR_EC
GO:0010715	0.00827	1	1	4	regulation of extracellular matrix disassembly	BP	1	FSCN1	down_AFEM_EC
GO:0002683	0.00828	1	2	126	negative regulation of immune system process	BP	0.775	HOXA9,ARG2	up_AORT_VSMC
GO:0031290	0.00828	1	1	4	retinal ganglion cell axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:1902668	0.00829	1	1	4	negative regulation of axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:0007399	0.0083	0.998	8	564	nervous system development	BP	0.733	LYN,HOXA3,ACSL4,SPG11,NRP2,SULF1,HOXA1,NEDD4	down_ACOR_EC
GO:0032620	0.00831	1	1	8	interleukin-17 production	BP	0.775	ARG2	up_AORT_VSMC
GO:0008625	0.00833	0.998	7	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	0.386	TNFAIP3,ATF3,CASP8,MADD,PMAIP1,SKIL,ARHGEF2	up_VCAV_EC
GO:0002673	0.00834	1	1	6	regulation of acute inflammatory response	BP	1	C6	up_VCAV_VSMC
GO:0032825	0.00835	1	1	2	positive regulation of natural killer cell	BP	0.795	TOX	up_VFEM_EC
GO:0031324	0.00836	0.998	9	735	negative regulation of cellular metabolic process	BP	0.733	ACVRL1,LYN,IGF1R,HOXA7,PRKAR2A,ELK3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0002431	0.00836	1	1	2	Fc receptor mediated stimulatory signaling	BP	0.733	LYN	down_ACOR_EC
GO:0050873	0.00837	0.999	3	18	brown fat cell differentiation	BP	1	LEP,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:2000515	0.00837	1	1	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	0.775	ARG2	up_AORT_VSMC
GO:0009166	0.00838	0.998	6	31	nucleotide catabolic process	BP	0.456	PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:0032680	0.00838	1	2	36	regulation of tumor necrosis factor production	BP	1	NR1H4,BPI	up_APUL_EC

GO:0009653	0.00839	0.998	6	773	anatomical structure morphogenesis	BP	1	HOXC10,EYA1,HOXA9,TBX15,HOXA11,SHOX2	up_VFEM_VSMC
GO:0071706	0.00839	1	2	40	tumor necrosis factor superfamily cytokine	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0021825	0.00839	1	1	4	substrate-dependent cerebral cortex tangential	BP	1	SLIT2	up_VPUL_VSMC
GO:0060603	0.0084	1	1	7	mammary gland duct morphogenesis	BP	0.775	ESR1	up_AORT_VSMC
GO:0050789	0.00841	0.997	21	3295	regulation of biological process	BP	0.795	HOXC10,EYA1,HOXA9,TOX,MAP2K6,AVPR1A,HOXA10,TRIM9,HOXB7,HOXA7,ENSCAFG00000018194,SIX1,YBX3,MAB21L1,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3	up_VFEM_EC
GO:0007416	0.00841	1	2	36	synapse assembly	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0072006	0.00842	1	2	59	nephron development	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0007219	0.00842	1	1	59	Notch signaling pathway	BP	1	GATA5	down_AFEM_VSMC
GO:0098528	0.00842	1	1	2	skeletal muscle fiber differentiation	BP	0.795	CYP26B1	up_VFEM_EC
GO:0071605	0.00843	1	2	3	monocyte chemotactic protein-1 production	BP	0.456	NR1H4,SOCS5	down_VSAP_EC
GO:0071637	0.00843	1	2	3	regulation of monocyte chemotactic protein-1	BP	0.456	NR1H4,SOCS5	down_VSAP_EC
GO:0071638	0.00843	1	2	3	negative regulation of monocyte chemotactic	BP	0.456	NR1H4,SOCS5	down_VSAP_EC
GO:0007267	0.00844	0.999	4	332	cell-cell signaling	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0060048	0.00844	1	1	30	cardiac muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0032609	0.00845	0.998	6	25	interferon-gamma production	BP	0.387	PDE4D,TLR4,GATA3,IRF8,TLR3,HMGB1	up_VCAV_EC
GO:0007043	0.00845	1	1	28	cell-cell junction assembly	BP	1	JUP	down_VFEM_VSMC
GO:0008582	0.00845	1	1	2	regulation of synaptic growth at neuromuscular	BP	0.795	SIX1	up_VFEM_EC
GO:0030910	0.00845	1	1	2	olfactory placode formation	BP	0.795	SIX1	up_VFEM_EC
GO:0031339	0.00845	1	1	2	negative regulation of vesicle fusion	BP	0.795	TRIM9	up_VFEM_EC
GO:0061055	0.00845	1	1	2	myotome development	BP	0.795	SIX1	up_VFEM_EC
GO:0071698	0.00845	1	1	2	olfactory placode development	BP	0.795	SIX1	up_VFEM_EC
GO:0071699	0.00845	1	1	2	olfactory placode morphogenesis	BP	0.795	SIX1	up_VFEM_EC
GO:0050673	0.00846	0.996	19	135	epithelial cell proliferation	BP	0.387	TNFAIP3,PDGFB,MEF2C,FERMT1,DLL4,GATA3,APLNR,EGFL7,MTSS1,BMP2,CAV2,PROX1,MCC,PRKD2,HMGB1,NRAS,NR4A1,VASH1,JCAD	up_VCAV_EC
GO:0009889	0.00846	0.997	11	1190	regulation of biosynthetic process	BP	0.853	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0033566	0.00846	1	1	1	gamma-tubulin complex localization	BP	1	MZT1	up_VPOR_EC
GO:0009605	0.00847	0.998	6	538	response to external stimulus	BP	1	NR1H4,RGS1,MRC1,CCL24,FLRT3,NEO1	up_VPUL_EC
GO:0035107	0.00847	1	2	60	appendage morphogenesis	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:0035108	0.00847	1	2	60	limb morphogenesis	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:1901605	0.00847866	0.9981	6	67	alpha-amino acid metabolic process	BP	0.96436359	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,AZIN2	up_ACOR_EC
GO:0055080	0.00848	0.999	3	176	cation homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:0071310	0.00848	1	2	634	cellular response to organic substance	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071495	0.00849	0.995	50	365	cellular response to endogenous stimulus	BP	0.934	SMAD6,ACTN2,LEP,LBH,GATA5,SKP2,PRKAA2,FERMT1,BMP4,FGFR2,MED14,CASTOR1,LATS2,CITED2,AR,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,ANKRD1,CTSB,AKAP6,CREBRF,UBR1,PTPN22,NPNT,APLP1,PTGDR,SESN3,PRKCE,FRS2,AGRN,FUT8,APP,PSEN1,TGFBR1,JUP,NR3C1,DUSP22,HPGD,NOD2,FAM107A,DDIT4,ENSCAFG00000018360,GNAQ,INPP5K,SH3BP4,PARK7,CRKL	up_ACOR_VSMC
GO:0016576	0.00849	1	1	2	histone dephosphorylation	BP	0.795	EYA1	up_VFEM_EC
GO:0048706	0.0085	0.997	11	59	embryonic skeletal system development	BP	0.387	EIF4A3,HOXA3,XYLT1,MMP14,HOXA7,HOXB7,HOXC6,HOXB5,TBX15,HOXA9,SIX4	down_ACOR_VSMC

GO:0007010	0.00852	0.995	53	441	cytoskeleton organization	BP	0.388	PLK2,TEK,HCLS1,KIT,ARHGEF15,ENSCAFG00000007112,AMOT,BAIAP2L1,MEF2C,EDN1,RAB11A,ARHGAP28,TMOD1,MTSS1,NECTIN2,MTOR,HOOK3,SLK,CEP68,PDZD8,NCKAP1,MZT1,PROX1,IQGAP2,ENSCAFG00000010224,EPB41,ELMO1,STMN1,FLNB,PAK2,SWAP70,NCK1,FES,SENP6,GCC2,TAOK1,CTNNA1,FMNL3,VPS54,ARPC5L,ARHGDIB,ZW10,ARHGAP26,ATRX,HAUS3,GAS2L3,TNFAIP1,TMOD3,ARHGEF2,FSCN1,FBXO5,ZMYM2,SASS6	up_VCAV_EC
GO:0006508	0.00852	0.995	42	483	proteolysis	BP	0.456	PRICKLE1,MYH9,PLK3,HSPA5,SERPINE1,SOCS5,HM13,PRKACB,HSP90B1,ENSCAFG00000005575,PGK1,TRIB3,PRCP,PTGS2,SEL1L,USP12,DNAJC10,UBA6,UCHL5,SPOPL,ADAM17,DNAJB9,CRYAB,APOE,USP48,LYN,DDIT3,FAM162A,CBLC,GSK3B,CUL2,REST,SPOP,DISC1,RAD23A,PAK2,A2M,TMTC3,SPINK2,RHBDF2,USP14,TNFAIP1	down_VSAP_EC
GO:0032269	0.00852	0.995	29	306	negative regulation of cellular protein metabolic process	BP	0.456	SERPINE1,SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,SESN2,PTGS2,DNAJC10,NXN,PTPN2,UCHL5,SPOPL,EIF4EBP1,CNOT7,CRYAB,APOE,LYN,STRAP,CBLC,ATF3,EIF2S1,CDYL,PAK2,A2M,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:0051239	0.00852	0.998	9	859	regulation of multicellular organismal process	BP	0.854	HOXA11,HOXA9,NETO1,GATM,HOXC10,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:1901863	0.00852	0.998	7	25	positive regulation of muscle tissue	BP	0.934	BMP4,FGFR2,GJA1,PPARGC1A,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0072520	0.00853	1	3	5	seminiferous tubule development	BP	0.934	ATRX,SPINK2,WDR48	up_ACOR_VSMC
GO:0008209	0.00854	1	1	8	androgen metabolic process	BP	0.78	ESR1	up_AORT_VSMC
GO:0061387	0.00855	1	2	18	regulation of extent of cell growth	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0021756	0.00856	1	1	6	striatum development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0016525	0.00857	0.998	7	38	negative regulation of angiogenesis	BP	0.456	SULF1,SERPINE1,SPARC,PGK1,THBS2,CTNNB1,STARD13	down_VSAP_EC
GO:2000181	0.00857	0.998	7	38	negative regulation of blood vessel	BP	0.456	SULF1,SERPINE1,SPARC,PGK1,THBS2,CTNNB1,STARD13	down_VSAP_EC
GO:0010453	0.00857	0.999	3	9	regulation of cell fate commitment	BP	1	BMPR1A,LMO4,LOXL3	down_VCAV_EC
GO:0071346	0.00857	1	2	41	cellular response to interferon-gamma	BP	1	MRC1,CCL24	up_VPUL_EC
GO:0035914	0.00858	0.998	6	22	skeletal muscle cell differentiation	BP	0.39	EPHB1,MEF2C,ATF3,FOXN2,NR1D2,CDON	up_VCAV_EC
GO:0003128	0.00858	1	1	6	heart field specification	BP	1	GATA5	up_VCAV_VSMC
GO:0070170	0.00858	1	1	1	regulation of tooth mineralization	BP	1	ASPN	up_VPOR_EC
GO:0070171	0.00858	1	1	1	negative regulation of tooth mineralization	BP	1	ASPN	up_VPOR_EC
GO:0030182	0.00859	0.999	3	327	neuron differentiation	BP	1	HOXC10,EYA1,IRX5	up_AFEM_VSMC
GO:0060689	0.00859	1	2	2	cell differentiation involved in salivary gland	BP	1	CLCN2,NFIB	up_VSAP_EC
GO:1901888	0.0086	0.998	7	29	regulation of cell junction assembly	BP	0.39	TEK,PRKCH,RAPGEF1,SLK,APOD,RAPGEF2,ENSCAFG00000002015	up_VCAV_EC
GO:0008406	0.0086	1	2	57	gonad development	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0045137	0.0086	1	2	57	development of primary sexual characteristics	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0003221	0.00861	1	1	3	right ventricular cardiac muscle tissue	BP	1	NKX2-5	up_VPOR_VSMC
GO:0055074	0.00862	0.996	17	95	calcium ion homeostasis	BP	0.934	ADRA1B,PLCG2,HTR2B,MICU2,ITPR1,F2RL1,DMPK,PRKCE,APP,PSEN1,CHD7,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,STC2	up_ACOR_VSMC
GO:1904063	0.00862	0.999	5	17	negative regulation of cation transmembrane	BP	0.392	NEDD4,CAV1,SLC30A1,GSTO1,REM1	down_ACOR_VSMC
GO:0030154	0.00863	0.999	5	1040	cell differentiation	BP	1	HOXC10,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:0010954	0.00864	1	1	6	positive regulation of protein processing	BP	1	C6	up_VCAV_VSMC
GO:1903319	0.00864	1	1	6	positive regulation of protein maturation	BP	1	C6	up_VCAV_VSMC
GO:0042711	0.00864	1	1	2	maternal behavior	BP	0.795	AVPR1A	up_VFEM_EC
GO:0060746	0.00864	1	1	2	parental behavior	BP	0.795	AVPR1A	up_VFEM_EC

GO:0051444	0.00865	1	1	6	negative regulation of ubiquitin-protein	BP	1	LIMK1	up_VCAV_VSMC
GO:0045773	0.00866	1	1	6	positive regulation of axon extension	BP	1	LIMK1	up_VCAV_VSMC
GO:0007625	0.00867	1	1	6	grooming behavior	BP	1	SLITRK5	up_VCAV_VSMC
GO:0042471	0.00868	1	2	34	ear morphogenesis	BP	0.795	EYA1,SIX1	up_VFEM_EC
GO:1904385	0.00868	1	1	6	cellular response to angiotensin	BP	1	CA2	up_VCAV_VSMC
GO:1990776	0.00868	1	1	6	response to angiotensin	BP	1	CA2	up_VCAV_VSMC
GO:0031424	0.00868	1	1	3	keratinization	BP	1	CYP26B1	up_VPOR_VSMC
GO:0045576	0.00869	0.999	4	12	mast cell activation	BP	0.393	KIT,NECTIN2,SNAP23,FES	up_VCAV_EC
GO:0038092	0.00869	1	1	4	nodal signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:0001659	0.00872	0.998	5	54	temperature homeostasis	BP	1	CMKLR1,HOXC10,LEP,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:0071286	0.00873	1	1	1	cellular response to magnesium ion	BP	1	FBP1	up_VPOR_EC
GO:0006793	0.008735436	0.99496	37	948	phosphorus metabolic process	BP	0.96436359	NR1H4,BRSK1,PLCL1,PKIB,THNSL2,SOX9,NMNAT2,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,CFI,GUCY1B1,GRK7,TNFRSF19,DCLK2,CHPT1,MAPK8IP2,MAVS,LRRC15,PIGS,LRP4,SH3RF3,AK7,LRRC4,ALDOC,RARRES2,STK32C,NRP1,AGPAT2,PRKCD,PPP1R26,DBNDD2,CCNYL1	up_ACOR_EC
GO:0070302	0.00874	0.996	15	78	regulation of stress-activated protein kinase signaling cascade	BP	0.934	LEP,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,PTPN22,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0010896	0.00874	1	1	1	regulation of triglyceride catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0010898	0.00874	1	1	1	positive regulation of triglyceride catabolic	BP	1	ABHD5	up_VPOR_EC
GO:0045638	0.00875	1	2	33	negative regulation of myeloid cell	BP	0.795	HOXA9,HOXA7	up_VFEM_EC
GO:0048754	0.00875	1	2	57	branching morphogenesis of an epithelial tube	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0005984	0.00875	1	1	3	disaccharide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046351	0.00875	1	1	3	disaccharide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043062	0.00877	0.998	7	99	extracellular structure organization	BP	1	CTSS,MFAP4,PLAGL2,GREM1,POSTN,RECK,FAP	up_AFEM_EC
GO:0035115	0.00877	1	1	12	embryonic forelimb morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0021978	0.00877	1	1	3	telencephalon regionalization	BP	1	EMX2	up_VFEM_VSMC
GO:0031126	0.00878	0.999	3	6	snoRNA 3'-end processing	BP	0.396	FBL,ENSCAFG00000019620,EXOSC5	down_ACOR_VSMC
GO:0006706	0.00878	1	2	3	steroid catabolic process	BP	0.463	APOE,YWHAH	down_VSAP_EC
GO:0007275	0.00879	0.997	11	1370	multicellular organism development	BP	1	NR1H4,TBX5,HOXA2,MAPK10,HOXA3,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:0060349	0.0088	0.997	9	38	bone morphogenesis	BP	1	HOXA11,PEX7,AXIN2,OSR2,INSIG2,RARG,SHOX2,TGFBR2,CITED2	up_VSAP_EC
GO:0070141	0.0088	1	1	2	response to UV-A	BP	0.795	MME	up_VFEM_EC
GO:0048645	0.00881	1	2	33	animal organ formation	BP	0.795	EYA1,SIX1	up_VFEM_EC
GO:0009404	0.00882	1	1	6	toxin metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0009111	0.00882	1	1	2	vitamin catabolic process	BP	0.795	CYP26B1	up_VFEM_EC
GO:1903350	0.00883	1	1	4	response to dopamine	BP	1	GABPA	down_AFEM_EC
GO:1903351	0.00883	1	1	4	cellular response to dopamine	BP	1	GABPA	down_AFEM_EC
GO:0031023	0.00884	0.997	11	58	microtubule organizing center organization	BP	0.397	HAUS8,NEK2,POC1A,WDR62,NUP62,PLK4,CDK2,SASS6,RBM14,KIF11,GEN1	down_ACOR_VSMC
GO:0007155	0.00884	0.998	6	324	cell adhesion	BP	0.763	ACVRL1,LYN,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0045926	0.00884	1	2	72	negative regulation of growth	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0048856	0.00885	1	4	1533	anatomical structure development	BP	1	HOXA3,TBX5,HOXA2,HOXB5	up_APUL_VSMC
GO:0042573	0.00885	1	1	4	retinoic acid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC

GO:0090257	0.00886	0.997	11	52	regulation of muscle system process	BP	0.934	TNNT2,FGF13,ADRA1B,KCNE3,GATA5,PDE5A,DMPK,NPNT,JUP,EDN1,DOCK5	up_ACOR_VSMC
GO:1903555	0.00886	1	2	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4,BPI	up_APUL_EC
GO:0006828	0.00886	1	1	3	manganese ion transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0032769	0.00886	1	1	2	negative regulation of monooxygenase activity	BP	0.857	CAV1	up_VSAP_VSMC
GO:0051001	0.00886	1	1	2	negative regulation of nitric-oxide synthase	BP	0.857	CAV1	up_VSAP_VSMC
GO:0086103	0.00886	1	1	2	G protein-coupled receptor signaling pathway involved in heart	BP	0.857	CAV1	up_VSAP_VSMC
GO:0072001	0.00887	0.999	3	104	renal system development	BP	0.857	HOXA11,EMX2,SALL1	up_VSAP_VSMC
GO:0042113	0.00888	0.997	12	64	B cell activation	BP	0.4	IL7R,KIT,TNFAIP3,MEF2C,TLR4,PELI1,HHEX,THOC1,SWAP70,MFNG,PLCG2,ATP11C	up_VCAV_EC
GO:0050673	0.00888	1	2	135	epithelial cell proliferation	BP	0.803	WNT7A,ESR1	up_AORT_VSMC
GO:0030038	0.00888093	0.99875	4	31	contractile actin filament bundle assembly	BP	0.96436359	ARHGAP6,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0043149	0.00888093	0.99875	4	31	stress fiber assembly	BP	0.96436359	ARHGAP6,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0072191	0.00889	1	1	2	ureter smooth muscle development	BP	0.795	SIX1	up_VFEM_EC
GO:0072193	0.00889	1	1	2	ureter smooth muscle cell differentiation	BP	0.795	SIX1	up_VFEM_EC
GO:0072198	0.00889	1	1	2	mesenchymal cell proliferation involved in	BP	0.795	SIX1	up_VFEM_EC
GO:0072199	0.00889	1	1	2	regulation of mesenchymal cell proliferation involved in	BP	0.795	SIX1	up_VFEM_EC
GO:0003151	0.0089	1	2	34	outflow tract morphogenesis	BP	0.795	EYA1,SIX1	up_VFEM_EC
GO:0009653	0.00892	0.999	4	773	anatomical structure morphogenesis	BP	0.803	HOXC10,HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0043031	0.00893	1	1	4	negative regulation of macrophage activation	BP	1	BPI	up_AORT_EC
GO:2000027	0.00895	1	2	72	regulation of animal organ morphogenesis	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0007010	0.00896	0.994	52	441	cytoskeleton organization	BP	0.402	FSCN1,FLNB,FMNL3,SMC1A,ZW10,CAPG,CENPA,FBXO5,BIRC5,CDK1,LIMA1,NF2,AURKB,STMN1,HAUS8,MAP3K20,NEK2,GAS2L3,PLK3,RCC1,POC1A,WDR62,ESPL1,SPC25,NDC80,RAC1,NUP62,EMP2,PDXP,PLK4,IQGAP2,CDC42EP4,SMC3,CDK2,STAG1,ENSCAFG00000005299,EZR,SASS6,RBM14,CORO1A,PHACTR4,CDC20,ASPM,MAST2,ARPC1B,ENSCAFG00000010224,ARHGEF2,KIF11,SIX4,TTLL1,GEN1,KIF24	down_ACOR_VSMC
GO:0001655	0.00896	1	2	116	urogenital system development	BP	0.803	ARG2,ESR1	up_AORT_VSMC
GO:0072697	0.00896	1	1	4	protein localization to cell cortex	BP	1	GPSM2	down_AFEM_EC
GO:0045765	0.00897	0.997	13	105	regulation of angiogenesis	BP	0.47	VEGFA,SULF1,SERPINE1,SPARC,JCAD,PGK1,PIK3C2A,HIF1A,THBS2,MTDH,CTNNB1,STARD13,NRP1	down_VSAP_EC
GO:1901362	0.00897	0.998	8	1293	organic cyclic compound biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0001656	0.00897	1	2	35	metanephros development	BP	0.795	EYA1,SIX1	up_VFEM_EC
GO:0051661	0.00897	1	1	4	maintenance of centrosome location	BP	1	GPSM2	down_AFEM_EC
GO:0001974	0.00897	1	1	13	blood vessel remodeling	BP	1	HOXA3	up_APUL_VSMC
GO:0072378	0.00898	1	2	2	blood coagulation, fibrin clot formation	BP	1	KLKB1,FBLN1	up_VSAP_EC
GO:0002042	0.00899	0.998	7	29	cell migration involved in sprouting angiogenesis	BP	0.404	PLK2,CLEC14A,DLL4,PIK3C2A,EPHB4,MAP3K3,JCAD	up_VCAV_EC
GO:0014902	0.00899	1	2	34	myotube differentiation	BP	0.863	STIM1,SHOX2	up_VSAP_VSMC
GO:1902626	0.00899	1	1	1	assembly of large subunit precursor of preribosome	BP	1	RSL24D1	up_VPOR_EC
GO:0032635	0.00901	1	2	37	interleukin-6 production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0030035	0.00901	1	1	4	microspike assembly	BP	1	FSCN1	down_AFEM_EC
GO:0032534	0.00901	1	1	4	regulation of microvillus assembly	BP	1	FSCN1	down_AFEM_EC

GO:2001236	0.00902	0.997	11	59	regulation of extrinsic apoptotic signaling	BP	0.404	TNFAIP3,ATF3,MADD,PAK2,BCL10,CTNNA1,PMAIP1,RIPK1,ITGA6,SKIL,ARHGEF2	up_VCAV_EC
GO:0046824	0.00902	1	1	30	positive regulation of nucleocytoplasmic	BP	1	JUP	down_VFEM_VSMC
GO:0060216	0.00902	1	1	3	definitive hemopoiesis	BP	1	HOXA9	up_VFEM_VSMC
GO:0044271	0.00903	0.999	6	1501	cellular nitrogen compound biosynthetic	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0099576	0.00903	1	2	2	regulation of protein catabolic process at postsynapse, modulating	BP	0.934	EGLN1,RNF19A	up_ACOR_VSMC
GO:0072073	0.00903	1	2	60	kidney epithelium development	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0032879	0.00904	0.994	62	767	regulation of localization	BP	0.471	ARHGEF2,VEGFA,SULF1,NR1H4,PLK3,HSPA5,SERPINE1,ACTN1,SPARC,ERO1A,PTPN14,ENPP1,JCAD,PTPN11,DPYSL3,TRIB3,PPP1R12A,PRCP,SESN2,REM1,WDR1,MYO1C,PIK3C2A,MSN,KIF5B,HIF1A,IWS1,YIPF5,ZPR1,PTPN2,YES1,ADAM17,CTNNB1,CRYAB,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,DDIT3,MMD,GSK3B,NKAIN1,NEXN,SH3GLB1,TAX1BP3,SDC4,HTT,REST,ABHD5,ZMYND8,CALM1,RAB11FIP1,LRRTM2,INHBA,SIX4,CDKN1A,NRP1,RHBDF2,YWHAH,HOMER1	down_VSAP_EC
GO:0090100	0.00904	1	2	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.773	ACVRL1,SULF1	down_ACOR_EC
GO:0045056	0.00904	1	1	5	transcytosis	BP	1	RAB11B	down_VPOR_EC
GO:0072507	0.00905	0.996	18	103	divalent inorganic cation homeostasis	BP	0.934	ADRA1B,PLCG2,HTR2B,CNNM2,MICU2,ITPR1,F2RL1,DMPK,PRKCE,APP,PSEN1,CHD7,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,STC2	up_ACOR_VSMC
GO:0022610	0.00906	0.998	6	326	biological adhesion	BP	0.773	ACVRL1,LYN,PDPN,HOXA7,SULF1,STX4	down_ACOR_EC
GO:0018198	0.00906	0.999	4	10	peptidyl-cysteine modification	BP	0.934	TMX3,OXR1,PARK7,ZDHHC21	up_ACOR_VSMC
GO:0098771	0.00907	0.999	3	180	inorganic ion homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:0042306	0.00907	1	1	31	regulation of protein import into nucleus	BP	1	JUP	down_VFEM_VSMC
GO:0007165	0.00909	0.993	111	1496	signal transduction	BP	0.471	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,NR1H4,HSPA5,SERPINE1,SOCS5,SGK1,ERO1A,PRKACB,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CASP3,HYOU1,WSB1,BCAR3,NUAK1,PTPN11,LRRC8A,TRIB3,FARP1,ILK,FHL2,PPP1R12A,PRCP,SMARCA4,SESN2,TGFBR1,PTGS2,REM1,MYO1C,PIK3C2A,CHSY1,UACA,HIF1A,CX3CL1,ENSCAFG00000000562,DNAJC10,TNIK,NXN,RGS2,PTPN2,EIF2B1,NEO1,PLCL1,MTDH,ESM1,ADAM17,AGRN,EIF4EBP1,SKAP2,CNOT7,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,STARD13,ENSCAFG00000002015,APOE,WWC3,PDE1A,ZC3H15,UBA5,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,TLN1,CBLC,ATF3,GSK3B,CDC37,ITGB3,SH3GLB1,TAX1BP3,MYO1E,KPNA1,HTT,MAPK10,SH2B3,RDH11,ARFGEF3,CALM1,DISC1,PAK2,CREB3L2,INHBA,CAMK2D,ENSCAFG00000018360,HIF1AN,BTK,CDKN1A,NRP1,SH3RF3,RHBDF2,YWHAH,TNFAIP1,MADD,SEC13,KDM3A,MID1	down_VSAP_EC
GO:0030033	0.00909	0.999	3	7	microvillus assembly	BP	0.471	FSCN1,TNIK,KLF5	down_VSAP_EC
GO:0051147	0.0091	0.997	9	44	regulation of muscle cell differentiation	BP	0.407	KIT,PDGFB,MEF2C,EDN1,MTOR,BMP2,PROX1,ENSCAFG00000010596,ZEB1	up_VCAV_EC
GO:0030325	0.0091	1	1	5	adrenal gland development	BP	1	CITED2	down_VPOR_EC
GO:0110020	0.009110875	0.9987	4	31	regulation of actomyosin structure organization	BP	0.96436359	ARHGAP6,ARHGAP28,PTGER4,NRP1	up_ACOR_EC
GO:0000725	0.00912	0.997	11	58	recombinational repair	BP	0.406	RPA1,PARPBP,GINS4,RAD54L,RAD51,TONSL,BRCA1,RBBP8,SMC6,H2AFX,GEN1	down_ACOR_VSMC
GO:0010466	0.00916	1	1	32	negative regulation of peptidase activity	BP	1	CST3	down_AORT_EC
GO:0010951	0.00916	1	1	32	negative regulation of endopeptidase activity	BP	1	CST3	down_AORT_EC
GO:0030154	0.00917	0.998	7	1040	cell differentiation	BP	1	HOXC10,EYA1,HOXA9,SPINK5,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048856	0.00919	0.999	6	1533	anatomical structure development	BP	1	HOXC10,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC

GO:0060421	0.00919	1	1	14	positive regulation of heart growth	BP	1	TBX5	up_APUL_VSMC
GO:0048706	0.0092	1	2	59	embryonic skeletal system development	BP	1	HOXA9,HOXC6	up_AORT_EC
GO:0033572	0.00922	1	1	5	transferrin transport	BP	1	RAB11B	down_VPOR_EC
GO:0071375	0.009228706	0.9979	6	68	cellular response to peptide hormone stimulus	BP	0.96436359	NR1H4,ENSCAFG00000004331,ACTN2,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0010870	0.00923	1	2	2	positive regulation of receptor biosynthetic	BP	0.409	EDN1,HIF1A	up_VCAV_EC
GO:0072359	0.00924	0.995	34	368	circulatory system development	BP	0.474	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,LTBP1,PTPN14,ERRFI1,JCAD,PGK1,PTPN11,TMED2,ILK,FHL2,PRCP,TGFBR1,PIK3C2A,HIF1A,THBS2,NXN,MTDH,ESM1,ACTA2,ADAMTS6,CTNNB1,STARD13,APOE,KLF5,DDIT3,NEXN,MYO1E,REST,NRP1	down_VSAP_EC
GO:0071363	0.00924	0.996	20	188	cellular response to growth factor stimulus	BP	0.474	VEGFA,SULF1,HSPA5,SPARC,JCAD,SNX25,PTPN11,ILK,TGFBR1,MYO1C,HIF1A,ZPR1,YES1,NEO1,ADAM17,CTNNB1,ENSCAFG00000002015,STRAP,ENSCAFG00000018360,NRP1	down_VSAP_EC
GO:0046631	0.00924	0.997	8	35	alpha-beta T cell activation	BP	0.409	IL6,GATA3,ARG2,MTOR,ELF4,ITPKB,HMGB1,BMX	up_VCAV_EC
GO:0060429	0.00924	0.999	4	341	epithelium development	BP	1	BARX1,NKX2-5,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0032092	0.00924	1	2	38	positive regulation of protein binding	BP	1	HOXA3,PLCL1	up_APUL_EC
GO:0030336	0.00927	0.999	3	86	negative regulation of cell migration	BP	0.779	ACVRL1,HOXA7,SULF1	down_ACOR_EC
GO:0048585	0.00928	0.994	42	475	negative regulation of response to stimulus	BP	0.474	ARHGEF2,PRICKLE1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,SNX25,HYOU1,PTPN11,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,NXN,RGS2,PTPN2,DDX39B,ADAM17,CNOT7,CTNNB1,APOE,WWC3,MMP28,LYN,STRAP,DDIT3,CBLC,ATF3,GSK3B,TAX1BP3,HTT,CALM1,A2M,HIF1AN,NRP1,USP14,TNFAIP1	down_VSAP_EC
GO:2000312	0.00928	1	1	2	regulation of kainate selective glutamate	BP	0.871	NETO1	up_VSAP_VSMC
GO:1905209	0.00929	1	1	13	positive regulation of cardiocyte differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0031399	0.00931	0.994	62	559	regulation of protein modification process	BP	0.409	EPHB1,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,IWS1,ATF3,RAPGEF1,TLR4,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,MTOR,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,SH3BP5,PPP1R2,ITPKB,PROX1,MADD,PAK2,PRKD2,SWAP70,TLR3,NCK1,OTUD4,NSD1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,CNOT7,HMGB1,BLM,SPTBN4,RIPK1,PDGFD,UBE2D1,KDM5A,KDM3A,ATRX,IVNS1ABP,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0051767	0.00931	1	2	2	nitric-oxide synthase biosynthetic process	BP	0.409	TLR4,EDN1	up_VCAV_EC
GO:0051769	0.00931	1	2	2	regulation of nitric-oxide synthase biosynthetic	BP	0.409	TLR4,EDN1	up_VCAV_EC
GO:0002224	0.00931	1	2	34	toll-like receptor signaling pathway	BP	0.871	TLR2,CAV1	up_VSAP_VSMC
GO:0097305	0.00931	1	1	31	response to alcohol	BP	1	JUP	down_VFEM_VSMC
GO:0034694	0.00933	0.999	4	9	response to prostaglandin	BP	0.953	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0032793	0.00934	0.999	3	6	positive regulation of CREB transcription factor	BP	0.41	RELN,PRKD2,CD200	up_VCAV_EC
GO:0030879	0.00935	1	2	34	mammary gland development	BP	0.871	HOXA9,CAV1	up_VSAP_VSMC
GO:0045823	0.00935	1	1	4	positive regulation of heart contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051252	0.00936	0.999	5	1051	regulation of RNA metabolic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0034341	0.00936	1	2	43	response to interferon-gamma	BP	1	MRC1,CCL24	up_VPUL_EC
GO:0060317	0.00936	1	1	11	cardiac epithelial to mesenchymal transition	BP	1	TGFBR1	down_VSAP_VSMC
GO:1904385	0.009361005	0.99968	2	6	cellular response to angiotensin	BP	0.96436359	ACTN2,PRKCD	up_ACOR_EC
GO:1990776	0.009361005	0.99968	2	6	response to angiotensin	BP	0.96436359	ACTN2,PRKCD	up_ACOR_EC
GO:0030968	0.00937	0.998	6	33	endoplasmic reticulum unfolded protein	BP	0.476	HSPA5,ERO1A,PTPN2,DDIT3,ATF3,CREB3L2	down_VSAP_EC

GO:0018335	0.00937	1	2	2	protein succinylation	BP	1	DLST,DLD	up_VSAP_EC
GO:0106077	0.00937	1	2	2	histone succinylation	BP	1	DLST,DLD	up_VSAP_EC
GO:1990144	0.00938	1	2	3	intrinsic apoptotic signaling pathway in	BP	0.476	HYOU1,BNIP3	down_VSAP_EC
GO:0008593	0.00938	1	1	33	regulation of Notch signaling pathway	BP	1	GATA5	down_VFEM_VSMC
GO:0003203	0.00938	1	1	11	endocardial cushion morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0034645	0.00939	0.997	13	1546	cellular macromolecule biosynthetic process	BP	0.871	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0003057	0.00939	1	1	2	regulation of the force of heart contraction by	BP	0.871	CAV1	up_VSAP_VSMC
GO:0048662	0.009397963	0.99914	3	18	negative regulation of smooth muscle cell	BP	0.96436359	NDRG2,PTGIR,CLSTN1	up_ACOR_EC
GO:0007517	0.00941	0.999	3	100	muscle organ development	BP	0.871	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0023051	0.009417702	0.99453	37	954	regulation of signaling	BP	0.96436359	CNTNAP4,SH3TC2,CDH3,NR1H4,BRSK1,PLCL1,SOX9,RGS1,NDRG2,KCNB1,FZD5,CCDC3,IFI6,DUSP26,DIXDC1,PTGIR,NOD2,PDE4A,SMAD6,ESM1,PAK3,TNFRSF19,ARHGDIB,ADAMTSL2,MAPK8IP2,MAVS,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0001501	0.00943	0.995	27	178	skeletal system development	BP	1	TBX15,HOXA11,HOXA7,PEX7,HOXA9,WNT11,AXIN2,OSR2,INSIG2,PPARGC1B,IRX5,HOXD3,HOXA6,OSR1,ZBTB16,RARG,HOXC4,ZEB1,FBXW4,SULF2,SHOX2,HOXC10,NFIB,ZFAND5,BGLAP,TGFBR2,CITED2	up_VSAP_EC
GO:1902903	0.00945	0.996	19	125	regulation of supramolecular fiber organization	BP	0.411	HCLS1,ARHGEF15,BAIAP2L1,MEF2C,EDN1,ARHGAP28,TMOD1,MTOR,NCKAP1,PROX1,IQGAP2,STMN1,SWAP70,NCK1,FES,TAOK1,ARPC5L,TMOD3,ARHGEF2	up_VCAV_EC
GO:0010594	0.00945	0.997	10	71	regulation of endothelial cell migration	BP	0.476	VEGFA,SPARC,JCAD,PRCP,PIK3C2A,HIF1A,ADAM17,STARD13,APOE,NRP1	down_VSAP_EC
GO:2000172	0.00945	1	1	2	regulation of branching morphogenesis of a nerve	BP	0.871	SHOX2	up_VSAP_VSMC
GO:0030279	0.00949	0.999	3	19	negative regulation of ossification	BP	1	TWIST2,GREM1,AXIN2	up_AFEM_EC
GO:0045843	0.00949	1	1	13	negative regulation of striated muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0016358	0.0095	0.997	9	58	dendrite development	BP	0.476	SIPA1L1,TNIK,UBA6,APOE,VLDLR,PAK2,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0046113	0.0095	1	2	2	nucleobase catabolic process	BP	1	GDA,ALDH6A1	up_VSAP_EC
GO:0003263	0.0095	1	1	4	cardioblast proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:0006468	0.00952	0.994	47	544	protein phosphorylation	BP	0.476	ARHGEF2,VEGFA,SOCS5,SGK1,ENPP1,ERRFI1,JCAD,SNX25,BCAR3,NUAK1,PTPN11,TRIB3,ILK,SESN2,PTGS2,DNAJC10,TNIK,PTPN2,YES1,PLCL1,ADAM17,CNOT7,MAGED1,CTNNB1,CDK8,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,HTT,MAPK10,EIF2S1,PAK2,INHBA,CAMK2D,BTK,CDKN1A,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:1902041	0.00953	0.998	6	23	regulation of extrinsic apoptotic signaling pathway via death	BP	0.411	TNFAIP3,ATF3,MADD,PMAIP1,SKIL,ARHGEF2	up_VCAV_EC
GO:0032400	0.00953	0.999	3	6	melanosome localization	BP	0.411	RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:0032401	0.00953	0.999	3	6	establishment of melanosome localization	BP	0.411	RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:0051875	0.00953	0.999	3	6	pigment granule localization	BP	0.411	RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:0051905	0.00953	0.999	3	6	establishment of pigment granule localization	BP	0.411	RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:0048645	0.00954	1	1	33	animal organ formation	BP	1	GATA5	down_VFEM_VSMC
GO:0001501	0.00956	0.997	10	178	skeletal system development	BP	1	TBX15,HOXA9,IRX5,HOXC10,XYLT1,HOXA7,GREM1,HOXA6,PTHLH,AXIN2	up_AFEM_EC
GO:0043009	0.00956	1	2	227	chordate embryonic development	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0051606	0.00956	1	1	33	detection of stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0010611	0.00956	1	1	11	regulation of cardiac muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC
GO:0014743	0.00956	1	1	11	regulation of muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC

GO:0090131	0.00957	1	2	3	mesenchyme migration	BP	0.476	ACTG2,ACTA2	down_VSAP_EC
GO:0051563	0.00958	1	2	2	smooth endoplasmic reticulum calcium ion	BP	0.966	APP,PSEN1	up_ACOR_VSMC
GO:1905908	0.00958	1	2	2	positive regulation of amyloid fibril formation	BP	0.966	APP,PSEN1	up_ACOR_VSMC
GO:0007409	0.00958	1	2	109	axonogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0060043	0.00958	1	1	14	regulation of cardiac muscle cell proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0110110	0.00959	1	2	34	positive regulation of animal organ	BP	0.841	HOXB7,SIX1	up_VFEM_EC
GO:0060914	0.00959	1	1	11	heart formation	BP	1	GATA5	down_VSAP_VSMC
GO:1904467	0.0096	1	1	8	regulation of tumor necrosis factor secretion	BP	0.856	ARG2	up_AORT_VSMC
GO:0018195	0.009604774	0.99966	2	6	peptidyl-arginine modification	BP	0.96436359	NR1H4,RIOX2	up_ACOR_EC
GO:0001568	0.00961	0.995	25	252	blood vessel development	BP	0.476	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,LTBP1,JCAD,PGK1,TMED2,PRCP,PIK3C2A,HIF1A,THBS2,MTDH,ESM1,ACTA2,ADAMTS6,CTNNB1,STARD13,APOE,KLF5,DDIT3,MYO1E,NRP1	down_VSAP_EC
GO:0000904	0.00961	0.995	20	181	cell morphogenesis involved in differentiation	BP	0.476	SIPA1L1,MYH9,ACTN1,PTPN11,FLNB,IFRD1,ILK,WDR1,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,ENSCAFG00000002015,PLOD3,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0003430	0.00961	1	2	2	growth plate cartilage chondrocyte growth	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:1904589	0.00963	1	1	33	regulation of protein import	BP	1	JUP	down_VFEM_VSMC
GO:0007369	0.00965	1	2	63	gastrulation	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0030335	0.00966	0.999	4	165	positive regulation of cell migration	BP	0.801	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0034764	0.009668803	0.99815	5	50	positive regulation of transmembrane transport	BP	0.96436359	NR1H4,ENSCAFG00000004331,ACTN2,RARRES2,AZIN2	up_ACOR_EC
GO:0002218	0.00968	0.997	10	53	activation of innate immune response	BP	0.417	TNFAIP3,TNIP1,TMEM173,TLR4,PELI1,RIOK3,TLR3,OTUD4,HMGB1,LSM14A	up_VCAV_EC
GO:0002191	0.00968	1	2	2	cap-dependent translational initiation	BP	1	EIF3D,NCK1	up_VSAP_EC
GO:0006538	0.00968	1	2	2	glutamate catabolic process	BP	1	GOT1,ADHFE1	up_VSAP_EC
GO:0031646	0.00968	1	1	7	positive regulation of neurological system	BP	0.859	WNT7A	up_AORT_VSMC
GO:0001952	0.0097	1	1	34	regulation of cell-matrix adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0042126	0.00971	1	2	2	nitrate metabolic process	BP	1	SUOX,MARC1	up_VSAP_EC
GO:0030198	0.00972	0.999	3	81	extracellular matrix organization	BP	0.801	PDPN,SULF1,CSGALNACT1	down_ACOR_EC
GO:0110110	0.00972	1	1	34	positive regulation of animal organ	BP	1	GATA5	down_VFEM_VSMC
GO:1900182	0.00973	1	1	33	positive regulation of protein localization to	BP	1	JUP	down_VFEM_VSMC
GO:0097191	0.00974	0.996	13	79	extrinsic apoptotic signaling pathway	BP	0.417	TNFAIP3,ATF3,CASP8,MADD,PAK2,TLR3,BCL10,CTNNA1,PMAIP1,RIPK1,ITGA6,SKIL,ARHGEF2	up_VCAV_EC
GO:0090287	0.00975	0.996	12	91	regulation of cellular response to growth factor	BP	0.478	VEGFA,SULF1,HSPA5,JCAD,SNX25,ILK,MYO1C,HIF1A,NEO1,ADAM17,CTNNB1,STRAP	down_VSAP_EC
GO:0071345	0.00976	0.995	27	210	cellular response to cytokine stimulus	BP	0.417	ACKR1,HCLS1,GBP5,KIT,CXCL8,LAPTM5,CXCR4,PDGFB,TMEM173,NLRC5,GATA3,IRF8,ST3GAL6,MAPK13,IFNGR1,FLNB,OTUD4,CREB1,CNOT7,ADIPOR2,RIPK1,LSM14A,HIF1A,KDM3A,ENSCAFG00000002015,ARHGEF2,TJP2	up_VCAV_EC
GO:1900426	0.00976	1	2	2	positive regulation of defense response to	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0043309	0.00976	1	2	2	regulation of eosinophil degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0043311	0.00976	1	2	2	positive regulation of eosinophil degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:1902566	0.00976	1	2	2	regulation of eosinophil activation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:1902568	0.00976	1	2	2	positive regulation of eosinophil activation	BP	1	F2RL1,STX4	up_VSAP_EC

GO:0048666	0.00977	0.995	26	258	neuron development	BP	0.478	SIPA1L1,SGK1,PTPN11,DPYSL3,IFRD1,KIF5B,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,APOE,LYN,GSK3B,VLDLR,SDC4,MAPK10,PRMT1,EXT1,DISC1,PAK2,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0008277	0.00977	0.998	7	31	regulation of G protein-coupled receptor signaling	BP	0.417	CXCL8,EDN1,APLNR,ACPP,CAV2,STMN1,RGS2	up_VCAV_EC
GO:0045667	0.00977	0.998	6	38	regulation of osteoblast differentiation	BP	1	BMPR1A,CLSTN1,GLI3,TWIST2,DDR2,GREM1	down_VCAV_EC
GO:0019933	0.009805067	0.99857	4	32	cAMP-mediated signaling	BP	0.96436359	SOX9,PTH1R,PTGIR,PDE4A	up_ACOR_EC
GO:0033135	0.00982	1	2	40	regulation of peptidyl-serine phosphorylation	BP	1	PLCL1,NTRK2	up_APUL_EC
GO:2000650	0.00982	1	1	2	negative regulation of sodium ion transmembrane	BP	0.801	NEDD4	down_ACOR_EC
GO:0032640	0.00983	1	2	39	tumor necrosis factor production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0050793	0.00985	0.998	7	731	regulation of developmental process	BP	1	TBX5,NR1H4,EVI2B,WIF1,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0042118	0.00985	1	1	4	endothelial cell activation	BP	1	HOXA9	up_AORT_EC
GO:0046622	0.00985	1	1	15	positive regulation of organ growth	BP	1	TBX5	up_APUL_VSMC
GO:0016070	0.00986	0.993	148	1479	RNA metabolic process	BP	0.436	ELK3,HMGB1,RNPS1,SREBF1,IRAK1,PTBP1,IL F3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2, HMGA1,EIF4A3,HNRNPUL1,EDC3,HNRNPD,S REBF2,HINFP,VARS,NEDD4,SRSF2,MED17,U2 AF2,INTS7,POLA1,MTDH,HEY1,SNRPB2,SF1,S RRT,NOP56,POLE,DDX23,NAB2,CDCA7L,FUS, BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,U2AF1 ,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1, EDC4,AURKB,NONO,HNRNPL,EZH2,GREM1,F BL,FEN1,SMARCC1,RNASEH2B,PLK3,SFSWAP, PCNA,DHX33,HOXA7,SMG9,SF3B4,PHF5A,UH RF1,CKS2,DIS3,GMNN,BRCA1,NOC4L,WDR62 ,FASTKD3,NOC2L,E2F8,FARSA,DDX51,ENSCA FG00000015065,PPARD,YBX3,HNRNPF,NCL, NUP62,DDX28,FOSL1,SUV39H1,RSL1D1,THU MPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP1 ,DHX15,CDK2,SMARCB1,DDX39B,CCNA2,ENS CAFG00000005299,EZR,SF3A2,DHX38,RBM1 4,RBM17,OSGEP,POLR3F,HOXA10,ERF,ENSC AFG00000019620,TCERG1,RARS,METTL1,SM ARCAL1,NOP14,TBX15,ELF4,PRMT5,PSMC1,C TH,NOP58,ARHGEF2,ENSCAFG00000015189, SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,H OXA9,GLI1,JMJD6,H2AFX,WDR33,ENSCAFG0 0000003222,CDC5L,EMG1,RNASEH2C,RTCB, EXOSC5,GEMIN7,HMGN1,SIX4,SF3A1,MED16	down_ACOR_VSMC
GO:0051240	0.00986	0.993	63	489	positive regulation of multicellular organismal process	BP	0.971	ADRA1B,VEGFD,TLR1,PLCG2,LEP,LBH,GATA5, CD83,HTR2B,MBP,FERMT1,BMP4,FGFR2,TP5 3BP1,GJA1,HRH1,TLR3,WASF3,PPARGC1A,PD E5A,CITED2,ISG15,CD274,ZNF365,SASH1,FGF 18,FAM210B,PLAC8B,F2RL1,HRH2,ENPP4,CL STN1,NRP1,PTPN22,NPNT,SMARCD3,SLITRK5 ,TBX20,TBX5,PRKCE,FZD3,FRS2,DAG1,APP,PS EN1,CHD7,JUP,DDR2,EDN1,NOD2,B2M,DISC 1,SCAMP5,MAP3K7,INPP5K,DOCK5,ERAP1,P ARK7,SLC8A1,IL18R1,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:1901214	0.00986	0.996	11	81	regulation of neuron death	BP	0.481	HYOU1,AARS,HIF1A,ZPR1,CTNNB1,APOE,DDIT3,GSK3B,EIF2S1,SIX4,NRP1	down_VSAP_EC
GO:1905939	0.0099	1	1	5	regulation of gonad development	BP	1	CITED2	down_VPOR_EC
GO:0045637	0.00991	0.997	9	73	regulation of myeloid cell differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,ZFP36L1,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0007100	0.00991	0.999	3	6	mitotic centrosome separation	BP	0.436	NEK2,NUP62,KIF11	down_ACOR_VSMC
GO:0009792	0.00991	1	2	231	embryo development ending in birth or egg	BP	1	HOXA3,HOXB5	up_APUL_VSMC
GO:0010804	0.009918494	0.99965	2	6	negative regulation of tumor necrosis factor-mediated signaling	BP	0.96436359	NR1H4,CCDC3	up_ACOR_EC
GO:0050706	0.00992	1	1	9	regulation of interleukin-1 beta secretion	BP	0.875	ARG2	up_AORT_VSMC
GO:1903706	0.00993	0.995	18	119	regulation of hemopoiesis	BP	0.422	HCLS1,IL7R,MEF2C,GATA3,HOXB8,CASP8,MTOR,ITPKB,FES,JAG1,CREB1,HMGB1,RIPK1,ATP11C,CUL4A,HIF1A,ZEB1,TJP2	up_VCAV_EC

GO:0045935	0.00994	0.993	57	491	positive regulation of nucleobase-containing compound metabolic process	BP	0.422	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,NOS2,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0001656	0.00995	1	2	35	metanephros development	BP	0.898	HOXA11,SALL1	up_VSAP_VSMC
GO:0006468	0.00996	0.993	61	544	protein phosphorylation	BP	0.422	EPHB1,PLK2,TEK,HCLS1,KIT,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,EPHB4,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,BMP2K,SH3BP5,ERC1,MAPK13,ITPKB,PROX1,ENSCAFG00000010596,MADD,PAK2,PRKD2,TLR3,NCK1,FES,NSD1,PTGS2,MMD,TOP1,RAPGEF2,CREB1,TAOK1,CNOT7,HMGB1,BLM,SPTBN4,RIPK1,PDGFD,BMX,LMTK2,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0019725	0.00996	0.994	35	245	cellular homeostasis	BP	0.971	RHOT1,ADRA1B,PLCG2,SLC26A7,HTR2B,PRDX4,PRKAA2,CLCN3,MICU2,TMX3,ITPR1,F2RL1,ERO1B,EGLN1,SLC12A7,LRRC8C,DMPK,ATP7A,ORMDL3,PRKCE,APP,PSEN1,CHD7,LAMP2,DMXL1,RAB11B,EDN1,DISC1,HERPUD1,TXNDC5,GAA,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0060708	0.00996	1	1	2	spongiotrophoblast differentiation	BP	0.898	GJB5	up_VSAP_VSMC
GO:0045333	0.00997	1	2	74	cellular respiration	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0000028	0.00998	0.999	3	9	ribosomal small subunit assembly	BP	1	RPS10,MRPS11,RPS27	down_VCAV_EC
GO:0030878	0.00998	1	1	13	thyroid gland development	BP	1	HOXA3	up_APUL_VSMC
GO:0071605	0.00998	1	1	3	monocyte chemotactic protein-1 production	BP	1	NR1H4	up_VPUL_EC
GO:0071637	0.00998	1	1	3	regulation of monocyte chemotactic protein-1	BP	1	NR1H4	up_VPUL_EC
GO:0071638	0.00998	1	1	3	negative regulation of monocyte chemotactic	BP	1	NR1H4	up_VPUL_EC
GO:0019934	0.009981409	0.99964	2	6	cGMP-mediated signaling	BP	0.96436359	AQP1,GUCY1B1	up_ACOR_EC
GO:0002689	0.00999	1	1	5	negative regulation of leukocyte chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0033627	0.01	0.998	5	22	cell adhesion mediated by integrin	BP	0.487	SERPINE1,ITGA2,PTPN11,ADAM17,LYN	down_VSAP_EC
GO:0002374	0.01	1	1	7	cytokine secretion involved in immune	BP	1	TLR2	up_AFEM_VSMC
GO:0048635	0.01	1	1	14	negative regulation of muscle organ	BP	1	TBX5	up_APUL_VSMC
GO:0060017	0.01	1	1	3	parathyroid gland development	BP	1	HOXA3	up_VPUL_EC
GO:0010614	0.01	1	1	5	negative regulation of cardiac muscle	BP	1	GATA5	up_VPUL_VSMC
GO:0014741	0.01	1	1	5	negative regulation of muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0055026	0.01	1	1	5	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0035295	0.0101	0.994	28	356	tube development	BP	1	ADAMTS2,HSPB6,PDGFRB,SMAD9,DCN,ANGPT1,SDC4,BMPR1A,LOX,LMO4,ANPEP,CLSTN1,SEMA3C,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,IFT57,CDH2,LOXL3,SPRED1,SHC1,RDH10,GREM1,CLIC4,THRB	down_VCAV_EC
GO:0006066	0.0101	0.996	16	89	alcohol metabolic process	BP	1	NAPEPLD,LIPC,INSIG2,GOT1,INPP5E,LMF1,PPIP5K1,GALK1,RETSAT,LCAT,PCBD1,TKFC,MVK,LIPE,CYB5R3,SOAT1	up_VSAP_EC
GO:0051252	0.0101	0.997	10	1051	regulation of RNA metabolic process	BP	0.898	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0043473	0.0101	0.998	7	28	pigmentation	BP	0.423	EDNRB,KIT,ADAMTS9,MEF2C,RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:1901224	0.0101	0.998	6	20	positive regulation of NIK/NF-kappaB signaling	BP	0.971	TLR3,SASH1,APP,NOD2,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0048002	0.0101	0.999	4	10	antigen processing and presentation of peptide	BP	0.971	DLA88,B2M,ERAP1,TAPBPL	up_ACOR_VSMC
GO:0009617	0.0101	0.999	3	133	response to bacterium	BP	1	NR1H4,RGS1,MRC1	up_VPUL_EC

GO:0034644	0.0101	1	2	32	cellular response to UV	BP	0.801	USP28,NEDD4	down_ACOR_EC
GO:0048645	0.0101	1	2	33	animal organ formation	BP	0.801	HOXA3,SULF1	down_ACOR_EC
GO:0048736	0.0101	1	2	66	appendage development	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:0060173	0.0101	1	2	66	limb development	BP	1	HOXC10,HOXA9	up_AORT_EC
GO:0042742	0.0101	1	2	39	defense response to bacterium	BP	1	NR1H4,BPI	up_APUL_EC
GO:0009952	0.0101	1	2	66	anterior/posterior pattern specification	BP	1	HOXA3,BARX1	up_VPOR_VSMC
GO:0002278	0.0101	1	1	3	eosinophil activation involved in immune	BP	0.801	STX4	down_ACOR_EC
GO:0002447	0.0101	1	1	3	eosinophil mediated immunity	BP	0.801	STX4	down_ACOR_EC
GO:0015884	0.0101	1	1	3	folic acid transport	BP	0.801	PDPN	down_ACOR_EC
GO:0043307	0.0101	1	1	3	eosinophil activation	BP	0.801	STX4	down_ACOR_EC
GO:0043308	0.0101	1	1	3	eosinophil degranulation	BP	0.801	STX4	down_ACOR_EC
GO:0046697	0.0101	1	1	5	decidualization	BP	1	CITED2	down_VPOR_EC
GO:0034134	0.0101	1	1	7	toll-like receptor 2 signaling pathway	BP	1	TLR2	up_AFEM_VSMC
GO:2000136	0.0101	1	1	7	regulation of cell proliferation involved in	BP	1	EYA1	up_AFEM_VSMC
GO:0021522	0.0101	1	1	8	spinal cord motor neuron differentiation	BP	0.883	HOXC10	up_AORT_VSMC
GO:0062009	0.0101	1	1	8	secondary palate development	BP	0.885	WNT7A	up_AORT_VSMC
GO:1901862	0.0101	1	1	14	negative regulation of muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:2000826	0.0101	1	1	14	regulation of heart morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:1901213	0.0101	1	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GATA5	up_VCAV_VSMC
GO:0010759	0.0101	1	1	5	positive regulation of macrophage chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0019627	0.0101	1	1	3	urea metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0072677	0.0101	1	1	3	eosinophil migration	BP	1	CCL24	up_VPUL_EC
GO:0003207	0.0101	1	1	5	cardiac chamber formation	BP	1	TBX5	up_VPUL_VSMC
GO:0060353	0.0101	1	1	2	regulation of cell adhesion molecule production	BP	0.898	CAV1	up_VSAP_VSMC
GO:0060355	0.0101	1	1	2	positive regulation of cell adhesion molecule	BP	0.898	CAV1	up_VSAP_VSMC
GO:0009719	0.0102	0.993	53	395	response to endogenous stimulus	BP	0.971	SMAD6,ACTN2,LEP,LBH,GATA5,SKP2,PRKAA2,FERMT1,BMP4,FGFR2,ABCA1,MED14,CASTOR1,LATS2,CITED2,RERG,AR,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,ANKRD1,MXRA5,CTSB,AKAP6,CREBRF,UBR1,PTPN22,NPNT,APLP1,PTGDR,SESN3,PRKCE,FRS2,AGRN,FUT8,APP,PSEN1,TGFBR1,JUP,NR3C1,DUSP22,HPGD,NOD2,FAM107A,DDIT4,ENSCAFG00000018360,GNAQ,INPP5K,SH3BP4,PARK7,CRKL	up_ACOR_VSMC
GO:0070997	0.0102	0.996	12	93	neuron death	BP	0.492	HYOU1,AARS,HIF1A,ZPR1,CTNNB1,APOE,DDIT3,FAM162A,GSK3B,EIF2S1,SIX4,NRP1	down_VSAP_EC
GO:0010810	0.0102	0.996	12	60	regulation of cell-substrate adhesion	BP	0.971	FERMT1,NRP1,NPNT,PRKCE,ECM2,JUP,DUSP22,NID1,FAM107A,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0045840	0.0102	0.999	4	12	positive regulation of mitotic nuclear division	BP	0.443	BIRC5,NUP62,ENSCAFG00000005299,UBE2C	down_ACOR_VSMC
GO:0030111	0.0102	0.999	3	108	regulation of Wnt signaling pathway	BP	0.898	SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0071363	0.0102	1	2	188	cellular response to growth factor stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0097709	0.0102	1	2	2	connective tissue replacement	BP	0.427	PPP3CA,HIF1A	up_VCAV_EC
GO:0006941	0.0102	1	1	36	striated muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0061323	0.0102	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0002828	0.0102	1	1	9	regulation of type 2 immune response	BP	0.888	ARG2	up_AORT_VSMC

GO:0003180	0.0102	1	1	7	aortic valve morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0010765	0.0102	1	1	5	positive regulation of sodium ion transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:2000463	0.0102	1	1	5	positive regulation of excitatory postsynaptic	BP	1	NETO1	up_VFEM_VSMC
GO:0018216	0.0102	1	1	3	peptidyl-arginine methylation	BP	1	NR1H4	up_VPUL_EC
GO:0051891	0.0102	1	1	3	positive regulation of cardioblast differentiation	BP	1	TBX5	up_VPUL_EC
GO:1904468	0.0102	1	1	3	negative regulation of tumor necrosis factor	BP	1	NR1H4	up_VPUL_EC
GO:0007616	0.0102	1	1	5	long-term memory	BP	1	LRRN4	up_VPUL_VSMC
GO:0055062	0.0102	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0003264	0.0102	1	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0003266	0.0102	1	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_VPUL_VSMC
GO:0072505	0.0102	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0072506	0.0102	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0048548	0.0102	1	1	2	regulation of pinocytosis	BP	0.898	CAV1	up_VSAP_VSMC
GO:0050716	0.010261442	0.99963	2	6	positive regulation of interleukin-1 secretion	BP	0.96436359	FZD5,NOD2	up_ACOR_EC
GO:0051239	0.0103	0.993	103	859	regulation of multicellular organismal process	BP	0.971	TNNT2,FGF13,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,SMAD6,PLCG2,LEP,PLCL1,LBH,KCNE3,GATA5,CD83,HTR2B,RASSF2,MBP,PRDX4,MLLT3,ITM2C,FERMT1,BMP4,LCAT,LNPK,FGFR2,TP53BP1,GJA1,ELF1,HRH1,TLR3,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,ISG15,ZNRF3,CD274,ZNF365,SASH1,TMEM108,FGF18,FAM210B,NDRG2,ATRN,P4HTM,PLAC8B,LIMS2,F2RL1,HRH2,ENPP4,EGLN1,CLSTN1,NRP1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,SMARCD3,EVL,SLITRK5,TBX20,TBX5,PRKCE,FZD3,FRS2,RNLS,DAG1,APP,LAMA3,PSEN1,TGFBR1,SYNJ2BP,CHD7,JUP,SIPA1L1,DDR2,WWC2,SSH3,EDN1,NOD2,ASAP1,B2M,DISC1,SCAMP5,TNFRSF11B,GAA,MAP3K7,INPP5K,CNOT4,DOCK5,ERAP1,PARK7,SLC8A1,STC2,IL18R1,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0051188	0.0103	0.996	15	81	cofactor biosynthetic process	BP	1	ACACB,NADK,ENSCAFG00000013986,COQ9,PDK2,GALK1,MOCOS,PCBD1,ACSS2,PNPO,DCAKD,CPOX,PNP,ZNF205,DDIT4	up_VSAP_EC
GO:0002683	0.0103	0.996	13	126	negative regulation of immune system process	BP	1	GPAM,PRNP,SDC4,FBN1,THY1,GLI3,ZFP36L1,BPI,LOXL3,RAB7B,A2M,TSC22D3,ZBTB16	down_VCAV_EC
GO:0050663	0.0103	0.996	11	52	cytokine secretion	BP	0.971	TLR1,LEP,HTR2B,MBP,FERMT1,ABCA1,CD274,F2RL1,PTPN22,NOD2,SCAMP5	up_ACOR_VSMC
GO:2000026	0.0103	0.998	5	560	regulation of multicellular organismal development	BP	1	NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:2000147	0.0103	0.998	4	169	positive regulation of cell motility	BP	0.801	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0051057	0.0103	0.999	4	11	positive regulation of small GTPase mediated signal transduction	BP	0.427	RELN,GPR4,ITPKB,CDON	up_VCAV_EC
GO:0045597	0.0103	0.999	4	253	positive regulation of cell differentiation	BP	1	TBX5,EVI2B,WIF1,ARHGEF2	up_VPUL_EC
GO:0071679	0.0103	0.999	3	5	commissural neuron axon guidance	BP	0.971	NRP1,FZD3,DAG1	up_ACOR_VSMC
GO:0014706	0.0103	1	2	112	striated muscle tissue development	BP	1	EYA1,BEND2	up_AFEM_VSMC
GO:0071706	0.0103	1	2	40	tumor necrosis factor superfamily cytokine	BP	1	NR1H4,BPI	up_APUL_EC
GO:0033632	0.0103	1	2	2	regulation of cell-cell adhesion mediated by	BP	0.427	PODXL,SWAP70	up_VCAV_EC
GO:0051962	0.0103	1	2	112	positive regulation of nervous system	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0021545	0.0103	1	2	21	cranial nerve development	BP	1	HOXA3,SEMA3A	up_VPOR_EC
GO:0035089	0.0103	1	1	5	establishment of apical/basal cell polarity	BP	1	FSCN1	down_AFEM_EC
GO:1905314	0.0103	1	1	12	semi-lunar valve development	BP	1	GATA5	down_VSAP_VSMC
GO:0001710	0.0103	1	1	7	mesodermal cell fate commitment	BP	1	EYA1	up_AFEM_VSMC

GO:0055021	0.0103	1	1	15	regulation of cardiac muscle tissue growth	BP	1	TBX5	up_APUL_VSMC
GO:0003209	0.0103	1	1	14	cardiac atrium morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0003230	0.0103	1	1	14	cardiac atrium development	BP	1	TBX5	up_APUL_VSMC
GO:0048384	0.0103	1	1	4	retinoic acid receptor signaling pathway	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048385	0.0103	1	1	4	regulation of retinoic acid receptor signaling	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003214	0.0103	1	1	3	cardiac left ventricle morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0031033	0.0103	1	1	3	myosin filament organization	BP	1	MYBPC2	up_VPUL_EC
GO:0033240	0.0103	1	1	3	positive regulation of cellular amine metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0072513	0.0103	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	TBX5	up_VPUL_EC
GO:1900122	0.0103	1	1	3	positive regulation of receptor binding	BP	1	HOXA3	up_VPUL_EC
GO:0048742	0.0103	1	1	2	regulation of skeletal muscle fiber development	BP	0.898	SHOX2	up_VSAP_VSMC
GO:0060056	0.0103	1	1	2	mammary gland involution	BP	0.898	CAV1	up_VSAP_VSMC
GO:0009059	0.0104	0.996	13	1563	macromolecule biosynthetic process	BP	0.898	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0034645	0.0104	0.998	6	1546	cellular macromolecule biosynthetic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:2000026	0.0104	0.998	6	560	regulation of multicellular organismal development	BP	1	TBX5,NR1H4,EVI2B,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0090050	0.0104	0.999	4	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	0.504	VEGFA,JCAD,PIK3C2A,NRP1	down_VSAP_EC
GO:0031347	0.0104	1	2	144	regulation of defense response	BP	0.9	ARG2,ESR1	up_AORT_VSMC
GO:0070428	0.0104	1	2	2	regulation of nucleotide-binding oligomerization domain containing 1	BP	0.43	TNFAIP3,TLR4	up_VCAV_EC
GO:2001013	0.0104	1	2	2	epithelial cell proliferation involved in renal tubule morphogenesis	BP	0.43	MEF2C,MTSS1	up_VCAV_EC
GO:0072088	0.0104	1	2	36	nephron epithelium morphogenesis	BP	0.898	HOXA11,SALL1	up_VSAP_VSMC
GO:2000027	0.0104	1	1	72	regulation of animal organ morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0007530	0.0104	1	1	5	sex determination	BP	1	CITED2	down_VPOR_EC
GO:0032402	0.0104	1	1	5	melanosome transport	BP	1	RAB11B	down_VPOR_EC
GO:0051904	0.0104	1	1	5	pigment granule transport	BP	1	RAB11B	down_VPOR_EC
GO:0042118	0.0104	1	1	4	endothelial cell activation	BP	1	HOXA9	up_VFEM_VSMC
GO:0000820	0.0104	1	1	3	regulation of glutamine family amino acid	BP	1	NR1H4	up_VPUL_EC
GO:1902667	0.0104	1	1	5	regulation of axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:0072006	0.0105	0.997	9	59	nephron development	BP	0.506	SULF1,ENSCAFG00000032470,ILK,HOXB7,ACTA2,MAGED1,CTNNB1,MYO1E,SIX4	down_VSAP_EC
GO:0055002	0.0105	0.997	9	45	striated muscle cell development	BP	0.432	MEF2C,EDN1,TMOD1,PPP3CA,MTOR,CAV2,PROX1,P2RX2,TMOD3	up_VCAV_EC
GO:1901222	0.0105	0.997	8	32	regulation of NIK/NF-kappaB signaling	BP	0.974	RASSF2,TLR3,SASH1,PTPN22,APP,NOD2,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051272	0.0105	0.998	4	170	positive regulation of cellular component	BP	0.801	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0034123	0.0105	0.999	4	10	positive regulation of toll-like receptor signaling	BP	0.974	TLR1,TLR3,F2RL1,PTPN22	up_ACOR_VSMC
GO:0009653	0.0105	0.999	3	773	anatomical structure morphogenesis	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0060501	0.0105	1	1	5	positive regulation of epithelial cell proliferation involved in lung	BP	1	SRSF6	down_AFEM_EC
GO:0030259	0.0105	1	1	5	lipid glycosylation	BP	1	GBGT1	down_VPOR_EC
GO:0010811	0.0105	1	1	36	positive regulation of cell-substrate adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0021615	0.0105	1	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	up_APUL_EC

GO:0051890	0.0105	1	1	4	regulation of cardioblast differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:1902713	0.0105	1	1	3	regulation of interferon-gamma secretion	BP	1	NR1H4	up_VPUL_EC
GO:0046794	0.0105	1	1	2	transport of virus	BP	0.899	CAV1	up_VSAP_VSMC
GO:0016310	0.010555302	0.99432	27	641	phosphorylation	BP	0.96436359	BRSK1,PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,GRK7,TNFRSF19,DCLK2,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,ALDOC,RARRES2,STK32C,NRP1,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0051186	0.0106	0.994	25	159	cofactor metabolic process	BP	1	ACSM3,ACACB,NADK,GOT1,ADHFE1,ENSCAFG00000013986,COQ9,PDK2,FXN,GALK1,CTNS,CLYBL,MOCOS,PCBD1,ACSS2,MVK,PNPO,DCAKD,CPOX,PNP,ZNF205,IDH1,HMOX1,ENSCAFG00000006478,DDIT4	up_VSAP_EC
GO:0046605	0.0106	0.997	7	30	regulation of centrosome cycle	BP	0.461	NEK2,POC1A,NUP62,PLK4,RBM14,KIF11,GEN1	down_ACOR_VSMC
GO:0035295	0.0106	0.998	5	356	tube development	BP	1	TBX5,HOXA3,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0030857	0.0106	0.998	5	15	negative regulation of epithelial cell	BP	1	HOXA7,DLL1,OSR1,ZEB1,ACVRL1	up_VSAP_EC
GO:0071363	0.0106	0.999	3	188	cellular response to growth factor stimulus	BP	1	FGF5,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0018216	0.0106	1	2	3	peptidyl-arginine methylation	BP	0.51	NR1H4,PRMT1	down_VSAP_EC
GO:2000403	0.0106	1	2	7	positive regulation of lymphocyte migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0019371	0.0106	1	2	2	cyclooxygenase pathway	BP	0.435	PTGS1,PTGS2	up_VCAV_EC
GO:0035270	0.0106	1	2	35	endocrine system development	BP	0.903	PITX1,SALL1	up_VSAP_VSMC
GO:0045605	0.0106	1	1	5	negative regulation of epidermal cell	BP	1	SRSF6	down_AFEM_EC
GO:0060065	0.0106	1	1	7	uterus development	BP	1	HOXA9	up_AFEM_VSMC
GO:1990774	0.0106	1	1	9	tumor necrosis factor secretion	BP	0.907	ARG2	up_AORT_VSMC
GO:0051482	0.0106	1	1	5	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-	BP	1	C3AR1	up_VPOR_VSMC
GO:0071624	0.0106	1	1	6	positive regulation of granulocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0090023	0.0106	1	1	6	positive regulation of neutrophil chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0021615	0.0106	1	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	up_VPUL_EC
GO:0046628	0.0106	1	1	3	positive regulation of insulin receptor signaling	BP	1	NR1H4	up_VPUL_EC
GO:0019932	0.0107	0.996	15	82	second-messenger-mediated signaling	BP	0.974	ADRA1B,ADGRD1,HTR2B,C28H10orf71,ABCA1,PDE5A,PTGIR,ADCY6,ITPR1,DMPK,RCAN2,APLP1,EDN1,NCALD,GNAQ	up_ACOR_VSMC
GO:0048699	0.0107	0.998	4	371	generation of neurons	BP	1	HOXC10,EYA1,EMX2,SHOX2	up_VFEM_VSMC
GO:0060485	0.0107	0.999	3	93	mesenchyme development	BP	0.801	ACVRL1,PDPN,NRP2	down_ACOR_EC
GO:0070848	0.0107	1	2	193	response to growth factor	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0010767	0.0107	1	1	2	regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage	BP	0.801	NEDD4	down_ACOR_EC
GO:0030388	0.0107	1	1	4	fructose 1,6-bisphosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC

GO:0010033	0.0108	0.992	93	772	response to organic substance	BP	0.974	TLR1,SMAD6,ACTN2,PLCG2,IFNGR1,LEP,LBH,AFF3,GATA5,CD83,SKP2,PRKAA2,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,EIF4A2,ATRX,MED14,CASTOR1,TLR3,LATS2,LPL,CITED2,TP53INP1,RERG,GLRB,ISG15,CD274,AR,PTGIR,SASH1,SLC2A5,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,KLHL20,ANKRD1,F2RL1,MXRA5,DAPK1,CTSB,AKAP6,P2RX7,CREBRF,NRP1,UBR1,PTPN22,NPNT,OS9,STT3B,EVL,APLP1,PTGDR,SESN3,CCDC3,PRKCE,FRS2,AGRN,FUT8,PARP9,APP,PSEN1,TGFBR1,JUP,CCL5,NR3C1,DUSP22,RAB11B,HPGD,NOD2,LRRC4,ARID5B,FAM107A,DDIT4,B2M,ENSCAFG00000018360,JKAMP,TNFRSF11B,HERPUD1,GNAQ,INPP5K,FAF2,PFKL,WFS1,DZIP3,SH3BP4,PARK7,STC2,CRKL	up_ACOR_VSMC
GO:0009790	0.0108	0.993	45	335	embryo development	BP	1	TBX15,HOXA11,FZD1,HOXA7,HOXA9,CDON,WNT11,HNF4A,AXIN2,OSR2,INSIG2,GJB5,LRIG3,IRX5,HOXD3,ABL1,DLL1,HOXA6,OSR1,FUZ,ZBTB16,RARG,HOXC4,RECK,PLPP3,AMBRA1,MFN2,ZFP36L1,FXN,IRX3,ZEB1,FBXW4,SULF2,SHOX2,HOXC10,LRP4,KDM2B,TAF8,ZFAND5,ACVRL1,TPRA1,TGFBR2,CITED2,KEAP1,LATS2	up_VSAP_EC
GO:0072503	0.0108	0.995	17	97	cellular divalent inorganic cation homeostasis	BP	0.974	ADRA1B,PLCG2,HTR2B,MICU2,ITPR1,F2RL1,DMPK,PRKCE,APP,PSEN1,CHD7,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,STC2	up_ACOR_VSMC
GO:0007159	0.0108	0.996	13	79	leukocyte cell-cell adhesion	BP	0.437	IL7R,SELP,SELE,TNIP1,STK10,SELL,GATA3,PELI1,ARG2,ITPKB,NCK1,BCL10,HMGB1	up_VCAV_EC
GO:0002221	0.0108	0.997	9	46	pattern recognition receptor signaling	BP	0.437	TNFAIP3,TNIP1,TLR4,PELI1,RIOK3,TLR3,OTUD4,HMGB1,LSM14A	up_VCAV_EC
GO:0002758	0.0108	0.997	9	46	innate immune response-activating signal	BP	0.437	TNFAIP3,TNIP1,TLR4,PELI1,RIOK3,TLR3,OTUD4,HMGB1,LSM14A	up_VCAV_EC
GO:0032611	0.0108	0.998	5	17	interleukin-1 beta production	BP	0.437	GBP5,TNFAIP3,TLR4,ARG2,ABCA1	up_VCAV_EC
GO:0045907	0.0108	0.999	3	6	positive regulation of vasoconstriction	BP	0.974	ADRA1B,HRH1,HRH2	up_ACOR_VSMC
GO:0071396	0.0108	0.999	3	134	cellular response to lipid	BP	1	NR1H4,MRC1,PTGER2	up_VPUL_EC
GO:0045638	0.0108	1	2	33	negative regulation of myeloid cell	BP	0.801	LYN,HOXA7	down_ACOR_EC
GO:2000404	0.0108	1	2	7	regulation of T cell migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0002467	0.0108	1	2	2	germinal center formation	BP	0.437	TNFAIP3,MEF2C	up_VCAV_EC
GO:0002634	0.0108	1	2	2	regulation of germinal center formation	BP	0.437	TNFAIP3,MEF2C	up_VCAV_EC
GO:0007411	0.0108	0.999	2	45	axon guidance	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0071222	0.0108	0.999	2	46	cellular response to lipopolysaccharide	BP	1	NR1H4,MRC1	up_VPUL_EC
GO:0097485	0.0108	0.999	2	45	neuron projection guidance	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0048565	0.0108	0.999	2	38	digestive tract development	BP	0.907	SALL1,SHOX2	up_VSAP_VSMC
GO:0060759	0.0108	0.999	2	37	regulation of response to cytokine stimulus	BP	0.907	TLR2,CAV1	up_VSAP_VSMC
GO:0071559	0.0108	1	1	75	response to transforming growth factor beta	BP	1	MXRA5	down_AORT_VSMC
GO:0002065	0.0108	1	1	37	columnar/cuboidal epithelial cell	BP	1	GATA5	down_VFEM_VSMC
GO:0071168	0.0108	1	1	9	protein localization to chromatin	BP	0.919	ESR1	up_AORT_VSMC
GO:0051926	0.0108	1	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0021602	0.0108	1	1	16	cranial nerve morphogenesis	BP	1	HOXA3	up_APUL_VSMC
GO:0055015	0.0108	1	1	5	ventricular cardiac muscle cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032237	0.0108	1	1	3	activation of store-operated calcium channel	BP	0.907	STIM1	up_VSAP_VSMC
GO:1901341	0.0108	1	1	3	positive regulation of store-operated calcium	BP	0.907	STIM1	up_VSAP_VSMC
GO:0009950	0.010839633	0.9996	2	6	dorsal/ventral axis specification	BP	0.96436359	SMAD6,LRP4	up_ACOR_EC

GO:0050896	0.0109	0.992	164	2346	response to stimulus	BP	0.514	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,ASNS,PLOD2,NR1H4,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,SOCS5,HM13,SPARC,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CBX5,CASP3,FAM49B,ENSCAFG00000003477,HYOU1,PGK1,WSB1,BCAR3,NUAK1,PTPN11,FLNB,COTL1,DPYSL3,LRRC8A,TRIB3,IFRD1,FARP1,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,SESN2,SRP54,TGFBR1,PTGS2,REM1,MYO1C,PIK3C2A,CHSY1,MSN,UACA,SEL1L,RPGR,KIF5B,HIF1A,CX3CL1,ENSCAFG00000000562,DNAJC10,TNIK,NXN,UBA6,RGS2,ZPR1,PTPN2,EIF2B1,PVR,YES1,NEO1,PLCL1,MTDH,ESM1,DDX39B,ADAM17,AGRN,ACTA2,EIF4EBP1,SKAP2,PDIA4,CNOT7,ADGRE5,MAGED1,DNAJB9,GNAQ,CTNNB1,KPNB1,SRP72,CRYAB,STARD13,ENSCAFG00000002015,TFRC,APOE,WWC3,KPNA4,PDE1A,ZC3H15,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,PLEKHG2,TLN1,SLC7A11,CBLC,ATF3,GSK3B,CDC37,GTF2H1,ITGB3,GBP5,SH3GLB1,TAX1BP3,MYO1E,SDC4,KPNA1,HTT,REST,RBBP8,MAPK10,EIF2S1,SH2B3,RDH11,ARFGEF3,EXT1,CALM1,DISC1,RAD23A,PAK2,CREB3L2,A2M,INHBA,CAMK2D,NR4A1,ENSCAFG00000018360,HI	down_VSAP_EC
GO:1902533	0.0109	0.993	38	271	positive regulation of intracellular signal transduction	BP	0.974	ADRA1B,LEP,MID1,HTR2B,RASSF2,C28H10orf71,NACC2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,ANKRD1,F2RL1,CRLF3,NRP1,PTPN22,NPNT,UNC5B,PRKCE,FRS2,PARP9,APP,PSEN1,CCL5,DUSP22,SIAH1,EDN1,NOD2,SH3RF3,SERINC3,MAP3K7,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0016051	0.0109	0.997	9	63	carbohydrate biosynthetic process	BP	0.514	ENPP1,TPI1,ENSCAFG00000032470,PGAM1,SESN2,PTPN2,PPP1R3C,ATF3,EXT1	down_VSAP_EC
GO:0006937	0.0109	0.997	9	40	regulation of muscle contraction	BP	0.974	TNNT2,FGF13,ADRA1B,KCNE3,PDE5A,DMPK,NPNT,JUP,DOCK5	up_ACOR_VSMC
GO:0032502	0.0109	0.997	9	1661	developmental process	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0032637	0.0109	0.997	7	26	interleukin-8 production	BP	0.974	TLR1,LEP,TLR3,F2RL1,PTPN22,NOD2,PARK7	up_ACOR_VSMC
GO:0070231	0.0109	0.998	5	18	T cell apoptotic process	BP	0.437	IL7R,ARG2,BCL10,RIPK1,HIF1A	up_VCAV_EC
GO:0061045	0.0109	0.999	4	12	negative regulation of wound healing	BP	0.437	PDGFB,CD34,KLKB1,TFPI	up_VCAV_EC
GO:0090208	0.0109	0.999	3	6	positive regulation of triglyceride metabolic	BP	0.471	SREBF1,CTDNEP1,ABHD5	down_ACOR_VSMC
GO:1903725	0.0109	0.999	2	30	regulation of phospholipid metabolic process	BP	0.801	LYN,ACSL3	down_ACOR_EC
GO:0007507	0.0109	1	2	194	heart development	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0090335	0.0109	1	2	7	regulation of brown fat cell differentiation	BP	1	LEP,NAPEPLD	up_AFEM_EC
GO:0008284	0.0109	1	2	238	positive regulation of cell proliferation	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0006044	0.0109	1	1	5	N-acetylglucosamine metabolic process	BP	1	EXTL2	down_AFEM_EC
GO:0021563	0.0109	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_VPOR_VSMC
GO:0050920	0.011	0.997	8	53	regulation of chemotaxis	BP	0.517	VEGFA,SERPINE1,PTPN2,ADAM17,MMP28,LYN,NRP1,USP14	down_VSAP_EC
GO:0009059	0.011	0.998	6	1563	macromolecule biosynthetic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0030511	0.011	0.999	4	10	positive regulation of transforming growth factor beta receptor	BP	0.974	FERMT1,CITED2,CDKN2B,NPNT	up_ACOR_VSMC
GO:1903846	0.011	0.999	4	10	positive regulation of cellular response to transforming growth	BP	0.974	FERMT1,CITED2,CDKN2B,NPNT	up_ACOR_VSMC
GO:0016558	0.011	0.999	4	10	protein import into peroxisome matrix	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:2000146	0.011	0.999	3	92	negative regulation of cell motility	BP	0.801	ACVRL1,HOXA7,SULF1	down_ACOR_EC
GO:0006029	0.011	0.999	2	29	proteoglycan metabolic process	BP	0.801	SULF1,CSGALNACT1	down_ACOR_EC
GO:0010712	0.011	1	2	7	regulation of collagen metabolic process	BP	1	MFAP4,FAP	up_AFEM_EC
GO:1902105	0.011	1	2	80	regulation of leukocyte differentiation	BP	1	TMEM176A,TMEM176B	up_VPUL_VSMC

GO:0072028	0.011	0.999	2	37	nephron morphogenesis	BP	0.908	HOXA11,SALL1	up_VSAP_VSMC
GO:0000463	0.011	1	1	3	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	0.801	WDR12	down_ACOR_EC
GO:0045671	0.011	1	1	8	negative regulation of osteoclast differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0048752	0.011	1	1	5	semicircular canal morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0048755	0.011	1	1	4	branching morphogenesis of a nerve	BP	1	SHOX2	up_VFEM_VSMC
GO:0014707	0.011	1	1	2	branchiomeric skeletal muscle development	BP	0.908	PITX1	up_VSAP_VSMC
GO:2000286	0.011	1	1	2	receptor internalization involved in canonical Wnt signaling pathway	BP	0.908	CAV1	up_VSAP_VSMC
GO:1903829	0.011088393	0.99699	7	91	positive regulation of cellular protein	BP	0.96436359	KCNB1,EDEM2,PLS1,TRIM8,MAVS,LRP4,PRKCD	up_ACOR_EC
GO:0050789	0.0111	0.991	346	3295	regulation of biological process	BP	0.974	SYNPO2L,EXPH5,TNNT2,SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,DNAJC6,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,CASP10,IFNGR1,LEP,PLCL1,LBH,DCBLD2,MAP3K8,MID1,KCNE3,GATA5,BCL2,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,PCGF5,ENSCAFG00000016285,HTR2B,RASSF2,TCAF1,MEIS2,USP6NL,FNDC5,MBP,ZRANB1,FBXL20,C28H10orf71,PRDX4,RECK,LIPT2,FEZ1,SKP2,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,LCAT,ZNF331,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,TM7SF3,FGFR2,TP53BP1,MX1,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TRPS1,TLR3,SH3RF2,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,RERG,GLRB,PKP4,ARHGAP29,CCNG2,ISG15,ZNRF3,ZNF782,CD274,ZNF365,PLPP2,MARCKSL1,AR,PTGIR,ZNF484,SARAF,SASH1,GPR155,LMO4,GTF3C1,PTPN3,TMEM108,ZNF572,FGF18,FAM210B,ARHGEF26,NDRG2,ATRN,P4HTM,TMX3,CHN2,CDKN2B,ADCY6,ZMYM2,ITPR1,GRK7,CST3,ZNF174,PLAC8B,KLHL20,LIMS2,BLNK,ANKRD1,PLEKHB2,F2RL1,HRH2,ADGRL1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,PPP2R5E,ERO1B,DAPK1,PKNOX	up_ACOR_VSMC
GO:0009725	0.0111	0.995	20	188	response to hormone	BP	0.521	NR1H4,ENPP1,PTPN11,TRIB3,FHL2,PRCP,SMARCA4,SESN2,MYO1C,MSN,PTPN2,AGRN,GNAQ,CTNNB1,UBA5,LYN,REST,NR4A1,YWHAH,KDM3A	down_VSAP_EC
GO:0070371	0.0111	0.995	16	91	ERK1 and ERK2 cascade	BP	0.974	HTR2B,BMP4,FGFR2,FGF18,NDRG2,F2RL1,NRP1,PTPN22,NPNT,FRS2,APP,SYNJ2BP,CCL5,DUSP26,ENSCAFG00000029553,CRKL	up_ACOR_VSMC
GO:0032502	0.0111	0.997	9	1661	developmental process	BP	1	HOXC10,EYA1,GATM,HOXA9,SPINK5,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006638	0.0111	0.997	7	30	neutral lipid metabolic process	BP	0.476	SREBF1,CTDNEP1,INSIG1,CAV1,ABHD5,LIPC,GK5	down_ACOR_VSMC
GO:0006639	0.0111	0.997	7	30	acylglycerol metabolic process	BP	0.476	SREBF1,CTDNEP1,INSIG1,CAV1,ABHD5,LIPC,GK5	down_ACOR_VSMC
GO:0006351	0.0111	0.997	7	1069	transcription, DNA-templated	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0034654	0.0111	0.999	4	1236	nucleobase-containing compound biosynthetic	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:1902106	0.0111	0.999	2	31	negative regulation of leukocyte differentiation	BP	0.801	LYN,HOXA7	down_ACOR_EC
GO:0071482	0.0111	0.999	2	34	cellular response to light stimulus	BP	0.801	USP28,NEDD4	down_ACOR_EC
GO:0071548	0.0111	1	2	7	response to dexamethasone	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0002730	0.0111	1	2	2	regulation of dendritic cell cytokine production	BP	0.441	TLR4,TLR3	up_VCAV_EC
GO:0045359	0.0111	1	2	2	positive regulation of interferon-beta	BP	0.441	TLR4,TLR3	up_VCAV_EC
GO:0061314	0.0111	1	2	2	Notch signaling involved in heart development	BP	0.441	DLL4,JAG1	up_VCAV_EC
GO:0010771	0.0111	0.999	2	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0048762	0.0111	1	1	77	mesenchymal cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0001759	0.0111	1	1	13	organ induction	BP	1	GATA5	down_VSAP_VSMC

GO:0006880	0.0111	1	1	4	intracellular sequestering of iron ion	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0097577	0.0111	1	1	4	sequestering of iron ion	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0032355	0.0111	1	1	10	response to estradiol	BP	0.931	ESR1	up_AORT_VSMC
GO:0060135	0.0111	1	1	10	maternal process involved in female pregnancy	BP	0.931	ESR1	up_AORT_VSMC
GO:0070233	0.0111	1	1	9	negative regulation of T cell apoptotic process	BP	0.931	ARG2	up_AORT_VSMC
GO:0042693	0.0111	1	1	4	muscle cell fate commitment	BP	1	NKX2-5	up_VPOR_VSMC
GO:2000096	0.0111	1	1	4	positive regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	ANKRD6	up_VPOR_VSMC
GO:0008356	0.0111	1	1	3	asymmetric cell division	BP	1	ARHGEF2	up_VPUL_EC
GO:0035690	0.01112454	0.99698	7	91	cellular response to drug	BP	0.96436359	SOX9,AQP1,AGRN,NOD2,PDE4A,GUCY1B1,PRKCD	up_ACOR_EC
GO:0034762	0.0112	0.995	20	122	regulation of transmembrane transport	BP	0.974	ACTN2,PLCG2,LEP,KCNE3,TCAF1,GJA1,PTPN3,DAPK1,CACNB3,AKAP6,KCNJ4,PRKCE,PSEN1,CHD7,EDN1,KCNC4,FXYD1,INPP5K,AZIN2,PARK7	up_ACOR_VSMC
GO:0060047	0.0112	0.998	5	57	heart contraction	BP	1	IRX5,CHRM2,THRB,BVES,DMPK	up_AFEM_EC
GO:1903599	0.0112	0.999	3	8	positive regulation of autophagy of	BP	0.521	HIF1A,CDC37,HTT	down_VSAP_EC
GO:0051452	0.0112	0.999	3	20	intracellular pH reduction	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0048646	0.0112	0.999	3	349	anatomical structure formation involved in	BP	1	GATA5,C6,TGFBI	up_VCAV_VSMC
GO:0045446	0.0112	0.999	2	32	endothelial cell differentiation	BP	0.801	ACVRL1,PDPN	down_ACOR_EC
GO:0048675	0.0112	0.999	2	26	axon extension	BP	0.801	SPG11,NRP2	down_ACOR_EC
GO:1903076	0.0112	0.999	2	32	regulation of protein localization to plasma	BP	0.801	ACSL3,STX4	down_ACOR_EC
GO:0010043	0.0112	1	2	7	response to zinc ion	BP	1	MT2A,ENSCAFG00000009113	up_AFEM_EC
GO:0060537	0.0112	1	2	117	muscle tissue development	BP	1	EYA1,BEND2	up_AFEM_VSMC
GO:0034144	0.0112	1	1	3	negative regulation of toll-like receptor 4 signaling	BP	0.801	LYN	down_ACOR_EC
GO:0048565	0.0112	1	1	38	digestive tract development	BP	1	GATA5	down_VFEM_VSMC
GO:0006956	0.0112	1	1	8	complement activation	BP	1	C6	up_VCAV_VSMC
GO:0043587	0.0112	1	1	4	tongue morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003211	0.0112	1	1	4	cardiac ventricle formation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051260	0.0113	0.995	15	100	protein homooligomerization	BP	0.444	GBP5,CDA,VWF,ACPP,LNX2,RIOK3,KCNJ2,EHD4,BCL10,GCH1,BLM,RIPK1,ALDH1A3,P2RX2,TNFAIP1	up_VCAV_EC
GO:0032774	0.0113	0.997	7	1073	RNA biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0097659	0.0113	0.997	7	1072	nucleic acid-templated transcription	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051093	0.0113	0.998	5	273	negative regulation of developmental process	BP	0.801	ACVRL1,LYN,HOXA7,SULF1,ASPN	down_ACOR_EC
GO:0035773	0.0113	0.998	5	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	RAB11B,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0032330	0.0113	0.999	3	20	regulation of chondrocyte differentiation	BP	1	GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:0072711	0.0113	0.999	3	5	cellular response to hydroxyurea	BP	0.444	TIMELESS,BLM,ATRX	up_VCAV_EC
GO:0046068	0.0113	0.999	3	5	cGMP metabolic process	BP	0.444	NPR1,GUCY1A1,GUCY1B1	up_VCAV_EC
GO:0050793	0.0113	1	2	731	regulation of developmental process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0070602	0.0113	1	2	3	regulation of centromeric sister chromatid cohesion	BP	0.525	NAA10,CTNNB1	down_VSAP_EC
GO:0061564	0.0113	1	2	119	axon development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0030593	0.0113	0.999	2	19	neutrophil chemotaxis	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0090103	0.0113	1	1	8	cochlea morphogenesis	BP	1	EYA1	up_AFEM_VSMC

GO:0021522	0.0113	1	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_AFEM_VSMC
GO:0021515	0.0113	1	1	9	cell differentiation in spinal cord	BP	0.931	HOXC10	up_AORT_VSMC
GO:0000820	0.0113	1	1	3	regulation of glutamine family amino acid	BP	1	NR1H4	up_APUL_EC
GO:0035136	0.0113	1	1	16	forelimb morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0021544	0.0113	1	1	8	subpallium development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0032228	0.0113	1	1	8	regulation of synaptic transmission, GABAergic	BP	1	CA2	up_VCAV_VSMC
GO:0009891	0.0114	0.992	59	521	positive regulation of biosynthetic process	BP	0.447	HCLS1,ADGRF5,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,RAB27A,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,PTGS2,CREB1,BCL10,CNOT7,HMGB1,AHR,NOS2,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0034765	0.0114	0.995	16	91	regulation of ion transmembrane transport	BP	0.976	ACTN2,PLCG2,KCNE3,TCAF1,GJA1,PTPN3,DAPK1,CACNB3,AKAP6,KCNJ4,PRKCE,PSEN1,CHD7,KCNC4,FXYD1,PARK7	up_ACOR_VSMC
GO:0042310	0.0114	0.998	6	21	vasoconstriction	BP	0.976	ADRA1B,HTR2B,HRH1,HRH2,EDN1,DOCK5	up_ACOR_VSMC
GO:0097756	0.0114	0.998	6	21	negative regulation of blood vessel diameter	BP	0.976	ADRA1B,HTR2B,HRH1,HRH2,EDN1,DOCK5	up_ACOR_VSMC
GO:0050793	0.0114	0.998	5	731	regulation of developmental process	BP	1	TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0006826	0.0114	0.998	5	15	iron ion transport	BP	1	RAB11B,SLC25A28,SCARA5,STEAP3,FTL	up_VSAP_EC
GO:0090287	0.0114	0.999	3	91	regulation of cellular response to growth factor	BP	0.801	ACVRL1,SULF1,ASPN	down_ACOR_EC
GO:0042127	0.0114	0.999	3	452	regulation of cell proliferation	BP	0.931	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0045893	0.0114	0.999	3	413	positive regulation of transcription, DNA-	BP	0.931	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0070848	0.0114	0.999	3	193	response to growth factor	BP	1	FGF5,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0014706	0.0114	0.999	3	112	striated muscle tissue development	BP	0.984	EYA1,SIX1,CYP26B1	up_VFEM_EC
GO:0045176	0.0114	1	2	3	apical protein localization	BP	0.529	SHROOM2,ARF4	down_VSAP_EC
GO:0045656	0.0114	1	1	3	negative regulation of monocyte differentiation	BP	0.801	HOXA7	down_ACOR_EC
GO:0060017	0.0114	1	1	3	parathyroid gland development	BP	0.801	HOXA3	down_ACOR_EC
GO:0006937	0.0114	1	1	40	regulation of muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0021696	0.0114	1	1	10	cerebellar cortex morphogenesis	BP	0.931	WNT7A	up_AORT_VSMC
GO:0046636	0.0114	1	1	10	negative regulation of alpha-beta T cell	BP	0.931	ARG2	up_AORT_VSMC
GO:0003229	0.0114	1	1	17	ventricular cardiac muscle tissue development	BP	1	TBX5	up_APUL_VSMC
GO:0060411	0.011496878	0.99824	4	33	cardiac septum morphogenesis	BP	0.96436359	GATA4,SMAD6,TBX5,NRP1	up_ACOR_EC
GO:0021700	0.0115	0.996	12	65	developmental maturation	BP	0.447	EDNRB,ARHGEF15,RELN,FERMT1,CDH5,GATA3,NTN4,SOX18,BMP2,SPTBN4,HIF1A,FBXO5	up_VCAV_EC
GO:0034654	0.0115	0.996	11	1236	nucleobase-containing compound biosynthetic	BP	0.919	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0030154	0.0115	0.998	6	1040	cell differentiation	BP	1	TBX5,GATA5,TMEM176A,TMEM176B,HOXB5,SLIT2	up_VPUL_VSMC
GO:1902680	0.0115	0.999	3	415	positive regulation of RNA biosynthetic process	BP	0.931	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:1903508	0.0115	0.999	3	415	positive regulation of nucleic acid-templated	BP	0.931	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0071356	0.0115	0.999	3	57	cellular response to tumor necrosis factor	BP	1	ARHGEF2,ENSCAFG00000002015,ENSCAFG00000032731	up_VPOR_EC
GO:0036257	0.0115	1	2	3	multivesicular body organization	BP	0.447	RAB11A,RAB27A	up_VCAV_EC
GO:0006813	0.0115	0.999	2	37	potassium ion transport	BP	0.919	NETO1,CAV1	up_VSAP_VSMC
GO:0010694	0.0115	1	1	3	positive regulation of alkaline phosphatase	BP	1	NPNT	up_APUL_EC

GO:1903052	0.0116	0.997	8	51	positive regulation of proteolysis involved in cellular protein catabolic	BP	0.531	PRICKLE1,PLK3,SOCS5,TRIB3,GSK3B,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:0007275	0.0116	0.997	8	1370	multicellular organism development	BP	1	HOXC10,EYA1,GATM,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0019395	0.0116	0.997	8	33	fatty acid oxidation	BP	1	PEX7,ACAA1,ACACB,PEX2,C1QTNF2,GCDH,EHHADH,LONP2	up_VSAP_EC
GO:0001658	0.0116	0.998	5	24	branching involved in ureteric bud	BP	0.531	ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0060412	0.0116	0.998	5	15	ventricular septum morphogenesis	BP	1	FZD1,WNT11,SAV1,TGFBR2,CITED2	up_VSAP_EC
GO:0002011	0.0116	0.999	2	28	morphogenesis of an epithelial sheet	BP	0.804	ACVRL1,PDPN	down_ACOR_EC
GO:0048844	0.0116	0.999	2	30	artery morphogenesis	BP	0.804	ACVRL1,HOXA1	down_ACOR_EC
GO:1900748	0.0116	1	2	3	positive regulation of vascular endothelial growth factor signaling	BP	0.531	JCAD,MYO1C	down_VSAP_EC
GO:0048640	0.0116	0.999	2	21	negative regulation of developmental growth	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0045165	0.0116	0.999	2	65	cell fate commitment	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0035313	0.0116	1	1	7	wound healing, spreading of epidermal cells	BP	0.933	WNT7A	up_AORT_VSMC
GO:0055025	0.0116	1	1	17	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0070836	0.0116	1	1	2	caveola assembly	BP	0.919	CAV1	up_VSAP_VSMC
GO:0032652	0.011607369	0.99885	3	18	regulation of interleukin-1 production	BP	0.96436359	NR1H4,FZD5,NOD2	up_ACOR_EC
GO:0043254	0.011628727	0.9959	10	164	regulation of protein complex assembly	BP	0.96436359	TMOD1,SMAD6,PAK3,PTGER4,PREB,CLSTN1,CLU,VPS16,PRKCD,TUBB4A	up_ACOR_EC
GO:0003206	0.011681482	0.99766	5	51	cardiac chamber morphogenesis	BP	0.96436359	GATA4,SMAD6,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0010562	0.0117	0.993	38	312	positive regulation of phosphorus metabolic process	BP	0.448	TEK,HCLS1,ADGRF5,KIT,PPP2R5A,MAP3K11,PDGFB,STK10,RELN,MEF2C,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,SH3GLB1,TLR3,PTGS2,MMD,RAPGEF2,TAOK1,HMGB1,NOS2,RIPK1,ITGA6,PDGFD,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0045937	0.0117	0.993	38	312	positive regulation of phosphate metabolic process	BP	0.448	TEK,HCLS1,ADGRF5,KIT,PPP2R5A,MAP3K11,PDGFB,STK10,RELN,MEF2C,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,SH3GLB1,TLR3,PTGS2,MMD,RAPGEF2,TAOK1,HMGB1,NOS2,RIPK1,ITGA6,PDGFD,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0006310	0.0117	0.995	15	93	DNA recombination	BP	0.498	HMGB1,RPA1,TRIP13,PARPBP,GINS4,RAD54L,RAD51,MND1,TONSL,BRCA1,TFRC,RBBP8,SMC6,H2AFX,GEN1	down_ACOR_VSMC
GO:0002285	0.0117	0.996	10	50	lymphocyte activation involved in immune	BP	0.448	IL6,TLR4,GATA3,RAB27A,MTOR,THOC1,SWAP70,MFNG,PLCG2,HMGB1	up_VCAV_EC
GO:0043536	0.0117	0.997	6	32	positive regulation of blood vessel endothelial	BP	0.532	VEGFA,JCAD,PIK3C2A,HIF1A,ADAM17,NRP1	down_VSAP_EC
GO:0006094	0.0117	0.998	5	24	gluconeogenesis	BP	0.532	TPI1,PGAM1,SESN2,PTPN2,ATF3	down_VSAP_EC
GO:1900044	0.0117	0.999	3	5	regulation of protein K63-linked ubiquitination	BP	0.992	SASH1,PTPN22,NOD2	up_ACOR_VSMC
GO:1903305	0.0117	0.999	2	36	regulation of regulated secretory pathway	BP	0.808	LYN,STX4	down_ACOR_EC
GO:0015014	0.0117	1	2	3	heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	BP	0.532	ENSCAFG00000032470,EXT1	down_VSAP_EC
GO:0055123	0.0117	1	1	40	digestive system development	BP	1	GATA5	down_VFEM_VSMC
GO:0006749	0.0117	1	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC
GO:0001502	0.0117	1	1	8	cartilage condensation	BP	0.936	WNT7A	up_AORT_VSMC
GO:0098743	0.0117	1	1	8	cell aggregation	BP	0.936	WNT7A	up_AORT_VSMC
GO:0046628	0.0117	1	1	3	positive regulation of insulin receptor signaling	BP	1	NR1H4	up_APUL_EC
GO:1902713	0.0117	1	1	3	regulation of interferon-gamma secretion	BP	1	NR1H4	up_APUL_EC
GO:0086011	0.0117	1	1	2	membrane repolarization during action potential	BP	0.919	CAV1	up_VSAP_VSMC

GO:0098903	0.0117	1	1	2	regulation of membrane repolarization during action potential	BP	0.919	CAV1	up_VSAP_VSMC
GO:0043207	0.011719558	0.99541	12	216	response to external biotic stimulus	BP	0.96436359	NR1H4,HMCN1,RGS1,FZD5,PTGIR,NOD2,PTGER4,MAVS,IFIT2,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0051707	0.011719558	0.99541	12	216	response to other organism	BP	0.96436359	NR1H4,HMCN1,RGS1,FZD5,PTGIR,NOD2,PTGER4,MAVS,IFIT2,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0071310	0.0118	0.997	8	634	cellular response to organic substance	BP	0.808	ACVRL1,LYN,IGF1R,NRP2,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0006342	0.0118	0.997	6	24	chromatin silencing	BP	0.499	ATAD2,UHRF1,SUV39H1,HAT1,HIST2H2AC,H2AFX	down_ACOR_VSMC
GO:0007275	0.0118	0.999	5	1370	multicellular organism development	BP	0.936	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0019438	0.0118	0.999	4	1258	aromatic compound biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0034035	0.0118	1	2	3	purine ribonucleoside bisphosphate metabolic	BP	0.532	ENPP1,PAPSS1	down_VSAP_EC
GO:0050427	0.0118	1	2	3	3'-phosphoadenosine 5'-phosphosulfate metabolic	BP	0.532	ENPP1,PAPSS1	down_VSAP_EC
GO:0003002	0.0118	0.999	2	118	regionalization	BP	1	HOXC6,GATA5	up_VCAV_VSMC
GO:0021603	0.0118	1	1	2	cranial nerve formation	BP	0.808	HOXA1	down_ACOR_EC
GO:0032400	0.0118	1	1	6	melanosome localization	BP	1	RAB11B	down_VPOR_EC
GO:0032401	0.0118	1	1	6	establishment of melanosome localization	BP	1	RAB11B	down_VPOR_EC
GO:0051875	0.0118	1	1	6	pigment granule localization	BP	1	RAB11B	down_VPOR_EC
GO:0051905	0.0118	1	1	6	establishment of pigment granule localization	BP	1	RAB11B	down_VPOR_EC
GO:0099550	0.0118	1	1	3	trans-synaptic signaling, modulating synaptic	BP	1	NTRK2	up_APUL_EC
GO:0033240	0.0118	1	1	3	positive regulation of cellular amine metabolic	BP	1	NR1H4	up_APUL_EC
GO:0003197	0.0118	1	1	16	endocardial cushion development	BP	1	TBX5	up_APUL_VSMC
GO:0055081	0.0118	1	1	17	anion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:1903779	0.0118	1	1	6	regulation of cardiac conduction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006002	0.0118	1	1	5	fructose 6-phosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0003161	0.0118	1	1	6	cardiac conduction system development	BP	1	TBX5	up_VPUL_VSMC
GO:0032272	0.011828334	0.99882	3	18	negative regulation of protein polymerization	BP	0.96436359	TMOD1,PRKCD,TUBB4A	up_ACOR_EC
GO:0009743	0.0119	0.996	9	40	response to carbohydrate	BP	1	HNF4A,RAB11B,LPL,ZFP36L1,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0048869	0.0119	0.998	5	1119	cellular developmental process	BP	1	HOXC10,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:0018130	0.0119	0.999	4	1261	heterocycle biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0035295	0.0119	0.999	3	356	tube development	BP	1	GATA5,C6,TGFBI	up_VCAV_VSMC
GO:0001952	0.0119	0.999	2	34	regulation of cell-matrix adhesion	BP	0.812	ACVRL1,HOXA7	down_ACOR_EC
GO:1902115	0.0119	0.999	2	77	regulation of organelle assembly	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:1901018	0.0119	1	2	2	positive regulation of potassium ion transmembrane	BP	1	ACTN2,AKAP6	up_ACOR_VSMC
GO:0007548	0.0119	0.999	2	68	sex differentiation	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0050890	0.0119	0.999	2	67	cognition	BP	1	GATM,NETO1	up_VFEM_VSMC
GO:0008584	0.0119	0.999	2	39	male gonad development	BP	0.926	HOXA11,HOXA9	up_VSAP_VSMC
GO:0046546	0.0119	0.999	2	39	development of primary male sexual	BP	0.926	HOXA11,HOXA9	up_VSAP_VSMC
GO:0050704	0.0119	1	1	11	regulation of interleukin-1 secretion	BP	0.939	ARG2	up_AORT_VSMC
GO:0099054	0.0119	1	1	9	presynapse assembly	BP	0.939	WNT7A	up_AORT_VSMC
GO:0014047	0.0119	1	1	3	glutamate secretion	BP	1	NTRK2	up_APUL_EC
GO:0003214	0.0119	1	1	3	cardiac left ventricle morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0018216	0.0119	1	1	3	peptidyl-arginine methylation	BP	1	NR1H4	up_APUL_EC

GO:0019627	0.0119	1	1	3	urea metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0031115	0.0119	1	1	3	negative regulation of microtubule	BP	1	TUBB4A	up_APUL_EC
GO:0051891	0.0119	1	1	3	positive regulation of cardioblast differentiation	BP	1	TBX5	up_APUL_EC
GO:0060017	0.0119	1	1	3	parathyroid gland development	BP	1	HOXA3	up_APUL_EC
GO:0071605	0.0119	1	1	3	monocyte chemotactic protein-1 production	BP	1	NR1H4	up_APUL_EC
GO:0071637	0.0119	1	1	3	regulation of monocyte chemotactic protein-1	BP	1	NR1H4	up_APUL_EC
GO:0071638	0.0119	1	1	3	negative regulation of monocyte chemotactic	BP	1	NR1H4	up_APUL_EC
GO:0072513	0.0119	1	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	TBX5	up_APUL_EC
GO:1904468	0.0119	1	1	3	negative regulation of tumor necrosis factor	BP	1	NR1H4	up_APUL_EC
GO:0042473	0.0119	1	1	5	outer ear morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0010648	0.011969521	0.99422	19	407	negative regulation of cell communication	BP	0.96436359	NR1H4,SOX9,NDRG2,KCNB1,CCDC3,IFI6,DUSP26,PTGIR,SMAD6,ADAMTSL2,MAPK8IP2,FIGNL1,LRRC15,LRP4,CLSTN1,LRRC4,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0045834	0.012	0.997	7	41	positive regulation of lipid metabolic process	BP	0.534	NR1H4,PTGS2,SLC45A3,APOE,LYN,SH3GLB1,ABHD5	down_VSAP_EC
GO:0045639	0.012	0.997	7	33	positive regulation of myeloid cell	BP	0.459	HCLS1,CASP8,FES,JAG1,CREB1,RIPK1,HIF1A	up_VCAV_EC
GO:0030198	0.012	0.997	6	81	extracellular matrix organization	BP	1	CTSS,MFAP4,GREM1,POSTN,RECK,FAP	up_AFEM_EC
GO:0003015	0.012	0.998	5	58	heart process	BP	1	IRX5,CHRM2,THRB,BVES,DMPK	up_AFEM_EC
GO:0032502	0.012	0.999	4	1661	developmental process	BP	1	HOXA3,TBX5,HOXA2,HOXB5	up_APUL_VSMC
GO:0051307	0.012	0.999	3	6	meiotic chromosome separation	BP	0.504	NCAPH,ESPL1,TTK	down_ACOR_VSMC
GO:0048598	0.012	0.999	3	207	embryonic morphogenesis	BP	1	HOXC10,HOXA9,DUSP2	up_AORT_EC
GO:0050801	0.012	0.999	3	200	ion homeostasis	BP	1	HOXA3,TRPC4,C3AR1	up_VPOR_VSMC
GO:1900084	0.012	1	2	3	regulation of peptidyl-tyrosine	BP	0.504	CAV1,GREM1	down_ACOR_VSMC
GO:0003002	0.012	0.999	2	118	regionalization	BP	1	HOXC10,HOXA9	up_AFEM_VSMC
GO:0016202	0.012	0.999	2	39	regulation of striated muscle tissue	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0048368	0.012	1	1	6	lateral mesoderm development	BP	1	CITED2	down_VPOR_EC
GO:1905207	0.012	1	1	17	regulation of cardiocyte differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0033674	0.0121	0.994	21	144	positive regulation of kinase activity	BP	0.459	TEK,KIT,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,NEDD9,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,SH3GLB1,MMD,RAPGEF2,RIPK1,PDGFD	up_VCAV_EC
GO:0045747	0.0121	0.998	5	18	positive regulation of Notch signaling pathway	BP	0.459	DLL4,TSPAN14,BMP2K,MFNG,JAG1	up_VCAV_EC
GO:0009066	0.0121	0.998	4	16	aspartate family amino acid metabolic process	BP	0.534	ASNS,PLOD2,NMNAT2,PLOD3	down_VSAP_EC
GO:0048699	0.0121	0.999	3	371	generation of neurons	BP	1	HOXC10,EYA1,IRX5	up_AFEM_VSMC
GO:0060349	0.0121	0.999	2	38	bone morphogenesis	BP	0.931	HOXA11,SHOX2	up_VSAP_VSMC
GO:0071467	0.0121	1	1	6	cellular response to pH	BP	1	RAB11B	down_VPOR_EC
GO:2000826	0.0121	1	1	14	regulation of heart morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0043403	0.0121	1	1	11	skeletal muscle tissue regeneration	BP	0.941	WNT7A	up_AORT_VSMC
GO:0061196	0.0121	1	1	3	fungiform papilla development	BP	1	SIX1	up_VFEM_EC
GO:0061197	0.0121	1	1	3	fungiform papilla morphogenesis	BP	1	SIX1	up_VFEM_EC
GO:0003264	0.0121	1	1	5	regulation of cardioblast proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:0003266	0.0121	1	1	5	regulation of secondary heart field cardioblast	BP	1	EYA1	up_VFEM_VSMC
GO:0010960	0.0121	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC

GO:0048012	0.012100722	0.9995	2	7	hepatocyte growth factor receptor signaling	BP	0.96436359	ESM1,NRP1	up_ACOR_EC
GO:0070848	0.0122	0.994	20	193	response to growth factor	BP	0.534	VEGFA,SULF1,HSPA5,SPARC,JCAD,SNX25,PTPN11,ILK,TGFBR1,MYO1C,HIF1A,ZPR1,YES1,NEO1,ADAM17,CTNNB1,ENSCAFG00000002015,STRAP,ENSCAFG00000018360,NRP1	down_VSAP_EC
GO:0010631	0.0122	0.995	14	118	epithelial cell migration	BP	0.534	VEGFA,MYH9,SPARC,JCAD,PTPN11,PRCP,PIK3C2A,HIF1A,ADAM17,ANLN,STARD13,APOE,STRAP,NRP1	down_VSAP_EC
GO:0090132	0.0122	0.995	14	118	epithelium migration	BP	0.534	VEGFA,MYH9,SPARC,JCAD,PTPN11,PRCP,PIK3C2A,HIF1A,ADAM17,ANLN,STARD13,APOE,STRAP,NRP1	down_VSAP_EC
GO:0072078	0.0122	0.997	6	33	nephron tubule morphogenesis	BP	0.534	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0010464	0.0122	0.997	6	21	regulation of mesenchymal cell	BP	1	WNT11,ZEB1,FBXW4,SHOX2,NFIB,TGFBR2	up_VSAP_EC
GO:2000112	0.0122	0.998	5	1119	regulation of cellular macromolecule biosynthetic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0010894	0.0122	0.999	3	9	negative regulation of steroid biosynthetic	BP	0.534	NR1H4,APOE,REST	down_VSAP_EC
GO:0045939	0.0122	0.999	3	9	negative regulation of steroid metabolic process	BP	0.534	NR1H4,APOE,REST	down_VSAP_EC
GO:0001655	0.0122	0.999	3	116	urogenital system development	BP	0.931	HOXA11,EMX2,SALL1	up_VSAP_VSMC
GO:1904502	0.0122	1	2	3	regulation of lipophagy	BP	0.534	SESN2,HTT	down_VSAP_EC
GO:1904504	0.0122	1	2	3	positive regulation of lipophagy	BP	0.534	SESN2,HTT	down_VSAP_EC
GO:0051099	0.0122	0.999	2	70	positive regulation of binding	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0055123	0.0122	0.999	2	40	digestive system development	BP	0.931	SALL1,SHOX2	up_VSAP_VSMC
GO:0045617	0.0122	1	1	3	negative regulation of keratinocyte	BP	0.813	HOXA7	down_ACOR_EC
GO:0097048	0.0122	1	1	2	dendritic cell apoptotic process	BP	0.813	LYN	down_ACOR_EC
GO:2000668	0.0122	1	1	2	regulation of dendritic cell apoptotic process	BP	0.813	LYN	down_ACOR_EC
GO:2000670	0.0122	1	1	2	positive regulation of dendritic cell apoptotic	BP	0.813	LYN	down_ACOR_EC
GO:0098815	0.0122	1	1	9	modulation of excitatory postsynaptic potential	BP	0.943	WNT7A	up_AORT_VSMC
GO:0060420	0.0122	1	1	18	regulation of heart growth	BP	1	TBX5	up_APUL_VSMC
GO:0061436	0.0122	1	1	5	establishment of skin barrier	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003128	0.0122	1	1	6	heart field specification	BP	1	GATA5	up_VPUL_VSMC
GO:0055083	0.0122	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0060038	0.012211164	0.99876	3	18	cardiac muscle cell proliferation	BP	0.96436359	FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0032527	0.012215222	0.99875	3	19	protein exit from endoplasmic reticulum	BP	0.96436359	EDEM2,PREB,HM13	up_ACOR_EC
GO:1901698	0.012217323	0.9948	14	266	response to nitrogen compound	BP	0.96436359	NR1H4,SOX9,AQP1,ENSCAFG00000004331,EDEM2,AGRN,NOD2,ACTN2,GUCY1B1,MAVS,FOXC2,RARRES2,HM13,PRKCD	up_ACOR_EC
GO:0050663	0.01223116	0.99752	5	52	cytokine secretion	BP	0.96436359	NR1H4,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0042981	0.0123	0.999	3	471	regulation of apoptotic process	BP	0.945	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0044057	0.0123	0.999	3	110	regulation of system process	BP	0.939	NETO1,IRX5,CAV1	up_VSAP_VSMC
GO:0030282	0.0123	0.999	2	37	bone mineralization	BP	0.813	HOXA3,ASPN	down_ACOR_EC
GO:0042092	0.0123	1	1	11	type 2 immune response	BP	0.945	ARG2	up_AORT_VSMC
GO:0001779	0.0123	1	1	3	natural killer cell differentiation	BP	1	TOX	up_VFEM_EC
GO:0021520	0.0123	1	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	up_VFEM_EC
GO:0031424	0.0123	1	1	3	keratinization	BP	1	CYP26B1	up_VFEM_EC
GO:0032823	0.0123	1	1	3	regulation of natural killer cell differentiation	BP	1	TOX	up_VFEM_EC

GO:0032268	0.012300452	0.99303	31	778	regulation of cellular protein metabolic process	BP	0.96436359	PLCL1,PKIB,SOX9,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,IFI6,DUSP26,NOD2,SMAD6,KLHL25,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,CLU,RARRES2,RNF114,NRP1,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0071260	0.012337874	0.99874	3	19	cellular response to mechanical stimulus	BP	0.96436359	SOX9,AQP1,PTGER4	up_ACOR_EC
GO:0048469	0.0124	0.997	7	31	cell maturation	BP	0.47	EDNRB,GATA3,NTN4,SOX18,SPTBN4,HIF1A,FBXO5	up_VCAV_EC
GO:0007095	0.0124	0.998	4	11	mitotic G2 DNA damage checkpoint	BP	0.52	CDK1,FANCI,TOPBP1,CLSPN	down_ACOR_VSMC
GO:0071901	0.0124	0.999	2	37	negative regulation of protein serine/threonine	BP	0.813	LYN,PRKAR2A	down_ACOR_EC
GO:1902993	0.0124	1	1	3	positive regulation of amyloid precursor protein catabolic process	BP	0.813	LYN	down_ACOR_EC
GO:0060038	0.0124	1	1	18	cardiac muscle cell proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0021800	0.0124	1	1	6	cerebral cortex tangential migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0009987	0.0125	0.99	448	5086	cellular process	BP	0.524	ELK3,SCD,ACSL3,PRPSAP1,FSCN1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,FLNB,POLE3,USP1,IRAK1,MCM7,RPA1,NCAPD2,ANLN,PTBP1,ILF3,DDX39A,STXBP6,CBX5,ENSCAFG00000016095,PPRC1,USP4,FMNL3,RACGAP1,SF3B2,ACSL4,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,TFPI,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,KIF2A,UBE2S,NEDD4,SRSF2,RRM1,WDR76,THOP1,MED17,U2AF2,ZW10,INTS7,QSOX2,ENSCAFG00000016482,MNDA,CAPG,SMC4,CENPA,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,HOXA3,ENSCAFG00000017264,NDC1,PPM1G,RRBP1,SNRPB2,CENPN,TOP3A,TRIP13,COLGALT1,SLC25A5,PPP1R15B,TIMM44,SF1,PARPBP,SGO1,POLA2,MPDU1,SRRT,GINS4,C1QTNF6,NOP56,SDC1,ARFGAP1,CTDNEP1,RAD54L,RANGAP1,POLE,FBXO5,DDX23,HSPA9,NAB2,SLC35C2,HNRNPH3,MRPS18B,RAN,B3GNT2,CFAP298,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,ENSCAFG00000030005,CAV1,CDK1,RFC5,CENPE,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,LIMA1,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,TXLNA,ENSCAFG00000008236,NF2,ANPEP,PFAS,	down_ACOR_VSMC
GO:0042221	0.0125	0.993	35	1012	response to chemical	BP	1	CMKLR1,MT2A,LEP,LBH,CRY2,ENSCAFG00000009113,RAB20,GAS1,ANGPT4,CD40,DLL1,CRYAB,CPNE7,PLXNA4,GPAM,FIBIN,CHRM2,TMEM100,GREM1,NFE2L1,AVPR1A,CAMK2A,GREM2,CYLD,POSTN,LRRC15,NR3C1,TBXA2R,ACKR4,PPARGC1A,CCL5,ADAM17,KANK1,ANXA11,SOD1	up_AFEM_EC
GO:0048513	0.0125	0.993	32	906	animal organ development	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,LEP,LBH,XYLT1,HOXA7,COL8A2,DLL1,CRYAB,PLXNA4,MAB21L1,THRB,TMEM100,GREM1,NFE2L1,OVOL1,HOXA6,CYLD,LUZP1,PTHLH,EVI2B,CNNM4,BVES,AXIN2,ACACB,PPARGC1A,GCNT4,FOSL2,TNC	up_AFEM_EC
GO:0072001	0.0125	0.995	11	104	renal system development	BP	1	SMAD9,KANK2,CLSTN1,PKD1,GLI3,GLIS2,PRKCSH,RDH10,GREM1,ZBTB16,SEC61A1	down_VCAV_EC
GO:0051241	0.0125	0.998	5	336	negative regulation of multicellular organismal	BP	1	HOXC10,HOXA9,MAP2K6,HOXA7,SIX1	up_VFEM_EC
GO:0032486	0.0125	0.999	3	6	Rap protein signal transduction	BP	0.472	RAPGEF1,RAP1A,RAPGEF2	up_VCAV_EC
GO:0014706	0.0125	0.999	3	112	striated muscle tissue development	BP	0.943	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0010033	0.0125	1	2	772	response to organic substance	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048634	0.0125	0.999	2	40	regulation of muscle organ development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0030336	0.0125	0.999	2	86	negative regulation of cell migration	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0042998	0.0125	1	1	3	positive regulation of Golgi to plasma membrane protein	BP	0.814	ACSL3	down_ACOR_EC
GO:0061162	0.0125	1	1	6	establishment of monopolar cell polarity	BP	1	FSCN1	down_AFEM_EC

GO:0061339	0.0125	1	1	6	establishment or maintenance of	BP	1	FSCN1	down_AFEM_EC
GO:2000482	0.0125	1	1	9	regulation of interleukin-8 secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0001541	0.0125	1	1	12	ovarian follicle development	BP	0.95	ESR1	up_AORT_VSMC
GO:0001709	0.0125	1	1	11	cell fate determination	BP	0.95	WNT7A	up_AORT_VSMC
GO:0048846	0.0125	1	1	6	axon extension involved in axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:1902284	0.0125	1	1	6	neuron projection extension involved in neuron projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0023057	0.012574299	0.99389	19	409	negative regulation of signaling	BP	0.96436359	NR1H4,SOX9,NDRG2,KCNB1,CCDC3,IFI6,DUSP26,PTGIR,SMAD6,ADAMTSL2,MAPK8IP2,FIGNL1,LRRC15,LRP4,CLSTN1,LRRC4,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0061351	0.0126	0.996	10	50	neural precursor cell proliferation	BP	0.473	EPHB1,DLL4,RAPGEF1,HOOK3,HHEX,PROX1,CTNNA1,HIF1A,ARHGEF2,CDON	up_VCAV_EC
GO:1903409	0.0126	0.997	6	24	reactive oxygen species biosynthetic process	BP	0.473	CD34,TLR4,NOS3,RAB27A,ARG2,NOS2	up_VCAV_EC
GO:0051254	0.0126	0.999	3	431	positive regulation of RNA metabolic process	BP	0.95	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0070887	0.0126	1	2	775	cellular response to chemical stimulus	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0060840	0.0126	0.999	2	42	artery development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0021515	0.0126	1	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_AFEM_VSMC
GO:0060260	0.0126	1	1	12	regulation of transcription initiation from RNA polymerase II promoter	BP	0.95	ESR1	up_AORT_VSMC
GO:0060872	0.0126	1	1	6	semicircular canal development	BP	1	EYA1	up_VFEM_VSMC
GO:0031399	0.012681148	0.99331	24	559	regulation of protein modification process	BP	0.96436359	PLCL1,PKIB,SOX9,NDRG2,ENSCAFG00000004331,FZD5,DUSP26,NOD2,SMAD6,PAK3,TNFRSF19,PIAS1,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,RARRES2,NRP1,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0060828	0.0127	0.997	6	82	regulation of canonical Wnt signaling pathway	BP	1	GREM1,FAM53B,CYLD,RECK,AXIN2,KANK1	up_AFEM_EC
GO:0008652	0.0127	0.998	5	24	cellular amino acid biosynthetic process	BP	0.546	ASNS,PLOD2,ALDH18A1,PLOD3,BCAT1	down_VSAP_EC
GO:1901607	0.0127	0.998	5	24	alpha-amino acid biosynthetic process	BP	0.546	ASNS,PLOD2,ALDH18A1,PLOD3,BCAT1	down_VSAP_EC
GO:0003008	0.0127	0.997	5	336	system process	BP	1	HOXC10,MAP2K6,MME,AVPR1A,SIX1	up_VFEM_EC
GO:0055086	0.0127	0.999	3	237	nucleobase-containing small molecule metabolic	BP	1	EXTL2,SUCLG2,NDUFA10	down_AFEM_EC
GO:0006935	0.0127	0.999	3	143	chemotaxis	BP	1	CCL24,FLRT3,NEO1	up_VPUL_EC
GO:0042330	0.0127	0.999	3	143	taxis	BP	1	CCL24,FLRT3,NEO1	up_VPUL_EC
GO:0000394	0.0127	1	1	6	RNA splicing, via endonucleolytic cleavage	BP	1	TSEN15	down_AFEM_EC
GO:0006388	0.0127	1	1	6	tRNA splicing, via endonucleolytic cleavage	BP	1	TSEN15	down_AFEM_EC
GO:1903055	0.0127	1	1	6	positive regulation of extracellular matrix	BP	1	FSCN1	down_AFEM_EC
GO:2000794	0.0127	1	1	6	regulation of epithelial cell proliferation involved in lung morphogenesis	BP	1	SRSF6	down_AFEM_EC
GO:0007252	0.0127	1	1	6	I-kappaB phosphorylation	BP	1	ERC1	up_AORT_EC
GO:0000578	0.0127	1	1	11	embryonic axis specification	BP	0.95	WNT7A	up_AORT_VSMC
GO:0021846	0.0127	1	1	11	cell proliferation in forebrain	BP	0.95	WNT7A	up_AORT_VSMC
GO:0051932	0.0127	1	1	9	synaptic transmission, GABAergic	BP	1	CA2	up_VCAV_VSMC
GO:0051093	0.0128	0.995	13	273	negative regulation of developmental process	BP	1	HOXA9,IRX3,LBH,ANGPT4,HOXA7,DLL1,TWIST2,THRB,GREM1,CYLD,TBXA2R,AXIN2,KANK1	up_AFEM_EC
GO:0009108	0.0128	0.995	13	68	coenzyme biosynthetic process	BP	1	ACACB,NADK,ENSCAFG00000013986,COQ9,PDK2,GALK1,MOCOS,PCBD1,ACSS2,PNPO,DCAKD,PNP,DDIT4	up_VSAP_EC
GO:0030534	0.0128	0.996	8	33	adult behavior	BP	1	LEP,GLRB,SLITRK5,APP,CHD7,CLN8,OXR1,PARK7	up_ACOR_VSMC
GO:0006612	0.0128	0.997	6	35	protein targeting to membrane	BP	0.546	TRAM1,SRP54,MYO1C,SSR1,SRPRA,SRP72	down_VSAP_EC

GO:0000902	0.0128	0.998	4	266	cell morphogenesis	BP	1	CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0098868	0.0128	0.999	3	11	bone growth	BP	1	THBS3,EVC,DDR2	down_VCAV_EC
GO:0060537	0.0128	0.999	3	117	muscle tissue development	BP	1	EYA1,SIX1,CYP26B1	up_VFEM_EC
GO:0009653	0.0128	1	2	773	anatomical structure morphogenesis	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0035507	0.0128	1	2	3	regulation of myosin-light-chain-phosphatase	BP	0.546	NUAK1,PPP1R12A	down_VSAP_EC
GO:0071219	0.0128	0.999	2	50	cellular response to molecule of bacterial	BP	1	NR1H4,MRC1	up_VPUL_EC
GO:0031128	0.0128	1	1	15	developmental induction	BP	1	GATA5	down_VSAP_VSMC
GO:2000144	0.0128	1	1	12	positive regulation of DNA-templated transcription,	BP	0.95	ESR1	up_AORT_VSMC
GO:0051248	0.0129	0.993	29	316	negative regulation of protein metabolic process	BP	0.549	SERPINE1,SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,SESN2,PTGS2,DNAJC10,NXN,PTPN2,UCHL5,SPOPL,EIF4EBP1,CNOT7,CRYAB,APOE,LYN,STRAP,CBLC,ATF3,EIF2S1,CDYL,PAK2,A2M,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:1902107	0.0129	0.996	9	47	positive regulation of leukocyte differentiation	BP	0.483	HCLS1,IL7R,GATA3,CASP8,ITPKB,CREB1,HMGB1,RIPK1,ATP11C	up_VCAV_EC
GO:0007080	0.0129	0.998	5	18	mitotic metaphase plate congression	BP	0.536	ZW10,KIF22,CDCA8,NDC80,NUP62	down_ACOR_VSMC
GO:0048639	0.0129	0.998	4	39	positive regulation of developmental growth	BP	1	LEP,DLL1,GPAM,ACACB	up_AFEM_EC
GO:0042310	0.0129	0.999	3	21	vasoconstriction	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0045851	0.0129	0.999	3	21	pH reduction	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0097756	0.0129	0.999	3	21	negative regulation of blood vessel diameter	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0060037	0.0129	1	1	9	pharyngeal system development	BP	1	EYA1	up_AFEM_VSMC
GO:0071493	0.0129	1	1	3	cellular response to UV-B	BP	1	MME	up_VFEM_EC
GO:0072095	0.0129	1	1	3	regulation of branch elongation involved in ureteric bud branching	BP	1	SIX1	up_VFEM_EC
GO:0021520	0.0129	1	1	3	spinal cord motor neuron cell fate specification	BP	0.968	HOXC10	up_VSAP_VSMC
GO:0003180	0.012982199	0.99944	2	7	aortic valve morphogenesis	BP	0.96436359	GATA4,SMAD6	up_ACOR_EC
GO:0008150	0.013	0.991	353	5646	biological_process	BP	0.552	ARHGEF2,COL15A1,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,SLC39A7,SHROOM2,TAGLN2,NR1H4,FMNL3,PLK3,C1QTNF6,ENSCAFG00000013214,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,HM13,SPARC,VASP,ANKRD50,GOLT1B,TRAM1,ENSCAFG00000009211,MEIS2,LTBP1,SGK1,ERO1A,PRKACB,HSP90B1,PTPN14,PTK7,SLC7A5,ENPP1,ERRFI1,SLC1A4,ENSCAFG00000005575,ITGA2,P4HA1,SEC24D,JCAD,TPM4,SNX25,CBX5,CASP3,FAM49B,SARS,ENSCAFG00000003477,HYOU1,PGK1,AKAP2,WSB1,BCAR3,NUAK1,PTPN11,EXOC5,ATP2B1,CORO1C,FSCN1,AARS,FLNB,SEC23A,MZT1,COTL1,TPI1,ENSCAFG00000032470,DPYSL3,ENSCAFG00000028814,LRRC8A,HOOK3,SLC38A1,TRIB3,PGAM1,IFRD1,FARP1,ENSCAFG00000007260,TMED2,PUM3,FKBP11,UGCG,PM20D2,FBLIM1,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,SRP54,TGFBR1,PTGS2,TMEM87B,REM1,WDR1,MYO1C,TMTC2,ENSCAFG00000031588,CANX,PPIB,CEMIP2,PIK3C2A,CHSY1,MSN,RAB6A,UACA,HOXB7,SEL1L,RPGR,KIF5B,ENSCAFG00000008716,LMAN1,HIF1A,HTR7,NDUFA4L2,FKBP10,CX3CL1,ENSCAFG00000000562,DYNLL1,TRA	down_VSAP_EC
GO:0009790	0.013	0.994	15	335	embryo development	BP	1	TBX15,HOXA9,IRX3,IRX5,HOXC10,XYLT1,HOXA7,DLL1,TMEM100,GREM1,GREM2,HOXA6,LUZP1,RECK,AXIN2	up_AFEM_EC
GO:0009749	0.013	0.996	8	34	response to glucose	BP	1	HNF4A,RAB11B,LPL,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0019932	0.013	0.997	6	82	second-messenger-mediated signaling	BP	1	CMKLR1,LMCD1,TMEM100,PTHLH,TBXA2R,DMPK	up_AFEM_EC
GO:0040017	0.013	0.998	4	180	positive regulation of locomotion	BP	0.835	LYN,IGF1R,PDPN,STX4	down_ACOR_EC

GO:0015985	0.013	0.998	4	13	energy coupled proton transport, down	BP	0.537	CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0015986	0.013	0.998	4	13	ATP synthesis coupled proton transport	BP	0.537	CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0051271	0.013	0.999	3	98	negative regulation of cellular component	BP	0.835	ACVRL1,HOXA7,SULF1	down_ACOR_EC
GO:0043067	0.013	0.999	3	479	regulation of programmed cell death	BP	0.964	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0007015	0.013	0.999	3	144	actin filament organization	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0003012	0.013	1	1	90	muscle system process	BP	1	GATA5	down_AFEM_VSMC
GO:0043535	0.013	1	1	45	regulation of blood vessel endothelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0045216	0.013	1	1	44	cell-cell junction organization	BP	1	JUP	down_VFEM_VSMC
GO:0060575	0.013	1	1	9	intestinal epithelial cell differentiation	BP	1	GATA5	up_VCAV_VSMC
GO:1905523	0.013	1	1	6	positive regulation of macrophage migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0030279	0.01308022	0.99863	3	19	negative regulation of ossification	BP	0.96436359	SOX9,SMAD6,LRP4	up_ACOR_EC
GO:0003181	0.013091447	0.99943	2	7	atrioventricular valve morphogenesis	BP	0.96436359	SMAD6,TBX5	up_ACOR_EC
GO:0034641	0.0131	0.999	5	2171	cellular nitrogen compound metabolic	BP	1	AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0010556	0.0131	0.998	5	1137	regulation of macromolecule	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:1901362	0.0131	0.999	4	1293	organic cyclic compound biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0046425	0.0131	0.999	2	39	regulation of JAK-STAT cascade	BP	0.835	LYN,ASPN	down_ACOR_EC
GO:0061196	0.0131	1	2	3	fungiform papilla development	BP	0.552	CTNNB1,SIX4	down_VSAP_EC
GO:0061197	0.0131	1	2	3	fungiform papilla morphogenesis	BP	0.552	CTNNB1,SIX4	down_VSAP_EC
GO:0034379	0.0131	1	1	3	very-low-density lipoprotein particle	BP	0.835	ACSL3	down_ACOR_EC
GO:0048025	0.0131	1	1	6	negative regulation of mRNA splicing, via	BP	1	SRSF6	down_AFEM_EC
GO:0051491	0.0131	1	1	6	positive regulation of filopodium assembly	BP	1	FSCN1	down_AFEM_EC
GO:1901071	0.0131	1	1	6	glucosamine-containing compound metabolic	BP	1	EXTL2	down_AFEM_EC
GO:0055017	0.0131	1	1	19	cardiac muscle tissue growth	BP	1	TBX5	up_APUL_VSMC
GO:0003176	0.0131	1	1	9	aortic valve development	BP	1	GATA5	up_VCAV_VSMC
GO:0019438	0.0132	0.996	11	1258	aromatic compound biosynthetic process	BP	0.986	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0070887	0.0132	0.997	7	775	cellular response to chemical stimulus	BP	1	NR1H4,MRC1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043124	0.0132	0.998	5	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	0.489	TNFAIP3,TNIP1,CASP8,RIOK3,RIPK1	up_VCAV_EC
GO:0048729	0.0132	0.999	3	209	tissue morphogenesis	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060284	0.0132	0.999	3	212	regulation of cell development	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0061041	0.0132	0.999	2	34	regulation of wound healing	BP	0.835	LYN,PDPN	down_ACOR_EC
GO:1905477	0.0132	0.999	2	32	positive regulation of protein localization to	BP	0.835	ACSL3,STX4	down_ACOR_EC
GO:0032504	0.0132	0.999	2	152	multicellular organism reproduction	BP	0.965	HOXA9,ESR1	up_AORT_VSMC
GO:0048609	0.0132	0.999	2	152	multicellular organismal reproductive process	BP	0.965	HOXA9,ESR1	up_AORT_VSMC
GO:1901861	0.0132	0.999	2	41	regulation of muscle tissue development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0021563	0.0132	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_APUL_EC
GO:0071955	0.0132	1	1	2	recycling endosome to Golgi transport	BP	1	GCC2	up_VPOR_EC
GO:0048387	0.0132	1	1	3	negative regulation of retinoic acid receptor	BP	1	CYP26B1	up_VFEM_EC
GO:0006775	0.0132	1	1	3	fat-soluble vitamin metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0050727	0.0133	0.995	12	74	regulation of inflammatory response	BP	0.491	GBP5,TNFAIP3,TNIP1,BCL6B,TLR4,GATA3,TLR3,APOD,PTGS2,NOS2,NR1D2,ENSCAFG00000025410	up_VCAV_EC

GO:0002274	0.0133	0.996	8	40	myeloid leukocyte activation	BP	0.491	ADGRF5,KIT,CXCL8,TLR4,NECTIN2,SNAP23,CD200,FES	up_VCAV_EC
GO:0006720	0.0133	0.997	6	25	isoprenoid metabolic process	BP	0.547	HMGCR,ENSCAFG00000018572,MVD,FDFT1,NUS1,PDSS1	down_ACOR_VSMC
GO:0046173	0.0133	0.997	5	19	polyol biosynthetic process	BP	0.491	SPTLC2,ITPKB,PLCG2,GCH1,IMPA1	up_VCAV_EC
GO:0048871	0.0133	0.999	3	120	multicellular organismal homeostasis	BP	1	HOXC10,MAP2K6,CYP26B1	up_VFEM_EC
GO:0051216	0.0133	0.999	2	70	cartilage development	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0098742	0.0133	1	1	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5	down_VFEM_VSMC
GO:0071599	0.0133	1	1	9	otic vesicle development	BP	1	EYA1	up_AFEM_VSMC
GO:0030812	0.0133	1	1	5	negative regulation of nucleotide catabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0045820	0.0133	1	1	5	negative regulation of glycolytic process	BP	1	FBP1	up_VFEM_VSMC
GO:0051195	0.0133	1	1	5	negative regulation of cofactor metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0051198	0.0133	1	1	5	negative regulation of coenzyme metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0071600	0.0133	1	1	5	otic vesicle morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0032879	0.0134	0.99	92	767	regulation of localization	BP	1	EXPH5,SH3TC2,FGF13,VEGFD,TLR1,DNAJC6,ACTN2,LGR6,PLCG2,LEP,KCNE3,HTR2B,TCAF1,USP6NL,MBP,FBXL20,RECK,PRKAA2,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,GJA1,SH3RF2,SEC24B,TP53INP1,ATXN2,CD274,AR,SARAF,SASH1,LMO4,PTPN3,FGF18,ITPR1,ANKRD1,F2RL1,DAPK1,CACNB3,AKAP6,CDKN1A,NRP1,PTPN22,LRPAP1,DMPK,OS9,SCP2,EVL,SPINT2,KCNJ4,TBX5,PRKCE,SCG5,DAG1,PARP9,APP,LAMA3,PSEN1,SEMA6D,SGSM2,SYNJ2BP,CHD7,JUP,CCL5,DDR2,DUSP22,RAB11B,EDN1,GTF2A1L,KCNC4,NOD2,FAM107A,JAM3,B2M,FXYD1,SCAMP5,INPP5K,RAB5C,PREPL,PFKL,WFS1,AZIN2,WASL,DOCK5,PARK7,STC2,BVES,RREB1,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0002521	0.0134	0.993	23	149	leukocyte differentiation	BP	1	HOXA7,PPARGC1B,ABL1,DLL1,ZBTB16,TOX,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,ZEB1,TFE3,FBXO7,CD83,ZFP36L2,PNP,PPP3CB,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0098542	0.0134	0.994	15	100	defense response to other organism	BP	0.491	LYZ,MX2,TMEM173,TLR4,NLRC5,IRF8,SERINC5,ARG2,RIOK3,TLR3,OAS3,CNOT7,NOS2,PMAIP1,LSM14A	up_VCAV_EC
GO:0030154	0.0134	0.995	11	1040	cell differentiation	BP	0.835	ACVRL1,LYN,ACSL4,SPG11,PDPN,NRP2,HOXA7,ANPEP,SULF1,ELK3,NEDD4	down_ACOR_EC
GO:0048731	0.0134	0.996	10	1247	system development	BP	1	NR1H4,TBX5,MAPK10,HOXA3,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDLIM3	up_APUL_EC
GO:1901998	0.0134	0.998	4	16	toxin transport	BP	0.558	HSPA5,COPB2,BNIP3,NRP1	down_VSAP_EC
GO:0000414	0.0134	1	2	2	regulation of histone H3-K36 methylation	BP	0.491	IWS1,NSD1	up_VCAV_EC
GO:0090091	0.0134	1	1	3	positive regulation of extracellular matrix	BP	0.835	PDPN	down_ACOR_EC
GO:0060485	0.0134	1	1	93	mesenchyme development	BP	1	GATA5	down_AFEM_VSMC
GO:0060602	0.0134	1	1	12	branch elongation of an epithelium	BP	0.977	ESR1	up_AORT_VSMC
GO:0007512	0.0134	1	1	6	adult heart development	BP	1	NKX2-5	up_VPOR_VSMC
GO:1902624	0.0134	1	1	7	positive regulation of neutrophil migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0030854	0.0134	1	1	4	positive regulation of granulocyte	BP	1	EVI2B	up_VPUL_EC
GO:0001649	0.0134894	0.99719	5	54	osteoblast differentiation	BP	0.96436359	PTH1R,SMAD6,FIGNL1,CLSTN1,TP53INP2	up_ACOR_EC
GO:0010468	0.0135	0.995	11	1270	regulation of gene expression	BP	0.993	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0018130	0.0135	0.995	11	1261	heterocycle biosynthetic process	BP	0.993	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0010035	0.0135	0.996	7	107	response to inorganic substance	BP	1	MT2A,ENSCAFG00000009113,CRYAB,CPNE7,FIBIN,ANXA11,SOD1	up_AFEM_EC
GO:0009653	0.0135	0.997	7	773	anatomical structure morphogenesis	BP	1	TBX5,HOXA3,MYBPC2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1902117	0.0135	0.997	6	32	positive regulation of organelle assembly	BP	0.562	FSCN1,MSN,DYNLL1,SH3GLB1,SDC4,HTT	down_VSAP_EC

GO:1901701	0.0135	0.998	4	271	cellular response to oxygen-containing	BP	1	NR1H4,MRC1,PTGER2,ARHGEF2	up_VPUL_EC
GO:0040013	0.0135	0.999	3	100	negative regulation of locomotion	BP	0.835	ACVRL1,HOXA7,SULF1	down_ACOR_EC
GO:0032530	0.0135	1	1	6	regulation of microvillus organization	BP	1	FSCN1	down_AFEM_EC
GO:0071803	0.0135	1	1	6	positive regulation of podosome assembly	BP	1	FSCN1	down_AFEM_EC
GO:0009612	0.0135	1	1	47	response to mechanical stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0033598	0.0135	1	1	11	mammary gland epithelial cell proliferation	BP	0.977	ESR1	up_AORT_VSMC
GO:0051123	0.0135	1	1	14	RNA polymerase II preinitiation complex	BP	0.977	ESR1	up_AORT_VSMC
GO:0003179	0.0135	1	1	19	heart valve morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0021545	0.0135	1	1	21	cranial nerve development	BP	1	HOXA3	up_APUL_VSMC
GO:0048168	0.0135	1	1	5	regulation of neuronal synaptic plasticity	BP	1	NETO1	up_VFEM_VSMC
GO:0071941	0.0135	1	1	4	nitrogen cycle metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0098543	0.0135	1	1	4	detection of other organism	BP	0.993	TLR2	up_VSAP_VSMC
GO:0016045	0.0135	1	1	4	detection of bacterium	BP	0.993	TLR2	up_VSAP_VSMC
GO:0048569	0.013509381	0.9994	2	7	post-embryonic animal organ development	BP	0.96436359	FZD5,EFEMP1	up_ACOR_EC
GO:0006654	0.013569774	0.9994	2	7	phosphatidic acid biosynthetic process	BP	0.96436359	NR1H4,AGPAT2	up_ACOR_EC
GO:0046473	0.013569774	0.9994	2	7	phosphatidic acid metabolic process	BP	0.96436359	NR1H4,AGPAT2	up_ACOR_EC
GO:0030277	0.013587612	0.9994	2	7	maintenance of gastrointestinal	BP	0.96436359	SOX9,NOD2	up_ACOR_EC
GO:0045862	0.0136	0.994	13	112	positive regulation of proteolysis	BP	0.563	PRICKLE1,MYH9,PLK3,SOCS5,TRIB3,APOE,LYN,FAM162A,GSK3B,REST,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:0031032	0.0136	0.995	11	61	actomyosin structure organization	BP	0.497	ARHGEF15,MEF2C,EDN1,ARHGAP28,TMOD1,MTOR,PROX1,EPB41,STMN1,TNFAIP1,TMOD3	up_VCAV_EC
GO:0021514	0.0136	1	2	4	ventral spinal cord interneuron	BP	1	LMO4,GLI3	down_VCAV_EC
GO:0048608	0.0136	0.999	2	129	reproductive structure development	BP	1	HOXA9,IRX5	up_AFEM_VSMC
GO:0048704	0.0136	0.999	2	46	embryonic skeletal system morphogenesis	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0015682	0.0136	1	1	7	ferric iron transport	BP	1	RAB11B	down_VPOR_EC
GO:0072512	0.0136	1	1	7	trivalent inorganic cation transport	BP	1	RAB11B	down_VPOR_EC
GO:0003197	0.0136	1	1	16	endocardial cushion development	BP	1	GATA5	down_VSAP_VSMC
GO:0003161	0.0136	1	1	6	cardiac conduction system development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0055062	0.0136	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:0072505	0.0136	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:0072506	0.0136	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:0045617	0.0136	1	1	3	negative regulation of keratinocyte	BP	1	HOXA7	up_VFEM_EC
GO:0006521	0.0136	1	1	4	regulation of cellular amino acid metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0032731	0.013637571	0.99939	2	7	positive regulation of interleukin-1 beta	BP	0.96436359	FZD5,NOD2	up_ACOR_EC
GO:0032232	0.013656058	0.99939	2	7	negative regulation of actin filament bundle	BP	0.96436359	ARHGAP6,ARHGAP28	up_ACOR_EC
GO:0051497	0.013656058	0.99939	2	7	negative regulation of stress fiber assembly	BP	0.96436359	ARHGAP6,ARHGAP28	up_ACOR_EC
GO:0048519	0.0137	0.995	14	1554	negative regulation of biological process	BP	0.835	ACVRL1,LYN,HOXA3,IGF1R,PDPN,HOXA7,PRKAR2A,USP28,ATRIP,SULF1,ELK3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0043542	0.0137	0.995	11	86	endothelial cell migration	BP	0.564	VEGFA,MYH9,SPARC,JCAD,PRCP,PIK3C2A,HIF1A,ADAM17,STARD13,APOE,NRP1	down_VSAP_EC
GO:0032675	0.0137	0.996	8	34	regulation of interleukin-6 production	BP	1	C5AR2,IL6R,IL17RC,F2RL1,MYD88,NLRX1,CYBA,MAVS	up_VSAP_EC
GO:0048869	0.0137	0.997	7	1119	cellular developmental process	BP	1	HOXC10,EYA1,HOXA9,SPINK5,EMX2,HOXA11,SHOX2	up_VFEM_VSMC

GO:0019219	0.0137	0.998	5	1151	regulation of nucleobase-containing compound metabolic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0051094	0.0137	0.998	4	388	positive regulation of developmental process	BP	1	NKX2-5,BAMBI,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0031145	0.0137	0.999	3	7	anaphase-promoting complex-dependent	BP	0.557	UBE2S,CDC20,UBE2C	down_ACOR_VSMC
GO:0043486	0.0137	0.999	3	7	histone exchange	BP	0.557	OIP5,CENPP,MIS18A	down_ACOR_VSMC
GO:0061548	0.0137	0.999	3	8	ganglion development	BP	0.564	CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:1904892	0.0137	0.999	2	40	regulation of STAT cascade	BP	0.835	LYN,ASPN	down_ACOR_EC
GO:1903530	0.0137	0.999	2	165	regulation of secretion by cell	BP	0.977	WNT7A,ARG2	up_AORT_VSMC
GO:0061138	0.0137	0.999	2	73	morphogenesis of a branching epithelium	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:2000027	0.0137	0.999	2	72	regulation of animal organ morphogenesis	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0071229	0.0137	0.999	2	51	cellular response to acid chemical	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0021649	0.0137	1	1	2	vestibulocochlear nerve structural organization	BP	0.835	NRP2	down_ACOR_EC
GO:0061552	0.0137	1	1	2	ganglion morphogenesis	BP	0.835	NRP2	down_ACOR_EC
GO:0097374	0.0137	1	1	2	sensory neuron axon guidance	BP	0.835	NRP2	down_ACOR_EC
GO:1904835	0.0137	1	1	2	dorsal root ganglion morphogenesis	BP	0.835	NRP2	down_ACOR_EC
GO:0003007	0.0137	1	1	94	heart morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0008016	0.0137	1	1	48	regulation of heart contraction	BP	1	JUP	down_VFEM_VSMC
GO:0048103	0.0137	1	1	10	somatic stem cell division	BP	0.977	WNT7A	up_AORT_VSMC
GO:0003207	0.0137	1	1	5	cardiac chamber formation	BP	1	NKX2-5	up_VPOR_VSMC
GO:2000052	0.0137	1	1	5	positive regulation of non-canonical Wnt signaling	BP	1	ANKRD6	up_VPOR_VSMC
GO:0045656	0.0137	1	1	3	negative regulation of monocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0034383	0.0137	1	1	4	low-density lipoprotein particle clearance	BP	1	NR1H4	up_VPUL_EC
GO:0051890	0.0137	1	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_VPUL_EC
GO:1903969	0.0137	1	1	3	regulation of response to macrophage colony-stimulating factor	BP	0.993	TLR2	up_VSAP_VSMC
GO:1903972	0.0137	1	1	3	regulation of cellular response to macrophage colony-stimulating factor	BP	0.993	TLR2	up_VSAP_VSMC
GO:0002062	0.0138	0.995	10	48	chondrocyte differentiation	BP	1	HOXA11,AXIN2,OSR2,OSR1,ZBTB16,RARG,SULF2,SHOX2,NFIB,TGFBR2	up_VSAP_EC
GO:0030111	0.0138	0.996	7	108	regulation of Wnt signaling pathway	BP	1	GREM1,FAM53B,CYLD,RECK,LGR6,AXIN2,KANK1	up_AFEM_EC
GO:0032502	0.0138	0.998	6	1661	developmental process	BP	1	HOXC10,TBX15,EYA1,HOXA9,BEND2,IRX5	up_AFEM_VSMC
GO:0006970	0.0138	0.997	5	23	response to osmotic stress	BP	0.567	ARHGEF2,PLK3,CASP3,LRRC8A,PTGS2	down_VSAP_EC
GO:0043502	0.0138	1	1	16	regulation of muscle adaptation	BP	1	GATA5	down_VSAP_VSMC
GO:2000514	0.0138	1	1	13	regulation of CD4-positive, alpha-beta T cell	BP	0.977	ARG2	up_AORT_VSMC
GO:0090191	0.0138	1	1	3	negative regulation of branching involved in ureteric bud	BP	1	SIX1	up_VFEM_EC
GO:0071073	0.0138	1	1	4	positive regulation of phospholipid biosynthetic	BP	1	NR1H4	up_VPUL_EC
GO:0003180	0.0138	1	1	7	aortic valve morphogenesis	BP	1	GATA5	up_VPUL_VSMC
GO:1900120	0.0138	1	1	7	regulation of receptor binding	BP	1	HOXA3	up_VPUL_VSMC
GO:0048169	0.0138	1	1	3	regulation of long-term neuronal synaptic	BP	0.993	NETO1	up_VSAP_VSMC
GO:0048523	0.0139	0.995	13	1399	negative regulation of cellular process	BP	0.835	ACVRL1,LYN,IGF1R,PDPN,HOXA7,PRKAR2A,USP28,ATRIP,SULF1,ELK3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0060442	0.0139	0.999	3	6	branching involved in prostate gland	BP	1	BMP4,FGFR2,FRS2	up_ACOR_VSMC

GO:0048598	0.0139	0.999	3	207	embryonic morphogenesis	BP	1	HOXA3,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0050678	0.0139	0.998	3	117	regulation of epithelial cell proliferation	BP	1	EYA1,SIX1,MTSS1	up_VFEM_EC
GO:0048871	0.0139	0.998	3	120	multicellular organismal homeostasis	BP	0.993	GATM,HOXC10,CAV1	up_VSAP_VSMC
GO:0060537	0.0139	0.998	3	117	muscle tissue development	BP	0.993	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0019896	0.0139	1	2	3	axonal transport of mitochondrion	BP	0.569	HIF1A,TRAK1	down_VSAP_EC
GO:1902306	0.0139	1	1	3	negative regulation of sodium ion	BP	0.835	NEDD4	down_ACOR_EC
GO:0060216	0.0139	1	1	3	definitive hemopoiesis	BP	1	HOXA9	up_VFEM_EC
GO:0003211	0.0139	1	1	4	cardiac ventricle formation	BP	1	TBX5	up_VPUL_EC
GO:0003263	0.0139	1	1	4	cardioblast proliferation	BP	1	TBX5	up_VPUL_EC
GO:0070857	0.0139	1	1	4	regulation of bile acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:1904251	0.0139	1	1	4	regulation of bile acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0003181	0.0139	1	1	7	atrioventricular valve morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0072170	0.013971849	0.99937	2	7	metanephric tubule development	BP	0.96436359	SOX9,AQP1	up_ACOR_EC
GO:0072207	0.013971849	0.99937	2	7	metanephric epithelium development	BP	0.96436359	SOX9,AQP1	up_ACOR_EC
GO:0072234	0.013971849	0.99937	2	7	metanephric nephron tubule development	BP	0.96436359	SOX9,AQP1	up_ACOR_EC
GO:0072243	0.013971849	0.99937	2	7	metanephric nephron epithelium development	BP	0.96436359	SOX9,AQP1	up_ACOR_EC
GO:0035556	0.01398193	0.99187	33	845	intracellular signal transduction	BP	0.96436359	NR1H4,BRSK1,PLCL1,SOX9,RHOU,PTH1R,NDRG2,AQP1,ENSCAFG00000004331,FZD5,DUSP26,PTGIR,NOD2,PDE4A,PLCE1,PAK3,GUCY1B1,TNFRSF19,ARHGDIB,DCLK2,MAPK8IP2,RAPGEF4,FIGNL1,LRRC15,SH3RF3,LRRC4,CLU,C23H3orf58,PRKACA,STK32C,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0050790	0.014	0.991	58	532	regulation of catalytic activity	BP	0.509	TEK,KIT,SELE,PPP2R5A,ARHGEF15,TNFAIP3,MAP3K11,AMOT,PDGFB,STK10,RELN,FGD6,MEF2C,RAPGEF1,TLR4,NLRC5,EDN1,RALB,NEDD9,CASP8,MTOR,MAP3K3,BMP2,HHEX,CHN2,PREX2,SLK,SH3BP5,PPP1R2,PROX1,IQGAP2,MADD,HMBOX1,PAK2,PRKD2,SH3GLB1,LDB2,PTGS2,MMD,RAPGEF2,BCL10,GCH1,HMGB1,TBC1D1,NOS2,PMAIP1,BLM,RIPK1,ITGA6,PDGFD,KDM5A,HIF1A,ALS2,ENSCAFG00000002015,FKBP15,PSMB9,RABGAP1,USP6NL	up_VCAV_EC
GO:0043603	0.014	0.992	29	372	cellular amide metabolic process	BP	1	GPAM,PRNP,UBA52,LARP6,COA1,SAMD4B,RPL23,RPL13,EIF3K,MRPL37,PARK7,RPL27A,EEF2,ZFP36L1,SEC11C,RNPEP,RPL27,MRPS11,ORMDL3,RPS27,ENSCAFG00000017708,ACSS2,PCSK6,ENSCAFG00000015122,PYM1,NAPEPLD,FOXO3,EIF4EBP1,ACAT1	down_VCAV_EC
GO:0006816	0.014	0.994	15	84	calcium ion transport	BP	1	PLCG2,HTR2B,TPC3,SARAF,MICU2,ITPR1,CACNB3,PRKCE,PSEN1,CHD7,INPP5K,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0022898	0.014	0.995	10	48	regulation of transmembrane	BP	1	ACTN2,PLCG2,KCNE3,TCAF1,PTPN3,DAPK1,CACNB3,AKAP6,FXYD1,PARK7	up_ACOR_VSMC
GO:0055001	0.014	0.995	9	47	muscle cell development	BP	0.509	MEF2C,EDN1,TMOD1,PPP3CA,MTOR,CAV2,PROX1,P2RX2,TMOD3	up_VCAV_EC
GO:0034405	0.014	0.998	4	11	response to fluid shear stress	BP	0.509	MEF2C,MTSS1,ABCA1,PTGS2	up_VCAV_EC
GO:0031639	0.014	0.999	3	9	plasminogen activation	BP	0.569	SERPINE1,ENSCAFG00000005575,PGK1	down_VSAP_EC
GO:0051704	0.014	0.999	3	476	multi-organism process	BP	0.977	HOXA9,ARG2,ESR1	up_AORT_VSMC
GO:0061458	0.014	0.999	2	131	reproductive system development	BP	1	HOXA9,IRX5	up_AFEM_VSMC
GO:0007268	0.014	0.999	2	130	chemical synaptic transmission	BP	1	SLITRK5,CA2	up_VCAV_VSMC
GO:0098916	0.014	0.999	2	130	anterograde trans-synaptic signaling	BP	1	SLITRK5,CA2	up_VCAV_VSMC
GO:0060993	0.014	0.999	2	42	kidney morphogenesis	BP	0.993	HOXA11,SALL1	up_VSAP_VSMC
GO:0010592	0.014	1	1	7	positive regulation of lamellipodium assembly	BP	1	FSCN1	down_AFEM_EC

GO:0001829	0.014	1	1	7	trophectodermal cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:0048665	0.014	1	1	6	neuron fate specification	BP	1	HOXC10	up_AORT_EC
GO:0032651	0.014	1	1	13	regulation of interleukin-1 beta production	BP	0.977	ARG2	up_AORT_VSMC
GO:0048663	0.014	1	1	13	neuron fate commitment	BP	0.977	HOXC10	up_AORT_VSMC
GO:0010667	0.014	1	1	5	negative regulation of cardiac muscle cell	BP	1	NKX2-5	up_VPOR_VSMC
GO:0043114	0.014	1	1	7	regulation of vascular permeability	BP	1	SLIT2	up_VPUL_VSMC
GO:1901213	0.014	1	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GATA5	up_VPUL_VSMC
GO:0035635	0.014	1	1	3	entry of bacterium into host cell	BP	0.993	CAV1	up_VSAP_VSMC
GO:2000535	0.014	1	1	3	regulation of entry of bacterium into host cell	BP	0.993	CAV1	up_VSAP_VSMC
GO:0007167	0.014068952	0.99391	14	274	enzyme linked receptor protein signaling pathway	BP	0.96436359	SH3TC2,CDH3,NR1H4,SOX9,ENSCAFG00000004331,PTGIR,RGMA,SMAD6,ESM1,ADAMTSL2,FOXC2,LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0051172	0.0141	0.996	8	663	negative regulation of nitrogen compound	BP	0.835	ACVRL1,LYN,IGF1R,HOXA7,PRKAR2A,ELK3,ASPN,NEDD4	down_ACOR_EC
GO:0009067	0.0141	0.999	3	9	aspartate family amino acid biosynthetic process	BP	0.569	ASNS,PLOD2,PLOD3	down_VSAP_EC
GO:0048489	0.0141	0.999	2	38	synaptic vesicle transport	BP	0.835	SPG11,STX4	down_ACOR_EC
GO:0097480	0.0141	0.999	2	38	establishment of synaptic vesicle localization	BP	0.835	SPG11,STX4	down_ACOR_EC
GO:1904375	0.0141	0.999	2	35	regulation of protein localization to cell	BP	0.835	ACSL3,STX4	down_ACOR_EC
GO:0042659	0.0141	1	2	4	regulation of cell fate specification	BP	1	BMPR1A,LMO4	down_VCAV_EC
GO:0048263	0.0141	1	2	4	determination of dorsal identity	BP	0.569	CTNNB1,DDIT3	down_VSAP_EC
GO:0034123	0.0141	1	1	10	positive regulation of toll-like receptor signaling	BP	1	TLR2	up_AFEM_VSMC
GO:1901099	0.0141	1	1	10	negative regulation of signal transduction in	BP	1	EYA1	up_AFEM_VSMC
GO:2001240	0.0141	1	1	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_AFEM_VSMC
GO:0048806	0.0141	1	1	10	genitalia development	BP	0.977	ESR1	up_AORT_VSMC
GO:0099172	0.0141	1	1	11	presynapse organization	BP	0.977	WNT7A	up_AORT_VSMC
GO:0061323	0.0141	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0043086	0.014110048	0.99488	10	170	negative regulation of catalytic activity	BP	0.96436359	PKIB,PCSK1N,IFI6,DUSP26,CST3,LRRC15,LRRC4,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0002793	0.014112616	0.99703	5	54	positive regulation of peptide secretion	BP	0.96436359	NR1H4,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0050714	0.014112616	0.99703	5	54	positive regulation of protein secretion	BP	0.96436359	NR1H4,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:1901701	0.014151493	0.99387	14	271	cellular response to oxygen-containing compound	BP	0.96436359	NR1H4,SOX9,AQP1,ENSCAFG00000004331,KCNB1,AGRN,NOD2,ACTN2,GUCY1B1,PTGER4,FOXC2,RARRES2,PRKACA,PRKCD	up_ACOR_EC
GO:0045927	0.0142	0.997	5	61	positive regulation of growth	BP	1	LEP,DLL1,GPAM,ACACB,ADAM17	up_AFEM_EC
GO:0097028	0.0142	0.998	4	11	dendritic cell differentiation	BP	1	TMEM176B,TMEM176A,F2RL1,PSEN1	up_ACOR_VSMC
GO:0044060	0.0142	0.999	3	9	regulation of endocrine process	BP	0.573	PTPN11,RAB11FIP1,INHBA	down_VSAP_EC
GO:0016486	0.0142	0.999	3	6	peptide hormone processing	BP	1	ERO1B,SCG5,PCSK6	up_ACOR_VSMC
GO:0000423	0.0142	0.999	3	6	mitophagy	BP	1	AMBRA1,MFN2,HTRA2	up_VSAP_EC
GO:0099537	0.0142	0.999	2	131	trans-synaptic signaling	BP	1	SLITRK5,CA2	up_VCAV_VSMC
GO:0014846	0.0142	1	1	2	esophagus smooth muscle contraction	BP	0.835	SULF1	down_ACOR_EC
GO:0090316	0.0142	1	1	48	positive regulation of intracellular protein	BP	1	JUP	down_VFEM_VSMC
GO:2000136	0.0142	1	1	7	regulation of cell proliferation involved in	BP	1	TBX5	up_VPUL_VSMC
GO:0055017	0.014224288	0.99846	3	19	cardiac muscle tissue growth	BP	0.96436359	FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0019220	0.0143	0.996	7	525	regulation of phosphate metabolic process	BP	0.835	ACVRL1,LYN,IGF1R,PRKAR2A,ACSL3,MYO1D,ASPN	down_ACOR_EC

GO:0051174	0.0143	0.996	7	525	regulation of phosphorus metabolic process	BP	0.835	ACVRL1,LYN,IGF1R,PRKAR2A,ACSL3,MYO1D,ASPN	down_ACOR_EC
GO:1901343	0.0143	0.996	7	42	negative regulation of vasculature development	BP	0.576	SULF1,SERPINE1,SPARC,PGK1,THBS2,CTNNB1,STARD13	down_VSAP_EC
GO:0048534	0.0143	0.999	3	262	hematopoietic or lymphoid organ	BP	1	HOXA3,TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0006399	0.0143	0.999	2	87	tRNA metabolic process	BP	1	DARS,TSEN15	down_AFEM_EC
GO:2000146	0.0143	0.999	2	92	negative regulation of cell motility	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0061307	0.0143	1	1	7	cardiac neural crest cell differentiation involved in heart development	BP	1	CITED2	down_VPOR_EC
GO:0061308	0.0143	1	1	7	cardiac neural crest cell development involved in heart development	BP	1	CITED2	down_VPOR_EC
GO:0071772	0.0143	1	1	50	response to BMP	BP	1	GATA5	down_VFEM_VSMC
GO:0071773	0.0143	1	1	50	cellular response to BMP stimulus	BP	1	GATA5	down_VFEM_VSMC
GO:0042551	0.0143	1	1	10	neuron maturation	BP	1	IRX5	up_AFEM_VSMC
GO:0090102	0.0143	1	1	10	cochlea development	BP	1	EYA1	up_AFEM_VSMC
GO:0032720	0.0143	1	1	13	negative regulation of tumor necrosis factor	BP	0.979	ARG2	up_AORT_VSMC
GO:0009605	0.0144	0.99	67	538	response to external stimulus	BP	1	VEGFD,SEMA5A,TLR1,PLCG2,LEP,TMEM255A,FEZ1,COCH,PRKAA2,MX1,ABCA1,GJA1,HRH1,CASTOR1,TLR3,PPARGC1A,GLRB,ISG15,PTGIR,SASH1,FGF18,CDKN2B,USP53,PLAC8B,ANKRD1,F2RL1,ENPP4,GABARAPL1,RBM4B,BNIP3,SLC17A5,CDKN1A,P2RX7,NRP1,PTPN22,GPM6A,ULK2,NPNT,UNC5B,SESN3,PRKCE,FZD3,DAG1,PARP9,APP,CHD7,PIK3C3,LAMP2,JUP,CCL5,SESN1,NOD2,FAM107A,DDIT4,JAM3,NAALADL2,B2M,SERINC3,TNFRSF11B,FEZ2,GNAQ,BMT2,WASL,ENSCAFG00000029553,PARK7,SLC8A1,ZFYVE1	up_ACOR_VSMC
GO:0009887	0.0144	0.991	42	314	animal organ morphogenesis	BP	1	TBX15,HOXA11,FZD1,THRB,HOXA7,PEX7,CDON,WNT11,AXIN2,OSR2,INSIG2,PPARGC1B,LIMS2,LRIG3,IRX5,HOXD3,SLC6A4,FGF7,ABL1,DLL1,HOXA6,OSR1,SAV1,RARG,STAT6,HOXC4,DLX3,MFN2,IRX3,ZEB1,SULF2,SHOX2,LRP4,E2F4,NTN4,KDM2B,NFIB,ZFAND5,ACVRL1,MAP2K2,TGFBR2,CITED2	up_VSAP_EC
GO:0048646	0.0144	0.992	32	349	anatomical structure formation involved in morphogenesis	BP	0.577	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,ACTN1,SPARC,PRKACB,PTPN14,ITGA2,JCAD,PGK1,PTPN11,ENSCAFG00000032470,TMED2,FHL2,PRCP,WDR1,PIK3C2A,HIF1A,THBS2,MTDH,ESM1,CTNNB1,STARD13,KLF5,SDC4,INHBA,SIX4,NRP1,COL12A1,MYBPC2	down_VSAP_EC
GO:1903532	0.0144	0.994	14	78	positive regulation of secretion by cell	BP	1	EXPH5,TLR1,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,EDN1,NOD2,SCAMP5	up_ACOR_VSMC
GO:0006418	0.0144	0.997	6	31	tRNA aminoacylation for protein translation	BP	0.577	CARS,SARS,AARS,YARS,TARS,NARS	down_VSAP_EC
GO:0070167	0.0144	0.997	5	29	regulation of biomineral tissue development	BP	1	BMPR1A,ASPN,DDR2,OMD,GREM1	down_VCAV_EC
GO:0007178	0.0144	0.998	3	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.841	ACVRL1,SULF1,ASPN	down_ACOR_EC
GO:0043144	0.0144	0.999	3	7	snoRNA processing	BP	0.582	FBL,ENSCAFG00000019620,EXOSC5	down_ACOR_VSMC
GO:0016074	0.0144	0.999	3	7	snoRNA metabolic process	BP	0.582	FBL,ENSCAFG00000019620,EXOSC5	down_ACOR_VSMC
GO:0016482	0.0144	0.998	3	63	cytosolic transport	BP	1	HOOK3,GCC2,TMEM87B	up_VPOR_EC
GO:0090280	0.0144	1	2	3	positive regulation of calcium ion import	BP	0.52	PDGFB,STC1	up_VCAV_EC
GO:0048640	0.0144	1	1	21	negative regulation of developmental growth	BP	1	TBX5	up_APUL_VSMC
GO:1903361	0.0144	1	1	3	protein localization to basolateral plasma	BP	1	CAV1	up_VSAP_VSMC

GO:0048519	0.0145	0.989	150	1554	negative regulation of biological process	BP	0.521	EPHB1,PLK2,EDNRB,TEK,HCLS1,IL7R,ADGRF5,KIT,PPP2R5A,CXCL8,PRKCH,ARHGEF15,IFRD1,DOCK4,TIE1,CDA,TNFAIP3,ADAMTS9,TNIP1,AMOT,PDGFB,PODXL,CD34,PDE4D,MOV10,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,GPR4,STC1,GATA3,MMP28,EDN1,HOXB8,APLNR,ARAP3,CTTNBP2NL,HOMER3,TFPI,IRF8,ARHGAP28,SOX18,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,FAM3C,MTSS1,GUCY1A1,ARG2,CASP8,MTOR,TENT2,HOOK3,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,CAV2,PREX2,TUT7,SH3BP5,CNOT6,RSC1A1,ENC1,ITPKB,GDPD5,RIOK3,ANGPT2,PROX1,UHRF2,ENSCAFG00000010224,MDFI,ENSCAFG00000010596,STMN1,HMBOX1,PAK2,MCC,THOC1,SWAP70,SMARCA4,APOD,PROCR,NCK1,TIMELESS,OTUD4,CD200,JAG1,PTGS2,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,PAN3,USP28,TAOK1,CTNNA1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,BLM,SPTBN4,RIPK1,ITGA6,RAD21,RAD17,RGS2,SKIL,MTA2,ARHGDIB,CUL4A,ZW10,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,HIST2H2AC,ARID5A,TOPBP1,ENSCAFG00000002015,VASH1,DCP2,TNFAIP1,IVNS1ABP,FKBP15,RGL2,TMOD3,ZEB1,ARHGEF2,PEAR1,FBXO5,	up_VCAV_EC
GO:0051091	0.0145	0.994	14	87	positive regulation of DNA-binding transcription factor activity	BP	0.52	HCLS1,KIT,PRKCH,TMEM173,RELN,EDN1,PPP3CA,PRKD2,SMARCA4,TLR3,CD200,BCL10,RIPK1,ARHGEF2	up_VCAV_EC
GO:0034333	0.0145	0.997	5	25	adherens junction assembly	BP	0.581	VEGFA,ACTN1,CTNNB1,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0009653	0.0145	0.997	5	773	anatomical structure morphogenesis	BP	1	HOXA3,TBX5,GATA5,HOXB5,SLIT2	up_VPUL_VSMC
GO:0090382	0.0145	0.999	2	8	phagosome maturation	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0043393	0.0145	0.999	2	77	regulation of protein binding	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0045619	0.0145	0.999	2	44	regulation of lymphocyte differentiation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0060485	0.0145	0.999	2	93	mesenchyme development	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:2000736	0.0145	1	1	21	regulation of stem cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0021563	0.0145	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_VPUL_EC
GO:0018108	0.0146	0.994	13	79	peptidyl-tyrosine phosphorylation	BP	0.522	HCLS1,KIT,PDGFB,RELN,NEDD9,YES1,MTOR,SH3BP5,FES,CNOT7,PDGFD,BMX,ARHGEF2	up_VCAV_EC
GO:1903829	0.0146	0.995	10	91	positive regulation of cellular protein	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,TRIM8,GLI3,PARK7,MAVS,GLIS2	down_VCAV_EC
GO:0022008	0.0146	0.998	4	406	neurogenesis	BP	1	HOXC10,EYA1,EMX2,SHOX2	up_VFEM_VSMC
GO:0099536	0.0146	0.999	2	133	synaptic signaling	BP	1	SLITRK5,CA2	up_VCAV_VSMC
GO:0045652	0.0146	1	1	7	regulation of megakaryocyte	BP	1	GABPA	down_AFEM_EC
GO:1900180	0.0146	1	1	50	regulation of protein localization to nucleus	BP	1	JUP	down_VFEM_VSMC
GO:0021978	0.0146	1	1	3	telencephalon regionalization	BP	1	EMX2	up_VSAP_VSMC
GO:0055093	0.0146	1	1	3	response to hyperoxia	BP	1	CAV1	up_VSAP_VSMC
GO:0071455	0.0146	1	1	3	cellular response to hyperoxia	BP	1	CAV1	up_VSAP_VSMC
GO:0007350	0.014631301	0.99933	2	7	blastoderm segmentation	BP	0.96436359	FZD5,NRP1	up_ACOR_EC
GO:0051271	0.014669661	0.99579	7	98	negative regulation of cellular component	BP	0.96436359	SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,TBX5,NRP1	up_ACOR_EC
GO:0003170	0.0147	0.997	6	25	heart valve development	BP	0.522	ADAMTS9,MEF2C,GATA3,MTOR,BMP2,JAG1	up_VCAV_EC
GO:0098801	0.0147	0.999	3	8	regulation of renal system process	BP	0.522	PDGFB,STC1,EDN1	up_VCAV_EC
GO:1901071	0.0147	0.999	3	6	glucosamine-containing compound metabolic	BP	1	RENBP,CHST7,GNPDA1	up_VSAP_EC
GO:0048305	0.0147	1	1	4	immunoglobulin secretion	BP	0.842	STX4	down_ACOR_EC
GO:0051023	0.0147	1	1	4	regulation of immunoglobulin secretion	BP	0.842	STX4	down_ACOR_EC
GO:0090386	0.0147	1	1	1	phagosome maturation involved in apoptotic cell	BP	0.842	SPG11	down_ACOR_EC

GO:0090387	0.0147	1	1	1	phagolysosome assembly involved in apoptotic cell clearance	BP	0.842	SPG11	down_ACOR_EC
GO:0090389	0.0147	1	1	1	phagosome-lysosome fusion involved in apoptotic cell clearance	BP	0.842	SPG11	down_ACOR_EC
GO:0003156	0.0147	1	1	20	regulation of animal organ formation	BP	1	TBX5	up_APUL_VSMC
GO:0048538	0.0147	1	1	20	thymus development	BP	1	HOXA3	up_APUL_VSMC
GO:0021871	0.0147	1	1	6	forebrain regionalization	BP	1	EMX2	up_VFEM_VSMC
GO:0071417	0.014754978	0.99494	9	142	cellular response to organonitrogen	BP	0.96436359	NR1H4,SOX9,AQP1,ENSCAFG00000004331,NOD2,ACTN2,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0048583	0.0148	0.989	83	1095	regulation of response to stimulus	BP	0.588	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,NR1H4,HSPA5,SERPINE1,SOCS5,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,FAM49B,HYOU1,NUAK1,PTPN11,TRIB3,FARP1,ILK,FHL2,PRCP,SMARCA4,SESN2,PTGS2,MYO1C,CHSY1,UACA,HIF1A,ENSCAFG00000000562,TNIK,NXN,RGS2,PTPN2,EIF2B1,PVR,NEO1,MTDH,ESM1,DDX39B,ADAM17,SKAP2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,APOE,WWC3,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,FAM162A,PLEKHG2,CBLC,ATF3,GSK3B,CDC37,GBP5,SH3GLB1,TAX1BP3,HTT,RDH11,ARFGEF3,CALM1,DISC1,PAK2,A2M,INHBA,HIF1AN,NRP1,SH3RF3,RHBDF2,USP14,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:0031589	0.0148	0.998	3	93	cell-substrate adhesion	BP	0.842	ACVRL1,PDPN,HOXA7	down_ACOR_EC
GO:0046607	0.0148	0.999	3	7	positive regulation of centrosome cycle	BP	0.594	POC1A,NUP62,PLK4	down_ACOR_VSMC
GO:1900122	0.0148	1	1	3	positive regulation of receptor binding	BP	0.842	HOXA3	down_ACOR_EC
GO:0050710	0.0148	1	1	13	negative regulation of cytokine secretion	BP	0.987	ARG2	up_AORT_VSMC
GO:0070232	0.0148	1	1	13	regulation of T cell apoptotic process	BP	0.987	ARG2	up_AORT_VSMC
GO:0033561	0.0148	1	1	6	regulation of water loss via skin	BP	1	CYP26B1	up_VPOR_VSMC
GO:0060347	0.0148	1	1	6	heart trabecula formation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006000	0.0148	1	1	5	fructose metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0032490	0.0148	1	1	4	detection of molecule of bacterial origin	BP	1	TLR2	up_VSAP_VSMC
GO:1901339	0.0148	1	1	4	regulation of store-operated calcium channel	BP	1	STIM1	up_VSAP_VSMC
GO:0043085	0.0149	0.991	38	323	positive regulation of catalytic activity	BP	0.527	TEK,KIT,SELE,MAP3K11,PDGFB,STK10,RELN,MEF2C,RAPGEF1,TLR4,EDN1,RALB,NEDD9,CASP8,MAP3K3,BMP2,SLK,PROX1,MADD,HMBOX1,PAK2,PRKD2,SH3GLB1,MMD,RAPGEF2,BCL10,GCH1,HMGB1,TBC1D1,NOS2,PMAIP1,RIPK1,ITGA6,PDGFD,ALS2,ENSCAFG00000002015,RABGAP1,USP6NL	up_VCAV_EC
GO:0030855	0.0149	0.992	27	183	epithelial cell differentiation	BP	1	FZD1,THRB,HOXA7,WNT11,HNF4A,ABL1,BTG1,DLL1,OSR1,ADAMTSL4,SAV1,KLF15,ANXA4,RILPL2,RARG,F2RL1,DLX3,ZFP36L1,ZEB1,MYD88,FRMD6,E2F4,NFIB,ACVRL1,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0034766	0.0149	0.997	5	19	negative regulation of ion transmembrane transport	BP	0.599	NEDD4,CAV1,SLC30A1,GSTO1,REM1	down_ACOR_VSMC
GO:0033209	0.0149	0.997	5	24	tumor necrosis factor-mediated signaling	BP	0.59	NR1H4,ILK,PTPN2,ADAM17,ENSCAFG00000002015	down_VSAP_EC
GO:0006690	0.0149	0.997	5	16	icosanoid metabolic process	BP	1	PTGES,DAGLB,ABHD16A,HPGD,ENSCAFG00000023820	up_VSAP_EC
GO:0050768	0.0149	0.998	3	66	negative regulation of neurogenesis	BP	1	HOOK3,SEMA3A,RNF6	up_VPOR_EC
GO:0007379	0.0149	0.999	3	6	segment specification	BP	1	DLL1,OSR1,IRX3	up_VSAP_EC
GO:0003413	0.0149	0.999	3	6	chondrocyte differentiation involved in endochondral bone	BP	1	AXIN2,RARG,TGFBR2	up_VSAP_EC
GO:0032101	0.0149	0.999	2	173	regulation of response to external stimulus	BP	0.987	ARG2,ESR1	up_AORT_VSMC
GO:0150018	0.0149	1	1	2	basal dendrite development	BP	1	SEMA3A	up_VPOR_EC
GO:0150019	0.0149	1	1	2	basal dendrite morphogenesis	BP	1	SEMA3A	up_VPOR_EC

GO:0150020	0.0149	1	1	2	basal dendrite arborization	BP	1	SEMA3A	up_VPOR_EC
GO:0051124	0.0149	1	1	4	synaptic growth at neuromuscular junction	BP	1	SIX1	up_VFEM_EC
GO:0060352	0.0149	1	1	3	cell adhesion molecule production	BP	1	CAV1	up_VSAP_VSMC
GO:0034762	0.014913371	0.99526	8	122	regulation of transmembrane transport	BP	0.96436359	NR1H4,ENSCAFG00000004331,KCNB1,ACTN2,MAPK8IP2,RARRES2,AZIN2,PM20D1	up_ACOR_EC
GO:0008347	0.015	0.998	3	11	glial cell migration	BP	1	NDN,CSPG4,GLI3	down_VCAV_EC
GO:0032689	0.015	0.999	3	8	negative regulation of interferon-gamma	BP	0.53	TLR4,GATA3,HMGB1	up_VCAV_EC
GO:0048514	0.015	0.998	3	214	blood vessel morphogenesis	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:1905214	0.015	0.999	3	6	regulation of RNA binding	BP	1	LARP6,CDK9,EIF3D	up_VSAP_EC
GO:1905216	0.015	0.999	3	6	positive regulation of RNA binding	BP	1	LARP6,CDK9,EIF3D	up_VSAP_EC
GO:0018158	0.015	0.999	2	4	protein oxidation	BP	1	PARK7,LOXL3	down_VCAV_EC
GO:0050776	0.015	0.999	2	173	regulation of immune response	BP	0.987	ARG2,ESR1	up_AORT_VSMC
GO:0050877	0.015	0.999	2	164	nervous system process	BP	0.987	HOXC10,WNT7A	up_AORT_VSMC
GO:0051046	0.015	0.999	2	174	regulation of secretion	BP	0.987	WNT7A,ARG2	up_AORT_VSMC
GO:0060348	0.015	0.999	2	78	bone development	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0003007	0.015	0.999	2	94	heart morphogenesis	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0048705	0.015	0.999	2	95	skeletal system morphogenesis	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0042130	0.015	1	1	13	negative regulation of T cell proliferation	BP	0.987	ARG2	up_AORT_VSMC
GO:0060419	0.015	1	1	22	heart growth	BP	1	TBX5	up_APUL_VSMC
GO:1900120	0.015	1	1	7	regulation of receptor binding	BP	1	HOXA3	up_VPOR_VSMC
GO:0006907	0.015	1	1	3	pinocytosis	BP	1	CAV1	up_VSAP_VSMC
GO:0035239	0.0151	0.991	28	299	tube morphogenesis	BP	0.592	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,PRKACB,JCAD,PGK1,ENSCAFG00000032470,TMED2,ILK,PRCP,PIK3C2A,HOXB7,HIF1A,THBS2,MTDH,ESM1,MAGED1,CTNNB1,STARD13,APOE,KLF5,MYO1E,SDC4,SIX4,NRP1	down_VSAP_EC
GO:0070887	0.0151	0.992	28	775	cellular response to chemical stimulus	BP	1	CMKLR1,MT2A,LEP,LBH,CRY2,ENSCAFG00000009113,RAB20,GAS1,ANGPT4,DLL1,CPNE7,PLXNA4,CHRM2,TMEM100,GREM1,NFE2L1,AVPR1A,CAMK2A,GREM2,CYLD,POSTN,LRRC15,NR3C1,PPARGC1A,CCL5,ADAM17,KANK1,SOD1	up_AFEM_EC
GO:0016052	0.0151	0.996	6	34	carbohydrate catabolic process	BP	0.592	PGK1,TPI1,PGAM1,HIF1A,ALDOC,GALE	down_VSAP_EC
GO:0031326	0.0151	0.998	5	1176	regulation of cellular biosynthetic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0031400	0.0151	0.997	4	205	negative regulation of protein modification	BP	0.847	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0009081	0.0151	0.999	3	6	branched-chain amino acid metabolic process	BP	1	ALDH6A1,BCKDHB,ENSCAFG00000002977	up_VSAP_EC
GO:0006486	0.0151	0.999	2	91	protein glycosylation	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0043413	0.0151	0.999	2	91	macromolecule glycosylation	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0048705	0.0151	0.999	2	95	skeletal system morphogenesis	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0071229	0.0151	0.999	2	51	cellular response to acid chemical	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0022602	0.0151	1	1	13	ovulation cycle process	BP	0.987	ESR1	up_AORT_VSMC
GO:1903556	0.0151	1	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	0.987	ARG2	up_AORT_VSMC
GO:0033631	0.0151	1	1	4	cell-cell adhesion mediated by integrin	BP	1	NPNT	up_APUL_EC
GO:0043031	0.0151	1	1	4	negative regulation of macrophage activation	BP	1	BPI	up_APUL_EC
GO:0014855	0.0151	1	1	22	striated muscle cell proliferation	BP	1	TBX5	up_APUL_VSMC

GO:0032026	0.0151	1	1	2	response to magnesium ion	BP	1	FBP1	up_VPOR_EC
GO:0000188	0.0151	1	1	3	inactivation of MAPK activity	BP	1	CAV1	up_VSAP_VSMC
GO:0060216	0.0151	1	1	3	definitive hemopoiesis	BP	1	HOXA9	up_VSAP_VSMC
GO:0048598	0.0152	0.993	18	207	embryonic morphogenesis	BP	1	SDC4,FBN1,BMPR1A,LMO4,RECK,COL6A1,NAGLU,TBX15,HOXC4,LAMA3,TLX2,GLI3,ZFP36L1,IFT57,IRX5,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0019362	0.0152	0.996	6	35	pyridine nucleotide metabolic process	BP	0.592	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0046496	0.0152	0.996	6	35	nicotinamide nucleotide metabolic process	BP	0.592	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0032677	0.0152	0.997	6	22	regulation of interleukin-8 production	BP	1	C5AR2,ANXA4,F2RL1,MAPKBP1,ZNF580,MAVS	up_VSAP_EC
GO:0048008	0.0152	0.997	5	24	platelet-derived growth factor receptor signaling	BP	0.592	VEGFA,PTPN11,PTPN2,MYO1E,NRP1	down_VSAP_EC
GO:0002183	0.0152	0.997	5	16	cytoplasmic translational initiation	BP	1	EIF3G,EIF3K,EIF3L,EIF3D,NCK1	up_VSAP_EC
GO:0001954	0.0152	0.998	4	17	positive regulation of cell-matrix adhesion	BP	0.592	VEGFA,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:0010592	0.0152	0.999	3	7	positive regulation of lamellipodium assembly	BP	0.533	MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0060914	0.0152	1	1	11	heart formation	BP	1	EYA1	up_AFEM_VSMC
GO:0007214	0.0152	1	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	up_APUL_EC
GO:0071073	0.0152	1	1	4	positive regulation of phospholipid biosynthetic	BP	1	NR1H4	up_APUL_EC
GO:1904396	0.0152	1	1	4	regulation of neuromuscular junction	BP	1	SIX1	up_VFEM_EC
GO:0045665	0.015218598	0.99673	5	55	negative regulation of neuron differentiation	BP	0.96436359	SOX9,DIXDC1,RGMA,LRP4,NRP1	up_ACOR_EC
GO:0046324	0.015260998	0.9983	3	20	regulation of glucose import	BP	0.96436359	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0002790	0.0153	0.992	21	133	peptide secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,LMF1,RAB11B,PASK,STEAP3,KCNB1,RAF1,PNP,MAPKBP1,STX4,PPP3CB,MAVS,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0007219	0.0153	0.995	10	59	Notch signaling pathway	BP	0.533	DLL4,EGFL7,TSPAN14,BMP2,HHEX,BMP2K,GDPD5,MFNG,JAG1,PEAR1	up_VCAV_EC
GO:0007229	0.0153	0.996	6	32	integrin-mediated signaling pathway	BP	0.592	ITGA2,PTPN11,ILK,TLN1,ITGB3,NRP1	down_VSAP_EC
GO:0072384	0.0153	0.997	5	24	organelle transport along microtubule	BP	0.592	KIF5B,HIF1A,TRAK1,HTT,AP3S1	down_VSAP_EC
GO:0002376	0.0153	0.997	5	622	immune system process	BP	1	HOXA3,BARX1,NKX2-5,CYP26B1,C3AR1	up_VPOR_VSMC
GO:2000249	0.0153	0.998	4	12	regulation of actin cytoskeleton	BP	0.533	TEK,BAIAP2L1,FES,ARHGDIB	up_VCAV_EC
GO:0003128	0.0153	0.999	3	6	heart field specification	BP	1	GATA5,BMP4,SMARCD3	up_ACOR_VSMC
GO:0034612	0.0153	0.998	3	63	response to tumor necrosis factor	BP	1	ARHGEF2,ENSCAFG00000002015,ENSCAFG00000032731	up_VPOR_EC
GO:0002274	0.0153	0.999	2	40	myeloid leukocyte activation	BP	0.848	LYN,STX4	down_ACOR_EC
GO:1990791	0.0153	1	2	3	dorsal root ganglion development	BP	0.592	CTNNB1,NRP1	down_VSAP_EC
GO:0010959	0.0153	0.999	2	79	regulation of metal ion transport	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0050855	0.0153	1	1	4	regulation of B cell receptor signaling	BP	0.848	LYN	down_ACOR_EC
GO:0050861	0.0153	1	1	4	positive regulation of B cell receptor signaling	BP	0.848	LYN	down_ACOR_EC
GO:0033539	0.0153	1	1	7	fatty acid beta-oxidation using acyl-CoA	BP	1	ETFA	down_AFEM_EC
GO:0070229	0.0153	1	1	13	negative regulation of lymphocyte apoptotic	BP	0.993	ARG2	up_AORT_VSMC
GO:0006521	0.0153	1	1	4	regulation of cellular amino acid metabolic	BP	1	NR1H4	up_APUL_EC
GO:0030809	0.0153	1	1	6	negative regulation of nucleotide biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:1900372	0.0153	1	1	6	negative regulation of purine nucleotide	BP	1	FBP1	up_VFEM_VSMC
GO:2001170	0.0153	1	1	6	negative regulation of ATP biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0001667	0.0154	0.993	16	146	ameboidal-type cell migration	BP	0.594	VEGFA,MYH9,SPARC,JCAD,PTPN11,ILK,PRCP,PIK3C2A,HIF1A,ADAM17,ANLN,STARD13,APOE,STRAP,SDC4,NRP1	down_VSAP_EC
GO:0009142	0.0154	0.996	7	46	nucleoside triphosphate biosynthetic process	BP	0.594	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5,CMPK1	down_VSAP_EC

GO:0090304	0.0154	0.997	6	1694	nucleic acid metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0045597	0.0154	0.997	4	253	positive regulation of cell differentiation	BP	1	TBX5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0006812	0.0154	0.998	3	222	cation transport	BP	1	HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0008015	0.0154	0.998	3	120	blood circulation	BP	1	IRX5,CAV1,F5	up_VSAP_VSMC
GO:0003158	0.0154	0.999	2	38	endothelium development	BP	0.849	ACVRL1,PDPN	down_ACOR_EC
GO:0045747	0.0154	1	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	down_VSAP_VSMC
GO:0060443	0.0154	1	1	13	mammary gland morphogenesis	BP	0.997	ESR1	up_AORT_VSMC
GO:0055024	0.0154	1	1	22	regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0072376	0.0154	1	1	11	protein activation cascade	BP	1	C6	up_VCAV_VSMC
GO:0051960	0.0155	0.992	22	216	regulation of nervous system development	BP	0.594	ARHGEF2,SIPA1L1,PRKACB,DPYSL3,HOOK3,IFRD1,HIF1A,SLC45A3,TNIK,ZPR1,UST,CTNNB1,APOE,LYN,MMD,VLDLR,REST,DISC1,LRRTM2,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0048638	0.0155	0.993	15	82	regulation of developmental growth	BP	1	LEP,BMP4,FGFR2,LATS2,ATRN,PLAC8B,NRP1,ULK2,TBX20,TBX5,APP,CHD7,WWC2,EDN1,STC2	up_ACOR_VSMC
GO:0009746	0.0155	0.995	8	35	response to hexose	BP	1	HNF4A,RAB11B,LPL,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0034284	0.0155	0.995	8	35	response to monosaccharide	BP	1	HNF4A,RAB11B,LPL,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0045893	0.0155	0.998	4	413	positive regulation of transcription, DNA-	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0022008	0.0155	0.998	3	406	neurogenesis	BP	1	HOXC10,EYA1,IRX5	up_AFEM_VSMC
GO:0007602	0.0155	0.999	2	4	phototransduction	BP	0.596	GNAQ,RDH11	down_VSAP_EC
GO:0048667	0.0155	0.999	2	140	cell morphogenesis involved in neuron	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0031646	0.0155	1	1	7	positive regulation of neurological system	BP	1	NETO1	up_VFEM_VSMC
GO:0008286	0.015565218	0.99738	4	36	insulin receptor signaling pathway	BP	0.96436359	NR1H4,ENSCAFG00000004331,FOXC2,PRKCD	up_ACOR_EC
GO:0048585	0.0156	0.99	53	475	negative regulation of response to stimulus	BP	0.541	PLK2,IL7R,CXCL8,TNFAIP3,TNIP1,PDGFB,CD34,PDE4D,FERMT1,ATF3,KLKB1,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,MMP28,APLNR,ARAP3,HOMER3,TFPI,EGFL7,FIGNL1,ARG2,CASP8,MTOR,MAP3K3,BMP2,HHEX,PREX2,GDPD5,RIOK3,ANGPT2,STMN1,MCC,THOC1,SMARCA4,APOD,NCK1,OTUD4,PTGS2,CTDSPL2,CTNNA1,CNOT7,RIPK1,ITGA6,RGS2,SKIL,HIF1A,TNFAIP1,IVNS1ABP,ARHGEF2,PEAR1	up_VCAV_EC
GO:0046328	0.0156	0.994	12	61	regulation of JNK cascade	BP	1	RASSF2,TLR3,SH3RF2,SASH1,F2RL1,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0032502	0.0156	0.995	11	1661	developmental process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,HOXA2,MYBPC2,WIF1,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0048593	0.0156	0.997	4	41	camera-type eye morphogenesis	BP	1	IRX5,COL8A2,DLL1,THRB	up_AFEM_EC
GO:0032501	0.0156	0.999	4	1782	multicellular organismal process	BP	1	HOXA3,TBX5,HOXA2,HOXB5	up_APUL_VSMC
GO:0060219	0.0156	0.999	2	4	camera-type eye photoreceptor cell	BP	1	THY1,THRB	down_VCAV_EC
GO:0051239	0.0156	1	2	859	regulation of multicellular organismal process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0051146	0.0156	0.999	2	76	striated muscle cell differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0051657	0.0156	1	1	7	maintenance of organelle location	BP	1	GPSM2	down_AFEM_EC
GO:1990126	0.0156	1	1	8	retrograde transport, endosome to plasma	BP	1	RAB11B	down_VPOR_EC
GO:0014896	0.0156	1	1	18	muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC
GO:0014897	0.0156	1	1	18	striated muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC
GO:0003300	0.0156	1	1	18	cardiac muscle hypertrophy	BP	1	GATA5	down_VSAP_VSMC
GO:0070897	0.0156	1	1	16	transcription preinitiation complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0003263	0.0156	1	1	4	cardioblast proliferation	BP	1	TBX5	up_APUL_EC
GO:0010611	0.0156	1	1	11	regulation of cardiac muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC

GO:0014743	0.0156	1	1	11	regulation of muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC
GO:0048643	0.0156	1	1	7	positive regulation of skeletal muscle tissue	BP	1	SHOX2	up_VFEM_VSMC
GO:1903044	0.0156	1	1	3	protein localization to membrane raft	BP	1	CAV1	up_VSAP_VSMC
GO:0038061	0.0157	0.995	8	34	NIK/NF-kappaB signaling	BP	1	RASSF2,TLR3,SASH1,PTPN22,APP,NOD2,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0070059	0.0157	0.997	5	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	0.6	ERO1A,HYOU1,DNAJC10,PTPN2,DDIT3	down_VSAP_EC
GO:0035295	0.0157	0.997	5	356	tube development	BP	1	EYA1,HOXB7,HOXA7,SIX1,MTSS1	up_VFEM_EC
GO:0008285	0.0157	0.997	4	201	negative regulation of cell proliferation	BP	0.865	ACVRL1,LYN,PDPN,SULF1	down_ACOR_EC
GO:0003013	0.0157	0.998	3	121	circulatory system process	BP	1	IRX5,CAV1,F5	up_VSAP_VSMC
GO:0034433	0.0157	0.999	2	4	steroid esterification	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0034434	0.0157	0.999	2	4	sterol esterification	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0034435	0.0157	0.999	2	4	cholesterol esterification	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0007389	0.0157	0.999	2	137	pattern specification process	BP	1	HOXC6,GATA5	up_VCAV_VSMC
GO:0046661	0.0157	0.999	2	45	male sex differentiation	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0030033	0.0157	1	1	7	microvillus assembly	BP	1	FSCN1	down_AFEM_EC
GO:0071801	0.0157	1	1	7	regulation of podosome assembly	BP	1	FSCN1	down_AFEM_EC
GO:0032717	0.0157	1	1	7	negative regulation of interleukin-8 production	BP	1	BPI	up_AORT_EC
GO:0003211	0.0157	1	1	4	cardiac ventricle formation	BP	1	TBX5	up_APUL_EC
GO:0034383	0.0157	1	1	4	low-density lipoprotein particle clearance	BP	1	NR1H4	up_APUL_EC
GO:0046548	0.0157	1	1	4	retinal rod cell development	BP	1	NTRK2	up_APUL_EC
GO:0060914	0.0157	1	1	11	heart formation	BP	1	GATA5	up_VCAV_VSMC
GO:0098722	0.0157	1	1	2	asymmetric stem cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:0010960	0.0157	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:0060841	0.0157	1	1	6	venous blood vessel development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0090399	0.0157	1	1	4	replicative senescence	BP	1	MME	up_VFEM_EC
GO:0050829	0.0157	1	1	8	defense response to Gram-negative bacterium	BP	1	IL22RA1	up_VPUL_VSMC
GO:0016264	0.0157	1	1	3	gap junction assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0032680	0.01571387	0.99734	4	36	regulation of tumor necrosis factor production	BP	0.96436359	NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC
GO:0051128	0.015746715	0.9909	31	790	regulation of cellular component organization	BP	0.96436359	CNTNAP4,TMOD1,BRSK1,PKIB,CALY,RHOU,ARHGAP6,SYNPO2,FZD5,DIXDC1,RGMA,SMAD6,PLS1,ACTN2,ARHGAP28,ESM1,PAK3,PTGER4,ARHGDIB,PREB,MAVS,LRP4,CLSTN1,LRRC4,CLU,CHMP4B,VPS16,NRP1,PRKCD,PYGO2,TUBB4A	up_ACOR_EC
GO:0055114	0.0158	0.992	24	157	oxidation-reduction process	BP	1	PEX7,ACAA1,ACACB,PEX2,DLST,C1QTNF2,COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,PHKA2,FXN,GCDH,NDUFS2,PASK,EHHADH,LONP2,MTFR1L,ENSCAFG00000001866,IDH1,IDH3A,ENSCAFG00000006639,NDUFV1,HMOX1	up_VSAP_EC
GO:0040011	0.0158	0.992	20	505	locomotion	BP	1	CMKLR1,ANGPT4,HOXA7,PLXNA4,TWIST2,HCK,GREM1,HTR1D,CAMK2A,LRRC15,RECK,TBXA2R,BVES,LGR6,ACKR4,RAB7A,CCL5,FAP,ADAM17,KANK1	up_AFEM_EC
GO:0071695	0.0158	0.995	9	45	anatomical structure maturation	BP	0.545	EDNRB,FERMT1,CDH5,GATA3,NTN4,BMP2,SPTBN4,HIF1A,FBXO5	up_VCAV_EC
GO:0055024	0.0158	0.996	6	22	regulation of cardiac muscle tissue	BP	1	BMP4,FGFR2,TBX20,TBX5,FRS2,EDN1	up_ACOR_VSMC
GO:1902680	0.0158	0.998	4	415	positive regulation of RNA biosynthetic process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:1903508	0.0158	0.998	4	415	positive regulation of nucleic acid-templated	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC

GO:0045668	0.0158	0.998	4	11	negative regulation of osteoblast differentiation	BP	1	TWIST2,AXIN2,HDAC7,LIMD1	up_VSAP_EC
GO:0002043	0.0158	0.999	3	7	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	0.545	DLL4,APLNR,JCAD	up_VCAV_EC
GO:0034755	0.0158	0.999	2	4	iron ion transmembrane transport	BP	1	SCARA5,ARHGAP1	down_VCAV_EC
GO:0044057	0.0158	1	1	110	regulation of system process	BP	1	GATA5	down_AFEM_VSMC
GO:0046822	0.0158	1	1	53	regulation of nucleocytoplasmic	BP	1	JUP	down_VFEM_VSMC
GO:0009593	0.0158	1	1	11	detection of chemical stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0048333	0.0158	1	1	12	mesodermal cell differentiation	BP	1	EYA1	up_AFEM_VSMC
GO:0060964	0.0158	1	1	13	regulation of gene silencing by miRNA	BP	1	ESR1	up_AORT_VSMC
GO:0051890	0.0158	1	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_APUL_EC
GO:0070857	0.0158	1	1	4	regulation of bile acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0071941	0.0158	1	1	4	nitrogen cycle metabolic process	BP	1	NR1H4	up_APUL_EC
GO:1904251	0.0158	1	1	4	regulation of bile acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0043254	0.0159	0.992	22	164	regulation of protein complex assembly	BP	0.545	HCLS1,GBP5,SELP,BAIAP2L1,TLR4,IRF8,TMOD1,MTOR,CNOT6,NCKAP1,RIOK3,IQGAP2,STMN1,NCK1,FES,SENP6,PAN3,HMGB1,PMAIP1,ARPC5L,TMOD3,FSCN1	up_VCAV_EC
GO:0048568	0.0159	0.992	20	148	embryonic organ development	BP	0.545	HOXB7,PCDH12,KIT,CXCL8,PDGFB,MEF2C,CHD7,GATA3,EDN1,HOXB8,SOX18,HHEX,PROX1,MDFI,HOXB5,HIF1A,ALDH1A3,RBBP6,VASH1,ZEB1	up_VCAV_EC
GO:0030098	0.0159	0.993	15	87	lymphocyte differentiation	BP	1	ABL1,DLL1,ZBTB16,TOX,STAT6,PATZ1,ZFP36L1,PIK3R1,ZEB1,FBXO7,CD83,ZFP36L2,PNP,PPP3CB,TGFBR2	up_VSAP_EC
GO:0006401	0.0159	0.993	14	88	RNA catabolic process	BP	0.629	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,ENSCAFG00000015189,RNASEH2C,EXOSC5	down_ACOR_VSMC
GO:0110020	0.0159	0.996	7	31	regulation of actomyosin structure organization	BP	0.546	ARHGEF15,MEF2C,EDN1,ARHGAP28,MTOR,PROX1,STMN1	up_VCAV_EC
GO:0010038	0.0159	0.997	5	62	response to metal ion	BP	1	MT2A,ENSCAFG00000009113,CPNE7,FIBIN,ANXA11	up_AFEM_EC
GO:0060004	0.0159	0.999	3	6	reflex	BP	1	GJA1,GLRB,NPNT	up_ACOR_VSMC
GO:0002761	0.0159	0.999	2	36	regulation of myeloid leukocyte differentiation	BP	0.87	LYN,HOXA7	down_ACOR_EC
GO:0060740	0.0159	1	1	13	prostate gland epithelium morphogenesis	BP	1	ESR1	up_AORT_VSMC
GO:0021517	0.0159	1	1	12	ventral spinal cord development	BP	1	HOXC10	up_AORT_VSMC
GO:0003208	0.0159	1	1	24	cardiac ventricle morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0003203	0.0159	1	1	11	endocardial cushion morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0021542	0.0159	1	1	6	dentate gyrus development	BP	1	EMX2	up_VFEM_VSMC
GO:1903828	0.015995754	0.99727	4	38	negative regulation of cellular protein	BP	0.96436359	ACTN2,DCLK2,LRRC15,TP53INP2	up_ACOR_EC
GO:0046903	0.016	0.99	35	255	secretion	BP	1	EXPH5,TLR1,LEP,SLC26A7,HTR2B,MBP,FBXL20,FERMT1,SYT16,TM7SF3,ABCA1,GJA1,CD274,STX11,ANKRD1,F2RL1,HRH2,PTPN22,PRKCE,SCG5,PSEN1,PCSK6,CHD7,CCL5,RAB11B,EDN1,KCNC4,NOD2,SCAMP5,SCRN2,CFI,PREPL,PFKL,PARK7,LMF1	up_ACOR_VSMC
GO:0030278	0.016	0.995	8	66	regulation of ossification	BP	1	BMPR1A,CLSTN1,GLI3,TWIST2,DDR2,OMD,GREM1,ZBTB16	down_VCAV_EC
GO:0032677	0.016	0.996	6	22	regulation of interleukin-8 production	BP	1	TLR1,TLR3,F2RL1,PTPN22,NOD2,PARK7	up_ACOR_VSMC
GO:0009889	0.016	0.997	5	1190	regulation of biosynthetic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0032663	0.016	0.997	5	19	regulation of interleukin-2 production	BP	0.546	TNFAIP3,PDE4D,GATA3,HOMER3,PRKD2	up_VCAV_EC
GO:0003002	0.016	0.997	4	118	regionalization	BP	1	BARX1,HOXA3,SEMA3A,ACVR2A	up_VPOR_EC
GO:0010769	0.016	0.998	3	69	regulation of cell morphogenesis involved	BP	1	ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0034762	0.016	0.998	3	122	regulation of transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC

GO:0071674	0.016	0.999	2	23	mononuclear cell migration	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0009913	0.016	0.999	2	47	epidermal cell differentiation	BP	1	HOXA7,CYP26B1	up_VFEM_EC
GO:0002089	0.016	1	1	8	lens morphogenesis in camera-type eye	BP	1	CITED2	down_VPOR_EC
GO:0021517	0.016	1	1	12	ventral spinal cord development	BP	1	HOXC10	up_AFEM_VSMC
GO:0050702	0.016	1	1	13	interleukin-1 beta secretion	BP	1	ARG2	up_AORT_VSMC
GO:0006972	0.016	1	1	2	hyperosmotic response	BP	1	ARHGEF2	up_VPOR_EC
GO:0010891	0.016	1	1	2	negative regulation of sequestering of	BP	1	ABHD5	up_VPOR_EC
GO:0071474	0.016	1	1	2	cellular hyperosmotic response	BP	1	ARHGEF2	up_VPOR_EC
GO:0060413	0.016	1	1	8	atrial septum morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0003283	0.016	1	1	8	atrial septum development	BP	1	TBX5	up_VPUL_VSMC
GO:0044854	0.016	1	1	3	plasma membrane raft assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0044857	0.016	1	1	3	plasma membrane raft organization	BP	1	CAV1	up_VSAP_VSMC
GO:0001932	0.0161	0.99	47	416	regulation of protein phosphorylation	BP	0.546	EPHB1,TEK,HCLS1,KIT,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,ATF3,RAPGEF1,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,ITPKB,PROX1,MADD,PAK2,PRKD2,TLR3,NCK1,NSD1,PTGS2,MMD,RAPGEF2,TAOK1,CNOT7,HMGB1,BLM,SPTBN4,RIPK1,PDGFD,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0014070	0.0161	0.991	23	172	response to organic cyclic compound	BP	0.546	PDGFB,P2RX7,TMEM173,SELL,PDE4D,MEF2C,TIPARP,RAPGEF1,RALB,TFPI,PELI1,BMP2,RIOK3,PAK2,SMARCA4,TLR3,RAPGEF2,CTNNA1,PMAIP1,BLM,UFSP2,KDM3A,P2RX2	up_VCAV_EC
GO:0032102	0.0161	0.994	11	67	negative regulation of response to external	BP	0.546	TNFAIP3,PDGFB,CD34,KLKB1,GATA3,MMP28,TFPI,ARG2,RIOK3,ANGPT2,APOD	up_VCAV_EC
GO:1903523	0.0161	0.998	4	10	negative regulation of blood circulation	BP	1	KCNE3,PDE5A,RNLS,DOCK5	up_ACOR_VSMC
GO:0007252	0.0161	0.999	3	6	I-kappaB phosphorylation	BP	0.546	TLR4,ERC1,TLR3	up_VCAV_EC
GO:0034447	0.0161	0.999	2	4	very-low-density lipoprotein particle	BP	0.613	APOE,VLDLR	down_VSAP_EC
GO:0048675	0.0161	0.999	2	26	axon extension	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0051271	0.0161	0.999	2	98	negative regulation of cellular component	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0032703	0.0161	1	1	8	negative regulation of interleukin-2 production	BP	1	HDAC7	down_VPOR_EC
GO:0060047	0.0161	1	1	57	heart contraction	BP	1	JUP	down_VFEM_VSMC
GO:0072606	0.0161	1	1	12	interleukin-8 secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0042698	0.0161	1	1	14	ovulation cycle	BP	1	ESR1	up_AORT_VSMC
GO:0055083	0.0161	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:0072102	0.0161	1	1	4	glomerulus morphogenesis	BP	1	MTSS1	up_VFEM_EC
GO:1903817	0.0161	1	1	3	negative regulation of voltage-gated potassium	BP	1	CAV1	up_VSAP_VSMC
GO:0001501	0.0162	0.992	16	178	skeletal system development	BP	1	NOTCH2,SMAD9,NAB2,FBN1,THBS3,BMPR1A,TBX15,HOXC4,HAPLN3,VCAN,GLI3,ENSCAFG00000017708,IRX5,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0032092	0.0162	1	1	38	positive regulation of protein binding	BP	1	PLCL1	down_VFEM_EC
GO:0060071	0.0162	1	1	14	Wnt signaling pathway, planar cell polarity	BP	1	WNT7A	up_AORT_VSMC
GO:0014912	0.0162	1	1	8	negative regulation of smooth muscle cell	BP	1	SLIT2	up_VPUL_VSMC
GO:0046621	0.0162	1	1	8	negative regulation of organ growth	BP	1	TBX5	up_VPUL_VSMC
GO:1902105	0.0163	0.993	13	80	regulation of leukocyte differentiation	BP	0.549	HCLS1,IL7R,GATA3,CASP8,MTOR,ITPKB,CREB1,HMGB1,RIPK1,ATP11C,CUL4A,ZEB1,TJP2	up_VCAV_EC
GO:0019219	0.0163	0.996	7	1151	regulation of nucleobase-containing compound metabolic process	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC

GO:0048869	0.0163	0.997	6	1119	cellular developmental process	BP	1	TBX5,GATA5,TMEM176A,TMEM176B,HOXB5,SLIT2	up_VPUL_VSMC
GO:0070085	0.0163	0.999	2	95	glycosylation	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0007160	0.0163	1	1	56	cell-matrix adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0007338	0.0163	1	1	16	single fertilization	BP	1	HOXA9	up_AORT_VSMC
GO:0043586	0.0163	1	1	6	tongue development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0032332	0.0163	1	1	6	positive regulation of chondrocyte	BP	1	HOXA11	up_VFEM_VSMC
GO:1901362	0.0164	0.994	11	1293	organic cyclic compound biosynthetic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0019319	0.0164	0.997	5	26	hexose biosynthetic process	BP	0.621	TPI1,PGAM1,SESN2,PTPN2,ATF3	down_VSAP_EC
GO:0007259	0.0164	0.999	2	42	JAK-STAT cascade	BP	0.891	LYN,ASPN	down_ACOR_EC
GO:0002221	0.0164	0.999	2	46	pattern recognition receptor signaling	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0002758	0.0164	0.999	2	46	innate immune response-activating signal	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0001893	0.0164	1	1	8	maternal placenta development	BP	1	CITED2	down_VPOR_EC
GO:0003015	0.0164	1	1	58	heart process	BP	1	JUP	down_VFEM_VSMC
GO:0010092	0.0164	1	1	19	specification of animal organ identity	BP	1	GATA5	down_VSAP_VSMC
GO:0003179	0.0164	1	1	19	heart valve morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0060795	0.0164	1	1	12	cell fate commitment involved in formation of	BP	1	EYA1	up_AFEM_VSMC
GO:0061028	0.0164	1	1	14	establishment of endothelial barrier	BP	1	WNT7A	up_AORT_VSMC
GO:0045844	0.0164	1	1	24	positive regulation of striated muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0048636	0.0164	1	1	24	positive regulation of muscle organ	BP	1	TBX5	up_APUL_VSMC
GO:0007320	0.0164	1	1	2	insemination	BP	1	ACVR2A	up_VPOR_EC
GO:0007620	0.0164	1	1	2	copulation	BP	1	ACVR2A	up_VPOR_EC
GO:2000484	0.0164	1	1	4	positive regulation of interleukin-8 secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0098542	0.01640875	0.99518	7	100	defense response to other organism	BP	0.96436359	NR1H4,NOD2,MAVS,IFIT2,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0009719	0.0165	0.996	6	395	response to endogenous stimulus	BP	0.891	ACVRL1,LYN,IGF1R,SULF1,ASPN,NEDD4	down_ACOR_EC
GO:0007031	0.0165	0.997	4	20	peroxisome organization	BP	1	SCP2,PEX5,MAVS,LONP2	down_VCAV_EC
GO:0045746	0.0165	0.997	4	14	negative regulation of Notch signaling pathway	BP	0.555	DLL4,EGFL7,GDPD5,PEAR1	up_VCAV_EC
GO:0044089	0.0165	0.999	2	170	positive regulation of cellular component	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0007596	0.0165	0.999	2	47	blood coagulation	BP	1	CAV1,F5	up_VSAP_VSMC
GO:0034135	0.0165	1	1	4	regulation of toll-like receptor 2 signaling	BP	0.891	LYN	down_ACOR_EC
GO:0010447	0.0165	1	1	8	response to acidic pH	BP	1	RAB11B	down_VPOR_EC
GO:0043534	0.0165	1	1	57	blood vessel endothelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:1903522	0.0165	1	1	58	regulation of blood circulation	BP	1	JUP	down_VFEM_VSMC
GO:0042474	0.0165	1	1	11	middle ear morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0022603	0.0166	0.991	28	301	regulation of anatomical structure morphogenesis	BP	0.628	VEGFA,SIPA1L1,SULF1,MYH9,FMNL3,SERPINE1,SPARC,JCAD,PGK1,AKAP2,IFRD1,WDR1,PIK3C2A,MSN,HOXB7,HIF1A,THBS2,TNIK,MTDH,UST,MAGED1,CTNNB1,STARD13,ENSCAFG00000002015,BNIP3,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0055085	0.0166	0.991	23	284	transmembrane transport	BP	1	PRNP,FOLR2,FXYD1,CLIP3,ENSCAFG00000014978,AKT2,SLC39A6,CACNB3,ATP5MC1,THY1,PEX5,MFSD3,ATP6V0C,PARK7,SLC17A9,SCARA5,SLC2A10,CYBA,SPNS1,SEC61B,ARHGAP1,LONP2,CLIC4	down_VCAV_EC

GO:0050877	0.0166	0.991	22	164	nervous system process	BP	0.556	EPHB1,PLK2,KIT,PTCHD1,ATP8A1,RELN,MEF2C,CHD7,HOXB8,HOMER3,PPP3CA,TMEM150C,NAV2,ACPP,MMP24,CREB1,GCH1,SPTBN4,HIF1A,ALDH1A3,DOP1B,P2RX2	up_VCAV_EC
GO:0001568	0.0166	0.993	12	252	blood vessel development	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,RECK,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0034440	0.0166	0.995	8	35	lipid oxidation	BP	1	PEX7,ACAA1,ACACB,PEX2,C1QTNF2,GCDH,EHHADH,LONP2	up_VSAP_EC
GO:0046928	0.0166	0.998	3	23	regulation of neurotransmitter	BP	1	KCNC4,CHRM2,CAMK2A	up_AFEM_EC
GO:0045649	0.0166	0.998	3	8	regulation of macrophage differentiation	BP	0.556	HCLS1,CASP8,RIPK1	up_VCAV_EC
GO:0006167	0.0166	1	1	2	AMP biosynthetic process	BP	0.891	TNRC6B	down_ACOR_EC
GO:0044208	0.0166	1	1	2	'de novo' AMP biosynthetic process	BP	0.891	TNRC6B	down_ACOR_EC
GO:0032927	0.0166	1	1	2	positive regulation of activin receptor signaling	BP	1	ACVR2A	up_VPOR_EC
GO:0060011	0.0166	1	1	2	Sertoli cell proliferation	BP	1	ACVR2A	up_VPOR_EC
GO:0006617	0.0166	1	1	2	SRP-dependent cotranslational protein targeting to membrane,	BP	1	SRP54	up_VPOR_EC
GO:0014841	0.0166	1	1	4	skeletal muscle satellite cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0014842	0.0166	1	1	4	regulation of skeletal muscle satellite cell	BP	1	SIX1	up_VFEM_EC
GO:0014856	0.0166	1	1	4	skeletal muscle cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0014857	0.0166	1	1	4	regulation of skeletal muscle cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0031295	0.0166	1	1	3	T cell costimulation	BP	1	CAV1	up_VSAP_VSMC
GO:0009968	0.016654157	0.99183	18	392	negative regulation of signal transduction	BP	0.96436359	NR1H4,SOX9,NDRG2,CCDC3,IFI6,DUSP26,PTGIR,SMAD6,ADAMTSL2,MAPK8IP2,FIGNL1,LRRC15,LRP4,CLSTN1,LRRC4,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0008285	0.0167	0.991	20	201	negative regulation of cell proliferation	BP	0.628	SULF1,SPARC,PTPN14,ILK,PTPN2,SKAP2,CNOT7,MAGED1,CTNNB1,APOE,LYN,STRAP,PDS5B,TAX1BP3,SDC4,REST,ENSCAFG00000017326,INHBA,BTK,CDKN1A	down_VSAP_EC
GO:0042221	0.0167	0.995	8	1012	response to chemical	BP	1	NR1H4,MRC1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1,MXRA5	up_VPUL_EC
GO:0035270	0.0167	0.995	8	35	endocrine system development	BP	1	WNT11,HNF4A,IL6R,HOXD3,DLL1,RAF1,MAP2K2,CITED2	up_VSAP_EC
GO:0007157	0.0167	0.998	4	12	heterophilic cell-cell adhesion via plasma membrane cell adhesion	BP	0.559	SELP,SELE,NECTIN2,CD200	up_VCAV_EC
GO:0090190	0.0167	0.998	3	10	positive regulation of branching involved in ureteric bud	BP	0.629	HOXB7,MAGED1,SIX4	down_VSAP_EC
GO:0044703	0.0167	0.999	2	172	multi-organism reproductive process	BP	1	HOXA9,ESR1	up_AORT_VSMC
GO:0040013	0.0167	0.999	2	100	negative regulation of locomotion	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0030851	0.0167	1	1	8	granulocyte differentiation	BP	1	CITED2	down_VPOR_EC
GO:0007219	0.0167	1	1	59	Notch signaling pathway	BP	1	GATA5	down_VFEM_VSMC
GO:0045793	0.0167	1	1	4	positive regulation of cell size	BP	1	PRR16	up_VSAP_VSMC
GO:0006469	0.016711957	0.99564	6	78	negative regulation of protein kinase activity	BP	0.96436359	PKIB,DUSP26,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0051902	0.016718356	1	1	1	negative regulation of mitochondrial	BP	0.96436359	IFI6	up_ACOR_EC
GO:1904180	0.016718356	1	1	1	negative regulation of membrane depolarization	BP	0.96436359	IFI6	up_ACOR_EC
GO:0010758	0.016746609	0.99914	2	8	regulation of macrophage chemotaxis	BP	0.96436359	MMP28,RARRES2	up_ACOR_EC
GO:0099072	0.016774117	0.99914	2	8	regulation of postsynaptic membrane neurotransmitter	BP	0.96436359	CALY,PORCN	up_ACOR_EC
GO:0009887	0.0168	0.993	14	314	animal organ morphogenesis	BP	1	TBX15,IRX3,IRX5,HOXA7,COL8A2,DLL1,THRB,TMEM100,GREM1,HOXA6,CNNM4,AXIN2,GCNT4,TNC	up_AFEM_EC
GO:0050730	0.0168	0.994	11	66	regulation of peptidyl-tyrosine phosphorylation	BP	0.559	HCLS1,KIT,PDGFB,RELN,NEDD9,YES1,MTOR,SH3BP5,CNOT7,PDGFD,ARHGEF2	up_VCAV_EC
GO:0051240	0.0168	0.996	6	489	positive regulation of multicellular organismal	BP	1	HOXA11,NETO1,GATM,TLR2,CAV1,SHOX2	up_VSAP_VSMC

GO:0010941	0.0168	0.998	3	524	regulation of cell death	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:2001214	0.0168	1	2	3	positive regulation of vasculogenesis	BP	0.559	CD34,RAPGEF2	up_VCAV_EC
GO:0003002	0.0168	1	1	118	regionalization	BP	1	GATA5	down_AFEM_VSMC
GO:0022027	0.0168	1	1	2	interkinetic nuclear migration	BP	1	HOOK3	up_VPOR_EC
GO:0010664	0.0168	1	1	6	negative regulation of striated muscle cell	BP	1	NKX2-5	up_VPOR_VSMC
GO:0034162	0.0168	1	1	5	toll-like receptor 9 signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:1903555	0.016867718	0.99708	4	37	regulation of tumor necrosis factor superfamily cytokine	BP	0.96436359	NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC
GO:0045860	0.0169	0.992	19	132	positive regulation of protein kinase activity	BP	0.559	KIT,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,NEDD9,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,MMD,RAPGEF2,RIPK1,PDGFD	up_VCAV_EC
GO:0030155	0.0169	0.992	16	180	regulation of cell adhesion	BP	1	GPAM,FBLN2,PRNP,SDC4,RHOD,ENSCAFG00000014978,TFE3,LAMA3,THY1,GLI3,EDIL3,LOXL3,GREM1,RAC2,ZBTB16,ECM2	down_VCAV_EC
GO:1901342	0.0169	0.993	13	114	regulation of vasculature development	BP	0.633	VEGFA,SULF1,SERPINE1,SPARC,JCAD,PGK1,PIK3C2A,HIF1A,THBS2,MTDH,CTNNB1,STARD13,NRP1	down_VSAP_EC
GO:0002224	0.0169	0.995	7	34	toll-like receptor signaling pathway	BP	0.559	TNFAIP3,TNIP1,TLR4,PELI1,TLR3,OTUD4,HMGB1	up_VCAV_EC
GO:0051299	0.0169	0.998	3	7	centrosome separation	BP	0.659	NEK2,NUP62,KIF11	down_ACOR_VSMC
GO:0048513	0.0169	0.999	3	906	animal organ development	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0002520	0.0169	0.998	3	279	immune system development	BP	1	HOXA3,TMEM176A,TMEM176B	up_VPUL_VSMC
GO:1905330	0.0169	0.999	2	48	regulation of morphogenesis of an	BP	1	HOXB7,SIX1	up_VFEM_EC
GO:0042996	0.0169	1	1	4	regulation of Golgi to plasma membrane	BP	0.9	ACSL3	down_ACOR_EC
GO:0017145	0.0169	1	1	13	stem cell division	BP	1	WNT7A	up_AORT_VSMC
GO:0060512	0.0169	1	1	14	prostate gland morphogenesis	BP	1	ESR1	up_AORT_VSMC
GO:1905314	0.0169	1	1	12	semi-lunar valve development	BP	1	GATA5	up_VCAV_VSMC
GO:0010159	0.0169	1	1	2	specification of animal organ position	BP	1	HOXA3	up_VPOR_EC
GO:2000095	0.0169	1	1	6	regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	ANKRD6	up_VPOR_VSMC
GO:1900084	0.0169	1	1	3	regulation of peptidyl-tyrosine	BP	1	CAV1	up_VSAP_VSMC
GO:0032331	0.01695558	0.99912	2	8	negative regulation of chondrocyte	BP	0.96436359	SOX9,EFEMP1	up_ACOR_EC
GO:0061037	0.01695558	0.99912	2	8	negative regulation of cartilage development	BP	0.96436359	SOX9,EFEMP1	up_ACOR_EC
GO:0032620	0.016969193	0.99912	2	8	interleukin-17 production	BP	0.96436359	NR1H4,NOD2	up_ACOR_EC
GO:0051094	0.017	0.989	50	388	positive regulation of developmental process	BP	1	HOXA11,NAPEPLD,CDON,CD274,AXIN2,WASF3,OSR2,AMIGO1,ENPP2,LRRN3,PPARGC1B,ACACB,DDHD1,ZHX3,HOXD3,FGF7,ABL1,BTG1,HDAC7,DLL1,OSR1,MAP3K5,SAV1,HPSE,ANKRD54,ZBTB16,TOX,CCBE1,STAT6,DDR2,ZFP36L1,IRX3,ZEB1,SHOX2,SASH1,GDPD5,CD83,KDM2B,YPEL3,PNP,CYB5D2,ACVRL1,FLOT1,NCK1,HMOX1,MAP2K2,TGFBR2,CITED2,TRADD,LBH	up_VSAP_EC
GO:0002694	0.017	0.992	18	126	regulation of leukocyte activation	BP	0.559	IL7R,ADGRF5,TNFAIP3,MEF2C,TLR4,GATA3,PELI1,ARG2,NECTIN2,ITPKB,THOC1,NCK1,CD200,FES,BCL10,HMGB1,ATP11C,ZEB1	up_VCAV_EC
GO:0051607	0.017	0.994	10	58	defense response to virus	BP	0.559	MX2,TMEM173,NLRC5,SERINC5,RIOK3,TLR3,OAS3,CNOT7,PMAIP1,LSM14A	up_VCAV_EC
GO:0061333	0.017	0.996	6	35	renal tubule morphogenesis	BP	0.635	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0010972	0.017	0.997	5	18	negative regulation of G2/M transition of mitotic	BP	0.559	TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0003073	0.017	0.997	5	20	regulation of systemic arterial blood pressure	BP	0.559	PRCP,PDGFB,EDN1,NAV2,P2RX2	up_VCAV_EC
GO:1900026	0.017	0.998	4	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	NRP1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0070206	0.017	0.998	4	11	protein trimerization	BP	1	C1QTNF2,SCARA5,CLYBL,HTRA2	up_VSAP_EC

GO:0003184	0.017	0.999	3	6	pulmonary valve morphogenesis	BP	1	SMAD6,BMP4,TBX20	up_ACOR_VSMC
GO:0097696	0.017	0.999	2	43	STAT cascade	BP	0.903	LYN,ASPN	down_ACOR_EC
GO:0060850	0.017	1	2	3	regulation of transcription involved in cell fate	BP	0.559	PPARG,PROX1	up_VCAV_EC
GO:0033135	0.017	1	1	40	regulation of peptidyl-serine phosphorylation	BP	1	PLCL1	down_VFEM_EC
GO:0002832	0.017	1	1	15	negative regulation of response to biotic	BP	1	ARG2	up_AORT_VSMC
GO:0060997	0.017	1	1	14	dendritic spine morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0019433	0.017	1	1	2	triglyceride catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0034454	0.017	1	1	2	microtubule anchoring at centrosome	BP	1	HOOK3	up_VPOR_EC
GO:0051006	0.017	1	1	2	positive regulation of lipoprotein lipase activity	BP	1	ABHD5	up_VPOR_EC
GO:0061365	0.017	1	1	2	positive regulation of triglyceride lipase activity	BP	1	ABHD5	up_VPOR_EC
GO:0032816	0.017	1	1	4	positive regulation of natural killer cell	BP	1	TOX	up_VFEM_EC
GO:0055026	0.017	1	1	5	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:1903706	0.0171	0.992	19	119	regulation of hemopoiesis	BP	1	HOXA7,HOXA9,PPARGC1B,ABL1,DLL1,ANKRD54,ZBTB16,TOX,RARG,ZFP36L1,PIK3R1,MYC,ZEB1,TFE3,FBXO7,CD83,ZFP36L2,PNP,TGFBR2	up_VSAP_EC
GO:0045740	0.0171	0.997	4	12	positive regulation of DNA replication	BP	0.667	PCNA,E2F8,CDK2,GLI1	down_ACOR_VSMC
GO:0048562	0.0171	0.999	2	102	embryonic organ morphogenesis	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0106106	0.0171	0.999	2	48	cold-induced thermogenesis	BP	1	HOXC10,MAP2K6	up_VFEM_EC
GO:0120161	0.0171	0.999	2	48	regulation of cold-induced thermogenesis	BP	1	HOXC10,MAP2K6	up_VFEM_EC
GO:0003156	0.0171	1	1	20	regulation of animal organ formation	BP	1	GATA5	down_VSAP_VSMC
GO:0043171	0.0171	1	1	8	peptide catabolic process	BP	1	LNPEP	up_AORT_EC
GO:1901863	0.0171	1	1	25	positive regulation of muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0006171	0.0171	1	1	5	cAMP biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0046058	0.0171	1	1	5	cAMP metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0072643	0.0171	1	1	5	interferon-gamma secretion	BP	1	NR1H4	up_VPUL_EC
GO:0009306	0.0172	0.991	20	127	protein secretion	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FERMT1,TM7SF3,ABCA1,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,CCL5,RAB11B,NOD2,SCAMP5,PFKL,PARK7,LMF1	up_ACOR_VSMC
GO:0032720	0.0172	0.997	4	13	negative regulation of tumor necrosis factor	BP	0.564	TNFAIP3,CD34,TLR4,ARG2	up_VCAV_EC
GO:0097479	0.0172	0.999	2	41	synaptic vesicle localization	BP	0.905	SPG11,STX4	down_ACOR_EC
GO:0019221	0.0172	0.999	2	102	cytokine-mediated signaling pathway	BP	1	IL22RA1,SLIT2	up_VPUL_VSMC
GO:0072009	0.0172	0.999	2	48	nephron epithelium development	BP	1	HOXA11,SALL1	up_VSAP_VSMC
GO:0010810	0.0172	1	1	60	regulation of cell-substrate adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0044319	0.0172	1	1	12	wound healing, spreading of cells	BP	1	WNT7A	up_AORT_VSMC
GO:0003401	0.0172	1	1	15	axis elongation	BP	1	ESR1	up_AORT_VSMC
GO:0090504	0.0172	1	1	12	epiboly	BP	1	WNT7A	up_AORT_VSMC
GO:0090505	0.0172	1	1	12	epiboly involved in wound healing	BP	1	WNT7A	up_AORT_VSMC
GO:0042483	0.0172	1	1	2	negative regulation of odontogenesis	BP	1	ASPN	up_VPOR_EC
GO:0006699	0.0172	1	1	5	bile acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0018212	0.0173	0.993	13	81	peptidyl-tyrosine modification	BP	0.564	HCLS1,KIT,PDGFB,RELN,NEDD9,YES1,MTOR,SH3BP5,FES,CNOT7,PDGFD,BMX,ARHGEF2	up_VCAV_EC
GO:0001678	0.0173	0.995	7	29	cellular glucose homeostasis	BP	1	RAB11B,PIK3R1,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0001885	0.0173	0.997	5	19	endothelial cell development	BP	0.564	PDE4D,RAPGEF1,STC1,SOX18,RAPGEF2	up_VCAV_EC

GO:0018401	0.0173	0.999	2	4	peptidyl-proline hydroxylation to 4-	BP	0.644	P4HB,P4HA1	down_VSAP_EC
GO:0048562	0.0173	0.999	2	102	embryonic organ morphogenesis	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0007599	0.0173	0.999	2	48	hemostasis	BP	1	CAV1,F5	up_VSAP_VSMC
GO:2000480	0.0173	1	1	4	negative regulation of cAMP-dependent protein	BP	0.905	PRKAR2A	down_ACOR_EC
GO:0033119	0.0173	1	1	8	negative regulation of RNA splicing	BP	1	SRSF6	down_AFEM_EC
GO:2000772	0.0173	1	1	15	regulation of cellular senescence	BP	1	ARG2	up_AORT_VSMC
GO:0005985	0.0173	1	1	2	sucrose metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0005986	0.0173	1	1	2	sucrose biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0060681	0.0173	1	1	4	branch elongation involved in ureteric bud	BP	1	SIX1	up_VFEM_EC
GO:0072106	0.0173	1	1	4	regulation of ureteric bud formation	BP	1	SIX1	up_VFEM_EC
GO:0072107	0.0173	1	1	4	positive regulation of ureteric bud formation	BP	1	SIX1	up_VFEM_EC
GO:1905278	0.0173	1	1	4	positive regulation of epithelial tube formation	BP	1	SIX1	up_VFEM_EC
GO:2000136	0.0173	1	1	7	regulation of cell proliferation involved in	BP	1	EYA1	up_VFEM_VSMC
GO:0003264	0.0173	1	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_VPUL_EC
GO:0003207	0.0173	1	1	5	cardiac chamber formation	BP	1	TBX5	up_VPUL_EC
GO:0003266	0.0173	1	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_VPUL_EC
GO:1901617	0.0174	0.994	10	60	organic hydroxy compound biosynthetic	BP	0.564	GATA3,SPTLC2,BMP2,ITPKB,PROX1,RAPGEF2,PLCG2,GCH1,LBR,IMPA1	up_VCAV_EC
GO:0032501	0.0174	0.995	9	1782	multicellular organismal process	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0001503	0.0174	0.998	3	109	ossification	BP	0.905	HOXA3,CSGALNACT1,ASPN	down_ACOR_EC
GO:0010557	0.0174	0.998	3	492	positive regulation of macromolecule biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0016339	0.0174	0.999	3	6	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion	BP	0.564	PCDH12,SELP,SELL	up_VCAV_EC
GO:0060055	0.0174	0.998	3	8	angiogenesis involved in wound healing	BP	0.564	PRCP,GPR4,ADIPOR2	up_VCAV_EC
GO:0048513	0.0174	1	2	906	animal organ development	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0043931	0.0174	0.999	2	9	ossification involved in bone maturation	BP	1	XYLT1,GREM1	up_AFEM_EC
GO:0070977	0.0174	0.999	2	9	bone maturation	BP	1	XYLT1,GREM1	up_AFEM_EC
GO:0060136	0.0174	1	1	4	embryonic process involved in female	BP	0.905	ACSL4	down_ACOR_EC
GO:0010837	0.0174	1	1	8	regulation of keratinocyte proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0070986	0.0174	1	1	9	left/right axis specification	BP	1	CITED2	down_VPOR_EC
GO:0003222	0.0174	1	1	6	ventricular trabecula myocardium	BP	1	NKX2-5	up_VPOR_VSMC
GO:0042118	0.0174	1	1	4	endothelial cell activation	BP	1	HOXA9	up_VFEM_EC
GO:0048384	0.0174	1	1	4	retinoic acid receptor signaling pathway	BP	1	CYP26B1	up_VFEM_EC
GO:0048385	0.0174	1	1	4	regulation of retinoic acid receptor signaling	BP	1	CYP26B1	up_VFEM_EC
GO:0055062	0.0174	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0072505	0.0174	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0072506	0.0174	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0055002	0.0175	0.995	7	45	striated muscle cell development	BP	0.649	ACTN1,FHL2,WDR1,NEXN,SIX4,MYBPC2,HOMER1	down_VSAP_EC
GO:0097327	0.0175	0.996	6	25	response to antineoplastic agent	BP	0.564	PDGFB,MAPK13,TIMELESS,CTNNA1,BLM,ATRX	up_VCAV_EC
GO:0099518	0.0175	0.997	4	17	vesicle cytoskeletal trafficking	BP	0.649	MYO1C,KIF5B,HTT,AP3S1	down_VSAP_EC
GO:0001881	0.0175	0.997	4	11	receptor recycling	BP	1	PSEN1,RAB11B,LMTK2,BVES	up_ACOR_VSMC

GO:0009952	0.0175	0.998	3	66	anterior/posterior pattern specification	BP	1	BARX1,HOXA3,ACVR2A	up_VPOR_EC
GO:0030856	0.0175	0.999	2	41	regulation of epithelial cell differentiation	BP	0.905	ACVRL1,HOXA7	down_ACOR_EC
GO:1903707	0.0175	0.999	2	48	negative regulation of hemopoiesis	BP	1	HOXA9,HOXA7	up_VFEM_EC
GO:0050830	0.0175	1	1	12	defense response to Gram-positive bacterium	BP	1	TLR2	up_AFEM_VSMC
GO:0035115	0.0175	1	1	12	embryonic forelimb morphogenesis	BP	1	HOXA9	up_AFEM_VSMC
GO:0060147	0.0175	1	1	14	regulation of posttranscriptional gene	BP	1	ESR1	up_AORT_VSMC
GO:0060966	0.0175	1	1	14	regulation of gene silencing by RNA	BP	1	ESR1	up_AORT_VSMC
GO:0048752	0.0175	1	1	5	semicircular canal morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0010758	0.0175	1	1	8	regulation of macrophage chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0090022	0.0175	1	1	9	regulation of neutrophil chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0042118	0.0175	1	1	4	endothelial cell activation	BP	1	HOXA9	up_VSAP_VSMC
GO:0032869	0.017552243	0.99608	5	57	cellular response to insulin stimulus	BP	0.96436359	NR1H4,ENSCAFG00000004331,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:1903362	0.0176	0.993	12	100	regulation of cellular protein catabolic process	BP	0.65	PRICKLE1,PLK3,SOCS5,TRIB3,MSN,UCHL5,APOE,GSK3B,DISC1,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0032640	0.0176	0.995	8	39	tumor necrosis factor production	BP	0.564	TNFAIP3,CD34,TLR4,ARG2,TLR3,HMGB1,RIPK1,ARHGEF2	up_VCAV_EC
GO:0071241	0.0176	0.995	8	42	cellular response to inorganic substance	BP	0.564	MEF2C,TJP1,ITPKB,TIMELESS,GUCY1B1,CREB1,BLM,ATRX	up_VCAV_EC
GO:0071322	0.0176	0.995	7	29	cellular response to carbohydrate stimulus	BP	1	RAB11B,ZFP36L1,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0007405	0.0176	0.996	6	21	neuroblast proliferation	BP	1	FGFR2,ACSL6,SMARCD3,FZD3,FRS2,DISC1	up_ACOR_VSMC
GO:0002027	0.0176	0.996	5	20	regulation of heart rate	BP	0.564	PDE4D,EDN1,KCNJ2,GCH1,SPTBN4	up_VCAV_EC
GO:1902914	0.0176	0.997	4	11	regulation of protein polyubiquitination	BP	1	SKP2,SASH1,PTPN22,NOD2	up_ACOR_VSMC
GO:0045935	0.0176	0.998	3	491	positive regulation of nucleobase-containing compound metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:1990126	0.0176	1	1	8	retrograde transport, endosome to plasma	BP	1	ANKRD50	down_AFEM_EC
GO:0048596	0.0176	1	1	9	embryonic camera-type eye morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0006048	0.0176	1	1	2	UDP-N-acetylglucosamine biosynthetic process	BP	1	GNPNAT1	up_VPOR_EC
GO:0046349	0.0176	1	1	2	amino sugar biosynthetic process	BP	1	GNPNAT1	up_VPOR_EC
GO:0090022	0.0176	1	1	9	regulation of neutrophil chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0048557	0.0176	1	1	7	embryonic digestive tract morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0043412	0.017638181	0.9889	44	1225	macromolecule modification	BP	0.96436359	NR1H4,BRSK1,PLCL1,PKIB,SOX9,GALNT5,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,DUSP26,NOD2,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0022604	0.0177	0.992	14	122	regulation of cell morphogenesis	BP	0.65	VEGFA,SIPA1L1,MYH9,FMNL3,SPARC,AKAP2,IFRD1,WDR1,MSN,TNIK,UST,ENSCAFG00000002015,NRP1,YWHAH	down_VSAP_EC
GO:0034329	0.0177	0.993	11	60	cell junction assembly	BP	0.566	TEK,PRKCH,OCLN,RAPGEF1,TJP1,SLK,APOD,RAPGEF2,CTNNA1,ENSCAFG00000002015,FSCN1	up_VCAV_EC
GO:0032501	0.0177	0.995	9	1782	multicellular organismal process	BP	1	HOXC10,EYA1,GATM,HOXA9,NETO1,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:2000060	0.0177	0.995	7	45	positive regulation of ubiquitin-dependent protein catabolic process	BP	0.65	PRICKLE1,PLK3,SOCS5,TRIB3,GSK3B,DISC1,RAD23A	down_VSAP_EC
GO:0034381	0.0177	0.998	3	10	plasma lipoprotein particle clearance	BP	0.65	NR1H4,APOE,VLDLR	down_VSAP_EC
GO:0048532	0.0177	0.999	2	9	anatomical structure arrangement	BP	1	DLL1,PLXNA4	up_AFEM_EC
GO:0072611	0.0177	1	2	3	interleukin-13 secretion	BP	0.564	GATA3,ARG2	up_VCAV_EC
GO:2000665	0.0177	1	2	3	regulation of interleukin-13 secretion	BP	0.564	GATA3,ARG2	up_VCAV_EC

GO:1990266	0.0177	0.999	2	24	neutrophil migration	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0048839	0.0177	0.999	2	50	inner ear development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0014904	0.0177	1	1	12	myotube cell development	BP	1	BEND2	up_AFEM_VSMC
GO:0048741	0.0177	1	1	12	skeletal muscle fiber development	BP	1	BEND2	up_AFEM_VSMC
GO:0099560	0.0177	1	1	5	synaptic membrane adhesion	BP	1	FLRT3	up_VPUL_EC
GO:0051246	0.017732955	0.98957	32	832	regulation of protein metabolic process	BP	0.96436359	PLCL1,PKIB,SOX9,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,IFI6,DUSP26,NOD2,SMAD6,KLHL25,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,LRRC15,LRP4,SH3RF3,LRRC4,CLU,RARRES2,RNF114,NRP1,AZIN2,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0032228	0.017776087	0.99906	2	8	regulation of synaptic transmission, GABAergic	BP	0.96436359	CNTNAP4,PLCL1	up_ACOR_EC
GO:0045165	0.0178	0.993	11	65	cell fate commitment	BP	0.566	IL6,PPARG,MEF2C,DLL4,GATA3,SOX18,MTOR,BMP2,PROX1,ARHGEF2,CDON	up_VCAV_EC
GO:0007610	0.0178	0.998	3	146	behavior	BP	1	SLITRK5,NTRK2,HOXA1	up_APUL_EC
GO:0034329	0.0178	1	1	60	cell junction assembly	BP	1	JUP	down_VFEM_VSMC
GO:0060065	0.0178	1	1	7	uterus development	BP	1	HOXA9	up_AORT_EC
GO:0090175	0.0178	1	1	15	regulation of establishment of planar	BP	1	WNT7A	up_AORT_VSMC
GO:0061323	0.0178	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0003176	0.0178	1	1	9	aortic valve development	BP	1	GATA5	up_VPUL_VSMC
GO:0009888	0.0179	0.991	21	545	tissue development	BP	1	IRX3,LEP,LBH,HOXA7,DLL1,THRB,TMEM100,GREM1,OVOL1,POSTN,LUZP1,PTHLH,CNNM4,BVES,LGR6,AXIN2,PPARGC1A,ADAM17,GCNT4,FOSL2,TNC	up_AFEM_EC
GO:0006090	0.0179	0.996	5	26	pyruvate metabolic process	BP	0.654	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0060914	0.0179	0.997	4	11	heart formation	BP	1	GATA5,BMP4,SMARCD3,TBX5	up_ACOR_VSMC
GO:0070229	0.0179	0.997	4	13	negative regulation of lymphocyte apoptotic	BP	0.57	IL7R,ARG2,BCL10,HIF1A	up_VCAV_EC
GO:1903034	0.0179	0.999	2	40	regulation of response to wounding	BP	0.905	LYN,PDPN	down_ACOR_EC
GO:0030855	0.0179	0.999	2	183	epithelial cell differentiation	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0048812	0.0179	0.999	2	151	neuron projection morphogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0014831	0.0179	1	1	3	gastro-intestinal system smooth muscle	BP	0.905	SULF1	down_ACOR_EC
GO:0071800	0.0179	1	1	8	podosome assembly	BP	1	FSCN1	down_AFEM_EC
GO:0003170	0.0179	1	1	25	heart valve development	BP	1	TBX5	up_APUL_VSMC
GO:0060575	0.0179	1	1	9	intestinal epithelial cell differentiation	BP	1	GATA5	up_VPUL_VSMC
GO:2000738	0.0179	1	1	9	positive regulation of stem cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0009888	0.017941488	0.99035	23	545	tissue development	BP	0.96436359	CDH3,NR1H4,TMOD1,GATA4,BRSK1,SOX9,PTH1R,AQP1,FZD5,SMAD6,ACTN2,DLX3,TNFRSF19,ADAMTSL2,FOXC2,TBX5,LRP4,CLSTN1,C23H3orf58,NRP1,ARHGEF26,PYGO2,EFEMP1	up_ACOR_EC
GO:0030239	0.017997635	0.99785	3	21	myofibril assembly	BP	0.96436359	MYOZ2,TMOD1,ACTN2	up_ACOR_EC
GO:0044249	0.018	0.993	14	1851	cellular biosynthetic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0050867	0.018	0.992	13	83	positive regulation of cell activation	BP	0.571	IL7R,SELP,MEF2C,TLR4,GATA3,PELI1,NECTIN2,ITPKB,NCK1,CD200,BCL10,HMGB1,ATP11C	up_VCAV_EC
GO:0000212	0.018	0.998	3	7	meiotic spindle organization	BP	0.695	FBXO5,ESPL1,ASPM	down_ACOR_VSMC
GO:0050680	0.018	0.999	2	44	negative regulation of epithelial cell proliferation	BP	0.905	ACVRL1,SULF1	down_ACOR_EC
GO:2001204	0.018	0.999	2	5	regulation of osteoclast development	BP	1	NOTCH2,FBN1	down_VCAV_EC
GO:0002176	0.018	0.999	2	3	male germ cell proliferation	BP	1	PRDX4,SPINK2	up_ACOR_VSMC

GO:0036093	0.018	0.999	2	3	germ cell proliferation	BP	1	PRDX4,SPINK2	up_ACOR_VSMC
GO:0046850	0.018	0.999	2	9	regulation of bone remodeling	BP	1	LEP,GREM1	up_AFEM_EC
GO:0060839	0.018	1	1	4	endothelial cell fate commitment	BP	0.905	PDPN	down_ACOR_EC
GO:0072148	0.018	1	1	4	epithelial cell fate commitment	BP	0.905	PDPN	down_ACOR_EC
GO:0006833	0.018	1	1	5	water transport	BP	0.905	PDPN	down_ACOR_EC
GO:0045766	0.018	1	1	63	positive regulation of angiogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0055003	0.018	1	1	7	cardiac myofibril assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0098581	0.018	1	1	5	detection of external biotic stimulus	BP	1	TLR2	up_VSAP_VSMC
GO:0044087	0.018001466	0.99149	16	339	regulation of cellular component biogenesis	BP	0.96436359	TMOD1,ARHGAP6,SYNPO2,FZD5,SMAD6,ARHGAP28,PAK3,PTGER4,PREB,CLSTN1,CLU,CHMP4B,VPS16,NRP1,PRKCD,TUBB4A	up_ACOR_EC
GO:0043039	0.0181	0.995	6	33	tRNA aminoacylation	BP	0.66	CARS,SARS,AARS,YARS,TARS,NARS	down_VSAP_EC
GO:0051254	0.0181	0.997	4	431	positive regulation of RNA metabolic process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0016055	0.0181	0.998	3	134	Wnt signaling pathway	BP	1	SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0198738	0.0181	0.998	3	134	cell-cell signaling by wnt	BP	1	SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0031214	0.0181	0.999	2	45	biomineral tissue development	BP	0.905	HOXA3,ASPN	down_ACOR_EC
GO:0045683	0.0181	0.999	2	9	negative regulation of epidermis development	BP	1	HOXA7,DLL1	up_AFEM_EC
GO:0002062	0.0181	0.999	2	48	chondrocyte differentiation	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0043500	0.0181	1	1	21	muscle adaptation	BP	1	GATA5	down_VSAP_VSMC
GO:1903426	0.0181	1	1	17	regulation of reactive oxygen species	BP	1	ARG2	up_AORT_VSMC
GO:0010002	0.0181	1	1	9	cardioblast differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0009719	0.0182	0.989	35	395	response to endogenous stimulus	BP	0.66	ARHGEF2,SULF1,NR1H4,HSPA5,SOCS5,ENPP1,SNX25,PTPN11,TRIB3,ILK,FHL2,PRCP,SMARCA4,SESN2,TGFBR1,MYO1C,MSN,ZPR1,PTPN2,YES1,NEO1,ADAM17,AGRN,GNAQ,CTNNB1,ENSCAFG00000002015,APOE,UBA5,LYN,STRAP,REST,NR4A1,ENSCAFG00000018360,YWHAH,KDM3A	down_VSAP_EC
GO:0031589	0.0182	0.992	16	93	cell-substrate adhesion	BP	1	SMAD6,ACTN2,FERMT1,NRP1,NPNT,PRKCE,ECM2,JUP,DUSP22,NID1,FAM107A,JAM3,DOCK5,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0021700	0.0182	0.996	5	65	developmental maturation	BP	1	IRX5,XYLT1,LGI4,GREM1,RECK	up_AFEM_EC
GO:0048519	0.0182	0.997	5	1554	negative regulation of biological process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0046825	0.0182	0.997	4	16	regulation of protein export from nucleus	BP	0.66	PTPN14,PTPN11,IWS1,GSK3B	down_VSAP_EC
GO:0002021	0.0182	0.999	2	9	response to dietary excess	BP	1	LEP,PPARGC1A	up_AFEM_EC
GO:0042246	0.0182	1	1	17	tissue regeneration	BP	1	WNT7A	up_AORT_VSMC
GO:2000107	0.0182	1	1	16	negative regulation of leukocyte apoptotic	BP	1	ARG2	up_AORT_VSMC
GO:0008356	0.0182	1	1	3	asymmetric cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:0042573	0.0182	1	1	4	retinoic acid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0072189	0.0182	1	1	4	ureter development	BP	1	SIX1	up_VFEM_EC
GO:0036005	0.0182	1	1	4	response to macrophage colony-stimulating factor	BP	1	TLR2	up_VSAP_VSMC
GO:0036006	0.0182	1	1	4	cellular response to macrophage colony-	BP	1	TLR2	up_VSAP_VSMC
GO:0042532	0.0182	1	1	4	negative regulation of tyrosine phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0022603	0.0183	0.988	40	301	regulation of anatomical structure morphogenesis	BP	1	HOXA11,FZD1,THRB,WNT11,HNF4A,WASF3,ENPP2,LIMS2,DDHD1,SLIT2,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,CDC42EP5,PLXNA4,CDC42EP2,CCBE1,TBXA2R,SULF2,SHOX2,SASH1,LRP4,DPYSL2,NTN4,LIMD1,FBLN1,NFIB,PQBP1,TTL,ACVRL1,FLOT1,HMOX1,MAP2K2,TGFBR2,CITED2	up_VSAP_EC

GO:0034220	0.0183	0.99	27	188	ion transmembrane transport	BP	1	ACTN2,PLCG2,SLC26A7,KCNE3,HTR2B,TCAF1,GJA1,PTPN3,CLCN3,MICU2,ITPR1,DAPK1,CACNB3,AKAP6,LRRC8C,KCNJ4,PRKCE,PSEN1,CHD7,CLN8,ATP6V0E1,KCNC4,FXYD1,SLC25A12,NDUFA4L2,PARK7,SLC8A1	up_ACOR_VSMC
GO:0031323	0.0183	0.993	15	1788	regulation of cellular metabolic process	BP	0.905	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,SULF1,ELK3,HOXA1,ACSL3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0009062	0.0183	0.996	5	31	fatty acid catabolic process	BP	1	AKT2,ACAA1,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:0007187	0.0183	0.997	4	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	GPR1,CHRM2,HTR1D,PTHLH	up_AFEM_EC
GO:0098901	0.0183	0.998	3	7	regulation of cardiac muscle cell action	BP	1	FGF13,KCNE3,JUP	up_ACOR_VSMC
GO:0032388	0.0183	1	1	62	positive regulation of intracellular transport	BP	1	JUP	down_VFEM_VSMC
GO:0021522	0.0183	1	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_AORT_EC
GO:2000142	0.0183	1	1	17	regulation of DNA-templated transcription,	BP	1	ESR1	up_AORT_VSMC
GO:0061218	0.0183	1	1	4	negative regulation of mesonephros	BP	1	SIX1	up_VFEM_EC
GO:1902204	0.018362751	1	1	1	positive regulation of hepatocyte growth factor receptor signaling	BP	0.96436359	ESM1	up_ACOR_EC
GO:0045058	0.0184	0.997	4	12	T cell selection	BP	0.582	IL6,GATA3,MTOR,ITPKB	up_VCAV_EC
GO:0008284	0.0184	0.997	4	238	positive regulation of cell proliferation	BP	1	EYA1,SIX1,MAB21L1,TIAM1	up_VFEM_EC
GO:0009584	0.0184	0.999	2	4	detection of visible light	BP	0.666	GNAQ,RDH11	down_VSAP_EC
GO:0002931	0.0184	0.999	2	9	response to ischemia	BP	1	CAMK2A,BVES	up_AFEM_EC
GO:0010766	0.0184	1	1	4	negative regulation of sodium ion transport	BP	0.905	NEDD4	down_ACOR_EC
GO:0007026	0.0184	1	1	8	negative regulation of microtubule	BP	1	TAOK1	up_AORT_EC
GO:0050772	0.0184	1	1	13	positive regulation of axonogenesis	BP	1	LIMK1	up_VCAV_VSMC
GO:0048755	0.0184	1	1	4	branching morphogenesis of a nerve	BP	1	SHOX2	up_VSAP_VSMC
GO:0050804	0.0185	0.992	15	87	modulation of chemical synaptic transmission	BP	1	PLCL1,FBXL20,HRH1,TMEM108,EGLN1,DMPK,PRKCE,RNF19A,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,PREPL	up_ACOR_VSMC
GO:0099177	0.0185	0.992	15	87	regulation of trans-synaptic signaling	BP	1	PLCL1,FBXL20,HRH1,TMEM108,EGLN1,DMPK,PRKCE,RNF19A,APP,PSEN1,EDN1,KCNC4,LRRC4,FAM107A,PREPL	up_ACOR_VSMC
GO:0019219	0.0185	0.994	10	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0006081	0.0185	0.996	5	27	cellular aldehyde metabolic process	BP	0.667	TPI1,PGAM1,REST,RDH11,KDM3A	down_VSAP_EC
GO:0072710	0.0185	0.998	3	6	response to hydroxyurea	BP	0.583	TIMELESS,BLM,ATRX	up_VCAV_EC
GO:0097329	0.0185	0.998	3	6	response to antimetabolite	BP	0.583	TIMELESS,BLM,ATRX	up_VCAV_EC
GO:0030099	0.0185	0.998	3	133	myeloid cell differentiation	BP	1	HOXA9,HOXB7,HOXA7	up_VFEM_EC
GO:0007519	0.0185	0.999	2	49	skeletal muscle tissue development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:1902745	0.0185	1	1	9	positive regulation of lamellipodium	BP	1	FSCN1	down_AFEM_EC
GO:0051238	0.0185	1	1	7	sequestering of metal ion	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:2001224	0.0185	1	1	5	positive regulation of neuron migration	BP	1	ARHGEF2	up_VPUL_EC
GO:0051354	0.0185	1	1	4	negative regulation of oxidoreductase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0098911	0.0185	1	1	4	regulation of ventricular cardiac muscle cell action	BP	1	CAV1	up_VSAP_VSMC
GO:2000463	0.0185	1	1	5	positive regulation of excitatory postsynaptic	BP	1	NETO1	up_VSAP_VSMC
GO:0031326	0.0186	0.995	7	1176	regulation of cellular biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042632	0.0186	0.995	6	27	cholesterol homeostasis	BP	0.715	SREBF2,RALY,INSIG1,CAV1,LIPC,NUS1	down_ACOR_VSMC
GO:0006661	0.0186	0.995	6	23	phosphatidylinositol biosynthetic process	BP	1	PIP5K1B,PLCG2,HTR2B,PIGN,PIGS,PIGG	up_ACOR_VSMC

GO:0006337	0.0186	0.998	3	7	nucleosome disassembly	BP	0.715	SMARCC1,SMARCB1,GRWD1	down_ACOR_VSMC
GO:0032986	0.0186	0.998	3	7	protein-DNA complex disassembly	BP	0.715	SMARCC1,SMARCB1,GRWD1	down_ACOR_VSMC
GO:0032754	0.0186	0.999	2	3	positive regulation of interleukin-5 production	BP	0.584	PDE4D,GATA3	up_VCAV_EC
GO:0006816	0.0186	0.999	2	84	calcium ion transport	BP	1	HOXA3,TRPC4	up_VPOR_VSMC
GO:0021575	0.0186	1	1	15	hindbrain morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0021587	0.0186	1	1	15	cerebellum morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0035116	0.0186	1	1	15	embryonic hindlimb morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0120163	0.0186	1	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_AORT_VSMC
GO:0021675	0.0186	1	1	29	nerve development	BP	1	HOXA3	up_APUL_VSMC
GO:0035640	0.0186	1	1	7	exploration behavior	BP	1	CHL1	up_VPOR_VSMC
GO:0006805	0.0186	1	1	8	xenobiotic metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0008045	0.0186	1	1	9	motor neuron axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:0038166	0.0186	1	1	4	angiotensin-activated signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0003283	0.018642737	0.99899	2	8	atrial septum development	BP	0.96436359	GATA4,TBX5	up_ACOR_EC
GO:0060413	0.018642737	0.99899	2	8	atrial septum morphogenesis	BP	0.96436359	GATA4,TBX5	up_ACOR_EC
GO:0043066	0.0187	0.99	24	253	negative regulation of apoptotic process	BP	0.673	ARHGEF2,VEGFA,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,HYOU1,AARS,FHL2,PTGS2,HIF1A,ZPR1,MTDH,CTNNB1,CRYAB,BNIP3,GSK3B,HTT,GLO1,PAK2,SIX4,NRP1,ARF4	down_VSAP_EC
GO:0009306	0.0187	0.99	20	127	protein secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,LMF1,RAB11B,STEAP3,KCNB1,RAF1,PNP,MAPKBP1,STX4,PPP3CB,MAVS,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0051049	0.0187	0.991	19	479	regulation of transport	BP	1	LEP,KCNC4,CRY2,RAB20,GAS1,DLL1,CRYAB,KCND1,GPAM,CHRM2,GREM1,CAMK2A,FXYD1,REEP2,BVES,RAB7A,CCL5,DMPK,CLIC4	up_AFEM_EC
GO:0046890	0.0187	0.994	9	51	regulation of lipid biosynthetic process	BP	0.584	ADGRF5,PDGFB,MTOR,SAMD8,BMP2,PROX1,ENSCAFG00000010596,PTGS2,CREB1	up_VCAV_EC
GO:1901342	0.0187	0.994	7	114	regulation of vasculature development	BP	1	LEP,ANGPT4,DLL1,F3,TMEM100,GREM1,TBXA2R	up_AFEM_EC
GO:1901880	0.0187	0.996	5	19	negative regulation of protein depolymerization	BP	0.584	TMOD1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0072358	0.0187	0.997	4	268	cardiovascular system development	BP	1	HOXA3,SLITRK5,NTRK2,HOXA1	up_APUL_EC
GO:0015012	0.0187	0.998	3	9	heparan sulfate proteoglycan biosynthetic	BP	0.672	ENSCAFG00000032470,CTNNB1,EXT1	down_VSAP_EC
GO:0061035	0.0187	0.998	3	24	regulation of cartilage development	BP	1	GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:0000290	0.0187	0.998	3	8	deadenylation-dependent decapping of nuclear-transcribed mRNA	BP	0.584	PAN3,CNOT7,DCP2	up_VCAV_EC
GO:0008284	0.0187	0.998	3	238	positive regulation of cell proliferation	BP	1	HOXA3,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0045596	0.0187	0.999	2	186	negative regulation of cell differentiation	BP	1	HOXA9,WNT7A	up_AORT_VSMC
GO:0007623	0.0187	0.999	2	55	circadian rhythm	BP	1	HTR7,NTRK2	up_APUL_EC
GO:0050803	0.0187	0.999	2	55	regulation of synapse structure or activity	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0050807	0.0187	0.999	2	55	regulation of synapse organization	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:1903589	0.0187	0.999	2	3	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	0.584	APLNR,JCAD	up_VCAV_EC
GO:0035019	0.0187	1	1	16	somatic stem cell population maintenance	BP	1	WNT7A	up_AORT_VSMC
GO:0050701	0.0187	1	1	16	interleukin-1 secretion	BP	1	ARG2	up_AORT_VSMC
GO:0001759	0.0187	1	1	13	organ induction	BP	1	GATA5	up_VCAV_VSMC
GO:0019748	0.0187	1	1	13	secondary metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0048752	0.0187	1	1	5	semicircular canal morphogenesis	BP	1	EYA1	up_VFEM_EC

GO:0033483	0.0187	1	1	4	gas homeostasis	BP	1	CAV1	up_VSAP_VSMC
GO:0042391	0.018762353	0.99498	6	81	regulation of membrane potential	BP	0.96436359	KCNB1,IFI6,INSYN1,ACTN2,USP53,MAPK8IP2	up_ACOR_EC
GO:0016050	0.0188	0.991	17	119	vesicle organization	BP	0.584	ATP8A1,RAB11A,RAB27A,NECTIN2,HOOK3,SNAP23,CAV2,ABCA1,SNX2,CREB1,STX11,TBC1D1,DNAJC13,ALS2,RABGAP1,FBXO5,USP6NL	up_VCAV_EC
GO:0006302	0.0188	0.991	15	97	double-strand break repair	BP	0.721	RPA1,POLA1,TRIP13,PARPBP,GINS4,RAD54L,RAD51,TIMELESS,MND1,TONSL,BRCA1,RBBP8,SMC6,H2AFX,GEN1	down_ACOR_VSMC
GO:1903035	0.0188	0.997	4	14	negative regulation of response to wounding	BP	0.584	PDGFB,CD34,KLKB1,TFPI	up_VCAV_EC
GO:1990845	0.0188	0.999	2	51	adaptive thermogenesis	BP	1	HOXC10,MAP2K6	up_VFEM_EC
GO:0071216	0.0188	0.999	2	61	cellular response to biotic stimulus	BP	1	NR1H4,MRC1	up_VPUL_EC
GO:0010572	0.0188	1	1	4	positive regulation of platelet activation	BP	0.905	PDPN	down_ACOR_EC
GO:0034505	0.0188	1	1	4	tooth mineralization	BP	0.905	ASPN	down_ACOR_EC
GO:0035909	0.0188	1	1	14	aorta morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0051128	0.0189	0.987	62	790	regulation of cellular component organization	BP	0.673	ARHGEF2,VEGFA,SIPA1L1,MYH9,FMNL3,SERPINE1,SPARC,ENPP1,AKAP2,PTPN11,FSCN1,DPYSL3,IFRD1,FBLIM1,SMARCA4,ANKRA2,SESN2,WDR1,MYO1C,MSN,LMAN1,HIF1A,DYNLL1,TUBB,IWS1,TNIK,NAA10,ESM1,ADAM17,UST,ACTR3,CTNNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,IGFBP7,KLF5,LYN,BNIP3,TWF1,FAM162A,PLEKHG2,GSK3B,VLDLR,NEXN,CDC37,GBP5,SH3GLB1,SDC4,HTT,DISC1,LRRTM2,CAPG,INHBA,SIX4,CDKN1A,NRP1,ARF4,YWHAH,KDM3A,MID1	down_VSAP_EC
GO:0031328	0.0189	0.987	57	512	positive regulation of cellular biosynthetic process	BP	0.584	HCLS1,ADGRF5,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,PTGS2,BCL10,CNOT7,HMGB1,AHR,NOS2,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0061041	0.0189	0.995	7	34	regulation of wound healing	BP	0.584	SELP,PDGFB,CD34,KLKB1,TLR4,TFPI,MTOR	up_VCAV_EC
GO:0061097	0.0189	0.996	5	27	regulation of protein tyrosine kinase activity	BP	0.673	SOCS5,ERRFI1,PTPN2,ADAM17,CBLC	down_VSAP_EC
GO:0010469	0.0189	0.996	5	26	regulation of signaling receptor activity	BP	0.673	SERPINE1,SOCS5,ERRFI1,ADAM17,CBLC	down_VSAP_EC
GO:0048856	0.0189	0.997	5	1533	anatomical structure development	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0006915	0.0189	0.998	3	550	apoptotic process	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:1990138	0.0189	0.999	2	35	neuron projection extension	BP	0.905	SPG11,NRP2	down_ACOR_EC
GO:2001242	0.0189	0.999	2	62	regulation of intrinsic apoptotic signaling	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0001886	0.0189	1	1	5	endothelial cell morphogenesis	BP	1	ARHGEF26	up_APUL_EC
GO:2000209	0.0189	1	1	5	regulation of anoikis	BP	1	NTRK2	up_APUL_EC
GO:2000811	0.0189	1	1	5	negative regulation of anoikis	BP	1	NTRK2	up_APUL_EC
GO:0016331	0.019	0.993	9	66	morphogenesis of embryonic epithelium	BP	0.673	PRICKLE1,SULF1,PRKACB,ENSCAFG00000032470,TMED2,HIF1A,CTNNB1,SDC4,SIX4	down_VSAP_EC
GO:0034620	0.019	0.995	6	38	cellular response to unfolded protein	BP	0.673	HSPA5,ERO1A,PTPN2,DDIT3,ATF3,CREB3L2	down_VSAP_EC
GO:0060306	0.019	0.998	3	7	regulation of membrane repolarization	BP	1	KCNE3,GJA1,AKAP6	up_ACOR_VSMC
GO:0086009	0.019	0.998	3	7	membrane repolarization	BP	1	KCNE3,GJA1,AKAP6	up_ACOR_VSMC
GO:0001516	0.019	0.998	3	7	prostaglandin biosynthetic process	BP	0.585	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:0046457	0.019	0.998	3	7	prostanoid biosynthetic process	BP	0.585	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:0007423	0.019	0.999	2	155	sensory organ development	BP	1	EYA1,IRX5	up_AFEM_VSMC
GO:0050817	0.019	0.999	2	50	coagulation	BP	1	CAV1,F5	up_VSAP_VSMC

GO:1902991	0.019	1	1	5	regulation of amyloid precursor protein	BP	0.905	LYN	down_ACOR_EC
GO:0042473	0.019	1	1	5	outer ear morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0048523	0.019047841	0.98772	49	1399	negative regulation of cellular process	BP	0.96436359	NR1H4,TMOD1,BRSK1,TRPS1,PKIB,SOX9,ARHGAP6,PTH1R,PCSK1N,NDRG2,AQP1,KCNB1,FZD5,CCDC3,IFI6,SEMA6D,DUSP26,DIXDC1,PTGIR,RGMA,SMAD6,ACTN2,ZMYND8,ARHGAP28,MMP28,BCL2,PTGER4,ARHGDIB,CST3,PIAS1,ADAMTSL2,MAPK8IP2,FOXC2,FIGNL1,LRRC15,TBX5,LRP4,CLSTN1,LRRC4,CLU,CHMP4B,RIOX2,NRP1,PRKCD,PPP1R26,PM20D1,DBNDD2,EFEMP1,TUBB4A	up_ACOR_EC
GO:0009966	0.019093011	0.98862	33	868	regulation of signal transduction	BP	0.96436359	SH3TC2,CDH3,NR1H4,SOX9,RGS1,NDRG2,FZD5,CCDC3,IFI6,DUSP26,DIXDC1,PTGIR,NOD2,PDE4A,SMAD6,ESM1,PAK3,TNFRSF19,ARHGDIB,ADAMTSL2,MAPK8IP2,MAVS,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,C23H3orf58,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0065008	0.0191	0.985	121	1056	regulation of biological quality	BP	1	FGF13,RHOT1,ADRA1B,ACTN2,PLCG2,LEP,PLCL1,SLC26A7,KCNE3,CDC7,HTR2B,RASSF2,MBP,FBXL20,PRDX4,PRKAA2,BMP4,LCAT,TPC3,LNPK,TM7SF3,NPPB,CNNM2,ABCA1,GJA1,SCARB2,ATRX,HRH1,WASF3,PPARGC1A,CITED2,MAOA,ISG15,ZNF365,SLC2A5,STX11,PTPN3,TMEM108,CLCN3,FAM210B,P4HTM,MICU2,TMX3,ADCY6,USP53,ITPR1,PLAC8B,F2RL1,HRH2,STN1,ENPP4,ERO1B,BNIP3,EGLN1,SLC12A7,AKAP6,JMY,CLSTN1,LRRC8C,NRP1,ULK2,DMPK,OS9,ATP7A,ORMDL3,EVL,SLITRK5,PTGDR,SESN3,MOXD1,PRKCE,DKKL1,SCG5,POLR2M,RNLS,DAG1,APP,PSEN1,PCSK6,CHD7,LAMP2,JUP,DMXL1,CCL5,CLN8,RAB11B,SSH3,EDN1,KCNC4,NOD2,LRRC4,FAM107A,INSYN1,JAM3,B2M,DISC1,AP2B1,PLIN2,FXYD1,NCALD,HERPUD1,TXNDC5,GAA,SUN1,GNAQ,INPP5K,PREPL,PFKL,WFS1,WDR48,WASL,ATP2C1,NAIF1,DOCK5,ERAP1,PARK7,SLC8A1,STC2,IL18R1,HMBOX1,BVES	up_ACOR_VSMC
GO:0065007	0.0191	0.993	21	3499	biological regulation	BP	1	HOXC10,EYA1,HOXA9,TOX,MAP2K6,AVPR1A,HOXA10,TRIM9,HOXB7,HOXA7,ENSCAFG00000018194,SIX1,YBX3,MAB21L1,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3	up_VFEM_EC
GO:0008202	0.0191	0.992	14	80	steroid metabolic process	BP	1	LIPC,INSIG2,ACAA1,SULT1A1,HSD17B14,HSD3B7,HSD17B8,LMF1,LCAT,DHRS9,MVK,LIPE,CYB5R3,SOAT1	up_VSAP_EC
GO:0035148	0.0191	0.993	9	66	tube formation	BP	0.673	PRICKLE1,VEGFA,PRKACB,ENSCAFG00000032470,TMED2,HIF1A,CTNNB1,SDC4,SIX4	down_VSAP_EC
GO:0010821	0.0191	0.994	7	49	regulation of mitochondrion	BP	0.673	HIF1A,BNIP3,FAM162A,GSK3B,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0030514	0.0191	0.998	3	12	negative regulation of BMP signaling pathway	BP	1	FBN1,CHRDL1,GREM1	down_VCAV_EC
GO:0140115	0.0191	0.999	2	3	export across plasma membrane	BP	1	KCNE3,FXYD1	up_ACOR_VSMC
GO:0002009	0.0191	0.999	2	177	morphogenesis of an epithelium	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0008016	0.0191	0.999	2	48	regulation of heart contraction	BP	1	IRX5,CAV1	up_VSAP_VSMC
GO:0002888	0.0191	1	1	5	positive regulation of myeloid leukocyte	BP	0.905	STX4	down_ACOR_EC
GO:0021615	0.0191	1	1	3	glossopharyngeal nerve morphogenesis	BP	0.905	HOXA3	down_ACOR_EC
GO:0030889	0.0191	1	1	4	negative regulation of B cell proliferation	BP	0.905	LYN	down_ACOR_EC
GO:2000116	0.0191	1	1	67	regulation of cysteine-type endopeptidase	BP	1	CST3	down_AORT_EC
GO:0032722	0.0191	1	1	14	positive regulation of chemokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0048643	0.0191	1	1	7	positive regulation of skeletal muscle tissue	BP	1	CYP26B1	up_VPOR_VSMC

GO:0048523	0.0192	0.986	102	1399	negative regulation of cellular process	BP	0.673	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,ERO1A,PRKACB,PTPN14,ENPP1,ERRFI1,SNX25,CBX5,HYOU1,PTPN11,AARS,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,NAA10,NXN,RGS2,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,PEG3,MTDH,DDX39B,ADAM17,EIF4EBP1,SKAP2,CNOT7,MAGED1,CTNNB1,CRYAB,STARD13,ENSCAFG00000002015,APOE,WWC3,KLF5,MMP28,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,CBLC,ATF3,GSK3B,VLDLR,TAX1BP3,SDC4,HTT,REST,ENSCAFG00000017326,ZMYND8,EIF2S1,PRMT1,ARFGEF3,CALM1,RAB11FIP1,GLO1,CDYL,PAK2,LRRTM2,A2M,CAPG,INHBA,NR4A1,HIF1AN,BTK,SIX4,CDKN1A,NRP1,SPINK2,RHBDF2,USP14,ARF4,YWHAH,TNFAIP1,KDM3A,MID1	down_VSAP_EC
GO:0001503	0.0192	0.992	11	109	ossification	BP	1	NAB2,THBS3,BMPR1A,CLSTN1,ASPN,GLI3,TWIST2,DDR2,OMD,GREM1,ZBTB16	down_VCAV_EC
GO:0048593	0.0192	0.994	8	41	camera-type eye morphogenesis	BP	0.587	EPHB1,PROX1,TSPAN12,JAG1,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0071706	0.0192	0.994	8	40	tumor necrosis factor superfamily cytokine	BP	0.587	TNFAIP3,CD34,TLR4,ARG2,TLR3,HMGB1,RIPK1,ARHGEF2	up_VCAV_EC
GO:0034332	0.0192	0.996	5	32	adherens junction organization	BP	1	NUMBL,RHOD,RASSF8,THY1,GREM1	down_VCAV_EC
GO:0001754	0.0192	0.998	3	12	eye photoreceptor cell differentiation	BP	1	NAGLU,THY1,THRB	down_VCAV_EC
GO:2000251	0.0192	0.998	3	7	positive regulation of actin cytoskeleton	BP	0.587	TEK,BAIAP2L1,FES	up_VCAV_EC
GO:0038089	0.0192	0.999	2	4	positive regulation of cell migration by vascular endothelial growth factor	BP	0.673	VEGFA,MYO1C	down_VSAP_EC
GO:0010715	0.0192	1	1	4	regulation of extracellular matrix disassembly	BP	0.905	PDPN	down_ACOR_EC
GO:0001732	0.0192	1	1	9	formation of cytoplasmic translation initiation	BP	1	EIF3M	down_AFEM_EC
GO:0045616	0.0192	1	1	9	regulation of keratinocyte differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0032924	0.0192	1	1	9	activin receptor signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:0060042	0.0192	1	1	14	retina morphogenesis in camera-type eye	BP	1	IRX5	up_AFEM_VSMC
GO:0010692	0.0192	1	1	5	regulation of alkaline phosphatase activity	BP	1	NPNT	up_APUL_EC
GO:0010659	0.0192	1	1	7	cardiac muscle cell apoptotic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010665	0.0192	1	1	7	regulation of cardiac muscle cell apoptotic	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060712	0.0192	1	1	4	spongiotrophoblast layer development	BP	1	GJB5	up_VSAP_VSMC
GO:0007160	0.0193	0.994	8	56	cell-matrix adhesion	BP	0.673	VEGFA,SERPINE1,ACTN1,ILK,CTNNB1,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:0072524	0.0193	0.995	6	37	pyridine-containing compound metabolic	BP	0.673	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0046364	0.0193	0.996	5	27	monosaccharide biosynthetic process	BP	0.673	TPI1,PGAM1,SESN2,PTPN2,ATF3	down_VSAP_EC
GO:0042461	0.0193	0.998	3	12	photoreceptor cell development	BP	1	NAGLU,THY1,THRB	down_VCAV_EC
GO:0008283	0.0193	0.998	3	545	cell proliferation	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0031328	0.0193	0.998	3	512	positive regulation of cellular biosynthetic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0010721	0.0193	0.998	3	73	negative regulation of cell development	BP	1	HOOK3,SEMA3A,RNF6	up_VPOR_EC
GO:0007135	0.0193	0.999	2	3	meiosis II	BP	0.728	DSN1,SGO2	down_ACOR_VSMC
GO:0045144	0.0193	0.999	2	3	meiotic sister chromatid segregation	BP	0.728	DSN1,SGO2	down_ACOR_VSMC
GO:0061983	0.0193	0.999	2	3	meiosis II cell cycle process	BP	0.728	DSN1,SGO2	down_ACOR_VSMC
GO:0042481	0.0193	1	1	5	regulation of odontogenesis	BP	0.905	ASPN	down_ACOR_EC
GO:0032652	0.0193	1	1	18	regulation of interleukin-1 production	BP	1	ARG2	up_AORT_VSMC
GO:0051965	0.0193	1	1	17	positive regulation of synapse assembly	BP	1	WNT7A	up_AORT_VSMC
GO:0090342	0.0193	1	1	17	regulation of cell aging	BP	1	ARG2	up_AORT_VSMC

GO:0055062	0.0193	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0072505	0.0193	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0072506	0.0193	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0051154	0.0193	1	1	7	negative regulation of striated muscle cell	BP	1	NKX2-5	up_VPOR_VSMC
GO:0055065	0.0194	0.99	22	145	metal ion homeostasis	BP	1	ADRA1B,PLCG2,HTR2B,CNNM2,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,EDN1,B2M,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0050808	0.0194	0.991	16	93	synapse organization	BP	1	WASF3,GLRB,ZNF365,TMEM108,EGLN1,CACNB3,NRP1,DMPK,SLITRK5,DAG1,APP,PSEN1,LRRC4,DISC1,WASL,CRKL	up_ACOR_VSMC
GO:1903311	0.0194	0.992	12	72	regulation of mRNA metabolic process	BP	0.728	RNPS1,HNRNPD,SRSF2,U2AF2,THRAP3,HNRNPL,SF3B4,FASTKD3,RBM14,WTAP,JMJD6,SF3A1	down_ACOR_VSMC
GO:0048513	0.0194	0.996	6	906	animal organ development	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0060350	0.0194	0.995	6	23	endochondral bone morphogenesis	BP	1	HOXA11,PEX7,AXIN2,RARG,SHOX2,TGFBR2	up_VSAP_EC
GO:0045143	0.0194	0.997	4	13	homologous chromosome segregation	BP	0.728	ENSCAFG00000017264,NDC1,TRIP13,ESPL1	down_ACOR_VSMC
GO:0006953	0.0194	0.998	3	7	acute-phase response	BP	0.591	F8,IL6,PTGS2	up_VCAV_EC
GO:0060685	0.0194	1	1	4	regulation of prostatic bud formation	BP	0.905	SULF1	down_ACOR_EC
GO:0060686	0.0194	1	1	4	negative regulation of prostatic bud formation	BP	0.905	SULF1	down_ACOR_EC
GO:0060502	0.0194	1	1	9	epithelial cell proliferation involved in lung	BP	1	SRSF6	down_AFEM_EC
GO:0030511	0.0194	1	1	10	positive regulation of transforming growth factor beta receptor	BP	1	CITED2	down_VPOR_EC
GO:1903846	0.0194	1	1	10	positive regulation of cellular response to transforming growth	BP	1	CITED2	down_VPOR_EC
GO:0072132	0.0194	1	1	23	mesenchyme morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0032945	0.0194	1	1	17	negative regulation of mononuclear cell	BP	1	ARG2	up_AORT_VSMC
GO:0050672	0.0194	1	1	17	negative regulation of lymphocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0043584	0.0194	1	1	5	nose development	BP	1	SIX1	up_VFEM_EC
GO:0010033	0.019424129	0.98867	30	772	response to organic substance	BP	0.96436359	NR1H4,SOX9,FNDC4,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,CCDC3,AGRN,PTGIR,NOD2,RGMA,SMAD6,ACTN2,PAK3,PTGER4,ADAMTSL2,MAVS,FOXC2,LRRC15,IFIT2,LRP4,LRRC4,CLU,RARRES2,PRKACA,NRP1,HM13,PRKCD	up_ACOR_EC
GO:0065008	0.0195	0.985	105	1056	regulation of biological quality	BP	0.593	EPHB1,PLK2,EDNRB,HCLS1,IL7R,ADGRF5,SELP,KIT,PRCP,F8,ARHGEF15,IFRD1,CP,DOCK4,TNFAIP3,ATP8A1,LRRC8D,PDGFB,BAIAP2L1,ATP2B1,RELN,VWF,CD34,PDE4D,MEF2C,CHD7,KLKB1,TIPARP,TLR4,NOS3,GPR4,STC1,GATA3,EDN1,RAB11A,APLNR,ARAP3,RAB27A,SLC39A8,SNCAIP,PTGS1,TFPI,TMOD1,PPP3CA,GUCY1A1,MTOR,NAV2,TENT2,SNAP23,MMRN1,LRRC8C,BMP2,SLC12A7,PDZD8,ABCA1,ITPKB,NCKAP1,IQGAP2,STMN1,HMBOX1,SH3GLB1,SWAP70,SMARCA4,NCK1,KCNJ2,EXOC5,LDB2,PDIA5,FES,PTGS2,PLCG2,CREB1,BCL10,USP28,TAOK1,FMNL3,STX11,SMG7,GCH1,VPS54,ADIPOR2,HMGB1,NOS2,PMAIP1,ARPC5L,BLM,SPTBN4,SMC5,USP13,SKIL,MCU,PDGFD,NR1D2,HIF1A,KDM3A,ALS2,ITGB3,ATRX,ALDH1A3,HP1BP3,P2RX2,DCP2,ATP2A1,TMOD3,PEAR1	up_VCAV_EC
GO:0051785	0.0195	0.997	4	14	positive regulation of nuclear division	BP	0.728	BIRC5,NUP62,ENSCAFG00000005299,UBE2C	down_ACOR_VSMC
GO:0044314	0.0195	0.999	2	3	protein K27-linked ubiquitination	BP	0.728	UBE2S,UBE2T	down_ACOR_VSMC
GO:0010888	0.0195	0.999	2	4	negative regulation of lipid storage	BP	0.677	PTPN2,ABHD5	down_VSAP_EC
GO:0120039	0.0195	0.999	2	158	plasma membrane bounded cell projection	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0045683	0.0195	1	1	9	negative regulation of epidermis development	BP	1	SRSF6	down_AFEM_EC

GO:0032757	0.0195	1	1	14	positive regulation of interleukin-8 production	BP	1	TLR2	up_AFEM_VSMC
GO:0048146	0.0195	1	1	18	positive regulation of fibroblast proliferation	BP	1	ESR1	up_AORT_VSMC
GO:0003264	0.0195	1	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_APUL_EC
GO:0003266	0.0195	1	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_APUL_EC
GO:0090103	0.0195	1	1	8	cochlea morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0098815	0.0195	1	1	9	modulation of excitatory postsynaptic potential	BP	1	NETO1	up_VFEM_VSMC
GO:0048736	0.0196	0.992	12	66	appendage development	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4,PRKAB1	up_VSAP_EC
GO:0060173	0.0196	0.992	12	66	limb development	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4,PRKAB1	up_VSAP_EC
GO:0009892	0.0196	0.993	9	835	negative regulation of metabolic process	BP	0.905	ACVRL1,LYN,IGF1R,HOXA7,PRKAR2A,ELK3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0072088	0.0196	0.995	6	36	nephron epithelium morphogenesis	BP	0.677	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0006879	0.0196	0.995	6	23	cellular iron ion homeostasis	BP	1	FXN,MYC,SCARA5,FTL,HMOX1,NCOA4	up_VSAP_EC
GO:0032875	0.0196	0.998	3	7	regulation of DNA endoreduplication	BP	0.728	SMC1A,E2F8,SMC3	down_ACOR_VSMC
GO:0010803	0.0196	0.998	3	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	0.677	NR1H4,PTPN2,ADAM17	down_VSAP_EC
GO:0060338	0.0196	0.998	3	10	regulation of type I interferon-mediated	BP	0.679	PTPN2,CNOT7,CDC37	down_VSAP_EC
GO:0021675	0.0196	0.999	2	29	nerve development	BP	1	HOXA3,SEMA3A	up_VPOR_EC
GO:0021824	0.0196	1	1	3	cerebral cortex tangential migration using cell-axon interactions	BP	0.905	NRP2	down_ACOR_EC
GO:0021828	0.0196	1	1	3	gonadotrophin-releasing hormone neuronal migration to the	BP	0.905	NRP2	down_ACOR_EC
GO:0021856	0.0196	1	1	3	hypothalamic tangential migration using cell-axon interactions	BP	0.905	NRP2	down_ACOR_EC
GO:0021886	0.0196	1	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	0.905	NRP2	down_ACOR_EC
GO:0021888	0.0196	1	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	0.905	NRP2	down_ACOR_EC
GO:0021979	0.0196	1	1	3	hypothalamus cell differentiation	BP	0.905	NRP2	down_ACOR_EC
GO:0035290	0.0196	1	1	3	trunk segmentation	BP	0.905	NRP2	down_ACOR_EC
GO:0036484	0.0196	1	1	3	trunk neural crest cell migration	BP	0.905	NRP2	down_ACOR_EC
GO:0036486	0.0196	1	1	3	ventral trunk neural crest cell migration	BP	0.905	NRP2	down_ACOR_EC
GO:0097490	0.0196	1	1	3	sympathetic neuron projection extension	BP	0.905	NRP2	down_ACOR_EC
GO:0097491	0.0196	1	1	3	sympathetic neuron projection guidance	BP	0.905	NRP2	down_ACOR_EC
GO:1901166	0.0196	1	1	3	neural crest cell migration involved in autonomic nervous system	BP	0.905	NRP2	down_ACOR_EC
GO:1903375	0.0196	1	1	3	facioacoustic ganglion development	BP	0.905	NRP2	down_ACOR_EC
GO:0007389	0.0196	1	1	137	pattern specification process	BP	1	GATA5	down_AFEM_VSMC
GO:0048821	0.0196	1	1	10	erythrocyte development	BP	1	CITED2	down_VPOR_EC
GO:0003207	0.0196	1	1	5	cardiac chamber formation	BP	1	TBX5	up_APUL_EC
GO:0072643	0.0196	1	1	5	interferon-gamma secretion	BP	1	NR1H4	up_APUL_EC
GO:0032612	0.019699196	0.99756	3	22	interleukin-1 production	BP	0.96436359	NR1H4,FZD5,NOD2	up_ACOR_EC
GO:0030032	0.0197	0.996	5	19	lamellipodium assembly	BP	0.599	KIT,MTOR,NCKAP1,NCK1,FSCN1	up_VCAV_EC
GO:0060986	0.0197	0.998	3	10	endocrine hormone secretion	BP	0.68	PTPN11,RAB11FIP1,INHBA	down_VSAP_EC
GO:0051961	0.0197	0.997	3	73	negative regulation of nervous system	BP	1	HOOK3,SEMA3A,RNF6	up_VPOR_EC

GO:0045834	0.0197	0.999	2	41	positive regulation of lipid metabolic process	BP	0.905	LYN,ACSL3	down_ACOR_EC
GO:0048858	0.0197	0.999	2	159	cell projection morphogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0001503	0.0197	0.999	2	109	ossification	BP	1	HOXA3,PHEX	up_VPUL_VSMC
GO:1904018	0.0197	1	1	69	positive regulation of vasculature development	BP	1	JUP	down_VFEM_VSMC
GO:0032613	0.0197	1	1	14	interleukin-10 production	BP	1	TLR2	up_AFEM_VSMC
GO:0006699	0.0197	1	1	5	bile acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0034162	0.0197	1	1	5	toll-like receptor 9 signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0021522	0.0197	1	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_VFEM_VSMC
GO:0003171	0.0197	1	1	10	atrioventricular valve development	BP	1	TBX5	up_VPUL_VSMC
GO:0048522	0.0198	0.994	10	1484	positive regulation of cellular process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,WIF1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0090288	0.0198	0.995	6	44	negative regulation of cellular response to growth factor stimulus	BP	1	DCN,VASN,FBN1,CHRDL1,ASPN,GREM1	down_VCAV_EC
GO:0006811	0.0198	0.996	5	330	ion transport	BP	0.906	LYN,HOXA3,PDPN,ACSL3,NEDD4	down_ACOR_EC
GO:1904738	0.0198	0.998	3	6	vascular associated smooth muscle cell	BP	0.599	DOCK4,PDGFB,MEF2C	up_VCAV_EC
GO:1904752	0.0198	0.998	3	6	regulation of vascular associated smooth muscle	BP	0.599	DOCK4,PDGFB,MEF2C	up_VCAV_EC
GO:0060019	0.0198	0.999	2	5	radial glial cell differentiation	BP	1	GLI3,CDH2	down_VCAV_EC
GO:1903011	0.0198	0.999	2	5	negative regulation of bone development	BP	1	FBN1,GREM1	down_VCAV_EC
GO:0003160	0.0198	0.999	2	3	endocardium morphogenesis	BP	0.599	SOX18,PROX1	up_VCAV_EC
GO:0006606	0.0198	1	1	67	protein import into nucleus	BP	1	JUP	down_VFEM_VSMC
GO:0055026	0.0198	1	1	5	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0021559	0.0198	1	1	3	trigeminal nerve development	BP	1	SEMA3A	up_VPOR_EC
GO:0021636	0.0198	1	1	3	trigeminal nerve morphogenesis	BP	1	SEMA3A	up_VPOR_EC
GO:0021637	0.0198	1	1	3	trigeminal nerve structural organization	BP	1	SEMA3A	up_VPOR_EC
GO:0021785	0.0198	1	1	3	branchiomotor neuron axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:1902287	0.0198	1	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0055012	0.0198	1	1	8	ventricular cardiac muscle cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060261	0.0198	1	1	8	positive regulation of transcription initiation from RNA polymerase II	BP	1	NKX2-5	up_VPOR_VSMC
GO:1900449	0.0198	1	1	9	regulation of glutamate receptor signaling	BP	1	NETO1	up_VFEM_VSMC
GO:0009607	0.019847977	0.99163	12	232	response to biotic stimulus	BP	0.96436359	NR1H4,HMCN1,RGS1,FZD5,PTGIR,NOD2,PTGER4,MAVS,IFIT2,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0050789	0.0199	0.992	23	3295	regulation of biological process	BP	0.907	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,PDPN,NRP2,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,IPO7,ATRIP,SULF1,ELK3,HOXA1,ACSL3,WDR12,STX4,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0070527	0.0199	0.998	3	10	platelet aggregation	BP	0.685	LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:1901223	0.0199	1	1	10	negative regulation of NIK/NF-kappaB signaling	BP	1	HDAC7	down_VPOR_EC
GO:2001239	0.0199	1	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	EYA1	up_AFEM_VSMC
GO:0061551	0.0199	1	1	5	trigeminal ganglion development	BP	1	SIX1	up_VFEM_EC
GO:0023052	0.02	0.992	14	1602	signaling	BP	0.907	ACVRL1,LYN,IGF1R,SPG11,PDPN,NRP2,HIVEP2,USP28,IPO7,SULF1,WDR12,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0034641	0.02	0.995	9	2171	cellular nitrogen compound metabolic	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0009889	0.02	0.995	7	1190	regulation of biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC

GO:0051894	0.02	0.998	3	10	positive regulation of focal adhesion assembly	BP	0.685	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0009891	0.02	0.998	3	521	positive regulation of biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0000289	0.02	0.998	3	7	nuclear-transcribed mRNA poly(A) tail shortening	BP	0.602	CNOT6,PAN3,CNOT7	up_VCAV_EC
GO:0060538	0.02	0.999	2	51	skeletal muscle organ development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0048535	0.02	1	1	5	lymph node development	BP	0.907	PDPN	down_ACOR_EC
GO:0071867	0.02	1	1	9	response to monoamine	BP	1	GABPA	down_AFEM_EC
GO:0071868	0.02	1	1	9	cellular response to monoamine stimulus	BP	1	GABPA	down_AFEM_EC
GO:0071869	0.02	1	1	9	response to catecholamine	BP	1	GABPA	down_AFEM_EC
GO:0071870	0.02	1	1	9	cellular response to catecholamine stimulus	BP	1	GABPA	down_AFEM_EC
GO:0060135	0.02	1	1	10	maternal process involved in female pregnancy	BP	1	CITED2	down_VPOR_EC
GO:0018195	0.02	1	1	6	peptidyl-arginine modification	BP	1	NR1H4	up_VPUL_EC
GO:0010638	0.0201	0.989	26	207	positive regulation of organelle organization	BP	0.604	TEK,ARHGEF15,PDGFB,BAIAP2L1,GATA3,EDN1,RALB,MTOR,CNOT6,NCKAP1,PROX1,IQGAP2,HMBOX1,PRKD2,SH3GLB1,SWAP70,NCK1,FES,PAN3,PMAIP1,ARPC5L,SMC5,RAD21,HIF1A,ATRX,FSCN1	up_VCAV_EC
GO:0060428	0.0201	0.996	5	17	lung epithelium development	BP	1	THRB,FGF7,SAV1,NFIB,MAP2K2	up_VSAP_EC
GO:0060669	0.0201	0.997	4	12	embryonic placenta morphogenesis	BP	1	FGFR2,SPINT1,ENSCAFG00000006238,SPINT2	up_ACOR_VSMC
GO:0032611	0.0201	1	1	17	interleukin-1 beta production	BP	1	ARG2	up_AORT_VSMC
GO:2000826	0.0201	1	1	14	regulation of heart morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0010575	0.0201	1	1	8	positive regulation of vascular endothelial growth factor production	BP	1	C3AR1	up_VPOR_VSMC
GO:0010804	0.0201	1	1	6	negative regulation of tumor necrosis factor-mediated signaling	BP	1	NR1H4	up_VPUL_EC
GO:0003161	0.0201	1	1	6	cardiac conduction system development	BP	1	TBX5	up_VPUL_EC
GO:0043434	0.020102501	0.99454	6	80	response to peptide hormone	BP	0.96436359	NR1H4,ENSCAFG00000004331,ACTN2,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0001819	0.0202	0.99	19	120	positive regulation of cytokine production	BP	1	WNT11,CD274,IL6R,ABL1,IL17RC,HPSE,CCBE1,F2RL1,PIK3R1,SULF2,MYD88,NLRX1,TKFC,CD83,ZNF580,CYBA,PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0070838	0.0202	0.99	16	96	divalent metal ion transport	BP	1	PLCG2,HTR2B,TPC3,NIPAL3,SARAF,MICU2,ITPR1,CACNB3,PRKCE,PSEN1,CHD7,INPP5K,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0051258	0.0202	0.991	14	94	protein polymerization	BP	0.606	HCLS1,MX2,BAIAP2L1,TMOD1,MTOR,NCKAP1,MZT1,IQGAP2,STMN1,NCK1,FES,ARPC5L,TMOD3,FBXO5	up_VCAV_EC
GO:0046165	0.0202	0.994	8	42	alcohol biosynthetic process	BP	0.739	LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1,NUS1	down_ACOR_VSMC
GO:1901800	0.0202	0.994	7	46	positive regulation of proteasomal protein catabolic process	BP	0.692	PRICKLE1,PLK3,SOCS5,TRIB3,GSK3B,RAD23A,TMTC3	down_VSAP_EC
GO:0055025	0.0202	0.996	5	17	positive regulation of cardiac muscle tissue	BP	1	BMP4,FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0016572	0.0202	0.997	4	13	histone phosphorylation	BP	0.739	CDK1,AURKB,HASPIN,CCNA2	down_ACOR_VSMC
GO:0071384	0.0202	0.997	4	12	cellular response to corticosteroid stimulus	BP	1	CREBRF,NR3C1,FAM107A,DDIT4	up_ACOR_VSMC
GO:0071385	0.0202	0.997	4	12	cellular response to glucocorticoid stimulus	BP	1	CREBRF,NR3C1,FAM107A,DDIT4	up_ACOR_VSMC
GO:0012501	0.0202	0.998	3	561	programmed cell death	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0006355	0.0202	1	2	974	regulation of transcription, DNA-	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071073	0.0202	1	1	4	positive regulation of phospholipid biosynthetic	BP	0.913	ACSL3	down_ACOR_EC
GO:0032528	0.0202	1	1	9	microvillus organization	BP	1	FSCN1	down_AFEM_EC
GO:0043124	0.0202	1	1	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	ESR1	up_AORT_VSMC
GO:0060079	0.0202	1	1	15	excitatory postsynaptic potential	BP	1	WNT7A	up_AORT_VSMC

GO:0070664	0.0202	1	1	18	negative regulation of leukocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0046620	0.0202	1	1	30	regulation of organ growth	BP	1	TBX5	up_APUL_VSMC
GO:0048246	0.0202	1	1	9	macrophage chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0060413	0.0202	1	1	8	atrial septum morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003283	0.0202	1	1	8	atrial septum development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0097120	0.0202	1	1	9	receptor localization to synapse	BP	1	NETO1	up_VFEM_VSMC
GO:0010984	0.0202	1	1	6	regulation of lipoprotein particle clearance	BP	1	NR1H4	up_VPUL_EC
GO:0006929	0.0202	1	1	10	substrate-dependent cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0007169	0.020218582	0.99222	10	178	transmembrane receptor protein tyrosine kinase	BP	0.96436359	SH3TC2,CDH3,NR1H4,SOX9,ENSCAFG00000004331,PTGIR,ESM1,FOXC2,NRP1,PRKCD	up_ACOR_EC
GO:0001936	0.0203	0.994	7	49	regulation of endothelial cell proliferation	BP	0.694	VEGFA,SULF1,SPARC,JCAD,TGFBR1,ADAM17,APOE	down_VSAP_EC
GO:1903506	0.0203	1	2	977	regulation of nucleic acid-templated transcription	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0045861	0.0203	1	1	71	negative regulation of proteolysis	BP	1	CST3	down_AORT_EC
GO:0051170	0.0203	1	1	69	import into nucleus	BP	1	JUP	down_VFEM_VSMC
GO:0030852	0.0203	1	1	6	regulation of granulocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0032692	0.0203	1	1	6	negative regulation of interleukin-1 production	BP	1	NR1H4	up_VPUL_EC
GO:0055090	0.0203	1	1	6	acylglycerol homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0070328	0.0203	1	1	6	triglyceride homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0021884	0.0203	1	1	10	forebrain neuron development	BP	1	SLIT2	up_VPUL_VSMC
GO:0030325	0.0203	1	1	5	adrenal gland development	BP	1	SALL1	up_VSAP_VSMC
GO:0070391	0.0203	1	1	5	response to lipoteichoic acid	BP	1	TLR2	up_VSAP_VSMC
GO:0071223	0.0203	1	1	5	cellular response to lipoteichoic acid	BP	1	TLR2	up_VSAP_VSMC
GO:0007045	0.020382812	0.99743	3	23	cell-substrate adherens junction assembly	BP	0.96436359	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0048041	0.020382812	0.99743	3	23	focal adhesion assembly	BP	0.96436359	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0009792	0.0204	0.988	32	231	embryo development ending in birth or egg hatching	BP	1	TBX15,HOXA11,FZD1,HOXA7,HOXA9,WNT11,AXIN2,OSR2,GJB5,IRX5,HOXD3,ABL1,DLL1,HOXA6,OSR1,FUZ,RARG,AMBRA1,MFN2,ZFP36L1,FXN,ZEB1,SULF2,SHOX2,KDM2B,TAF8,ZFAND5,ACVRL1,TGFBR2,CITED2,KEAP1,LATS2	up_VSAP_EC
GO:0090087	0.0204	0.988	27	185	regulation of peptide transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,MBP,FERMT1,BMP4,TM7SF3,CD274,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,PSEN1,CHD7,JUP,CCL5,NOD2,SCAMP5,INPP5K,PFKL,PARK7,PTPN14	up_ACOR_VSMC
GO:0006636	0.0204	0.997	4	14	unsaturated fatty acid biosynthetic process	BP	0.612	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0045926	0.0204	0.997	3	72	negative regulation of growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC
GO:0030509	0.0204	0.999	2	47	BMP signaling pathway	BP	0.922	ACVRL1,SULF1	down_ACOR_EC
GO:2001141	0.0204	1	2	979	regulation of RNA biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0033629	0.0204	0.999	2	4	negative regulation of cell adhesion mediated by	BP	0.695	SERPINE1,PTPN11	down_VSAP_EC
GO:0106106	0.0204	1	1	48	cold-induced thermogenesis	BP	1	PLCL1	down_VFEM_EC
GO:0120161	0.0204	1	1	48	regulation of cold-induced thermogenesis	BP	1	PLCL1	down_VFEM_EC
GO:0010594	0.0204	1	1	71	regulation of endothelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:2000826	0.0204	1	1	14	regulation of heart morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0006749	0.0204	1	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	up_VCAV_VSMC
GO:1905521	0.0204	1	1	9	regulation of macrophage migration	BP	1	C3AR1	up_VPOR_VSMC

GO:0035774	0.0204	1	1	6	positive regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_VPUL_EC
GO:0044271	0.0205	0.992	12	1501	cellular nitrogen compound biosynthetic	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0006890	0.0205	0.996	4	18	retrograde vesicle-mediated transport, Golgi	BP	0.698	RAB6A,COPB2,HTT,ARF4	down_VSAP_EC
GO:0007628	0.0205	0.997	4	11	adult walking behavior	BP	1	GLRB,CHD7,CLN8,OXR1	up_ACOR_VSMC
GO:1901863	0.0205	0.997	3	25	positive regulation of muscle tissue	BP	1	DLL1,GREM1,PPARGC1A	up_AFEM_EC
GO:0050673	0.0205	0.997	3	135	epithelial cell proliferation	BP	1	EYA1,SIX1,MTSS1	up_VFEM_EC
GO:0015980	0.0205	0.999	2	106	energy derivation by oxidation of organic	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0021515	0.0205	1	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_AORT_EC
GO:0070231	0.0205	1	1	18	T cell apoptotic process	BP	1	ARG2	up_AORT_VSMC
GO:0060788	0.0205	1	1	5	ectodermal placode formation	BP	1	SIX1	up_VFEM_EC
GO:0071697	0.0205	1	1	5	ectodermal placode morphogenesis	BP	1	SIX1	up_VFEM_EC
GO:0043549	0.0206	0.988	30	244	regulation of kinase activity	BP	0.614	TEK,KIT,PPP2R5A,TNFAIP3,MAP3K11,PDGFB,STK10,RELN,TLR4,NLRC5,EDN1,RALB,NEDD9,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,PROX1,MADD,PAK2,SH3GLB1,LDB2,MMD,RAPGEF2,BLM,RIPK1,PDGFD	up_VCAV_EC
GO:0006875	0.0206	0.989	20	129	cellular metal ion homeostasis	BP	1	ADRA1B,PLCG2,HTR2B,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:1901576	0.0206	0.992	14	1877	organic substance biosynthetic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0009451	0.0206	0.992	10	59	RNA modification	BP	0.748	NOP56,TRUB2,FBL,THUMPD2,OSGEP,ENSCAFG00000019620,METTL1,NOP58,WTAP,EMG1	down_ACOR_VSMC
GO:0008203	0.0206	0.993	8	37	cholesterol metabolic process	BP	1	LIPC,INSIG2,LMF1,LCAT,MVK,LIPE,CYB5R3,SOAT1	up_VSAP_EC
GO:1903556	0.0206	0.997	4	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	0.614	TNFAIP3,CD34,TLR4,ARG2	up_VCAV_EC
GO:0032703	0.0206	0.998	3	8	negative regulation of interleukin-2 production	BP	0.614	TNFAIP3,GATA3,HOMER3	up_VCAV_EC
GO:0036022	0.0206	0.999	2	4	limb joint morphogenesis	BP	0.698	SULF1,CTNNB1	down_VSAP_EC
GO:0006874	0.0206	0.999	2	91	cellular calcium ion homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0043271	0.0206	1	1	28	negative regulation of ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0042473	0.0206	1	1	5	outer ear morphogenesis	BP	1	EYA1	up_VFEM_EC
GO:0032640	0.020606327	0.9962	4	39	tumor necrosis factor production	BP	0.96436359	NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC
GO:0019932	0.020614546	0.99436	6	82	second-messenger-mediated signaling	BP	0.96436359	SOX9,PTH1R,AQP1,PTGIR,PDE4A,GUCY1B1	up_ACOR_EC
GO:0050770	0.020619748	0.9962	4	39	regulation of axonogenesis	BP	0.96436359	BRSK1,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0031329	0.0207	0.989	23	241	regulation of cellular catabolic process	BP	0.699	PRICKLE1,PLK3,SOCS5,TRIB3,PGAM1,SESN2,MSN,HIF1A,UCHL5,SMG7,MTDH,CNOT7,APOE,BNIP3,GSK3B,CDC37,SH3GLB1,HTT,ABHD5,DISC1,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0002791	0.0207	0.99	17	104	regulation of peptide secretion	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,CHD7,CCL5,NOD2,SCAMP5,PFKL	up_ACOR_VSMC
GO:0022603	0.0207	0.998	3	301	regulation of anatomical structure morphogenesis	BP	1	TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:0018216	0.0207	0.999	2	3	peptidyl-arginine methylation	BP	0.749	PRMT1,PRMT5	down_ACOR_VSMC
GO:0031998	0.0207	0.999	2	5	regulation of fatty acid beta-oxidation	BP	1	AKT2,LONP2	down_VCAV_EC
GO:0060346	0.0207	0.999	2	5	bone trabecula formation	BP	1	THBS3,GREM1	down_VCAV_EC
GO:0031114	0.0207	1	1	9	regulation of microtubule depolymerization	BP	1	TAOK1	up_AORT_EC
GO:0050829	0.0207	1	1	8	defense response to Gram-negative bacterium	BP	1	BPI	up_AORT_EC
GO:0050919	0.0207	1	1	10	negative chemotaxis	BP	1	SLIT2	up_VPUL_VSMC

GO:0032760	0.020761855	0.99737	3	22	positive regulation of tumor necrosis factor	BP	0.96436359	FZD5,NOD2,MAVS	up_ACOR_EC
GO:1903557	0.020761855	0.99737	3	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	0.96436359	FZD5,NOD2,MAVS	up_ACOR_EC
GO:0009880	0.020799091	0.99737	3	22	embryonic pattern specification	BP	0.96436359	FZD5,SMAD6,NRP1	up_ACOR_EC
GO:2000058	0.0208	0.993	9	68	regulation of ubiquitin-dependent protein catabolic process	BP	0.701	PRICKLE1,PLK3,SOCS5,TRIB3,UCHL5,GSK3B,DISC1,RAD23A,USP14	down_VSAP_EC
GO:0010628	0.0208	0.998	3	527	positive regulation of gene expression	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0001936	0.0208	0.999	2	49	regulation of endothelial cell proliferation	BP	0.926	ACVRL1,SULF1	down_ACOR_EC
GO:0048771	0.0208	0.999	2	43	tissue remodeling	BP	0.926	ACVRL1,HOXA3	down_ACOR_EC
GO:0071356	0.0208	0.999	2	57	cellular response to tumor necrosis factor	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0060429	0.0208	0.999	2	341	epithelium development	BP	1	TBX5,HOXB5	up_APUL_VSMC
GO:1990791	0.0208	1	1	3	dorsal root ganglion development	BP	0.926	NRP2	down_ACOR_EC
GO:0009268	0.0208	1	1	10	response to pH	BP	1	RAB11B	down_VPOR_EC
GO:0060872	0.0208	1	1	6	semicircular canal development	BP	1	HOXA1	up_APUL_EC
GO:0010960	0.0208	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0055083	0.0208	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0042473	0.0208	1	1	5	outer ear morphogenesis	BP	1	SALL1	up_VSAP_VSMC
GO:0010468	0.0209	0.996	5	1270	regulation of gene expression	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0002052	0.0209	0.998	3	9	positive regulation of neuroblast proliferation	BP	0.701	HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0033194	0.0209	0.998	3	7	response to hydroperoxide	BP	1	TP53INP1,DAPK1,OXR1	up_ACOR_VSMC
GO:0007423	0.0209	0.997	3	155	sensory organ development	BP	1	ZDHHC16,NTRK2,HOXA1	up_APUL_EC
GO:0061724	0.0209	0.999	2	4	lipophagy	BP	0.701	SESN2,HTT	down_VSAP_EC
GO:0061448	0.0209	0.999	2	89	connective tissue development	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0045603	0.0209	1	1	5	positive regulation of endothelial cell	BP	0.926	ACVRL1	down_ACOR_EC
GO:0016579	0.0209	1	1	49	protein deubiquitination	BP	1	USP12	down_VFEM_EC
GO:0003344	0.0209	1	1	6	pericardium morphogenesis	BP	1	FLRT3	up_VPUL_EC
GO:0006796	0.021	0.984	93	938	phosphate-containing compound metabolic process	BP	0.621	EPHB1,PLK2,TEK,HCLS1,NPR1,ADGRF5,KIT,PPP2R5A,PANK3,PRKCH,CDA,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,NLRC5,GK5,EDN1,RALB,APLNR,CTTNBP2NL,PIPOX,NEDD9,SERINC5,ADSS,YES1,GUCY1A1,SPTLC2,EPHB4,MTOR,ACPP,SAMD8,MAP3K3,BMP2,HHEX,PREX2,SLK,BMP2K,SH3BP5,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,ENSCAFG00000010596,MADD,PAK2,PRKD2,SH3GLB1,SWAP70,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,LDB2,SLC25A25,FES,NSD1,GUCY1B1,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,TAOK1,CNOT7,DCK,HMGB1,NOS2,BLM,SPTBN4,RIPK1,ITGA6,RAD17,IMPA1,PDGFD,PIP5K1B,BMX,HIF1A,LMTK2,FKBP15,JCAD,ARHGEF2,CDON	up_VCAV_EC

GO:0006464	0.021	0.985	86	1162	cellular protein modification process	BP	0.701	ARHGEF2,PRICKLE1,VEGFA,P4HB,PLOD2,NR1H4,HSPA5,SOCS5,SGK1,ERO1A,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,WSB1,BCAR3,NUAK1,PTPN11,TRIB3,PUM3,ILK,PPP1R12A,SESN2,PTGS2,PPIB,USP12,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,PLCL1,TTLL7,ADAM17,CNOT7,MAGED1,CTNNB1,CDK8,APOE,PLOD3,USP48,UBA5,LYN,STRAP,BACH1,ASPH,CCNYL1,STT3A,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,CALM1,CDYL,PAK2,INHBA,CAMK2D,HIF1AN,BTK,CDKN1A,NRP1,SH3RF3,USP14,ARF4,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:0036211	0.021	0.985	86	1162	protein modification process	BP	0.701	ARHGEF2,PRICKLE1,VEGFA,P4HB,PLOD2,NR1H4,HSPA5,SOCS5,SGK1,ERO1A,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,WSB1,BCAR3,NUAK1,PTPN11,TRIB3,PUM3,ILK,PPP1R12A,SESN2,PTGS2,PPIB,USP12,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,PLCL1,TTLL7,ADAM17,CNOT7,MAGED1,CTNNB1,CDK8,APOE,PLOD3,USP48,UBA5,LYN,STRAP,BACH1,ASPH,CCNYL1,STT3A,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,CALM1,CDYL,PAK2,INHBA,CAMK2D,HIF1AN,BTK,CDKN1A,NRP1,SH3RF3,USP14,ARF4,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:2000026	0.021	0.986	46	560	regulation of multicellular organismal development	BP	0.701	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,NR1H4,SERPINE1,SOCS5,SPARC,PRKACB,ERRFI1,JCAD,PGK1,DPYSL3,HOOK3,IFRD1,TGFBR1,PIK3C2A,HOXB7,HIF1A,SLC45A3,THBS2,TNIK,ZPR1,PTPN2,EVI2B,MTDH,UST,MAGED1,CTNNB1,STARD13,TFRC,APOE,LYN,STRAP,DDIT3,MMD,VLDLR,REST,PRMT1,DISC1,LRRTM2,INHBA,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0033962	0.021	0.997	4	12	cytoplasmic mRNA processing body assembly	BP	0.621	CNOT6,PAN3,CNOT7,LSM14A	up_VCAV_EC
GO:0006613	0.021	0.998	3	12	cotranslational protein targeting to membrane	BP	1	SSR2,SSR3,SEC61B	down_VCAV_EC
GO:0006273	0.021	0.999	2	3	lagging strand elongation	BP	0.758	POLA1,FEN1	down_ACOR_VSMC
GO:0032055	0.021	0.999	2	4	negative regulation of translation in response to	BP	0.701	SESN2,EIF2S1	down_VSAP_EC
GO:0097527	0.021	0.999	2	3	necroptotic signaling pathway	BP	0.621	TLR3,RIPK1	up_VCAV_EC
GO:1903053	0.021	1	1	10	regulation of extracellular matrix organization	BP	1	FSCN1	down_AFEM_EC
GO:2000027	0.021	1	1	72	regulation of animal organ morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:0055007	0.021	1	1	31	cardiac muscle cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0061436	0.021	1	1	5	establishment of skin barrier	BP	1	CYP26B1	up_VFEM_EC
GO:0007252	0.021	1	1	6	I-kappaB phosphorylation	BP	1	TLR2	up_VSAP_VSMC
GO:0072012	0.021071517	0.99874	2	9	glomerulus vasculature development	BP	0.96436359	AQP1,FOXC2	up_ACOR_EC
GO:0010628	0.0211	0.985	58	527	positive regulation of gene expression	BP	0.621	HCLS1,IL7R,KIT,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,DLL4,TLR4,NLRC5,GATA3,EDN1,RAB27A,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ENSCAFG00000002015,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0001654	0.0211	0.99	16	110	eye development	BP	0.621	EPHB1,ARHGEF15,CHD7,DLL4,GATA3,TMOD1,PROX1,TSPAN12,SMARCA4,SLC25A25,JAG1,SKIL,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0048880	0.0211	0.99	16	110	sensory system development	BP	0.621	EPHB1,ARHGEF15,CHD7,DLL4,GATA3,TMOD1,PROX1,TSPAN12,SMARCA4,SLC25A25,JAG1,SKIL,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0150063	0.0211	0.99	16	110	visual system development	BP	0.621	EPHB1,ARHGEF15,CHD7,DLL4,GATA3,TMOD1,PROX1,TSPAN12,SMARCA4,SLC25A25,JAG1,SKIL,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC

GO:0001822	0.0211	0.992	10	98	kidney development	BP	1	SMAD9,KANK2,CLSTN1,PKD1,GLI3,GLIS2,RDH10,GREM1,ZBTB16,SEC61A1	down_VCAV_EC
GO:0050863	0.0211	0.993	8	69	regulation of T cell activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0043038	0.0211	0.994	6	34	amino acid activation	BP	0.701	CARS,SARS,AARS,YARS,TARS,NARS	down_VSAP_EC
GO:0010562	0.0211	0.996	4	312	positive regulation of phosphorus metabolic	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0045937	0.0211	0.996	4	312	positive regulation of phosphate metabolic	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0098662	0.0211	0.997	3	131	inorganic cation transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0090288	0.0211	0.999	2	44	negative regulation of cellular response to growth factor stimulus	BP	0.926	SULF1,ASPN	down_ACOR_EC
GO:0051186	0.0211	0.999	2	159	cofactor metabolic process	BP	1	CYP1A1,ENSCAFG00000028814	up_VCAV_VSMC
GO:2000010	0.0211	1	1	5	positive regulation of protein localization to cell	BP	0.926	STX4	down_ACOR_EC
GO:0030516	0.0211	1	1	15	regulation of axon extension	BP	1	LIMK1	up_VCAV_VSMC
GO:0002762	0.0211	1	1	15	negative regulation of myeloid leukocyte	BP	1	LRRC17	up_VCAV_VSMC
GO:0050732	0.0212	0.996	4	18	negative regulation of peptidyl-tyrosine	BP	0.702	SOCS5,ERRFI1,PTPN2,CBLC	down_VSAP_EC
GO:0001659	0.0212	0.999	2	54	temperature homeostasis	BP	1	HOXC10,MAP2K6	up_VFEM_EC
GO:0061502	0.0212	1	1	3	early endosome to recycling endosome	BP	0.926	MYO1D	down_ACOR_EC
GO:0001881	0.0212	1	1	11	receptor recycling	BP	1	RAB11B	down_VPOR_EC
GO:0006936	0.0212	1	1	74	muscle contraction	BP	1	JUP	down_VFEM_VSMC
GO:0035196	0.0212	1	1	16	production of miRNAs involved in gene silencing	BP	1	ESR1	up_AORT_VSMC
GO:0032501	0.02128002	0.98578	60	1782	multicellular organismal process	BP	0.96436359	SH3TC2,CPAMD8,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TBX18,PLCL1,SOX9,PTH1R,PCSK1N,NDRG2,AQP1,ENSCAFG00000004331,FZD5,SEMA6D,GNAO1,DIXDC1,PDLIM3,NOD2,IL33,RGMA,LHX9,PDE4A,INSYN1,SMAD6,PLS1,ACTN2,RNLS,ESM1,PTGDS,PAK3,DLX3,TRIM8,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,USP53,MAPK8IP2,MAVS,FOXC2,FIGNL1,TBX5,LRP4,CLSTN1,C23H3orf58,CHMP4B,TP53INP2,RARRES2,NRP1,AGPAT2,PRKCD,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1	up_ACOR_EC
GO:1901698	0.0213	0.987	33	266	response to nitrogen compound	BP	0.624	TNFAIP3,PPARG,P2RX7,BAIAP2L1,TMEM173,SELL,PDE4D,MEF2C,RAPGEF1,TLR4,RALB,PELI1,MTOR,ABCA1,MAPK13,RIOK3,TLR3,NCK1,TIMELESS,JAG1,GUCY1B1,RAPGEF2,CREB1,CTNNA1,PMAIP1,BLM,USP13,PDGFD,ATRX,NR4A1,P2RX2,ZEB1,ARHGEF2	up_VCAV_EC
GO:0010467	0.0213	0.996	6	1787	gene expression	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0055013	0.0213	0.996	5	17	cardiac muscle cell development	BP	1	ACTN2,BMP4,NEBL,EDN1,BVES	up_ACOR_VSMC
GO:0072606	0.0213	0.997	4	12	interleukin-8 secretion	BP	1	C5AR2,ANXA4,F2RL1,MAPKBP1	up_VSAP_EC
GO:0048646	0.0213	0.999	2	349	anatomical structure formation involved in	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0036022	0.0213	1	1	4	limb joint morphogenesis	BP	0.928	SULF1	down_ACOR_EC
GO:0045668	0.0213	1	1	11	negative regulation of osteoblast differentiation	BP	1	HDAC7	down_VPOR_EC
GO:0034499	0.0213	1	1	3	late endosome to Golgi transport	BP	1	GCC2	up_VPOR_EC
GO:0014855	0.021307998	0.99728	3	22	striated muscle cell proliferation	BP	0.96436359	FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0061448	0.0214	0.99	15	89	connective tissue development	BP	1	HOXA11,AXIN2,OSR2,HOXD3,EBF2,OSR1,ZBTB16,RARG,HOXC4,ZEB1,FBXW4,SULF2,SHOX2,NFIB,TGFBR2	up_VSAP_EC
GO:0001838	0.0214	0.993	8	56	embryonic epithelial tube formation	BP	0.709	PRICKLE1,PRKACB,ENSCAFG00000032470,TMED2,HIF1A,CTNNB1,SDC4,SIX4	down_VSAP_EC
GO:0001935	0.0214	0.999	2	50	endothelial cell proliferation	BP	0.928	ACVRL1,SULF1	down_ACOR_EC
GO:0035860	0.0214	1	1	4	glial cell-derived neurotrophic factor	BP	0.928	SULF1	down_ACOR_EC
GO:1902803	0.0214	1	1	20	regulation of synaptic vesicle transport	BP	1	WNT7A	up_AORT_VSMC

GO:2000300	0.0214	1	1	20	regulation of synaptic vesicle exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:1902622	0.0214	1	1	11	regulation of neutrophil migration	BP	1	SLIT2	up_VPUL_VSMC
GO:2000209	0.0214	1	1	5	regulation of anoikis	BP	1	CAV1	up_VSAP_VSMC
GO:2000811	0.0214	1	1	5	negative regulation of anoikis	BP	1	CAV1	up_VSAP_VSMC
GO:0048246	0.021406736	0.99871	2	9	macrophage chemotaxis	BP	0.96436359	MMP28,RARRES2	up_ACOR_EC
GO:1905521	0.021442726	0.99871	2	9	regulation of macrophage migration	BP	0.96436359	MMP28,RARRES2	up_ACOR_EC
GO:0050679	0.0215	0.992	10	62	positive regulation of epithelial cell proliferation	BP	0.628	TNFAIP3,PDGFB,APLNR,EGFL7,BMP2,PROX1,PRKD2,HMGB1,NRAS,JCAD	up_VCAV_EC
GO:0045646	0.0215	0.996	4	19	regulation of erythrocyte differentiation	BP	0.71	HIF1A,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0050702	0.0215	0.997	4	13	interleukin-1 beta secretion	BP	0.627	GBP5,TLR4,ARG2,ABCA1	up_VCAV_EC
GO:0072604	0.0215	0.997	4	12	interleukin-6 secretion	BP	1	C5AR2,IL17RC,F2RL1,MAVS	up_VSAP_EC
GO:0009653	0.0215	0.998	3	773	anatomical structure morphogenesis	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0042221	0.0215	1	2	1012	response to chemical	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048705	0.0215	0.999	2	95	skeletal system morphogenesis	BP	1	HOXA3,CYP26B1	up_VPOR_VSMC
GO:0001101	0.0215	0.999	2	65	response to acid chemical	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0002218	0.0215	0.999	2	53	activation of innate immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0009225	0.0215	1	1	10	nucleotide-sugar metabolic process	BP	1	EXTL2	down_AFEM_EC
GO:0003170	0.0215	1	1	25	heart valve development	BP	1	GATA5	down_VSAP_VSMC
GO:0035567	0.0215	1	1	19	non-canonical Wnt signaling pathway	BP	1	WNT7A	up_AORT_VSMC
GO:0003281	0.0215	1	1	30	ventricular septum development	BP	1	TBX5	up_APUL_VSMC
GO:0045670	0.0215	1	1	16	regulation of osteoclast differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0010831	0.0215	1	1	9	positive regulation of myotube differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:2000050	0.0215	1	1	8	regulation of non-canonical Wnt signaling	BP	1	ANKRD6	up_VPOR_VSMC
GO:0099173	0.021511039	0.99598	4	40	postsynapse organization	BP	0.96436359	PAK3,LRP4,LRRC4,NRP1	up_ACOR_EC
GO:0060419	0.021525195	0.99724	3	22	heart growth	BP	0.96436359	FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0051094	0.0216	0.99	16	388	positive regulation of developmental process	BP	1	CMKLR1,IRX3,LEP,LBH,ANGPT4,DLL1,F3,GPAM,TMEM100,GREM1,CYLD,EVI2B,AXIN2,ACACB,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:0043269	0.0216	0.997	3	135	regulation of ion transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0045055	0.0216	0.999	2	52	regulated exocytosis	BP	0.933	LYN,STX4	down_ACOR_EC
GO:0048799	0.0216	0.999	2	10	animal organ maturation	BP	1	XYLT1,GREM1	up_AFEM_EC
GO:0003007	0.0216	0.999	2	94	heart morphogenesis	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0050847	0.0216	1	1	2	progesterone receptor signaling pathway	BP	0.934	NEDD4	down_ACOR_EC
GO:0043588	0.0216	1	1	74	skin development	BP	1	JUP	down_VFEM_VSMC
GO:0031128	0.0216	1	1	15	developmental induction	BP	1	GATA5	up_VCAV_VSMC
GO:0072075	0.0216	1	1	5	metanephric mesenchyme	BP	1	SIX1	up_VFEM_EC
GO:0036445	0.0216	1	1	6	neuronal stem cell division	BP	1	ARHGEF2	up_VPUL_EC
GO:0055057	0.0216	1	1	6	neuroblast division	BP	1	ARHGEF2	up_VPUL_EC
GO:0031294	0.0216	1	1	4	lymphocyte costimulation	BP	1	CAV1	up_VSAP_VSMC
GO:0019732	0.021673752	1	1	1	antifungal humoral response	BP	0.96436359	RARRES2	up_ACOR_EC
GO:0061760	0.021673752	1	1	1	antifungal innate immune response	BP	0.96436359	RARRES2	up_ACOR_EC

GO:0023051	0.0217	0.984	110	954	regulation of signaling	BP	1	SH3TC2,ADRA1B,TLR1,SMAD6,LGR6,LEP,PLCL1,LBH,MID1,GATA5,HTR2B,RASSF2,ZRANB1,FBXL20,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,ELF1,HRH1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,ZNRF3,AR,PTGIR,SASH1,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ITPR1,LIMS2,ANKRD1,F2RL1,DAPK1,BNIP3,EGLN1,CRLF3,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,DMPK,NPNT,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,FRS2,RNF19A,SCG5,RGS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,CHD7,SIPA1L1,CCL5,WWC2,DUSP22,SIAH1,RAB11B,EDN1,SESN1,KCNC4,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,DDIT4,DISC1,SH3RF3,SERINC3,USP20,HERPUD1,MAP3K7,INPP5K,PREPL,BMT2,PFKL,WFS1,SH3BP4,ENSCAFG00000029553,PARK7,IL18R1,BVES,CRKL	up_ACOR_VSMC
GO:0022610	0.0217	0.99	14	326	biological adhesion	BP	1	LEP,CDH18,HOXA7,DLL1,GPAM,GREM1,CYLD,POSTN,LRRC15,ICAM5,BVES,ADAM17,KANK1,TNC	up_AFEM_EC
GO:0055001	0.0217	0.993	7	47	muscle cell development	BP	0.713	ACTN1,FHL2,WDR1,NEXN,SIX4,MYBPC2,HOMER1	down_VSAP_EC
GO:0055072	0.0217	0.994	7	30	iron ion homeostasis	BP	1	FXN,SLC25A28,MYC,SCARA5,FTL,HMOX1,NCOA4	up_VSAP_EC
GO:0071838	0.0217	0.999	2	3	cell proliferation in bone marrow	BP	0.633	MEF2C,MAP3K3	up_VCAV_EC
GO:1990845	0.0217	1	1	51	adaptive thermogenesis	BP	1	PLCL1	down_VFEM_EC
GO:0007501	0.0217	1	1	5	mesodermal cell fate specification	BP	1	EYA1	up_VFEM_EC
GO:0045605	0.0217	1	1	5	negative regulation of epidermal cell	BP	1	HOXA7	up_VFEM_EC
GO:0009595	0.0217	1	1	6	detection of biotic stimulus	BP	1	TLR2	up_VSAP_VSMC
GO:0001765	0.0217	1	1	4	membrane raft assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0060429	0.0218	0.986	44	341	epithelium development	BP	1	HOXA11,FZD1,THRB,HOXA7,WNT11,HNF4A,AXIN2,SLIT2,FGF7,ABL1,BTG1,DLL1,OSR1,FUZ,ADAMTSL4,SAV1,KLF15,ANXA4,HPSE,RILPL2,RARG,STAT6,AMBRA1,F2RL1,DLX3,ZFP36L1,IRX3,ZEB1,MYD88,LRP4,FRMD6,E2F4,NTN4,KDM2B,NFIB,ARHGAP12,ACVRL1,MAP2K2,TGFBR2,CITED2,TRADD,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0030278	0.0218	0.991	12	66	regulation of ossification	BP	1	TWIST2,AXIN2,OSR2,ZHX3,HDAC7,OSR1,ZBTB16,DDR2,OMD,LRP4,LIMD1,BGLAP	up_VSAP_EC
GO:0016192	0.0218	0.994	6	452	vesicle-mediated transport	BP	0.938	LYN,SPG11,ACSL3,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0050873	0.0218	0.995	5	18	brown fat cell differentiation	BP	1	LEP,FNDC5,PPARGC1A,PLAC8B,BNIP3	up_ACOR_VSMC
GO:0019722	0.0218	0.996	4	45	calcium-mediated signaling	BP	1	CMKLR1,LMCD1,TMEM100,DMPK	up_AFEM_EC
GO:0031214	0.0218	0.996	4	45	biomineral tissue development	BP	1	GREM1,PTHLH,CNNM4,AXIN2	up_AFEM_EC
GO:0045663	0.0218	0.998	3	7	positive regulation of myoblast differentiation	BP	1	CDON,BTG1,MAP3K5	up_VSAP_EC
GO:0045056	0.0218	0.999	2	5	transcytosis	BP	1	LRP1,LRPAP1	down_VCAV_EC
GO:0045657	0.0218	0.999	2	5	positive regulation of monocyte differentiation	BP	1	CLSTN1,ZFP36L1	down_VCAV_EC
GO:0048706	0.0218	0.999	2	59	embryonic skeletal system development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0032990	0.0218	0.999	2	167	cell part morphogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0043616	0.0218	1	1	10	keratinocyte proliferation	BP	1	SRSF6	down_AFEM_EC
GO:2001293	0.0218	1	1	1	malonyl-CoA metabolic process	BP	1	ACACB	up_AFEM_EC
GO:2001295	0.0218	1	1	1	malonyl-CoA biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0021615	0.0218	1	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	up_VPOR_EC
GO:0003203	0.0218	1	1	11	endocardial cushion morphogenesis	BP	1	GATA5	up_VPUL_VSMC
GO:0007501	0.0218	1	1	5	mesodermal cell fate specification	BP	1	HOXA11	up_VSAP_VSMC

GO:0045595	0.0219	0.985	58	469	regulation of cell differentiation	BP	1	HOXA11,THRB,HOXA7,NAPEPLD,TWIST2,HOXA9,CDON,AXIN2,PPARGC1B,SLIT2,ZHX3,HOXD3,ABL1,BTG1,HDAC7,EMP2,DLL1,OSR1,MAP3K5,SAV1,PLXNA4,ANKRD54,ZBTB16,TOX,RARG,DDR2,ZFP36L1,PIK3R1,TIAM1,MYC,IRX3,ZEB1,SHOX2,RTN4RL1,TFE3,LRP4,DPYSL2,GDPD5,ZADH2,FBXO7,LIMD1,CDK9,CD83,FBLN1,ZFP36L2,PLEKHB2,PNP,TAF8,CYB5D2,PQBP1,TTL,ACVRL1,FLOT1,NCK1,MAP2K2,TGFBR2,LBH,KEAP1	up_VSAP_EC
GO:0006936	0.0219	0.991	13	74	muscle contraction	BP	1	TNNT2,ADRA1B,ACTN2,KCNE3,HTR2B,PDE5A,DMPK,NPNT,TBX20,JUP,EDN1,GAA,DOCK5	up_ACOR_VSMC
GO:0032963	0.0219	0.996	4	18	collagen metabolic process	BP	0.714	SERPINH1,HIF1A,PLOD3,P3H4	down_VSAP_EC
GO:0019752	0.0219	0.997	3	283	carboxylic acid metabolic process	BP	1	ETFA,DARS,SUCLG2	down_AFEM_EC
GO:0007283	0.0219	0.999	2	91	spermatogenesis	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0021648	0.0219	1	1	3	vestibulocochlear nerve morphogenesis	BP	0.938	NRP2	down_ACOR_EC
GO:0003407	0.0219	1	1	15	neural retina development	BP	1	IRX5	up_AFEM_VSMC
GO:0060872	0.0219	1	1	6	semicircular canal development	BP	1	EYA1	up_VFEM_EC
GO:0071600	0.0219	1	1	5	otic vesicle morphogenesis	BP	1	EYA1	up_VFEM_EC
GO:0021515	0.0219	1	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_VFEM_VSMC
GO:0003176	0.021938141	0.99866	2	9	aortic valve development	BP	0.96436359	GATA4,SMAD6	up_ACOR_EC
GO:0071706	0.021967522	0.99587	4	40	tumor necrosis factor superfamily cytokine	BP	0.96436359	NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC
GO:0006518	0.022	0.988	23	290	peptide metabolic process	BP	1	PRNP,UBA52,LARP6,COA1,SAMD4B,RPL23,RPL13,EIF3K,MRPL37,PARK7,RPL27A,EEF2,ZFP36L1,SEC11C,RNPEP,RPL27,MRPS11,RPS27,PCSK6,ENSCAFG00000015122,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0045732	0.022	0.992	10	78	positive regulation of protein catabolic process	BP	0.714	PRICKLE1,PLK3,SOCS5,TRIB3,MSN,APOE,GSK3B,DISC1,RAD23A,TMTC3	down_VSAP_EC
GO:0032635	0.022	0.993	8	37	interleukin-6 production	BP	1	C5AR2,IL6R,IL17RC,F2RL1,MYD88,NLRX1,CYBA,MAVS	up_VSAP_EC
GO:0048262	0.022	0.999	2	5	determination of dorsal/ventral asymmetry	BP	0.714	CTNNB1,DDIT3	down_VSAP_EC
GO:0030889	0.022	0.999	2	4	negative regulation of B cell proliferation	BP	0.714	LYN,BTK	down_VSAP_EC
GO:0033144	0.022	0.999	2	10	negative regulation of intracellular steroid hormone receptor	BP	1	LBH,CRY2	up_AFEM_EC
GO:0060739	0.022	1	1	1	mesenchymal-epithelial cell signaling involved in prostate gland	BP	1	TNC	up_AFEM_EC
GO:0010573	0.022	1	1	9	vascular endothelial growth factor production	BP	1	C3AR1	up_VPOR_VSMC
GO:0010574	0.022	1	1	9	regulation of vascular endothelial growth factor	BP	1	C3AR1	up_VPOR_VSMC
GO:0010658	0.022	1	1	8	striated muscle cell apoptotic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010662	0.022	1	1	8	regulation of striated muscle cell apoptotic	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006044	0.022	1	1	5	N-acetylglucosamine metabolic process	BP	1	CHST7	up_VFEM_EC
GO:1901016	0.022	1	1	9	regulation of potassium ion transmembrane transporter activity	BP	1	NETO1	up_VFEM_VSMC
GO:0034329	0.022054863	0.99477	5	60	cell junction assembly	BP	0.96436359	NR1H4,ARHGAP6,FZD5,ACTN2,NRP1	up_ACOR_EC
GO:0072073	0.022098453	0.99476	5	60	kidney epithelium development	BP	0.96436359	SOX9,AQP1,SMAD6,FOXC2,CLSTN1	up_ACOR_EC
GO:0048608	0.0221	0.989	20	129	reproductive structure development	BP	1	LEP,GATA4,PRDX4,BMP4,FGFR2,ATRX,CITED2,SPINT1,CTSB,EGLN1,ENSCAFG00000006238,SPINT2,FRS2,CHD7,SPINK2,ARID5B,DMC1,SERPINB5,LHX9,WDR48	up_ACOR_VSMC
GO:0001935	0.0221	0.993	7	50	endothelial cell proliferation	BP	0.714	VEGFA,SULF1,SPARC,JCAD,TGFBR1,ADAM17,APOE	down_VSAP_EC
GO:0072028	0.0221	0.994	6	37	nephron morphogenesis	BP	0.714	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0097306	0.0221	0.994	6	22	cellular response to alcohol	BP	1	PRKAA2,TP53INP1,ADCY6,PTGDR,PRKCE,JUP	up_ACOR_VSMC

GO:0007044	0.0221	0.995	5	27	cell-substrate junction assembly	BP	0.714	VEGFA,ACTN1,ENSCAFG00000002015,TLN1, NRP1	down_VSAP_EC
GO:0051239	0.0221	0.996	5	859	regulation of multicellular organismal process	BP	1	TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0061213	0.0221	0.997	3	11	positive regulation of mesonephros	BP	0.714	HOXB7,MAGED1,SIX4	down_VSAP_EC
GO:0009888	0.0221	0.998	3	545	tissue development	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0009101	0.0221	0.999	2	113	glycoprotein biosynthetic process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0036037	0.0221	0.999	2	3	CD8-positive, alpha-beta T cell activation	BP	1	CD274,PTPN22	up_ACOR_VSMC
GO:2001185	0.0221	0.999	2	3	regulation of CD8-positive, alpha-beta T cell	BP	1	CD274,PTPN22	up_ACOR_VSMC
GO:0071621	0.0221	0.998	2	27	granulocyte chemotaxis	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0060485	0.0221	0.999	2	93	mesenchyme development	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0001822	0.0221	0.999	2	98	kidney development	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0021960	0.0221	0.999	2	3	anterior commissure morphogenesis	BP	1	PLXNA4,NFIB	up_VSAP_EC
GO:0001885	0.0221	1	1	19	endothelial cell development	BP	1	WNT7A	up_AORT_VSMC
GO:0031050	0.0221	1	1	17	dsRNA processing	BP	1	ESR1	up_AORT_VSMC
GO:0070918	0.0221	1	1	17	production of small RNA involved in gene silencing	BP	1	ESR1	up_AORT_VSMC
GO:0050922	0.0221	1	1	11	negative regulation of chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0060039	0.0221	1	1	11	pericardium development	BP	1	TBX5	up_VPUL_VSMC
GO:0048869	0.0222	0.992	11	1119	cellular developmental process	BP	0.945	ACVRL1,LYN,ACSL4,SPG11,PDPN,NRP2,HOXA 7,ANPEP,SULF1,ELK3,NEDD4	down_ACOR_EC
GO:0045833	0.0222	0.994	6	29	negative regulation of lipid metabolic process	BP	0.645	PPP2R5A,PDGFB,BMP2,PROX1,ENSCAFG000 00010596,APOD	up_VCAV_EC
GO:0050777	0.0222	0.994	6	28	negative regulation of immune response	BP	0.644	IL7R,TNFAIP3,NLRC5,ARG2,THOC1,CNOT7	up_VCAV_EC
GO:0044271	0.0222	0.998	4	1501	cellular nitrogen compound biosynthetic	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0006952	0.0222	0.996	4	319	defense response	BP	1	NR1H4,MRC1,CCL24,ARHGEF2	up_VPUL_EC
GO:0001765	0.0222	0.999	2	4	membrane raft assembly	BP	0.781	CAV1,EMP2	down_ACOR_VSMC
GO:0042551	0.0222	0.999	2	10	neuron maturation	BP	1	IRX5,LGI4	up_AFEM_EC
GO:0046320	0.0222	0.999	2	10	regulation of fatty acid oxidation	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0072678	0.0222	0.999	2	10	T cell migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0051346	0.0222	1	1	78	negative regulation of hydrolase activity	BP	1	CST3	down_AORT_EC
GO:0048762	0.0222	1	1	77	mesenchymal cell differentiation	BP	1	GATA5	down_VFEM_VSMC
GO:0045446	0.0222	1	1	32	endothelial cell differentiation	BP	1	HOXB5	up_APUL_VSMC
GO:0021824	0.0222	1	1	3	cerebral cortex tangential migration using cell-axon interactions	BP	1	SEMA3A	up_VPOR_EC
GO:0021828	0.0222	1	1	3	gonadotrophin-releasing hormone neuronal migration to the	BP	1	SEMA3A	up_VPOR_EC
GO:0021856	0.0222	1	1	3	hypothalamic tangential migration using cell-axon interactions	BP	1	SEMA3A	up_VPOR_EC
GO:0021886	0.0222	1	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	SEMA3A	up_VPOR_EC
GO:0021888	0.0222	1	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	SEMA3A	up_VPOR_EC
GO:0021979	0.0222	1	1	3	hypothalamus cell differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0035290	0.0222	1	1	3	trunk segmentation	BP	1	SEMA3A	up_VPOR_EC
GO:0036484	0.0222	1	1	3	trunk neural crest cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0036486	0.0222	1	1	3	ventral trunk neural crest cell migration	BP	1	SEMA3A	up_VPOR_EC

GO:0097490	0.0222	1	1	3	sympathetic neuron projection extension	BP	1	SEMA3A	up_VPOR_EC
GO:0097491	0.0222	1	1	3	sympathetic neuron projection guidance	BP	1	SEMA3A	up_VPOR_EC
GO:1901166	0.0222	1	1	3	neural crest cell migration involved in autonomic nervous system	BP	1	SEMA3A	up_VPOR_EC
GO:1903375	0.0222	1	1	3	facioacoustic ganglion development	BP	1	SEMA3A	up_VPOR_EC
GO:1902622	0.0222	1	1	11	regulation of neutrophil migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0010611	0.0222	1	1	11	regulation of cardiac muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0014743	0.0222	1	1	11	regulation of muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0051240	0.0223	0.988	19	489	positive regulation of multicellular organismal process	BP	1	CMKLR1,IRX3,LEP,LBH,ANGPT4,DLL1,F3,GPAM,TMEM100,GREM1,AVPR1A,CYLD,TBXA2R,EVI2B,AXIN2,ACACB,PPARGC1A,ADAM17,AGPAT2	up_AFEM_EC
GO:0051222	0.0223	0.989	17	103	positive regulation of protein transport	BP	1	EXPH5,TLR1,LEP,HTR2B,TCAF1,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,PSEN1,JUP,NOD2,SCAMP5	up_ACOR_VSMC
GO:0072511	0.0223	0.989	16	97	divalent inorganic cation transport	BP	1	PLCG2,HTR2B,TPC3,NIPAL3,SARAF,MICU2,ITPR1,CACNB3,PRKCE,PSEN1,CHD7,INPP5K,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0006575	0.0223	0.992	10	53	cellular modified amino acid metabolic process	BP	1	PRDX4,ERO1B,EGLN1,ENSCAFG00000028814,P4HA1,SARDH,PCYOX1,SERINC3,SERINC1,PARK7	up_ACOR_VSMC
GO:0090150	0.0223	0.992	8	64	establishment of protein localization to membrane	BP	0.717	TRAM1,SRP54,MYO1C,SSR1,SRPRA,SRP72,SH3GLB1,BLZF1	down_VSAP_EC
GO:0002063	0.0223	0.995	5	18	chondrocyte development	BP	1	AXIN2,RARG,SULF2,SHOX2,TGFBR2	up_VSAP_EC
GO:0051926	0.0223	0.996	4	14	negative regulation of calcium ion transport	BP	0.781	HOXA3,SLC30A1,GSTO1,REM1	down_ACOR_VSMC
GO:0035926	0.0223	0.999	2	3	chemokine (C-C motif) ligand 2 secretion	BP	1	MBP,F2RL1	up_ACOR_VSMC
GO:2000725	0.0223	0.999	2	10	regulation of cardiac muscle cell differentiation	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0021644	0.0223	1	1	1	vagus nerve morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0021793	0.0223	1	1	1	chemorepulsion of branchiomotor axon	BP	1	PLXNA4	up_AFEM_EC
GO:0070228	0.0223	1	1	20	regulation of lymphocyte apoptotic process	BP	1	ARG2	up_AORT_VSMC
GO:0010960	0.0223	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0060037	0.0223	1	1	9	pharyngeal system development	BP	1	EYA1	up_VFEM_VSMC
GO:0021772	0.0223	1	1	11	olfactory bulb development	BP	1	SLIT2	up_VPUL_VSMC
GO:0021988	0.0223	1	1	11	olfactory lobe development	BP	1	SLIT2	up_VPUL_VSMC
GO:0060045	0.0223	1	1	11	positive regulation of cardiac muscle cell	BP	1	TBX5	up_VPUL_VSMC
GO:0001944	0.0224	0.99	12	263	vasculature development	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,RECK,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0035051	0.0224	0.993	8	41	cardiocyte differentiation	BP	0.649	MEF2C,EDN1,SOX18,MTOR,BMP2,PROX1,ENSCAFG00000010596,JAG1	up_VCAV_EC
GO:0002833	0.0224	0.996	4	12	positive regulation of response to biotic	BP	1	CD274,F2RL1,SASH1,CYBA	up_VSAP_EC
GO:0006357	0.0224	0.998	3	547	regulation of transcription by RNA polymerase II	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0002699	0.0224	0.998	2	46	positive regulation of immune effector process	BP	0.95	LYN,STX4	down_ACOR_EC
GO:0022618	0.0224	0.999	2	111	ribonucleoprotein complex assembly	BP	1	EIF3M,SRSF6	down_AFEM_EC
GO:0035295	0.0224	0.999	2	356	tube development	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0035136	0.0224	1	1	16	forelimb morphogenesis	BP	1	HOXA9	up_AFEM_VSMC
GO:2001014	0.0224	1	1	8	regulation of skeletal muscle cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048535	0.0224	1	1	5	lymph node development	BP	1	TOX	up_VFEM_EC
GO:0051047	0.022401141	0.99375	6	84	positive regulation of secretion	BP	0.96436359	NR1H4,AQP1,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0007154	0.0225	0.991	14	1622	cell communication	BP	0.95	ACVRL1,LYN,IGF1R,SPG11,PDPN,NRP2,HIVEP2,USP28,IPO7,SULF1,WDR12,STX4,ASPN,NEDD4	down_ACOR_EC

GO:0030182	0.0225	0.99	14	327	neuron differentiation	BP	1	IRX3,IRX5,HOXC10,LEP,DLL1,VXN,PLXNA4,NEFH,THRB,LGI4,CAMK2A,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0055092	0.0225	0.994	6	28	sterol homeostasis	BP	0.785	SREBF2,RALY,INSIG1,CAV1,LIPC,NUS1	down_ACOR_VSMC
GO:0071772	0.0225	0.998	2	50	response to BMP	BP	0.95	ACVRL1,SULF1	down_ACOR_EC
GO:0071773	0.0225	0.998	2	50	cellular response to BMP stimulus	BP	0.95	ACVRL1,SULF1	down_ACOR_EC
GO:0010803	0.0225	0.999	2	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	CYLD,ADAM17	up_AFEM_EC
GO:0048014	0.0225	0.999	2	3	Tie signaling pathway	BP	0.652	TEK,ANGPT2	up_VCAV_EC
GO:0007160	0.0225	0.998	2	56	cell-matrix adhesion	BP	1	HOXA7,TIAM1	up_VFEM_EC
GO:0031644	0.0225	1	1	19	regulation of neurological system process	BP	1	WNT7A	up_AORT_VSMC
GO:0060078	0.0225	1	1	17	regulation of postsynaptic membrane potential	BP	1	WNT7A	up_AORT_VSMC
GO:0099565	0.0225	1	1	17	chemical synaptic transmission, postsynaptic	BP	1	WNT7A	up_AORT_VSMC
GO:0050771	0.0225	1	1	11	negative regulation of axonogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0034141	0.0225	1	1	5	positive regulation of toll-like receptor 3 signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0061737	0.022519107	1	1	1	leukotriene signaling pathway	BP	0.96436359	RGS1	up_ACOR_EC
GO:0051932	0.022534655	0.99861	2	9	synaptic transmission, GABAergic	BP	0.96436359	CNTNAP4,PLCL1	up_ACOR_EC
GO:0006625	0.0226	0.996	4	12	protein targeting to peroxisome	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0015919	0.0226	0.996	4	12	peroxisomal membrane transport	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0043574	0.0226	0.996	4	12	peroxisomal transport	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0072662	0.0226	0.996	4	12	protein localization to peroxisome	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0072663	0.0226	0.996	4	12	establishment of protein localization to peroxisome	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0071402	0.0226	0.997	3	10	cellular response to lipoprotein particle	BP	0.725	SOCS5,ADAM17,APOE	down_VSAP_EC
GO:0060840	0.0226	0.998	2	42	artery development	BP	0.95	ACVRL1,HOXA1	down_ACOR_EC
GO:0051660	0.0226	0.999	2	3	establishment of centrosome localization	BP	0.788	EZR,CEP83	down_ACOR_VSMC
GO:0072608	0.0226	0.999	2	3	interleukin-10 secretion	BP	1	CD274,F2RL1	up_ACOR_VSMC
GO:0006576	0.0226	0.999	2	10	cellular biogenic amine metabolic process	BP	1	MOXD1,NAPEPLD	up_AFEM_EC
GO:0007611	0.0226	0.998	2	54	learning or memory	BP	1	NETO1,GATM	up_VSAP_VSMC
GO:0043502	0.0226	1	1	16	regulation of muscle adaptation	BP	1	GATA5	up_VCAV_VSMC
GO:0060600	0.0226	1	1	3	dichotomous subdivision of an epithelial terminal	BP	1	SEMA3A	up_VPOR_EC
GO:0060666	0.0226	1	1	3	dichotomous subdivision of terminal units involved in salivary gland	BP	1	SEMA3A	up_VPOR_EC
GO:0010656	0.0226	1	1	8	negative regulation of muscle cell apoptotic	BP	1	NKX2-5	up_VPOR_VSMC
GO:2000738	0.0226	1	1	9	positive regulation of stem cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048168	0.0226	1	1	5	regulation of neuronal synaptic plasticity	BP	1	NETO1	up_VSAP_VSMC
GO:0007423	0.022604646	0.99166	9	155	sensory organ development	BP	0.96436359	CPAMD8,TMOD1,SOX9,AQP1,FZD5,FOXC2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:2000778	0.0227	0.998	3	7	positive regulation of interleukin-6 secretion	BP	1	IL17RC,F2RL1,MAVS	up_VSAP_EC
GO:0048589	0.0227	0.999	2	188	developmental growth	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0035137	0.0227	1	1	18	hindlimb morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0051415	0.0227	1	1	3	microtubule nucleation by interphase microtubule organizing center	BP	1	MZT1	up_VPOR_EC
GO:0051418	0.0227	1	1	3	microtubule nucleation by microtubule organizing	BP	1	MZT1	up_VPOR_EC
GO:0006110	0.0227	1	1	9	regulation of glycolytic process	BP	1	FBP1	up_VFEM_VSMC

GO:0030811	0.0227	1	1	9	regulation of nucleotide catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043470	0.0227	1	1	9	regulation of carbohydrate catabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0099601	0.0227	1	1	10	regulation of neurotransmitter	BP	1	NETO1	up_VFEM_VSMC
GO:0032732	0.022790746	0.99858	2	9	positive regulation of interleukin-1 production	BP	0.96436359	FZD5,NOD2	up_ACOR_EC
GO:0034404	0.0228	0.993	7	50	nucleobase-containing small molecule	BP	0.729	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:1901606	0.0228	0.996	4	22	alpha-amino acid catabolic process	BP	1	THNSL2,ENSCAFG00000002977,GLS2,ACAT1	down_VCAV_EC
GO:0001523	0.0228	0.997	3	12	retinoid metabolic process	BP	1	CYP1B1,RETSAT,RDH10	down_VCAV_EC
GO:0052548	0.0228	1	1	80	regulation of endopeptidase activity	BP	1	CST3	down_AORT_EC
GO:0033059	0.0228	1	1	12	cellular pigmentation	BP	1	RAB11B	down_VPOR_EC
GO:0043276	0.0228	1	1	6	anoikis	BP	1	NTRK2	up_APUL_EC
GO:0060070	0.022870972	0.99281	7	105	canonical Wnt signaling pathway	BP	0.96436359	CDH3,SOX9,PORCN,FZD5,DIXDC1,LRP4,PYGO2	up_ACOR_EC
GO:0009653	0.0229	0.993	7	773	anatomical structure morphogenesis	BP	1	TBX5,HOXA3,ARHGEF26,SLITRK5,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:1902117	0.0229	0.993	7	32	positive regulation of organelle assembly	BP	0.654	EDN1,RALB,CNOT6,PROX1,SH3GLB1,PAN3,FSCN1	up_VCAV_EC
GO:0001568	0.0229	0.997	3	252	blood vessel development	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0009084	0.0229	0.998	3	7	glutamine family amino acid biosynthetic process	BP	1	GLUL,ENSCAFG00000016140,ASS1	up_VSAP_EC
GO:0008356	0.0229	0.999	2	3	asymmetric cell division	BP	0.796	ASPM,ARHGEF2	down_ACOR_VSMC
GO:0034137	0.0229	0.999	2	3	positive regulation of toll-like receptor 2 signaling	BP	1	TLR1,F2RL1	up_ACOR_VSMC
GO:0045357	0.0229	0.999	2	3	regulation of interferon-beta biosynthetic process	BP	0.654	TLR4,TLR3	up_VCAV_EC
GO:0036462	0.0229	0.999	2	4	TRAIL-activated apoptotic signaling pathway	BP	0.654	ATF3,CASP8	up_VCAV_EC
GO:0045350	0.0229	0.999	2	3	interferon-beta biosynthetic process	BP	0.654	TLR4,TLR3	up_VCAV_EC
GO:0060760	0.0229	1	1	17	positive regulation of response to cytokine	BP	1	TLR2	up_AFEM_VSMC
GO:0060411	0.0229	1	1	33	cardiac septum morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:1901652	0.022940365	0.99278	7	105	response to peptide	BP	0.96436359	NR1H4,ENSCAFG00000004331,NOD2,ACTN2,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0014902	0.023	0.993	7	34	myotube differentiation	BP	0.654	MEF2C,PPP3CA,MTOR,CAV2,ENSCAFG00000010596,P2RX2,CDON	up_VCAV_EC
GO:0001913	0.023	0.997	3	10	T cell mediated cytotoxicity	BP	0.654	IL7R,RAB27A,NECTIN2	up_VCAV_EC
GO:0051694	0.023	0.999	2	4	pointed-end actin filament capping	BP	0.654	TMOD1,TMOD3	up_VCAV_EC
GO:0044089	0.023	0.999	2	170	positive regulation of cellular component	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0021855	0.023	1	1	4	hypothalamus cell migration	BP	0.959	NRP2	down_ACOR_EC
GO:0001659	0.023	1	1	54	temperature homeostasis	BP	1	PLCL1	down_VFEM_EC
GO:0021695	0.023	1	1	20	cerebellar cortex development	BP	1	WNT7A	up_AORT_VSMC
GO:0003197	0.023	1	1	16	endocardial cushion development	BP	1	GATA5	up_VCAV_VSMC
GO:0060677	0.023	1	1	6	ureteric bud elongation	BP	1	SIX1	up_VFEM_EC
GO:0045019	0.023	1	1	5	negative regulation of nitric oxide biosynthetic	BP	1	CAV1	up_VSAP_VSMC
GO:1901017	0.023	1	1	5	negative regulation of potassium ion transmembrane	BP	1	CAV1	up_VSAP_VSMC
GO:1901380	0.023	1	1	5	negative regulation of potassium ion	BP	1	CAV1	up_VSAP_VSMC
GO:1904406	0.023	1	1	5	negative regulation of nitric oxide metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0006541	0.023079055	0.99855	2	9	glutamine metabolic process	BP	0.96436359	NR1H4,NIT2	up_ACOR_EC
GO:0043271	0.0231	0.994	6	28	negative regulation of ion transport	BP	0.801	NEDD4,HOXA3,CAV1,SLC30A1,GSTO1,REM1	down_ACOR_VSMC
GO:0032755	0.0231	0.994	6	24	positive regulation of interleukin-6 production	BP	1	IL6R,IL17RC,F2RL1,MYD88,CYBA,MAVS	up_VSAP_EC

GO:0001974	0.0231	0.996	4	13	blood vessel remodeling	BP	0.656	MEF2C,CHD7,DLL4,JAG1	up_VCAV_EC
GO:0021615	0.0231	0.999	2	3	glossopharyngeal nerve morphogenesis	BP	1	HOXD3,PLXNA4	up_VSAP_EC
GO:0051924	0.0231	0.998	2	53	regulation of calcium ion transport	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0021503	0.0231	1	1	1	neural fold bending	BP	1	LUZP1	up_AFEM_EC
GO:1903524	0.0231	1	1	11	positive regulation of blood circulation	BP	1	NKX2-5	up_VPOR_VSMC
GO:1905517	0.0231	1	1	10	macrophage migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0010831	0.0231	1	1	9	positive regulation of myotube differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:2000738	0.023101052	0.99855	2	9	positive regulation of stem cell differentiation	BP	0.96436359	SOX9,TBX5	up_ACOR_EC
GO:0033673	0.023127166	0.9935	6	84	negative regulation of kinase activity	BP	0.96436359	PKIB,DUSP26,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0090399	0.0232	0.999	2	4	replicative senescence	BP	0.735	SERPINE1,CDKN1A	down_VSAP_EC
GO:0048232	0.0232	0.998	2	95	male gamete generation	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0045605	0.0232	1	1	5	negative regulation of epidermal cell	BP	0.966	HOXA7	down_ACOR_EC
GO:0008343	0.0232	1	1	1	adult feeding behavior	BP	1	LEP	up_AFEM_EC
GO:1904478	0.0232	1	1	1	regulation of intestinal absorption	BP	1	LEP	up_AFEM_EC
GO:1904729	0.0232	1	1	1	regulation of intestinal lipid absorption	BP	1	LEP	up_AFEM_EC
GO:0030300	0.0232	1	1	1	regulation of intestinal cholesterol absorption	BP	1	LEP	up_AFEM_EC
GO:0032817	0.0232	1	1	1	regulation of natural killer cell proliferation	BP	1	LEP	up_AFEM_EC
GO:0070093	0.0232	1	1	1	negative regulation of glucagon secretion	BP	1	LEP	up_AFEM_EC
GO:0060004	0.0232	1	1	6	reflex	BP	1	NPNT	up_APUL_EC
GO:0021756	0.0232	1	1	6	striatum development	BP	1	SLITRK5	up_APUL_EC
GO:0055083	0.0232	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0035542	0.0232	1	1	6	regulation of SNARE complex assembly	BP	1	TRIM9	up_VFEM_EC
GO:0032682	0.0232	1	1	7	negative regulation of chemokine production	BP	1	NR1H4	up_VPUL_EC
GO:0051270	0.0233	0.99	13	296	regulation of cellular component movement	BP	1	CMKLR1,ANGPT4,HOXA7,PLXNA4,TWIST2,CAMK2A,LRRC15,RECK,TBXA2R,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0050707	0.0233	0.992	9	44	regulation of cytokine secretion	BP	1	TLR1,HTR2B,MBP,FERMT1,CD274,F2RL1,PTPN22,NOD2,SCAMP5	up_ACOR_VSMC
GO:0043619	0.0233	0.999	2	4	regulation of transcription from RNA polymerase II promoter in response to	BP	0.738	SESN2,HIF1A	down_VSAP_EC
GO:0072503	0.0233	0.998	2	97	cellular divalent inorganic cation homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:1903706	0.0233	0.998	2	119	regulation of hemopoiesis	BP	1	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0042391	0.0233	1	1	81	regulation of membrane potential	BP	1	JUP	down_VFEM_VSMC
GO:0030850	0.0233	1	1	20	prostate gland development	BP	1	ESR1	up_AORT_VSMC
GO:0016486	0.0233	1	1	6	peptide hormone processing	BP	1	PCSK1N	up_APUL_EC
GO:0048843	0.0233	1	1	3	negative regulation of axon extension involved in axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0035239	0.0234	0.987	23	299	tube morphogenesis	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,SDC4,BMPR1A,LOX,LMO4,ANPEP,CLSTN1,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,IFT57,CDH2,SPRED1,SHC1,RDH10,GREM1,CLIC4	down_VCAV_EC
GO:0044271	0.0234	0.993	8	1501	cellular nitrogen compound biosynthetic	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048871	0.0234	0.993	7	120	multicellular organismal homeostasis	BP	1	CMKLR1,HOXC10,LEP,DLL1,ACACB,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:0045639	0.0234	0.995	5	33	positive regulation of myeloid cell	BP	1	CLSTN1,ZFP36L1,RAB7B,FOXO3,ANKRD54	down_VCAV_EC
GO:1903393	0.0234	0.997	3	11	positive regulation of adherens junction	BP	0.738	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC

GO:1903707	0.0234	0.998	2	48	negative regulation of hemopoiesis	BP	0.966	LYN,HOXA7	down_ACOR_EC
GO:0052547	0.0234	1	1	82	regulation of peptidase activity	BP	1	CST3	down_AORT_EC
GO:0072659	0.0234	1	1	82	protein localization to plasma membrane	BP	1	JUP	down_VFEM_VSMC
GO:0071307	0.0234	1	1	1	cellular response to vitamin K	BP	1	POSTN	up_AFEM_EC
GO:2000393	0.0234	1	1	1	negative regulation of lamellipodium	BP	1	KANK1	up_AFEM_EC
GO:0035624	0.0234	1	1	1	receptor transactivation	BP	1	ADAM17	up_AFEM_EC
GO:0051088	0.0234	1	1	1	PMA-inducible membrane protein ectodomain	BP	1	ADAM17	up_AFEM_EC
GO:0071403	0.0234	1	1	1	cellular response to high density lipoprotein	BP	1	ADAM17	up_AFEM_EC
GO:1901098	0.0234	1	1	1	positive regulation of autophagosome	BP	1	CLEC16A	up_AFEM_EC
GO:1904766	0.0234	1	1	1	negative regulation of macroautophagy by TORC1 signaling	BP	1	CLEC16A	up_AFEM_EC
GO:0001708	0.0234	1	1	20	cell fate specification	BP	1	HOXC10	up_AORT_VSMC
GO:0007625	0.0234	1	1	6	grooming behavior	BP	1	SLITRK5	up_APUL_EC
GO:0060385	0.0234	1	1	3	axonogenesis involved in innervation	BP	1	SEMA3A	up_VPOR_EC
GO:0010002	0.0234	1	1	9	cardioblast differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:1901164	0.023417454	1	1	1	negative regulation of trophoblast cell migration	BP	0.96436359	ARHGDIB	up_ACOR_EC
GO:0050706	0.023461357	0.99852	2	9	regulation of interleukin-1 beta secretion	BP	0.96436359	FZD5,NOD2	up_ACOR_EC
GO:0033365	0.0235	0.986	33	276	protein localization to organelle	BP	0.814	SREBF1,RPA1,NEDD4,ZW10,CENPA,TIMM44,POLA2,CTDNEP1,RAN,INSIG1,CDK1,NF2,AURKB,EZH2,ENSCAFG00000011598,TRAM1,NDC80,IPO4,NUP62,NUP188,HASPIN,TOMM34,SAMM50,DMAP1,RAB35,EZR,TTK,KNL1,PMPCA,TINF2,CCT4,SIX4,MTBP	down_ACOR_VSMC
GO:2000026	0.0235	0.987	21	560	regulation of multicellular organismal development	BP	1	HOXA9,IRX3,LEP,LBH,ANGPT4,HOXA7,DLL1,F3,PLXNA4,THRB,LGI4,TMEM100,GREM1,CAMK2A,CYLD,PTHLH,TBXA2R,EVI2B,AXIN2,ACACB,KANK1	up_AFEM_EC
GO:0070838	0.0235	0.989	14	96	divalent metal ion transport	BP	0.663	CALCRL,PDGFB,ATP2B1,PDE4D,CHD7,STC1,APLNR,SLC39A8,PPP3CA,KCNJ2,SLC25A25,PLCG2,MCU,ATP2A1	up_VCAV_EC
GO:0097581	0.0235	0.994	6	26	lamellipodium organization	BP	0.662	KIT,MTOR,NCKAP1,SNX2,NCK1,FSCN1	up_VCAV_EC
GO:0045859	0.0235	0.996	4	219	regulation of protein kinase activity	BP	0.966	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0033619	0.0235	0.996	4	19	membrane protein proteolysis	BP	0.738	MYH9,HM13,ADAM17,APOE	down_VSAP_EC
GO:0048704	0.0235	0.995	4	46	embryonic skeletal system morphogenesis	BP	1	TBX15,IRX5,HOXA7,HOXA6	up_AFEM_EC
GO:0015682	0.0235	0.998	3	7	ferric iron transport	BP	1	RAB11B,LMTK2,B2M	up_ACOR_VSMC
GO:0072512	0.0235	0.998	3	7	trivalent inorganic cation transport	BP	1	RAB11B,LMTK2,B2M	up_ACOR_VSMC
GO:0045597	0.0235	0.997	3	253	positive regulation of cell differentiation	BP	1	NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0051252	0.0235	1	2	1051	regulation of RNA metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1902946	0.0235	0.999	2	4	protein localization to early endosome	BP	0.738	MSN,NRP1	down_VSAP_EC
GO:2001199	0.0235	0.999	2	3	negative regulation of dendritic cell	BP	1	TMEM176B,TMEM176A	up_ACOR_VSMC
GO:0072008	0.0235	0.999	2	4	glomerular mesangial cell differentiation	BP	0.662	PDGFB,GPR4	up_VCAV_EC
GO:0072144	0.0235	0.999	2	4	glomerular mesangial cell development	BP	0.662	PDGFB,GPR4	up_VCAV_EC
GO:0070838	0.0235	0.998	2	96	divalent metal ion transport	BP	1	HOXA3,TRPC4	up_VPOR_VSMC
GO:1900151	0.0235	0.999	2	3	regulation of nuclear-transcribed mRNA catabolic process,	BP	1	ZFP36L2,TNRC6C	up_VSAP_EC
GO:1900153	0.0235	0.999	2	3	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	ZFP36L2,TNRC6C	up_VSAP_EC

GO:0060513	0.0235	1	1	5	prostatic bud formation	BP	0.966	SULF1	down_ACOR_EC
GO:0034330	0.0235	1	1	80	cell junction organization	BP	1	JUP	down_VFEM_VSMC
GO:0060244	0.0235	1	1	1	negative regulation of cell proliferation involved in contact inhibition	BP	1	FAP	up_AFEM_EC
GO:1902362	0.0235	1	1	1	melanocyte apoptotic process	BP	1	FAP	up_AFEM_EC
GO:0010710	0.0235	1	1	1	regulation of collagen catabolic process	BP	1	FAP	up_AFEM_EC
GO:0010716	0.0235	1	1	1	negative regulation of extracellular matrix	BP	1	FAP	up_AFEM_EC
GO:0016925	0.0235	1	1	16	protein sumoylation	BP	1	EYA1	up_AFEM_VSMC
GO:0035774	0.0235	1	1	6	positive regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_APUL_EC
GO:0140059	0.0235	1	1	3	dendrite arborization	BP	1	SEMA3A	up_VPOR_EC
GO:0061550	0.0235	1	1	6	cranial ganglion development	BP	1	SIX1	up_VFEM_EC
GO:0071599	0.0235	1	1	9	otic vesicle development	BP	1	EYA1	up_VFEM_VSMC
GO:0003181	0.0235	1	1	7	atrioventricular valve morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0086005	0.0235	1	1	5	ventricular cardiac muscle cell action potential	BP	1	CAV1	up_VSAP_VSMC
GO:0002690	0.0236	0.997	3	26	positive regulation of leukocyte chemotaxis	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:2000026	0.0236	0.997	3	560	regulation of multicellular organismal development	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0098780	0.0236	0.998	3	7	response to mitochondrial depolarisation	BP	1	AMBRA1,MFN2,HTRA2	up_VSAP_EC
GO:0046688	0.0236	0.999	2	5	response to copper ion	BP	1	PRNP,PARK7	down_VCAV_EC
GO:0035907	0.0236	1	1	5	dorsal aorta development	BP	0.966	ACVRL1	down_ACOR_EC
GO:0035912	0.0236	1	1	5	dorsal aorta morphogenesis	BP	0.966	ACVRL1	down_ACOR_EC
GO:0001757	0.0236	1	1	1	somite specification	BP	1	DLL1	up_AFEM_EC
GO:0002085	0.0236	1	1	1	inhibition of neuroepithelial cell	BP	1	DLL1	up_AFEM_EC
GO:1901860	0.0236	1	1	1	positive regulation of mitochondrial DNA metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0007386	0.0236	1	1	1	compartment pattern specification	BP	1	DLL1	up_AFEM_EC
GO:0014807	0.0236	1	1	1	regulation of somitogenesis	BP	1	DLL1	up_AFEM_EC
GO:0021688	0.0236	1	1	1	cerebellar molecular layer formation	BP	1	DLL1	up_AFEM_EC
GO:0021693	0.0236	1	1	1	cerebellar Purkinje cell layer structural	BP	1	DLL1	up_AFEM_EC
GO:0021698	0.0236	1	1	1	cerebellar cortex structural organization	BP	1	DLL1	up_AFEM_EC
GO:0045168	0.0236	1	1	1	cell-cell signaling involved in cell fate commitment	BP	1	DLL1	up_AFEM_EC
GO:0045608	0.0236	1	1	1	negative regulation of inner ear auditory receptor cell	BP	1	DLL1	up_AFEM_EC
GO:0045632	0.0236	1	1	1	negative regulation of mechanoreceptor	BP	1	DLL1	up_AFEM_EC
GO:0046331	0.0236	1	1	1	lateral inhibition	BP	1	DLL1	up_AFEM_EC
GO:0048630	0.0236	1	1	1	skeletal muscle tissue growth	BP	1	DLL1	up_AFEM_EC
GO:0048631	0.0236	1	1	1	regulation of skeletal muscle tissue growth	BP	1	DLL1	up_AFEM_EC
GO:0048633	0.0236	1	1	1	positive regulation of skeletal muscle tissue	BP	1	DLL1	up_AFEM_EC
GO:0060853	0.0236	1	1	1	Notch signaling pathway involved in arterial endothelial cell fate	BP	1	DLL1	up_AFEM_EC
GO:0097102	0.0236	1	1	1	endothelial tip cell fate specification	BP	1	DLL1	up_AFEM_EC
GO:2000981	0.0236	1	1	1	negative regulation of inner ear receptor cell	BP	1	DLL1	up_AFEM_EC

GO:0010984	0.0236	1	1	6	regulation of lipoprotein particle clearance	BP	1	NR1H4	up_APUL_EC
GO:0032692	0.0236	1	1	6	negative regulation of interleukin-1 production	BP	1	NR1H4	up_APUL_EC
GO:0055090	0.0236	1	1	6	acylglycerol homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0070328	0.0236	1	1	6	triglyceride homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0051496	0.0236	1	1	17	positive regulation of stress fiber assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0030217	0.0237	0.99	11	65	T cell differentiation	BP	0.665	IL7R,KIT,IL6,CHD7,DLL4,GATA3,MTOR,ITPKB,HMGB1,BMX,ZEB1	up_VCAV_EC
GO:0007166	0.0237	0.995	5	686	cell surface receptor signaling pathway	BP	1	FGF5,BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0002521	0.0237	0.997	3	149	leukocyte differentiation	BP	1	TOX,HOXA7,CYP26B1	up_VFEM_EC
GO:0016321	0.0237	0.999	2	3	female meiosis chromosome segregation	BP	0.814	NCAPH,TTK	down_ACOR_VSMC
GO:0097421	0.0237	0.999	2	3	liver regeneration	BP	0.814	EZH2,GLI1	down_ACOR_VSMC
GO:0043587	0.0237	0.999	2	4	tongue morphogenesis	BP	0.74	CTNNB1,SIX4	down_VSAP_EC
GO:0001921	0.0237	0.999	2	3	positive regulation of receptor recycling	BP	1	PSEN1,BVES	up_ACOR_VSMC
GO:1902259	0.0237	0.999	2	3	regulation of delayed rectifier potassium	BP	1	KCNE3,AKAP6	up_ACOR_VSMC
GO:0006120	0.0237	1	1	12	mitochondrial electron transport, NADH to	BP	1	NDUFA10	down_AFEM_EC
GO:2000008	0.0237	1	1	12	regulation of protein localization to cell surface	BP	1	RAB11B	down_VPOR_EC
GO:0006589	0.0237	1	1	1	octopamine biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0014722	0.0237	1	1	1	regulation of skeletal muscle contraction by calcium ion signaling	BP	1	DMPK	up_AFEM_EC
GO:0014852	0.0237	1	1	1	regulation of skeletal muscle contraction by neural stimulation via	BP	1	DMPK	up_AFEM_EC
GO:0014853	0.0237	1	1	1	regulation of excitatory postsynaptic membrane potential involved in skeletal muscle	BP	1	DMPK	up_AFEM_EC
GO:0046333	0.0237	1	1	1	octopamine metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0051823	0.0237	1	1	1	regulation of synapse structural plasticity	BP	1	DMPK	up_AFEM_EC
GO:0007095	0.0237	1	1	11	mitotic G2 DNA damage checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0061180	0.0237	1	1	20	mammary gland epithelium development	BP	1	ESR1	up_AORT_VSMC
GO:0032642	0.0237	1	1	22	regulation of chemokine production	BP	1	ARG2	up_AORT_VSMC
GO:0010804	0.0237	1	1	6	negative regulation of tumor necrosis factor-mediated signaling	BP	1	NR1H4	up_APUL_EC
GO:0018195	0.0237	1	1	6	peptidyl-arginine modification	BP	1	NR1H4	up_APUL_EC
GO:0003161	0.0237	1	1	6	cardiac conduction system development	BP	1	TBX5	up_APUL_EC
GO:0002526	0.0237	1	1	17	acute inflammatory response	BP	1	C6	up_VCAV_VSMC
GO:1900120	0.0237	1	1	7	regulation of receptor binding	BP	1	HOXA3	up_VPUL_EC
GO:0035115	0.0237	1	1	12	embryonic forelimb morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0040008	0.0238	0.986	26	179	regulation of growth	BP	1	LEP,DCBLD2,BMP4,CRIM1,FGFR2,GJA1,LATS2,RERG,ATRN,PLAC8B,CDKN1A,CRLF3,NRP1,ULK2,TBX20,TBX5,APP,CHD7,WWC2,EDN1,FAM107A,IGFBP7,WFS1,NAIF1,SH3BP4,STC2	up_ACOR_VSMC
GO:0035107	0.0238	0.99	11	60	appendage morphogenesis	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4	up_VSAP_EC
GO:0035108	0.0238	0.99	11	60	limb morphogenesis	BP	1	HOXA11,HOXA9,OSR2,OSR1,ZBTB16,RARG,RECK,FBXW4,SHOX2,HOXC10,LRP4	up_VSAP_EC
GO:0035384	0.0238	0.996	4	14	thioester biosynthetic process	BP	0.814	ACLY,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0071616	0.0238	0.996	4	14	acyl-CoA biosynthetic process	BP	0.814	ACLY,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:2001222	0.0238	0.996	4	11	regulation of neuron migration	BP	0.666	RELN,RAPGEF2,ARHGEF2,ZNF609	up_VCAV_EC

GO:0072359	0.0238	0.999	2	368	circulatory system development	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0022617	0.0238	1	1	11	extracellular matrix disassembly	BP	1	FSCN1	down_AFEM_EC
GO:0002541	0.0238	1	1	1	activation of plasma proteins involved in acute inflammatory response	BP	1	F3	up_AFEM_EC
GO:0010641	0.0238	1	1	1	positive regulation of platelet-derived growth factor receptor signaling	BP	1	F3	up_AFEM_EC
GO:0006478	0.0238	1	1	1	peptidyl-tyrosine sulfation	BP	1	TPST2	up_AFEM_EC
GO:0007338	0.0238	1	1	16	single fertilization	BP	1	HOXA9	up_AFEM_VSMC
GO:0010889	0.0238	1	1	3	regulation of sequestering of triglyceride	BP	1	ABHD5	up_VPOR_EC
GO:0006654	0.0238	1	1	7	phosphatidic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0046473	0.0238	1	1	7	phosphatidic acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:1905314	0.0238	1	1	12	semi-lunar valve development	BP	1	GATA5	up_VPUL_VSMC
GO:0006950	0.0239	0.982	109	1102	response to stress	BP	0.666	ACKR1,EPHB1,PLK2,GBP5,SELP,KIT,LYZ,PRCP,CXCL8,F8,IFRD1,CXCR4,IL6,TNFAIP3,MAP3K11,TNIP1,LRRC8D,MX2,PDGFB,BCL6B,STK10,SH2D3C,TMEM173,RELN,VWF,CD34,MEF2C,ATF3,KLKB1,TLR4,NLRC5,GPR4,GATA3,EDN1,RALB,RAB27A,PTGS1,TFPI,PSME4,IRF8,FIGNL1,PELI1,PPP3CA,SERINC5,MTSS1,ARG2,NECTIN2,MTOR,SNAP23,MMRN1,ELF4,MAP3K3,BMP2,SLK,ABCA1,MAPK13,RIOK3,FLNB,PAK2,THOC1,TLR3,OAS3,APOD,NCK1,TIMELESS,OTUD4,PDIA5,FES,GUCY1B1,PTGS2,ETAA1,BCL10,USP28,TAOK1,CNOT7,GCH1,ENSCAFG00000002897,ASF1A,ADIPOR2,HMGB1,NOS2,PMAIP1,BLM,RIPK1,SMC5,LSM14A,USP13,RAD21,RAD17,SKIL,PDGFD,CUL4A,BMX,NR1D2,ENSCAFG00000025410,HIF1A,ALS2,ITGB3,ATRX,HP1BP3,TOPBP1,P2RX2,RBBP6,VASH1,ATP2A1,ARHGEF2,PEAR1,ELK3,GINS4	up_VCAV_EC
GO:0032434	0.0239	0.992	8	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	0.744	PRICKLE1,PLK3,SOCS5,TRIB3,UCHL5,GSK3B,RAD23A,USP14	down_VSAP_EC
GO:0009966	0.0239	0.993	7	868	regulation of signal transduction	BP	1	NR1H4,RGS1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1904018	0.0239	0.994	5	69	positive regulation of vasculature development	BP	1	ANGPT4,DLL1,F3,TMEM100,GREM1	up_AFEM_EC
GO:0032757	0.0239	0.996	4	14	positive regulation of interleukin-8 production	BP	0.666	PRKD2,TLR3,BCL10,RIPK1	up_VCAV_EC
GO:1901575	0.0239	0.999	2	643	organic substance catabolic process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0097475	0.0239	0.999	2	4	motor neuron migration	BP	0.744	VEGFA,NRP1	down_VSAP_EC
GO:0003129	0.0239	0.999	2	3	heart induction	BP	1	GATA5,BMP4	up_ACOR_VSMC
GO:0042487	0.0239	0.999	2	3	regulation of odontogenesis of dentin-containing tooth	BP	1	BMP4,TNFRSF11B	up_ACOR_VSMC
GO:0000132	0.0239	1	1	11	establishment of mitotic spindle orientation	BP	1	GPSM2	down_AFEM_EC
GO:0051294	0.0239	1	1	11	establishment of spindle orientation	BP	1	GPSM2	down_AFEM_EC
GO:0015739	0.0239	1	1	1	sialic acid transport	BP	1	SLC17A5	up_AFEM_EC
GO:0099148	0.0239	1	1	1	regulation of synaptic vesicle docking	BP	1	CAMK2A	up_AFEM_EC
GO:0106020	0.0239	1	1	1	regulation of vesicle docking	BP	1	CAMK2A	up_AFEM_EC
GO:1990443	0.0239	1	1	1	peptidyl-threonine autophosphorylation	BP	1	CAMK2A	up_AFEM_EC
GO:0007619	0.0239	1	1	1	courtship behavior	BP	1	THRB	up_AFEM_EC
GO:0007621	0.0239	1	1	1	negative regulation of female receptivity	BP	1	THRB	up_AFEM_EC
GO:0008050	0.0239	1	1	1	female courtship behavior	BP	1	THRB	up_AFEM_EC
GO:0016081	0.0239	1	1	1	synaptic vesicle docking	BP	1	CAMK2A	up_AFEM_EC
GO:0034378	0.0239	1	1	1	chylomicron assembly	BP	1	PLAGL2	up_AFEM_EC

GO:0042480	0.0239	1	1	1	negative regulation of eye photoreceptor cell	BP	1	THRB	up_AFEM_EC
GO:0045924	0.0239	1	1	1	regulation of female receptivity	BP	1	THRB	up_AFEM_EC
GO:0060040	0.0239	1	1	1	retinal bipolar neuron differentiation	BP	1	IRX5	up_AFEM_EC
GO:0060180	0.0239	1	1	1	female mating behavior	BP	1	THRB	up_AFEM_EC
GO:0097474	0.0239	1	1	1	retinal cone cell apoptotic process	BP	1	THRB	up_AFEM_EC
GO:0034121	0.0239	1	1	22	regulation of toll-like receptor signaling	BP	1	ESR1	up_AORT_VSMC
GO:1900543	0.0239	1	1	9	negative regulation of purine nucleotide	BP	1	FBP1	up_VFEM_VSMC
GO:1903579	0.0239	1	1	9	negative regulation of ATP metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0033238	0.0239	1	1	7	regulation of cellular amine metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0060973	0.0239	1	1	7	cell migration involved in heart development	BP	1	FLRT3	up_VPUL_EC
GO:0061323	0.0239	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0002686	0.0239	1	1	12	negative regulation of leukocyte migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0030030	0.024	0.985	33	377	cell projection organization	BP	0.744	SIPA1L1,SGK1,PTPN11,EXOC5,FSCN1,DPYSL3,IFRD1,ILK,RPGR,KIF5B,DYNLL1,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,ANLN,APOE,KLF5,LYN,GSK3B,VLDLR,SDC4,HTT,PRMT1,EXT1,DISC1,PAK2,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0009058	0.024	0.991	14	1910	biosynthetic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0032409	0.024	0.991	10	52	regulation of transporter activity	BP	1	ACTN2,PLCG2,KCNE3,TCAF1,PTPN3,DAPK1,CACNB3,AKAP6,FXYD1,PARK7	up_ACOR_VSMC
GO:1902652	0.024	0.992	8	38	secondary alcohol metabolic process	BP	1	LIPC,INSIG2,LMF1,LCAT,MVK,LIPE,CYB5R3,SOAT1	up_VSAP_EC
GO:0060487	0.024	0.998	3	7	lung epithelial cell differentiation	BP	1	THRB,SAV1,NFIB	up_VSAP_EC
GO:0090647	0.024	0.999	2	3	modulation of age-related behavioral decline	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0071242	0.024	1	1	11	cellular response to ammonium ion	BP	1	GABPA	down_AFEM_EC
GO:0002118	0.024	1	1	1	aggressive behavior	BP	1	GCNT4	up_AFEM_EC
GO:0002121	0.024	1	1	1	inter-male aggressive behavior	BP	1	GCNT4	up_AFEM_EC
GO:0034769	0.024	1	1	1	basement membrane disassembly	BP	1	CTSS	up_AFEM_EC
GO:0060037	0.024	1	1	9	pharyngeal system development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010591	0.024	1	1	12	regulation of lamellipodium assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0048731	0.0241	0.994	7	1247	system development	BP	1	HOXC10,EYA1,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0055008	0.0241	0.994	6	24	cardiac muscle tissue morphogenesis	BP	1	TNNT2,FGFR2,ANKRD1,EGLN1,TBX20,CHD7	up_ACOR_VSMC
GO:0032069	0.0241	0.997	3	8	regulation of nuclease activity	BP	0.822	HMGB1,PCNA,HMGB2	down_ACOR_VSMC
GO:0001504	0.0241	0.998	3	7	neurotransmitter uptake	BP	1	PSEN1,CLN8,PARK7	up_ACOR_VSMC
GO:0072511	0.0241	0.998	2	97	divalent inorganic cation transport	BP	1	HOXA3,TRPC4	up_VPOR_VSMC
GO:0033157	0.0241	1	1	82	regulation of intracellular protein transport	BP	1	JUP	down_VFEM_VSMC
GO:0001992	0.0241	1	1	1	regulation of systemic arterial blood pressure by	BP	1	AVPR1A	up_AFEM_EC
GO:0055089	0.0241	1	1	7	fatty acid homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0060546	0.0241	1	1	7	negative regulation of necroptotic process	BP	1	ARHGEF2	up_VPUL_EC
GO:0060547	0.0241	1	1	7	negative regulation of necrotic cell death	BP	1	ARHGEF2	up_VPUL_EC
GO:2000136	0.0241	1	1	7	regulation of cell proliferation involved in	BP	1	TBX5	up_VPUL_EC
GO:0120033	0.0241	1	1	12	negative regulation of plasma membrane bounded cell projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0046328	0.024157669	0.99413	5	61	regulation of JNK cascade	BP	0.96436359	FZD5,NOD2,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC

GO:0015791	0.024182689	1	1	1	polyol transport	BP	0.96436359	AQP1	up_ACOR_EC
GO:0015793	0.024182689	1	1	1	glycerol transport	BP	0.96436359	AQP1	up_ACOR_EC
GO:0035377	0.024182689	1	1	1	transepithelial water transport	BP	0.96436359	AQP1	up_ACOR_EC
GO:0035378	0.024182689	1	1	1	carbon dioxide transmembrane transport	BP	0.96436359	AQP1	up_ACOR_EC
GO:0046878	0.024182689	1	1	1	positive regulation of saliva secretion	BP	0.96436359	AQP1	up_ACOR_EC
GO:0051458	0.024182689	1	1	1	corticotropin secretion	BP	0.96436359	AQP1	up_ACOR_EC
GO:0071288	0.024182689	1	1	1	cellular response to mercury ion	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072019	0.024182689	1	1	1	proximal convoluted tubule development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072020	0.024182689	1	1	1	proximal straight tubule development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072022	0.024182689	1	1	1	descending thin limb development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072032	0.024182689	1	1	1	proximal convoluted tubule segment 2	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072220	0.024182689	1	1	1	metanephric descending thin limb development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072229	0.024182689	1	1	1	metanephric proximal convoluted tubule	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072230	0.024182689	1	1	1	metanephric proximal straight tubule	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072232	0.024182689	1	1	1	metanephric proximal convoluted tubule	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072236	0.024182689	1	1	1	metanephric loop of Henle development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0072237	0.024182689	1	1	1	metanephric proximal tubule development	BP	0.96436359	AQP1	up_ACOR_EC
GO:0085018	0.024182689	1	1	1	maintenance of symbiont-containing vacuole by	BP	0.96436359	AQP1	up_ACOR_EC
GO:0070207	0.0242	0.997	3	7	protein homotrimerization	BP	1	SCARA5,CLYBL,HTRA2	up_VSAP_EC
GO:0090521	0.0242	0.999	2	3	glomerular visceral epithelial cell migration	BP	0.823	ANLN,NUP188	down_ACOR_VSMC
GO:0001525	0.0242	0.998	2	173	angiogenesis	BP	1	C6,TGFBI	up_VCAV_VSMC
GO:0003163	0.0242	1	1	1	sinoatrial node development	BP	1	BVES	up_AFEM_EC
GO:0060931	0.0242	1	1	1	sinoatrial node cell development	BP	1	BVES	up_AFEM_EC
GO:0007174	0.0242	1	1	1	epidermal growth factor catabolic process	BP	1	RAB7A	up_AFEM_EC
GO:0060921	0.0242	1	1	1	sinoatrial node cell differentiation	BP	1	BVES	up_AFEM_EC
GO:0051965	0.0242	1	1	17	positive regulation of synapse assembly	BP	1	SLITRK5	up_VCAV_VSMC
GO:1900122	0.0242	1	1	3	positive regulation of receptor binding	BP	1	HOXA3	up_VPOR_EC
GO:0071696	0.0242	1	1	6	ectodermal placode development	BP	1	SIX1	up_VFEM_EC
GO:0060548	0.024207215	0.98875	14	294	negative regulation of cell death	BP	0.96436359	NR1H4,SOX9,AQP1,IFI6,SMAD6,BCL2,MAPK8IP2,FOXC2,FIGNL1,CLU,CHMP4B,NRP1,PRKCD,PM20D1	up_ACOR_EC
GO:2001236	0.0243	0.992	8	59	regulation of extrinsic apoptotic signaling	BP	0.753	ARHGEF2,SERPINE1,ATF3,HTT,PAK2,INHBA,NRP1,MADD	down_VSAP_EC
GO:0045661	0.0243	0.995	5	18	regulation of myoblast differentiation	BP	1	CDON,BTG1,DLL1,MAP3K5,ZFP36L1	up_VSAP_EC
GO:0006351	0.0243	1	2	1069	transcription, DNA-templated	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0055118	0.0243	0.999	2	3	negative regulation of cardiac muscle	BP	1	KCNE3,PDE5A	up_ACOR_VSMC
GO:0001101	0.0243	0.998	2	65	response to acid chemical	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0070167	0.0243	0.998	2	29	regulation of biomineral tissue development	BP	1	ASPN,ACVR2A	up_VPOR_EC
GO:0006376	0.0243	1	1	11	mRNA splice site selection	BP	1	SRSF6	down_AFEM_EC
GO:0032596	0.0243	1	1	1	protein transport into membrane raft	BP	1	REEP2	up_AFEM_EC
GO:0050913	0.0243	1	1	1	sensory perception of bitter taste	BP	1	REEP2	up_AFEM_EC
GO:0050916	0.0243	1	1	1	sensory perception of sweet taste	BP	1	REEP2	up_AFEM_EC

GO:0051729	0.0243	1	1	1	germline cell cycle switching, mitotic to	BP	1	OVOL1	up_AFEM_EC
GO:0048874	0.0243	1	1	1	host-mediated regulation of intestinal microbiota	BP	1	NAPEPLD	up_AFEM_EC
GO:0051728	0.0243	1	1	1	cell cycle switching, mitotic to meiotic cell	BP	1	OVOL1	up_AFEM_EC
GO:0060184	0.0243	1	1	1	cell cycle switching	BP	1	OVOL1	up_AFEM_EC
GO:0070291	0.0243	1	1	1	N-acylethanolamine metabolic process	BP	1	NAPEPLD	up_AFEM_EC
GO:0070292	0.0243	1	1	1	N-acylphosphatidylethanola	BP	1	NAPEPLD	up_AFEM_EC
GO:0022603	0.0244	0.984	40	301	regulation of anatomical structure morphogenesis	BP	1	VEGFD,LEP,GATA5,CDC7,MBP,ZRANB1,MLLT3,BMP4,FGFR2,TLR3,SEC24B,WASF3,CITED2,ZNRF3,SASH1,FGF18,ZMYM2,LIMS2,MARCH5,BNIP3,EGLN1,NRP1,ULK2,TBX5,FZD3,FRS2,DAG1,PSEN1,SYNJ2BP,JUP,SIPA1L1,SSH3,EDN1,TNFRSF11B,DOCK5,ERAP1,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0051153	0.0244	0.993	6	28	regulation of striated muscle cell differentiation	BP	0.677	MEF2C,EDN1,MTOR,BMP2,PROX1,ENSCAFG00000010596	up_VCAV_EC
GO:0072604	0.0244	0.996	4	12	interleukin-6 secretion	BP	1	LEP,MBP,F2RL1,PTPN22	up_ACOR_VSMC
GO:0032467	0.0244	0.997	3	8	positive regulation of cytokinesis	BP	0.826	AURKB,CDC6,NUP62	down_ACOR_VSMC
GO:0050920	0.0244	0.998	2	53	regulation of chemotaxis	BP	0.994	LYN,STX4	down_ACOR_EC
GO:0032774	0.0244	1	2	1073	RNA biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0097659	0.0244	1	2	1072	nucleic acid-templated transcription	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0036376	0.0244	1	1	1	sodium ion export across plasma membrane	BP	1	FXYD1	up_AFEM_EC
GO:1903276	0.0244	1	1	1	regulation of sodium ion export across plasma	BP	1	FXYD1	up_AFEM_EC
GO:1903278	0.0244	1	1	1	positive regulation of sodium ion export across	BP	1	FXYD1	up_AFEM_EC
GO:0120163	0.0244	1	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_AFEM_VSMC
GO:0072393	0.0244	1	1	3	microtubule anchoring at microtubule organizing	BP	1	HOOK3	up_VPOR_EC
GO:0055023	0.0244	1	1	12	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0002790	0.024431716	0.99148	8	133	peptide secretion	BP	0.96436359	NR1H4,AQP1,KCNB1,FZD5,NOD2,PTGER4,PREB,MAVS	up_ACOR_EC
GO:0023056	0.0245	0.983	57	462	positive regulation of signaling	BP	1	ADRA1B,TLR1,LGR6,LEP,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,SKP2,NACC2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,TLR3,SH3RF2,PDE5A,CITED2,TP53INP1,SASH1,TMEM108,FGF18,CDKN2B,LIMS2,ANKRD1,F2RL1,BNIP3,CRLF3,CREBRF,NRP1,PTPN22,NPNT,UNC5B,PRKCE,FRS2,PARP9,APP,PSEN1,CCL5,DUSP22,SIAH1,EDN1,NOD2,FAM107A,DISC1,SH3RF3,SERINC3,MAP3K7,ENSCAFG00000029553,PARK7,IL18R1,BVES,CRKL	up_ACOR_VSMC
GO:0030334	0.0245	0.989	12	267	regulation of cell migration	BP	1	CMKLR1,ANGPT4,HOXA7,TWIST2,CAMK2A,LRRC15,RECK,TBXA2R,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0032534	0.0245	0.999	2	4	regulation of microvillus assembly	BP	0.756	FSCN1,KLF5	down_VSAP_EC
GO:0007525	0.0245	1	1	1	somatic muscle development	BP	1	HSPB2	up_AFEM_EC
GO:0002158	0.0245	1	1	1	osteoclast proliferation	BP	1	GREM1	up_AFEM_EC
GO:0002174	0.0245	1	1	1	mammary stem cell proliferation	BP	1	LBH	up_AFEM_EC
GO:0038098	0.0245	1	1	1	sequestering of BMP from receptor via BMP binding	BP	1	GREM2	up_AFEM_EC
GO:0046851	0.0245	1	1	1	negative regulation of bone remodeling	BP	1	GREM1	up_AFEM_EC
GO:0060300	0.0245	1	1	1	regulation of cytokine activity	BP	1	GREM2	up_AFEM_EC
GO:0090289	0.0245	1	1	1	regulation of osteoclast proliferation	BP	1	GREM1	up_AFEM_EC
GO:0090291	0.0245	1	1	1	negative regulation of osteoclast proliferation	BP	1	GREM1	up_AFEM_EC
GO:1904674	0.0245	1	1	1	positive regulation of somatic stem cell	BP	1	LBH	up_AFEM_EC

GO:1904675	0.0245	1	1	1	regulation of somatic stem cell division	BP	1	LBH	up_AFEM_EC
GO:1904677	0.0245	1	1	1	positive regulation of somatic stem cell division	BP	1	LBH	up_AFEM_EC
GO:2000035	0.0245	1	1	1	regulation of stem cell division	BP	1	LBH	up_AFEM_EC
GO:2000101	0.0245	1	1	1	regulation of mammary stem cell proliferation	BP	1	LBH	up_AFEM_EC
GO:2000103	0.0245	1	1	1	positive regulation of mammary stem cell	BP	1	LBH	up_AFEM_EC
GO:1901099	0.0245	1	1	10	negative regulation of signal transduction in	BP	1	EYA1	up_VFEM_VSMC
GO:2001240	0.0245	1	1	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_VFEM_VSMC
GO:0002755	0.0245	1	1	6	MyD88-dependent toll-like receptor signaling	BP	1	TLR2	up_VSAP_VSMC
GO:0050770	0.0246	0.992	8	39	regulation of axonogenesis	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,TTL,MAP2K2	up_VSAP_EC
GO:0032623	0.0246	0.994	5	21	interleukin-2 production	BP	0.68	TNFAIP3,PDE4D,GATA3,HOMER3,PRKD2	up_VCAV_EC
GO:0060284	0.0246	0.994	5	212	regulation of cell development	BP	1	HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0006984	0.0246	0.996	4	19	ER-nucleus signaling pathway	BP	0.759	HSPA5,PTPN2,DDIT3,GSK3B	down_VSAP_EC
GO:0060055	0.0246	0.997	3	8	angiogenesis involved in wound healing	BP	0.829	ADIPOR2,B4GALT1,PRCP	down_ACOR_VSMC
GO:0042255	0.0246	0.998	2	29	ribosome assembly	BP	1	RSL24D1,RPL10L	up_VPOR_EC
GO:0045602	0.0246	1	1	4	negative regulation of endothelial cell	BP	1	ACVRL1	down_ACOR_EC
GO:0050794	0.0247	0.98	321	3075	regulation of cellular process	BP	1	SYNPO2L,EXPH5,SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,DNAJC6,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,CASP10,IFNGR1,LEP,PLCL1,LBH,DCBLD2,MAP3K8,MID1,KCNE3,GATA5,BCL2,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,PCGF5,ENSCAFG00000016285,HTR2B,RASSF2,TCAF1,MEIS2,USP6NL,FNDC5,MBP,ZRANB1,FBXL20,C28H10orf71,PRDX4,RECK,LIPT2,FEZ1,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,LCAT,ZNF331,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,TM7SF3,FGFR2,TP53BP1,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TRPS1,TLR3,SH3RF2,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,RERG,GLRB,PKP4,ARHGAP29,CCNG2,ISG15,ZNRF3,ZNF782,CD274,ZNF365,PLPP2,MARCKSL1,AR,PTGIR,ZNF484,SASH1,GPR155,LMO4,GTF3C1,PTPN3,TMEM108,ZNF572,FGF18,FAM210B,ARHGEF26,NDRG2,P4HTM,TMX3,CHN2,CDKN2B,ADCY6,ZMYM2,ITPR1,GRK7,CST3,ZNF174,PLAC8B,KLHL20,LIMS2,BLNK,ANKRD1,PLEKHB2,F2RL1,ADGRL1,FAM129A,CAMK2D,MARCH5,PSEN2,PPP2R5E,ERO1B,DAPK1,PKNOX2,ARHGAP5,RBM4B,HKR1,BNIP3,EGLN1,NCEH1,AKAP6,CDK	up_ACOR_VSMC
GO:0006364	0.0247	0.989	13	87	rRNA processing	BP	0.831	NOP56,FBL,DIS3,NOC4L,RSL1D1,RRP1,ENSCAFG00000019620,NOP14,NOP58,ENSCAFG00000015189,EMG1,EXOSC5,NOB1	down_ACOR_VSMC
GO:0019395	0.0247	0.994	5	33	fatty acid oxidation	BP	1	AKT2,ACAA1,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:0050709	0.0247	0.994	5	28	negative regulation of protein secretion	BP	0.761	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0030154	0.0247	0.997	4	1040	cell differentiation	BP	1	HOXC10,HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:1903729	0.0247	0.997	3	7	regulation of plasma membrane organization	BP	1	AR,ASAP1,WASL	up_ACOR_VSMC
GO:0019400	0.0247	0.997	3	7	alditol metabolic process	BP	1	GOT1,GALK1,TKFC	up_VSAP_EC
GO:0002703	0.0247	0.998	2	47	regulation of leukocyte mediated immunity	BP	1	LYN,STX4	down_ACOR_EC
GO:1902991	0.0247	0.999	2	5	regulation of amyloid precursor protein	BP	0.761	APOE,LYN	down_VSAP_EC
GO:0007517	0.0247	0.998	2	100	muscle organ development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:1902459	0.0247	0.999	2	3	positive regulation of stem cell population	BP	1	KDM2B,LBH	up_VSAP_EC
GO:0072006	0.0247	0.998	2	59	nephron development	BP	1	HOXA11,SALL1	up_VSAP_VSMC

GO:0048048	0.0247	1	1	13	embryonic eye morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0043542	0.0247	1	1	86	endothelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0001657	0.024749809	0.99516	4	42	ureteric bud development	BP	0.96436359	SOX9,SMAD6,FOXC2,CLSTN1	up_ACOR_EC
GO:0072163	0.024749809	0.99516	4	42	mesonephric epithelium development	BP	0.96436359	SOX9,SMAD6,FOXC2,CLSTN1	up_ACOR_EC
GO:0072164	0.024749809	0.99516	4	42	mesonephric tubule development	BP	0.96436359	SOX9,SMAD6,FOXC2,CLSTN1	up_ACOR_EC
GO:0072111	0.0248	0.997	3	9	cell proliferation involved in kidney development	BP	0.682	PDGFB,GATA3,BMP2	up_VCAV_EC
GO:0030730	0.0248	0.999	2	4	sequestering of triglyceride	BP	0.761	ENPP1,ABHD5	down_VSAP_EC
GO:0043583	0.0248	0.998	2	59	ear development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0010591	0.0248	1	1	12	regulation of lamellipodium assembly	BP	1	FSCN1	down_AFEM_EC
GO:0030336	0.0248	1	1	86	negative regulation of cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0032612	0.0248	1	1	22	interleukin-1 production	BP	1	ARG2	up_AORT_VSMC
GO:0097061	0.0248	1	1	21	dendritic spine organization	BP	1	WNT7A	up_AORT_VSMC
GO:0032602	0.0248	1	1	23	chemokine production	BP	1	ARG2	up_AORT_VSMC
GO:0051047	0.0249	0.989	14	84	positive regulation of secretion	BP	1	EXPH5,TLR1,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,EDN1,NOD2,SCAMP5	up_ACOR_VSMC
GO:0030308	0.0249	0.992	7	49	negative regulation of cell growth	BP	0.761	ENPP1,IFRD1,SMARCA4,SESN2,INHBA,CDKN1A,NRP1	down_VSAP_EC
GO:0051145	0.0249	0.994	5	21	smooth muscle cell differentiation	BP	0.685	EDNRB,KIT,PDGFB,MEF2C,ZEB1	up_VCAV_EC
GO:0072606	0.0249	0.996	4	12	interleukin-8 secretion	BP	1	TLR1,LEP,F2RL1,PTPN22	up_ACOR_VSMC
GO:0098660	0.0249	0.997	3	141	inorganic ion transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0071826	0.0249	0.998	2	117	ribonucleoprotein complex subunit	BP	1	EIF3M,SRSF6	down_AFEM_EC
GO:0001501	0.0249	0.998	2	178	skeletal system development	BP	1	HOXC6,LRRC17	up_VCAV_VSMC
GO:0048144	0.0249	1	1	23	fibroblast proliferation	BP	1	ESR1	up_AORT_VSMC
GO:0048145	0.0249	1	1	23	regulation of fibroblast proliferation	BP	1	ESR1	up_AORT_VSMC
GO:0043276	0.0249	1	1	6	anoikis	BP	1	CAV1	up_VSAP_VSMC
GO:0015865	0.024950347	1	1	1	purine nucleotide transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0015866	0.024950347	1	1	1	ADP transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0015868	0.024950347	1	1	1	purine ribonucleotide transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0015880	0.024950347	1	1	1	coenzyme A transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0035349	0.024950347	1	1	1	coenzyme A transmembrane transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0051503	0.024950347	1	1	1	adenine nucleotide transport	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0071106	0.024950347	1	1	1	adenosine 3',5'-bisphosphate	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0072530	0.024950347	1	1	1	purine-containing compound	BP	0.96436359	SLC25A42	up_ACOR_EC
GO:0006915	0.025	0.984	44	550	apoptotic process	BP	0.763	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,ETV6,ERO1A,CASP3,HYOU1,EXOC5,AARS,FHL2,PTGS2,UACA,HIF1A,DNAJC10,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,GLO1,PAK2,INHBA,SIX4,CDKN1A,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0048644	0.025	0.993	7	31	muscle organ morphogenesis	BP	1	TNNT2,FGFR2,ANKRD1,EGLN1,TBX20,CHD7,ARID5B	up_ACOR_VSMC
GO:0090101	0.025	0.994	5	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	VASN,FBN1,CHRDL1,ASPN,GREM1	down_VCAV_EC
GO:0045595	0.025	0.997	3	469	regulation of cell differentiation	BP	1	LIMK1,GATA5,LRRC17	up_VCAV_VSMC

GO:0048536	0.025	1	1	12	spleen development	BP	1	CITED2	down_VPOR_EC
GO:0071380	0.025	1	1	7	cellular response to prostaglandin E stimulus	BP	1	PTGER2	up_VPUL_EC
GO:0048665	0.025	1	1	6	neuron fate specification	BP	1	HOXC10	up_VSAP_VSMC
GO:0032092	0.0251	0.992	8	38	positive regulation of protein binding	BP	1	PLCL1,BMP4,APP,PSEN1,AKTIP,B2M,HERPUD1,PARK7	up_ACOR_VSMC
GO:0007519	0.0251	0.992	7	49	skeletal muscle tissue development	BP	0.763	ACTN1,FLNB,CTNNB1,KLF5,ATF3,SIX4,HOMER1	down_VSAP_EC
GO:0042572	0.0251	0.999	2	5	retinol metabolic process	BP	1	CYP1B1,RETSAT	down_VCAV_EC
GO:0001696	0.0251	0.999	2	3	gastric acid secretion	BP	1	SLC26A7,HRH2	up_ACOR_VSMC
GO:0034612	0.0251	0.998	2	63	response to tumor necrosis factor	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0090385	0.0251	1	1	4	phagosome-lysosome fusion	BP	1	SPG11	down_ACOR_EC
GO:0007565	0.0251	1	1	23	female pregnancy	BP	1	ESR1	up_AORT_VSMC
GO:0044314	0.0251	1	1	3	protein K27-linked ubiquitination	BP	1	RNF6	up_VPOR_EC
GO:0090102	0.0251	1	1	10	cochlea development	BP	1	EYA1	up_VFEM_VSMC
GO:0048856	0.0252	0.992	10	1533	anatomical structure development	BP	1	TBX5,HOXA3,NR1H4,EVI2B,HOXA2,MYBPC2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0048584	0.0252	0.997	3	592	positive regulation of response to stimulus	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0046085	0.0252	0.999	2	5	adenosine metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:0019336	0.0252	0.999	2	3	phenol-containing compound catabolic	BP	1	MAOA,MOXD1	up_ACOR_VSMC
GO:0019614	0.0252	0.999	2	3	catechol-containing compound catabolic	BP	1	MAOA,MOXD1	up_ACOR_VSMC
GO:0042420	0.0252	0.999	2	3	dopamine catabolic process	BP	1	MAOA,MOXD1	up_ACOR_VSMC
GO:0042424	0.0252	0.999	2	3	catecholamine catabolic process	BP	1	MAOA,MOXD1	up_ACOR_VSMC
GO:1900122	0.0252	0.999	2	3	positive regulation of receptor binding	BP	1	PLCL1,B2M	up_ACOR_VSMC
GO:0000904	0.0252	0.998	2	181	cell morphogenesis involved in differentiation	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0061387	0.0252	1	1	18	regulation of extent of cell growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0019098	0.0252	1	1	6	reproductive behavior	BP	1	AVPR1A	up_VFEM_EC
GO:0071622	0.0252	1	1	13	regulation of granulocyte chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0019058	0.025240474	0.99379	5	64	viral life cycle	BP	0.96436359	ATG16L2,TRIM8,MAVS,LRRC15,CHMP4B	up_ACOR_EC
GO:0034330	0.0253	0.99	10	80	cell junction organization	BP	0.766	VEGFA,NR1H4,ACTN1,FSCN1,WDR1,MYO1C,CTNNB1,ENSCAFG00000002015,TLN1,NRP1	down_VSAP_EC
GO:0045844	0.0253	0.993	6	24	positive regulation of striated muscle tissue	BP	1	BMP4,FGFR2,GJA1,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0048636	0.0253	0.993	6	24	positive regulation of muscle organ	BP	1	BMP4,FGFR2,GJA1,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0048705	0.0253	0.993	6	95	skeletal system morphogenesis	BP	1	TBX15,IRX5,HOXA7,GREM1,HOXA6,AXIN2	up_AFEM_EC
GO:0051639	0.0253	0.999	2	4	actin filament network formation	BP	0.766	ACTN1,PLS3	down_VSAP_EC
GO:1901985	0.0253	1	1	11	positive regulation of protein acetylation	BP	1	TAOK1	up_AORT_EC
GO:0014896	0.0253	1	1	18	muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC
GO:0014897	0.0253	1	1	18	striated muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC
GO:0003300	0.0253	1	1	18	cardiac muscle hypertrophy	BP	1	GATA5	up_VCAV_VSMC
GO:0003215	0.0253	1	1	9	cardiac right ventricle morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0001990	0.0253	1	1	6	regulation of systemic arterial blood pressure by	BP	1	AVPR1A	up_VFEM_EC
GO:1905114	0.0254	0.991	8	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	GREM1,FAM53B,CYLD,RECK,LGR6,AXIN2,DMPK,KANK1	up_AFEM_EC
GO:0009611	0.0254	0.992	7	122	response to wounding	BP	1	F5,F3,TFPI2,LGR6,ADAM17,KANK1,TNC	up_AFEM_EC
GO:0033993	0.0254	0.997	3	186	response to lipid	BP	1	NR1H4,MRC1,PTGER2	up_VPUL_EC

GO:0071472	0.0254	0.999	2	3	cellular response to salt stress	BP	1	ZFP36L1,SLC12A6	up_VSAP_EC
GO:0034143	0.0254	1	1	6	regulation of toll-like receptor 4 signaling	BP	1	LYN	down_ACOR_EC
GO:0046928	0.0254	1	1	23	regulation of neurotransmitter	BP	1	WNT7A	up_AORT_VSMC
GO:0035270	0.0254	1	1	35	endocrine system development	BP	1	HOXA3	up_APUL_VSMC
GO:0006821	0.0254	1	1	18	chloride transport	BP	1	CA2	up_VCAV_VSMC
GO:0033561	0.0254	1	1	6	regulation of water loss via skin	BP	1	CYP26B1	up_VFEM_EC
GO:0072358	0.0255	0.989	12	268	cardiovascular system development	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,RECK,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0023061	0.0255	0.993	6	95	signal release	BP	1	LEP,KCNC4,CRY2,CHRM2,CAMK2A,CCL5	up_AFEM_EC
GO:0032642	0.0255	0.994	5	22	regulation of chemokine production	BP	0.699	ACKR1,TLR4,ARG2,TLR3,APOD	up_VCAV_EC
GO:0072350	0.0255	0.994	5	18	tricarboxylic acid metabolic process	BP	1	DLST,IDH1,IDH3A,ENSCAFG00000006639,ASS1	up_VSAP_EC
GO:0048729	0.0255	0.995	4	209	tissue morphogenesis	BP	1	ACVRL1,PDPN,NRP2,SULF1	down_ACOR_EC
GO:0016049	0.0255	0.996	3	124	cell growth	BP	1	ACVRL1,SPG11,NRP2	down_ACOR_EC
GO:0008219	0.0255	0.997	3	611	cell death	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0032504	0.0255	0.996	3	152	multicellular organism reproduction	BP	1	HOXA9,AVPR1A,CYP26B1	up_VFEM_EC
GO:0048609	0.0255	0.996	3	152	multicellular organismal reproductive process	BP	1	HOXA9,AVPR1A,CYP26B1	up_VFEM_EC
GO:0098655	0.0255	0.996	3	142	cation transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0043409	0.0255	0.998	2	54	negative regulation of MAPK cascade	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0003006	0.0255	0.998	2	180	developmental process involved in reproduction	BP	1	HOXA9,IRX5	up_AFEM_VSMC
GO:0032940	0.0255	0.998	2	231	secretion by cell	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0051091	0.0255	1	1	87	positive regulation of DNA-binding transcription factor activity	BP	1	JUP	down_VFEM_VSMC
GO:0046889	0.025542109	0.99648	3	24	positive regulation of lipid biosynthetic process	BP	0.96436359	NR1H4,CCDC3,PRKCD	up_ACOR_EC
GO:0010970	0.0256	0.992	7	48	transport along microtubule	BP	0.767	RPGR,KIF5B,HIF1A,DYNLL1,TRAK1,HTT,AP3S1	down_VSAP_EC
GO:0099111	0.0256	0.992	7	48	microtubule-based transport	BP	0.767	RPGR,KIF5B,HIF1A,DYNLL1,TRAK1,HTT,AP3S1	down_VSAP_EC
GO:0010827	0.0256	0.994	5	28	regulation of glucose transmembrane transport	BP	0.767	NR1H4,ENPP1,PTPN11,TRIB3,YES1	down_VSAP_EC
GO:0035249	0.0256	0.996	4	13	synaptic transmission, glutamatergic	BP	0.7	RELN,MEF2C,GRM8,ALS2	up_VCAV_EC
GO:0001842	0.0256	0.999	2	3	neural fold formation	BP	0.7	HIF1A,LUZP1	up_VCAV_EC
GO:0048562	0.0256	0.998	2	102	embryonic organ morphogenesis	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0042044	0.0256	1	1	6	fluid transport	BP	1	PDPN	down_ACOR_EC
GO:0006040	0.0256	1	1	12	amino sugar metabolic process	BP	1	EXTL2	down_AFEM_EC
GO:0060972	0.0256	1	1	13	left/right pattern formation	BP	1	CITED2	down_VPOR_EC
GO:0032715	0.0256	1	1	11	negative regulation of interleukin-6 production	BP	1	BPI	up_AORT_EC
GO:0045747	0.0256	1	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	up_VCAV_VSMC
GO:0030878	0.0256	1	1	13	thyroid gland development	BP	1	HOXA3	up_VPUL_VSMC
GO:0007595	0.0256	1	1	6	lactation	BP	1	CAV1	up_VSAP_VSMC

GO:0048519	0.0257	0.981	111	1554	negative regulation of biological process	BP	0.767	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,ERO1A,PRKACB,PTPN14,ENPP1,ERRFI1,SNX25,CBX5,HYOU1,PGK1,PTPN11,AARS,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,FHL2,BHLHE40,SMARCA4,SESN2,PTGS2,REM1,CHSY1,HIF1A,DYNLL1,THBS2,DNAJC10,NAA10,NXN,RGS2,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,EIF4EBP1,SKAP2,CNOT7,MAGED1,CTNNB1,CRYAB,STARD13,SND1,ENSCAFG00000002015,APOE,WWC3,KLF5,MMP28,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,CBLC,ATF3,GSK3B,VLDLR,TAX1BP3,SDC4,HTT,REST,ABHD5,ENSCAFG00000017326,ZMYND8,EIF2S1,PRMT1,ARFGEF3,CALM1,RAB11FIP1,GLO1,CDYL,PAK2,LRRTM2,A2M,CAPG,INHBA,NR4A1,HIF1AN,BTK,SIX4,CDKN1A,NRP1,SPINK2,RHBDF2,USP14,ARF4,YWHAH,TNFAIP1,KDM3A,MID1	down_VSAP_EC
GO:0001568	0.0257	0.986	20	252	blood vessel development	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,BMPR1A,LOX,RECK,ANPEP,SEMA3C,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,CDH2,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC
GO:0051403	0.0257	0.988	15	89	stress-activated MAPK cascade	BP	1	LEP,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,PTPN22,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0051146	0.0257	0.989	12	76	striated muscle cell differentiation	BP	0.7	MEF2C,EDN1,TMOD1,PPP3CA,MTOR,BMP2,CAV2,PROX1,ENSCAFG00000010596,P2RX2,TMOD3,CDON	up_VCAV_EC
GO:0010721	0.0257	0.991	8	73	negative regulation of cell development	BP	1	FBN1,BMPR1A,THY1,TLX2,GLI3,PRKCSH,THRB,RGMA	down_VCAV_EC
GO:0051241	0.0257	0.994	5	336	negative regulation of multicellular organismal	BP	1	ACVRL1,LYN,HOXA7,SULF1,ASPN	down_ACOR_EC
GO:0090049	0.0257	0.994	5	21	regulation of cell migration involved in sprouting angiogenesis	BP	0.701	PLK2,DLL4,PIK3C2A,MAP3K3,JCAD	up_VCAV_EC
GO:0055023	0.0257	0.996	4	12	positive regulation of cardiac muscle tissue	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0001944	0.0257	0.997	3	263	vasculature development	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0035089	0.0257	0.999	2	5	establishment of apical/basal cell polarity	BP	0.767	FSCN1,MSN	down_VSAP_EC
GO:0043302	0.0257	1	1	6	positive regulation of leukocyte degranulation	BP	1	STX4	down_ACOR_EC
GO:0044539	0.0257	1	1	5	long-chain fatty acid import	BP	1	ACSL3	down_ACOR_EC
GO:0005984	0.0257	1	1	3	disaccharide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0046351	0.0257	1	1	3	disaccharide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0008542	0.0257	1	1	13	visual learning	BP	1	LRRN4	up_VPUL_VSMC
GO:0071675	0.0257	1	1	13	regulation of mononuclear cell	BP	1	SLIT2	up_VPUL_VSMC
GO:0021871	0.0257	1	1	6	forebrain regionalization	BP	1	EMX2	up_VSAP_VSMC
GO:0072511	0.0258	0.988	14	97	divalent inorganic cation transport	BP	0.701	CALCRL,PDGFB,ATP2B1,PDE4D,CHD7,STC1,APLNR,SLC39A8,PPP3CA,KCNJ2,SLC25A25,PLCG2,MCU,ATP2A1	up_VCAV_EC
GO:0032413	0.0258	0.995	4	15	negative regulation of ion transmembrane transporter activity	BP	0.863	NEDD4,CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0060544	0.0258	0.997	3	8	regulation of necroptotic process	BP	0.701	PELI1,RIPK1,ARHGEF2	up_VCAV_EC
GO:0048729	0.0258	0.998	2	209	tissue morphogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0043270	0.0258	0.998	2	56	positive regulation of ion transport	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0035088	0.0258	1	1	12	establishment or maintenance of	BP	1	FSCN1	down_AFEM_EC
GO:0061245	0.0258	1	1	12	establishment or maintenance of bipolar	BP	1	FSCN1	down_AFEM_EC
GO:0031111	0.0258	1	1	11	negative regulation of microtubule polymerization or	BP	1	TAOK1	up_AORT_EC
GO:0060017	0.0258	1	1	3	parathyroid gland development	BP	1	HOXA3	up_VPOR_EC
GO:0001523	0.0258	1	1	12	retinoid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC

GO:0071622	0.0258	1	1	13	regulation of granulocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0060914	0.0258	1	1	11	heart formation	BP	1	EYA1	up_VFEM_VSMC
GO:0001759	0.0258	1	1	13	organ induction	BP	1	GATA5	up_VPUL_VSMC
GO:0031345	0.0259	0.993	6	46	negative regulation of cell projection organization	BP	1	PRNP,THY1,TLX2,PRKCSH,EVI5L,RGMA	down_VCAV_EC
GO:0099003	0.0259	0.998	2	50	vesicle-mediated transport in synapse	BP	1	SPG11,STX4	down_ACOR_EC
GO:0021562	0.0259	1	1	4	vestibulocochlear nerve development	BP	1	NRP2	down_ACOR_EC
GO:1990778	0.0259	1	1	91	protein localization to cell periphery	BP	1	JUP	down_VFEM_VSMC
GO:0060561	0.0259	1	1	11	apoptotic process involved in	BP	1	NKX2-5	up_VPOR_VSMC
GO:0045843	0.0259	1	1	13	negative regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:1905209	0.0259	1	1	13	positive regulation of cardiocyte differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0034333	0.025920972	0.99639	3	25	adherens junction assembly	BP	0.96436359	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0035262	0.025922746	1	1	1	gonad morphogenesis	BP	0.96436359	LHX9	up_ACOR_EC
GO:0090360	0.025937111	1	1	1	platelet-derived growth factor production	BP	0.96436359	NDRG2	up_ACOR_EC
GO:0090361	0.025937111	1	1	1	regulation of platelet-derived growth factor	BP	0.96436359	NDRG2	up_ACOR_EC
GO:0061458	0.026	0.986	20	131	reproductive system development	BP	1	LEP,GATA4,PRDX4,BMP4,FGFR2,ATRX,CITED2,SPINT1,CTSB,EGLN1,ENSCAFG00000006238,SPINT2,FRS2,CHD7,SPINK2,ARID5B,DMC1,SERPINB5,LHX9,WDR48	up_ACOR_VSMC
GO:0048705	0.026	0.988	14	95	skeletal system morphogenesis	BP	0.87	EIF4A3,HOXA3,NAB2,INSIG1,MMP14,GREM1,HOXA7,HOXB7,POC1A,HOXB5,SGPL1,TBX15,SERPINH1,SIX4	down_ACOR_VSMC
GO:0061028	0.026	0.995	4	14	establishment of endothelial barrier	BP	0.703	PDE4D,RAPGEF1,SOX18,RAPGEF2	up_VCAV_EC
GO:0007389	0.026	0.995	4	137	pattern specification process	BP	1	BARX1,HOXA3,SEMA3A,ACVR2A	up_VPOR_EC
GO:0060977	0.026	0.998	2	6	coronary vasculature morphogenesis	BP	1	PDGFRB,SPRED1	down_VCAV_EC
GO:0036023	0.026	0.999	2	3	embryonic skeletal limb joint morphogenesis	BP	1	OSR2,OSR1	up_VSAP_EC
GO:0072073	0.026	0.998	2	60	kidney epithelium development	BP	1	HOXA11,SALL1	up_VSAP_VSMC
GO:0046033	0.026	1	1	5	AMP metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0009880	0.026	1	1	22	embryonic pattern specification	BP	1	WNT7A	up_AORT_VSMC
GO:0022602	0.026	1	1	13	ovulation cycle process	BP	1	SLIT2	up_VPUL_VSMC
GO:0046360	0.026031548	1	1	1	2-oxobutyrate biosynthetic process	BP	0.96436359	THNSL2	up_ACOR_EC
GO:0046361	0.026031548	1	1	1	2-oxobutyrate metabolic process	BP	0.96436359	THNSL2	up_ACOR_EC
GO:1901617	0.0261	0.99	10	60	organic hydroxy compound biosynthetic	BP	0.87	SQLE,LSS,SREBF1,HMGCR,INSIG1,ENSCAFG00000018572,DHCR24,MVD,FDFT1,NUS1	down_ACOR_VSMC
GO:0044249	0.0261	0.995	6	1851	cellular biosynthetic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0006355	0.0261	0.993	6	974	regulation of transcription, DNA-	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060525	0.0261	0.999	2	3	prostate glandular acinus development	BP	1	FGFR2,FRS2	up_ACOR_VSMC
GO:0060526	0.0261	0.999	2	3	prostate glandular acinus morphogenesis	BP	1	FGFR2,FRS2	up_ACOR_VSMC
GO:0060527	0.0261	0.999	2	3	prostate epithelial cord arborization involved in prostate glandular acinus	BP	1	FGFR2,FRS2	up_ACOR_VSMC
GO:0040001	0.0261	1	1	12	establishment of mitotic spindle localization	BP	1	GPSM2	down_AFEM_EC
GO:0017158	0.0261	1	1	24	regulation of calcium ion-dependent exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0035710	0.0261	1	1	22	CD4-positive, alpha-beta T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0048639	0.0261	1	1	39	positive regulation of developmental growth	BP	1	TBX5	up_APUL_VSMC
GO:0009226	0.0261	1	1	3	nucleotide-sugar biosynthetic process	BP	1	GNPNAT1	up_VPOR_EC
GO:0051004	0.0261	1	1	3	regulation of lipoprotein lipase activity	BP	1	ABHD5	up_VPOR_EC

GO:2000271	0.0261	1	1	3	positive regulation of fibroblast apoptotic	BP	1	STK17B	up_VPOR_EC
GO:0030336	0.026124203	0.99245	6	86	negative regulation of cell migration	BP	0.96436359	SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,TBX5	up_ACOR_EC
GO:0040008	0.0262	0.99	9	179	regulation of growth	BP	1	MT2A,LEP,ENSCAFG00000009113,DLL1,PLXNA4,GPAM,DCUN1D3,ACACB,ADAM17	up_AFEM_EC
GO:0043010	0.0262	0.992	6	96	camera-type eye development	BP	1	IRX5,COL8A2,DLL1,CRYAB,MAB21L1,THRB	up_AFEM_EC
GO:0051209	0.0262	0.994	5	28	release of sequestered calcium ion into cytosol	BP	0.776	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0051283	0.0262	0.994	5	28	negative regulation of sequestering of calcium	BP	0.776	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0035239	0.0262	0.995	4	299	tube morphogenesis	BP	1	HOXA3,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0043436	0.0262	0.997	3	303	oxoacid metabolic process	BP	1	ETFA,DARS,SUCLG2	down_AFEM_EC
GO:0030513	0.0262	0.997	3	11	positive regulation of BMP signaling pathway	BP	0.776	SULF1,ILK,NEO1	down_VSAP_EC
GO:0035162	0.0262	0.997	3	8	embryonic hemopoiesis	BP	0.707	KIT,GATA3,HIF1A	up_VCAV_EC
GO:0060509	0.0262	0.999	2	3	type I pneumocyte differentiation	BP	1	THRB,NFIB	up_VSAP_EC
GO:0021517	0.0262	1	1	12	ventral spinal cord development	BP	1	HOXC10	up_AORT_EC
GO:0034754	0.0262	1	1	24	cellular hormone metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0099175	0.0262	1	1	21	regulation of postsynapse organization	BP	1	WNT7A	up_AORT_VSMC
GO:0001974	0.0262	1	1	13	blood vessel remodeling	BP	1	HOXA3	up_VPUL_VSMC
GO:0043267	0.0262	1	1	6	negative regulation of potassium ion transport	BP	1	CAV1	up_VSAP_VSMC
GO:0009605	0.026239257	0.98554	22	538	response to external stimulus	BP	0.96436359	NR1H4,SOX9,HMCN1,RGS1,PCSK1N,FNDC4,AQP1,FZD5,PTGIR,NOD2,IL33,RGMA,MMP28,PTGER4,ELMO2,USP53,MAVS,IFIT2,RARRES2,AGBL5,NRP1,PRKCD	up_ACOR_EC
GO:0060429	0.0263	0.984	30	341	epithelium development	BP	0.776	PRICKLE1,SULF1,TAGLN2,SERPINE1,PRKACB,PTK7,ERRFI1,CASP3,PGK1,EXOC5,FLNB,ENSCAFG00000032470,TMED2,ILK,WDR1,MSN,HOXB7,HIF1A,ADAM17,ACTA2,MAGED1,CTNNB1,STARD13,PLOD3,KLF5,MYO1E,SDC4,INHBA,SIX4,NRP1	down_VSAP_EC
GO:0032501	0.0263	0.991	11	1782	multicellular organismal process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,HOXA2,MYBPC2,CCL24,HTR7,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0032502	0.0263	0.996	5	1661	developmental process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0002685	0.0263	0.998	2	55	regulation of leukocyte migration	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0034975	0.0263	0.999	2	5	protein folding in endoplasmic reticulum	BP	0.776	ERO1A,DNAJC10	down_VSAP_EC
GO:0050727	0.0263	0.998	2	74	regulation of inflammatory response	BP	1	NR1H4,CCL24	up_VPUL_EC
GO:0003158	0.0263	1	1	38	endothelium development	BP	1	HOXB5	up_APUL_VSMC
GO:0030282	0.0263	1	1	37	bone mineralization	BP	1	HOXA3	up_APUL_VSMC
GO:0003179	0.0263	1	1	19	heart valve morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0021952	0.0263	1	1	13	central nervous system projection neuron	BP	1	SLIT2	up_VPUL_VSMC
GO:0050729	0.026388797	0.9963	3	25	positive regulation of inflammatory response	BP	0.96436359	NOD2,IL33,PTGER4	up_ACOR_EC
GO:0042327	0.0264	0.984	34	289	positive regulation of phosphorylation	BP	0.709	TEK,HCLS1,KIT,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,SH3GLB1,TLR3,PTGS2,MMD,RAPGEF2,TAOK1,HMGB1,RIPK1,ITGA6,PDGFD,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0051223	0.0264	0.985	26	181	regulation of protein transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,MBP,FERMT1,BMP4,TM7SF3,CD274,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,PSEN1,JUP,CCL5,NOD2,SCAMP5,INPP5K,PFKL,PARK7,PTPN14	up_ACOR_VSMC
GO:0045926	0.0264	0.99	9	72	negative regulation of growth	BP	0.776	ENPP1,IFRD1,SMARCA4,SESN2,HIF1A,WWC3,INHBA,CDKN1A,NRP1	down_VSAP_EC
GO:0106106	0.0264	0.995	4	48	cold-induced thermogenesis	BP	1	CMKLR1,HOXC10,LEP,PPARGC1A	up_AFEM_EC
GO:0120161	0.0264	0.995	4	48	regulation of cold-induced thermogenesis	BP	1	CMKLR1,HOXC10,LEP,PPARGC1A	up_AFEM_EC

GO:0034145	0.0264	0.999	2	3	positive regulation of toll-like receptor 4 signaling	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0071493	0.0264	0.999	2	3	cellular response to UV-B	BP	1	MFAP4,CDKN1A	up_ACOR_VSMC
GO:2001212	0.0264	0.999	2	4	regulation of vasculogenesis	BP	0.709	CD34,RAPGEF2	up_VCAV_EC
GO:0006936	0.0264	0.998	2	74	muscle contraction	BP	1	MYBPC2,HTR7	up_VPUL_EC
GO:0030855	0.0264	1	1	183	epithelial cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0098609	0.0264	1	1	181	cell-cell adhesion	BP	1	GATA5	down_AFEM_VSMC
GO:0014910	0.0264	1	1	13	regulation of smooth muscle cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0006793	0.0265	0.98	93	948	phosphorus metabolic process	BP	0.709	EPHB1,PLK2,TEK,HCLS1,NPR1,ADGRF5,KIT,PPP2R5A,PANK3,PRKCH,CDA,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,PDE4D,MEF2C,ATF3,RAPGEF1,TLR4,NLRC5,GK5,EDN1,RALB,APLNR,CTTNBP2NL,PIPOX,NEDD9,SERINC5,ADSS,YES1,GUCY1A1,SPTLC2,EPHB4,MTOR,ACPP,SAMD8,MAP3K3,BMP2,HHEX,PREX2,SLK,BMP2K,SH3BP5,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,ENSCAFG00000010596,MADD,PAK2,PRKD2,SH3GLB1,SWAP70,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,LDB2,SLC25A25,FES,NSD1,GUCY1B1,PTGS2,MMD,TOP1,RAPGEF2,PLCG2,CREB1,TAOK1,CNOT7,DCK,HMGB1,NOS2,BLM,SPTBN4,RIPK1,ITGA6,RAD17,IMPA1,PDGFD,PIP5K1B,BMX,HIF1A,LMTK2,FKBP15,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0043009	0.0265	0.984	31	227	chordate embryonic development	BP	1	TBX15,HOXA11,FZD1,HOXA7,HOXA9,WNT11,AXIN2,OSR2,GJB5,IRX5,HOXD3,ABL1,DLL1,HOXA6,OSR1,FUZ,RARG,AMBRA1,MFN2,ZFP36L1,ZEB1,SULF2,SHOX2,KDM2B,TAF8,ZFAND5,ACVRL1,TGFBR2,CITED2,KEAP1,LATS2	up_VSAP_EC
GO:0034767	0.0265	0.992	7	31	positive regulation of ion transmembrane transport	BP	1	ACTN2,PLCG2,TCAF1,AKAP6,PSEN1,FXYD1,PARK7	up_ACOR_VSMC
GO:1903506	0.0265	0.993	6	977	regulation of nucleic acid-templated transcription	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0106049	0.0265	0.999	2	4	regulation of cellular response to osmotic	BP	0.776	ARHGEF2,PTGS2	down_VSAP_EC
GO:1902218	0.0265	0.999	2	4	regulation of intrinsic apoptotic signaling pathway in response to	BP	0.776	ARHGEF2,PTGS2	down_VSAP_EC
GO:1902219	0.0265	0.999	2	4	negative regulation of intrinsic apoptotic signaling pathway in	BP	0.776	ARHGEF2,PTGS2	down_VSAP_EC
GO:0055062	0.0265	1	1	5	phosphate ion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:0072505	0.0265	1	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:0072506	0.0265	1	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:2000392	0.0265	1	1	4	regulation of lamellipodium	BP	1	PDPN	down_ACOR_EC
GO:1903829	0.0265	1	1	91	positive regulation of cellular protein	BP	1	JUP	down_VFEM_VSMC
GO:2000146	0.0265	1	1	92	negative regulation of cell motility	BP	1	JUP	down_VFEM_VSMC
GO:0032717	0.0265	1	1	7	negative regulation of interleukin-8 production	BP	1	BPI	up_APUL_EC
GO:1901071	0.0265	1	1	6	glucosamine-containing compound metabolic	BP	1	CHST7	up_VFEM_EC
GO:0051049	0.026561879	0.98577	20	479	regulation of transport	BP	0.96436359	SH3TC2,CDH3,NR1H4,CALY,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,NOD2,ACTN2,PTGER4,PREB,MAPK8IP2,MAVS,RARRES2,VPS16,AZIN2,PRKCD,PM20D1	up_ACOR_EC
GO:1905517	0.026578702	0.99817	2	10	macrophage migration	BP	0.96436359	MMP28,RARRES2	up_ACOR_EC
GO:0071333	0.026587631	0.99626	3	25	cellular response to glucose stimulus	BP	0.96436359	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0003171	0.026588257	0.99816	2	10	atrioventricular valve development	BP	0.96436359	SMAD6,TBX5	up_ACOR_EC
GO:0016055	0.026598006	0.99058	8	134	Wnt signaling pathway	BP	0.96436359	CDH3,SOX9,PORCN,FZD5,DIXDC1,LRP4,CLSTN1,PYGO2	up_ACOR_EC
GO:0198738	0.026598006	0.99058	8	134	cell-cell signaling by wnt	BP	0.96436359	CDH3,SOX9,PORCN,FZD5,DIXDC1,LRP4,CLSTN1,PYGO2	up_ACOR_EC

GO:0043067	0.0266	0.983	39	479	regulation of programmed cell death	BP	0.778	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,CASP3,HYOU1,AARS,FHL2,PTGS2,HIF1A,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,GLO1,PAK2,INHBA,SIX4,CDKN1A,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:1902751	0.0266	0.995	4	14	positive regulation of cell cycle G2/M phase	BP	0.883	CDK1,CDK4,DTL,CDC25A	down_ACOR_VSMC
GO:1903707	0.0266	0.995	4	48	negative regulation of hemopoiesis	BP	1	HOXA9,HOXA7,DLL1,CYLD	up_AFEM_EC
GO:0007350	0.0266	0.997	3	7	blastoderm segmentation	BP	1	NRP1,FRS2,PCSK6	up_ACOR_VSMC
GO:2000112	0.0266	1	2	1119	regulation of cellular macromolecule biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0019731	0.0266	0.999	2	3	antibacterial humoral response	BP	1	PLA2G6,JCHAIN	up_VSAP_EC
GO:0051451	0.0266	1	1	6	myoblast migration	BP	1	SIX1	up_VFEM_EC
GO:0060676	0.0266	1	1	6	ureteric bud formation	BP	1	SIX1	up_VFEM_EC
GO:0032689	0.0266	1	1	8	negative regulation of interferon-gamma	BP	1	NR1H4	up_VPUL_EC
GO:0021542	0.0266	1	1	6	dentate gyrus development	BP	1	EMX2	up_VSAP_VSMC
GO:1904385	0.0266	1	1	6	cellular response to angiotensin	BP	1	CAV1	up_VSAP_VSMC
GO:1990776	0.0266	1	1	6	response to angiotensin	BP	1	CAV1	up_VSAP_VSMC
GO:0003400	0.026642364	1	1	1	regulation of COPII vesicle coating	BP	0.96436359	PREB	up_ACOR_EC
GO:0090113	0.026642364	1	1	1	regulation of ER to Golgi vesicle-mediated transport by GTP	BP	0.96436359	PREB	up_ACOR_EC
GO:0009967	0.0267	0.982	54	435	positive regulation of signal transduction	BP	1	ADRA1B,TLR1,LGR6,LEP,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,SKP2,NACC2,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,CITED2,TP53INP1,SASH1,TMEM108,FGF18,CDKN2B,LIMS2,ANKRD1,F2RL1,BNIP3,CRLF3,CREBRF,NRP1,PTPN22,NPNT,UNC5B,PRKCE,FRS2,PARP9,APP,PSEN1,CCL5,DUSP22,SIAH1,EDN1,NOD2,DISC1,SH3RF3,SERINC3,MAP3K7,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0034097	0.0267	0.985	22	238	response to cytokine	BP	0.779	ARHGEF2,NR1H4,HSPA5,SOCS5,FLNB,DPYSL3,ILK,MYO1C,KIF5B,HIF1A,CX3CL1,PTPN2,ADAM17,CNOT7,ENSCAFG00000002015,TFRC,ZC3H15,KLF5,CDC37,GBP5,BTK,KDM3A	down_VSAP_EC
GO:0016458	0.0267	0.99	10	59	gene silencing	BP	0.888	ATAD2,SRRT,RAN,UHRF1,SUV39H1,CDK2,RBM14,HAT1,HIST2H2AC,H2AFX	down_ACOR_VSMC
GO:0042306	0.0267	0.992	7	31	regulation of protein import into nucleus	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP	up_ACOR_VSMC
GO:0045595	0.0267	0.995	4	469	regulation of cell differentiation	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006082	0.0267	0.996	3	305	organic acid metabolic process	BP	1	ETFA,DARS,SUCLG2	down_AFEM_EC
GO:0001945	0.0267	0.997	3	9	lymph vessel development	BP	0.71	SOX18,PROX1,VASH1	up_VCAV_EC
GO:0001946	0.0267	0.997	3	9	lymphangiogenesis	BP	0.71	SOX18,PROX1,VASH1	up_VCAV_EC
GO:0036303	0.0267	0.997	3	9	lymph vessel morphogenesis	BP	0.71	SOX18,PROX1,VASH1	up_VCAV_EC
GO:0048588	0.0267	0.998	2	44	developmental cell growth	BP	1	SPG11,NRP2	down_ACOR_EC
GO:0048255	0.0267	0.998	2	11	mRNA stabilization	BP	1	TENT5C,AXIN2	up_AFEM_EC
GO:0001818	0.0267	0.998	2	65	negative regulation of cytokine production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0050890	0.0267	0.998	2	67	cognition	BP	1	NTRK2,HOXA1	up_APUL_EC
GO:0034137	0.0267	0.999	2	3	positive regulation of toll-like receptor 2 signaling	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0042473	0.0267	1	1	5	outer ear morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0043030	0.0267	1	1	12	regulation of macrophage activation	BP	1	BPI	up_AORT_EC
GO:0021846	0.0267	1	1	11	cell proliferation in forebrain	BP	1	EMX2	up_VFEM_VSMC

GO:0030097	0.0268	0.985	23	244	hemopoiesis	BP	0.779	VEGFA,MYH9,ACTN1,SOCS5,ETV6,CASP3,PTPN11,WDR1,HOXB7,HIF1A,PTPN2,EVI2B,CTNNB1,ANLN,TFRC,LYN,MYO1E,REST,PRMT1,SH2B3,GLO1,INHBA,BTK	down_VSAP_EC
GO:0071559	0.0268	0.988	13	75	response to transforming growth factor beta	BP	1	SMAD6,FERMT1,CITED2,CDKN2B,ANKRD1,MXRA5,NPNT,FUT8,TGFBR1,NR3C1,DUSP22,HPGD,CRKL	up_ACOR_VSMC
GO:0072009	0.0268	0.992	7	48	nephron epithelium development	BP	0.779	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,MYO1E,SIX4	down_VSAP_EC
GO:2001141	0.0268	0.993	6	979	regulation of RNA biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0009888	0.0268	0.993	6	545	tissue development	BP	1	HOXA11,PITX1,SALL1,CAV1,SHOX2,GJB5	up_VSAP_VSMC
GO:1901535	0.0268	0.999	2	3	regulation of DNA demethylation	BP	0.712	GATA3,OTUD4	up_VCAV_EC
GO:0035690	0.0268	1	1	91	cellular response to drug	BP	1	JUP	down_VFEM_VSMC
GO:0060485	0.0268	1	1	93	mesenchyme development	BP	1	GATA5	down_VFEM_VSMC
GO:0009064	0.0268	1	1	23	glutamine family amino acid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0021563	0.0268	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	up_VPOR_EC
GO:0030851	0.0268	1	1	8	granulocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0032620	0.0268	1	1	8	interleukin-17 production	BP	1	NR1H4	up_VPUL_EC
GO:0071071	0.0268	1	1	8	regulation of phospholipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0035556	0.0269	0.981	65	845	intracellular signal transduction	BP	0.779	ARHGEF2,VEGFA,P4HB,SIPA1L1,ARHGAP31,NR1H4,SOCS5,SGK1,ERO1A,JCAD,CASP3,HYOU1,WSB1,BCAR3,NUAK1,PTPN11,TRIB3,FARP1,ILK,FHL2,SESN2,TGFBR1,PTGS2,PIK3C2A,UACA,HIF1A,DNAJC10,TNIK,PTPN2,PLCL1,MTDH,EIF4EBP1,CNOT7,MAGED1,GNAQ,CTNNB1,KPNB1,ENSCAFG00000002015,APOE,WWC3,LYN,BNIP3,DDIT3,PLEKHG2,CBLC,ATF3,GSK3B,TAX1BP3,HTT,MAPK10,SH2B3,ARFGEF3,CALM1,DISC1,PAK2,INHBA,CAMK2D,BTK,CDKN1A,NRP1,SH3RF3,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:0048732	0.0269	0.986	18	116	gland development	BP	1	HOXA9,WNT11,HNF4A,LIMS2,HOXD3,FGF7,ABL1,RARG,STAT6,SULF2,CLCN2,NTN4,RAF1,NFIB,MAP2K2,TGFBR2,CITED2,LBH	up_VSAP_EC
GO:0051171	0.0269	0.989	14	1697	regulation of nitrogen compound metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,SULF1,ELK3,HOXA1,ACSL3,ASPN,NEDD4	down_ACOR_EC
GO:0072329	0.0269	0.993	5	34	monocarboxylic acid catabolic process	BP	1	AKT2,ACAA1,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:0006366	0.0269	0.997	3	583	transcription by RNA polymerase II	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0099170	0.0269	0.999	2	3	postsynaptic modulation of chemical synaptic	BP	1	EGLN1,RNF19A	up_ACOR_VSMC
GO:0050650	0.0269	0.998	2	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC
GO:0006574	0.0269	0.999	2	3	valine catabolic process	BP	1	ALDH6A1,ENSCAFG00000002977	up_VSAP_EC
GO:0032693	0.0269	0.999	2	3	negative regulation of interleukin-10 production	BP	1	CD274,DLL1	up_VSAP_EC
GO:0072608	0.0269	0.999	2	3	interleukin-10 secretion	BP	1	CD274,F2RL1	up_VSAP_EC
GO:0070646	0.0269	1	1	63	protein modification by small protein removal	BP	1	USP12	down_VFEM_EC
GO:0009566	0.0269	1	1	24	fertilization	BP	1	HOXA9	up_AORT_VSMC
GO:0033238	0.0269	1	1	7	regulation of cellular amine metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0009312	0.0269	1	1	9	oligosaccharide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:2001169	0.0269	1	1	11	regulation of ATP biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0031953	0.0269	1	1	6	negative regulation of protein	BP	1	CAV1	up_VSAP_VSMC
GO:0044249	0.027	0.992	9	1851	cellular biosynthetic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:1901654	0.027	0.992	7	31	response to ketone	BP	1	PRKAA2,ADCY6,PTGDR,PRKCE,NR3C1,DDIT4,PARK7	up_ACOR_VSMC
GO:0006809	0.027	0.995	4	14	nitric oxide biosynthetic process	BP	0.713	CD34,TLR4,NOS3,NOS2	up_VCAV_EC

GO:0046209	0.027	0.995	4	14	nitric oxide metabolic process	BP	0.713	CD34,TLR4,NOS3,NOS2	up_VCAV_EC
GO:0050854	0.027	0.995	4	16	regulation of antigen receptor-mediated	BP	0.713	PRKCH,NECTIN2,PRKD2,BCL10	up_VCAV_EC
GO:0043269	0.027	0.996	3	135	regulation of ion transport	BP	1	LYN,HOXA3,NEDD4	down_ACOR_EC
GO:0051924	0.027	0.998	2	53	regulation of calcium ion transport	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0003415	0.027	0.999	2	3	chondrocyte hypertrophy	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:0060841	0.027	1	1	6	venous blood vessel development	BP	1	ACVRL1	down_ACOR_EC
GO:0031589	0.027	1	1	93	cell-substrate adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0010092	0.027	1	1	19	specification of animal organ identity	BP	1	GATA5	up_VCAV_VSMC
GO:1902285	0.027	1	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	SEMA3A	up_VPOR_EC
GO:0006808	0.027052226	1	1	1	regulation of nitrogen utilization	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0019676	0.027052226	1	1	1	ammonia assimilation cycle	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0019740	0.027052226	1	1	1	nitrogen utilization	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0034255	0.027052226	1	1	1	regulation of urea metabolic process	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0034971	0.027052226	1	1	1	histone H3-R17 methylation	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0038183	0.027052226	1	1	1	bile acid signaling pathway	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0038185	0.027052226	1	1	1	intracellular bile acid receptor signaling	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0045848	0.027052226	1	1	1	positive regulation of nitrogen utilization	BP	0.96436359	NR1H4	up_ACOR_EC
GO:1903314	0.027052226	1	1	1	regulation of nitrogen cycle metabolic process	BP	0.96436359	NR1H4	up_ACOR_EC
GO:1905693	0.027052226	1	1	1	regulation of phosphatidic acid biosynthetic process	BP	0.96436359	NR1H4	up_ACOR_EC
GO:1905695	0.027052226	1	1	1	positive regulation of phosphatidic acid biosynthetic process	BP	0.96436359	NR1H4	up_ACOR_EC
GO:2000211	0.027052226	1	1	1	regulation of glutamate metabolic process	BP	0.96436359	NR1H4	up_ACOR_EC
GO:2000213	0.027052226	1	1	1	positive regulation of glutamate metabolic	BP	0.96436359	NR1H4	up_ACOR_EC
GO:2001248	0.027052226	1	1	1	regulation of ammonia assimilation cycle	BP	0.96436359	NR1H4	up_ACOR_EC
GO:2001250	0.027052226	1	1	1	positive regulation of ammonia assimilation	BP	0.96436359	NR1H4	up_ACOR_EC
GO:0098629	0.027061226	1	1	1	trans-Golgi network membrane organization	BP	0.96436359	AZIN2	up_ACOR_EC
GO:0003290	0.027067801	1	1	1	atrial septum secundum morphogenesis	BP	0.96436359	GATA4	up_ACOR_EC
GO:1902310	0.027067801	1	1	1	positive regulation of peptidyl-serine	BP	0.96436359	DUSP26	up_ACOR_EC
GO:0003275	0.027091778	1	1	1	apoptotic process involved in outflow tract	BP	0.96436359	FOXC2	up_ACOR_EC
GO:0035470	0.027091778	1	1	1	positive regulation of vascular wound healing	BP	0.96436359	FOXC2	up_ACOR_EC
GO:0048342	0.027091778	1	1	1	paraxial mesodermal cell differentiation	BP	0.96436359	FOXC2	up_ACOR_EC
GO:0048343	0.027091778	1	1	1	paraxial mesodermal cell fate commitment	BP	0.96436359	FOXC2	up_ACOR_EC
GO:0072011	0.027091778	1	1	1	glomerular endothelium development	BP	0.96436359	FOXC2	up_ACOR_EC
GO:1902256	0.027091778	1	1	1	regulation of apoptotic process involved in outflow tract	BP	0.96436359	FOXC2	up_ACOR_EC
GO:1902257	0.027091778	1	1	1	negative regulation of apoptotic process involved in outflow tract	BP	0.96436359	FOXC2	up_ACOR_EC
GO:0007538	0.027096764	1	1	1	primary sex determination	BP	0.96436359	SOX9	up_ACOR_EC
GO:0007542	0.027096764	1	1	1	primary sex determination, germ-line	BP	0.96436359	SOX9	up_ACOR_EC
GO:0014034	0.027096764	1	1	1	neural crest cell fate commitment	BP	0.96436359	SOX9	up_ACOR_EC
GO:0014036	0.027096764	1	1	1	neural crest cell fate specification	BP	0.96436359	SOX9	up_ACOR_EC

GO:0018992	0.027096764	1	1	1	germ-line sex determination	BP	0.96436359	SOX9	up_ACOR_EC
GO:0019100	0.027096764	1	1	1	male germ-line sex determination	BP	0.96436359	SOX9	up_ACOR_EC
GO:0060221	0.027096764	1	1	1	retinal rod cell differentiation	BP	0.96436359	SOX9	up_ACOR_EC
GO:0060516	0.027096764	1	1	1	primary prostatic bud elongation	BP	0.96436359	SOX9	up_ACOR_EC
GO:0060517	0.027096764	1	1	1	epithelial cell proliferation involved in prostatic bud elongation	BP	0.96436359	SOX9	up_ACOR_EC
GO:0060784	0.027096764	1	1	1	regulation of cell proliferation involved in	BP	0.96436359	SOX9	up_ACOR_EC
GO:0072034	0.027096764	1	1	1	renal vesicle induction	BP	0.96436359	SOX9	up_ACOR_EC
GO:2000741	0.027096764	1	1	1	positive regulation of mesenchymal stem cell differentiation	BP	0.96436359	SOX9	up_ACOR_EC
GO:0007165	0.0271	0.989	13	1496	signal transduction	BP	1	ACVRL1,LYN,IGF1R,PDPN,NRP2,HIVEP2,USP28,IPO7,SULF1,WDR12,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0040011	0.0271	0.994	5	505	locomotion	BP	1	TBX5,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0072358	0.0271	0.996	3	268	cardiovascular system development	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0003418	0.0271	0.999	2	3	growth plate cartilage chondrocyte	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:0003431	0.0271	0.999	2	3	growth plate cartilage chondrocyte development	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:0140115	0.0271	0.999	2	3	export across plasma membrane	BP	1	KCNE3,FXYD1	up_VSAP_EC
GO:0051180	0.0271	1	1	7	vitamin transport	BP	1	PDPN	down_ACOR_EC
GO:0071363	0.0271	1	1	188	cellular response to growth factor stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0001825	0.0271	1	1	14	blastocyst formation	BP	1	CITED2	down_VPOR_EC
GO:1901224	0.0271	1	1	20	positive regulation of NIK/NF-kappaB signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0032092	0.0271	1	1	38	positive regulation of protein binding	BP	1	HOXA3	up_APUL_VSMC
GO:0060343	0.0271	1	1	11	trabecula formation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0045980	0.0271	1	1	10	negative regulation of nucleotide metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0003218	0.027138217	1	1	1	cardiac left ventricle formation	BP	0.96436359	TBX5	up_ACOR_EC
GO:0071612	0.027144544	1	1	1	IP-10 production	BP	0.96436359	MAVS	up_ACOR_EC
GO:0071651	0.027144544	1	1	1	positive regulation of chemokine (C-C motif)	BP	0.96436359	MAVS	up_ACOR_EC
GO:0071658	0.027144544	1	1	1	regulation of IP-10 production	BP	0.96436359	MAVS	up_ACOR_EC
GO:0071660	0.027144544	1	1	1	positive regulation of IP-10 production	BP	0.96436359	MAVS	up_ACOR_EC
GO:0001655	0.0272	0.989	11	116	urogenital system development	BP	1	SMAD9,KANK2,CLSTN1,PKD1,GLI3,GLIS2,PRKCSH,RDH10,GREM1,ZBTB16,SEC61A1	down_VCAV_EC
GO:0009887	0.0272	0.998	2	314	animal organ morphogenesis	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0002756	0.0272	0.999	2	3	MyD88-independent toll-like receptor signaling	BP	0.717	TLR4,TLR3	up_VCAV_EC
GO:0002645	0.0272	0.999	2	3	positive regulation of tolerance induction	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0035739	0.0272	0.999	2	3	CD4-positive, alpha-beta T cell proliferation	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0042983	0.0272	0.999	2	3	amyloid precursor protein biosynthetic process	BP	1	NECAB3,SOAT1	up_VSAP_EC
GO:0042984	0.0272	0.999	2	3	regulation of amyloid precursor protein	BP	1	NECAB3,SOAT1	up_VSAP_EC
GO:2000561	0.0272	0.999	2	3	regulation of CD4-positive, alpha-beta T cell	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0045656	0.0272	0.999	2	3	negative regulation of monocyte differentiation	BP	1	HOXA7,MYC	up_VSAP_EC
GO:0001709	0.0272	1	1	11	cell fate determination	BP	1	CYP26B1	up_VPOR_VSMC
GO:0032703	0.0272	1	1	8	negative regulation of interleukin-2 production	BP	1	NR1H4	up_VPUL_EC
GO:0070098	0.0272	1	1	14	chemokine-mediated signaling pathway	BP	1	SLIT2	up_VPUL_VSMC
GO:0031646	0.0272	1	1	7	positive regulation of neurological system	BP	1	NETO1	up_VSAP_VSMC

GO:0010669	0.027231185	0.9981	2	10	epithelial structure maintenance	BP	0.96436359	SOX9,NOD2	up_ACOR_EC
GO:0007517	0.0273	0.987	16	100	muscle organ development	BP	1	TNNT2,BMP4,FGFR2,GJA1,CITED2,ANKRD1,EGLN1,CHD2,TBX20,TBX5,FRS2,CHD7,EDN1,ARID5B,ID3,BVES	up_ACOR_VSMC
GO:0010632	0.0273	0.989	11	95	regulation of epithelial cell migration	BP	0.785	VEGFA,SPARC,JCAD,PRCP,PIK3C2A,HIF1A,ADAM17,STARD13,APOE,STRAP,NRP1	down_VSAP_EC
GO:0032729	0.0273	0.995	4	15	positive regulation of interferon-gamma	BP	0.717	PDE4D,TLR4,IRF8,TLR3	up_VCAV_EC
GO:0008284	0.0273	0.998	2	238	positive regulation of cell proliferation	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0016053	0.0273	0.998	2	97	organic acid biosynthetic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0046394	0.0273	0.998	2	97	carboxylic acid biosynthetic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0034370	0.0273	0.999	2	3	triglyceride-rich lipoprotein particle	BP	1	LIPC,LCAT	up_VSAP_EC
GO:0034372	0.0273	0.999	2	3	very-low-density lipoprotein particle	BP	1	LIPC,LCAT	up_VSAP_EC
GO:0002278	0.0273	0.999	2	3	eosinophil activation involved in immune	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0002447	0.0273	0.999	2	3	eosinophil mediated immunity	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0060216	0.0273	0.999	2	3	definitive hemopoiesis	BP	1	HOXA9,ZFP36L2	up_VSAP_EC
GO:0072047	0.0273	0.999	2	3	proximal/distal pattern formation involved in	BP	1	OSR1,IRX3	up_VSAP_EC
GO:0072081	0.0273	0.999	2	3	specification of nephron tubule identity	BP	1	OSR1,IRX3	up_VSAP_EC
GO:0072177	0.0273	0.999	2	3	mesonephric duct development	BP	1	WNT11,OSR1	up_VSAP_EC
GO:0043307	0.0273	0.999	2	3	eosinophil activation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0043308	0.0273	0.999	2	3	eosinophil degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0051895	0.0273	1	1	7	negative regulation of focal adhesion assembly	BP	1	ACVRL1	down_ACOR_EC
GO:1903392	0.0273	1	1	7	negative regulation of adherens junction	BP	1	ACVRL1	down_ACOR_EC
GO:2000243	0.0273	1	1	14	positive regulation of reproductive process	BP	1	CITED2	down_VPOR_EC
GO:0010632	0.0273	1	1	95	regulation of epithelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0046634	0.0273	1	1	24	regulation of alpha-beta T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0061323	0.0273	1	1	7	cell proliferation involved in heart morphogenesis	BP	1	TBX5	up_APUL_EC
GO:2000136	0.0273	1	1	7	regulation of cell proliferation involved in	BP	1	TBX5	up_APUL_EC
GO:0007140	0.0273	1	1	10	male meiotic nuclear division	BP	1	CYP26B1	up_VPOR_VSMC
GO:0051926	0.0273	1	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0048643	0.0273	1	1	7	positive regulation of skeletal muscle tissue	BP	1	SHOX2	up_VSAP_VSMC
GO:0086065	0.0273	1	1	6	cell communication involved in cardiac	BP	1	CAV1	up_VSAP_VSMC
GO:0045234	0.02730132	1	1	1	protein palmitoleylation	BP	0.96436359	PORCN	up_ACOR_EC
GO:0060061	0.027338152	1	1	1	Spemann organizer formation	BP	0.96436359	FZD5	up_ACOR_EC
GO:0060715	0.027338152	1	1	1	syncytiotrophoblast cell differentiation involved in labyrinthine layer	BP	0.96436359	FZD5	up_ACOR_EC
GO:0097360	0.027338152	1	1	1	chorionic trophoblast cell proliferation	BP	0.96436359	FZD5	up_ACOR_EC
GO:1901382	0.027338152	1	1	1	regulation of chorionic trophoblast cell	BP	0.96436359	FZD5	up_ACOR_EC
GO:0036509	0.027384624	1	1	1	trimming of terminal mannose on B branch	BP	0.96436359	EDEM2	up_ACOR_EC
GO:1904380	0.027384624	1	1	1	endoplasmic reticulum mannose trimming	BP	0.96436359	EDEM2	up_ACOR_EC
GO:0043605	0.027398898	1	1	1	cellular amide catabolic process	BP	0.96436359	PM20D1	up_ACOR_EC
GO:0035295	0.0274	0.983	31	356	tube development	BP	0.785	PRICKLE1,VEGFA,SULF1,MYH9,SERPINE1,SPARC,PRKACB,ERRFI1,JCAD,PGK1,ENSCAFG00000032470,TMED2,ILK,PRCP,PIK3C2A,HOXB7,HIF1A,THBS2,MTDH,ESM1,MAGED1,CTNNB1,STARD13,APOE,PLOD3,KLF5,MYO1E,SDC4,SIX4,NRP1,SPINK2	down_VSAP_EC

GO:0097193	0.0274	0.988	12	109	intrinsic apoptotic signaling pathway	BP	0.785	ARHGEF2,P4HB,ERO1A,CASP3,HYOU1,PTGS2,HIF1A,DNAJC10,PTPN2,BNIP3,DDIT3,CDKN1A	down_VSAP_EC
GO:0090189	0.0274	0.996	3	12	regulation of branching involved in ureteric bud	BP	0.785	HOXB7,MAGED1,SIX4	down_VSAP_EC
GO:0009790	0.0274	0.996	3	335	embryo development	BP	1	HOXA3,TBX5,HOXB5	up_VPUL_VSMC
GO:0032700	0.0274	0.999	2	4	negative regulation of interleukin-17 production	BP	0.717	TLR4,ARG2	up_VCAV_EC
GO:0060047	0.0274	0.998	2	57	heart contraction	BP	1	IRX5,CAV1	up_VSAP_VSMC
GO:0070168	0.0274	1	1	6	negative regulation of biomineral tissue	BP	1	ASPN	down_ACOR_EC
GO:0090169	0.0274	1	1	13	regulation of spindle assembly	BP	1	GPSM2	down_AFEM_EC
GO:0003007	0.0274	1	1	94	heart morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:0010717	0.0274	1	1	32	regulation of epithelial to mesenchymal transition	BP	1	TGFBR1	down_VSAP_VSMC
GO:0021510	0.0274	1	1	23	spinal cord development	BP	1	HOXC10	up_AORT_VSMC
GO:0006654	0.0274	1	1	7	phosphatidic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0046473	0.0274	1	1	7	phosphatidic acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0055089	0.0274	1	1	7	fatty acid homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0021517	0.0274	1	1	12	ventral spinal cord development	BP	1	HOXC10	up_VFEM_VSMC
GO:0032940	0.0275	0.984	27	231	secretion by cell	BP	0.717	GBP5,KIT,EXOC3L2,MEF2C,FERMT1,CHD7,TLR4,GATA3,EDN1,RAB11A,RAB27A,EXOC6,SNCAIP,ARG2,SNAP23,SCAMP1,RSC1A1,ABCA1,EXOC5,CD200,FES,CREB1,STX11,HMGB1,NOS2,MCU,HIF1A	up_VCAV_EC
GO:0072503	0.0275	0.987	14	97	cellular divalent inorganic cation homeostasis	BP	0.717	ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,ATP2A1	up_VCAV_EC
GO:0030258	0.0275	0.99	8	71	lipid modification	BP	1	ENSCAFG00000014978,AKT2,LCAT,ACAA1,PEX5,LONP2,SOAT1,ACAT1	down_VCAV_EC
GO:0060041	0.0275	0.991	8	41	retina development in camera-type eye	BP	0.717	ARHGEF15,CHD7,DLL4,PROX1,TSPAN12,SMARCA4,HIF1A,CDON	up_VCAV_EC
GO:0003008	0.0275	0.996	3	336	system process	BP	1	GATA5,LRRN4,SLIT2	up_VPUL_VSMC
GO:0010556	0.0275	1	2	1137	regulation of macromolecule	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1903524	0.0275	0.998	2	11	positive regulation of blood circulation	BP	1	AVPR1A,TBXA2R	up_AFEM_EC
GO:0035774	0.0275	1	1	6	positive regulation of insulin secretion involved in cellular response to	BP	1	STX4	down_ACOR_EC
GO:0017038	0.0275	1	1	96	protein import	BP	1	JUP	down_VFEM_VSMC
GO:0008585	0.0275	1	1	24	female gonad development	BP	1	ESR1	up_AORT_VSMC
GO:0046545	0.0275	1	1	24	development of primary female sexual	BP	1	ESR1	up_AORT_VSMC
GO:0045987	0.0275	1	1	7	positive regulation of smooth muscle	BP	1	NPNT	up_APUL_EC
GO:0003283	0.0275	1	1	8	atrial septum development	BP	1	TBX5	up_VPUL_EC
GO:0060413	0.0275	1	1	8	atrial septum morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0032332	0.0275	1	1	6	positive regulation of chondrocyte	BP	1	HOXA11	up_VSAP_VSMC
GO:0009653	0.0276	0.979	89	773	anatomical structure morphogenesis	BP	1	TBX15,HOXA11,FZD1,THRB,HOXA7,PEX7,HOXA9,CDON,WNT11,HNF4A,ACKR3,AXIN2,WASF3,OSR2,INSIG2,ENPP2,RADIL,PPARGC1B,GJB5,LIMS2,LRIG3,DDHD1,IRX5,SLIT2,HOXD3,SLC6A4,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,HOXA6,OSR1,CDC42EP5,FUZ,WARS2,SAV1,HPSE,PLXNA4,RILPL2,CDC42EP2,ZBTB16,RARG,CCBE1,STAT6,HOXC4,RECK,PLPP3,DLX3,MFN2,ZFP36L1,IRX3,ZEB1,FBXW4,TBXA2R,SULF2,SHOX2,SASH1,HOXC10,POLDIP2,LOX,LRP4,DPYSL2,FRMD6,E2F4,NTN4,LIMD1,KDM2B,FBLN1,HPGD,NFIB,ZFAND5,ANPEP,PQBP1,TTL,ARHGAP12,ACVRL1,FLOT1,PPP3CB,ULK1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,OGN,LATS2	up_VSAP_EC

GO:0071333	0.0276	0.993	6	25	cellular response to glucose stimulus	BP	1	RAB11B,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0006935	0.0276	0.994	4	143	chemotaxis	BP	1	C3AR1,SEMA3A,SEMA3D,ENSCAFG00000032731	up_VPOR_EC
GO:0042330	0.0276	0.994	4	143	taxis	BP	1	C3AR1,SEMA3A,SEMA3D,ENSCAFG00000032731	up_VPOR_EC
GO:0051656	0.0276	0.996	3	129	establishment of organelle localization	BP	1	LYN,SPG11,STX4	down_ACOR_EC
GO:2001014	0.0276	0.997	3	8	regulation of skeletal muscle cell differentiation	BP	0.717	EPHB1,MEF2C,NR1D2	up_VCAV_EC
GO:1903522	0.0276	0.998	2	58	regulation of blood circulation	BP	1	IRX5,CAV1	up_VSAP_VSMC
GO:0003181	0.0276	1	1	7	atrioventricular valve morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0032682	0.0276	1	1	7	negative regulation of chemokine production	BP	1	NR1H4	up_APUL_EC
GO:0016202	0.0276	1	1	39	regulation of striated muscle tissue	BP	1	TBX5	up_APUL_VSMC
GO:0007026	0.0276	1	1	8	negative regulation of microtubule	BP	1	ARHGEF2	up_VPUL_EC
GO:0060544	0.0276	1	1	8	regulation of necroptotic process	BP	1	ARHGEF2	up_VPUL_EC
GO:1904467	0.0276	1	1	8	regulation of tumor necrosis factor secretion	BP	1	NR1H4	up_VPUL_EC
GO:0007632	0.0276	1	1	14	visual behavior	BP	1	LRRN4	up_VPUL_VSMC
GO:1902742	0.0276	1	1	14	apoptotic process involved in development	BP	1	SLIT2	up_VPUL_VSMC
GO:0032570	0.0276	1	1	6	response to progesterone	BP	1	CAV1	up_VSAP_VSMC
GO:0051490	0.027648686	1	1	1	negative regulation of filopodium assembly	BP	0.96436359	PRKCD	up_ACOR_EC
GO:0060697	0.027648686	1	1	1	positive regulation of phospholipid catabolic	BP	0.96436359	PRKCD	up_ACOR_EC
GO:0110112	0.027648686	1	1	1	regulation of lipid transporter activity	BP	0.96436359	PRKCD	up_ACOR_EC
GO:0110113	0.027648686	1	1	1	positive regulation of lipid transporter activity	BP	0.96436359	PRKCD	up_ACOR_EC
GO:1900161	0.027648686	1	1	1	regulation of phospholipid scramblase activity	BP	0.96436359	PRKCD	up_ACOR_EC
GO:1900163	0.027648686	1	1	1	positive regulation of phospholipid scramblase	BP	0.96436359	PRKCD	up_ACOR_EC
GO:2000752	0.027648686	1	1	1	regulation of glucosylceramide	BP	0.96436359	PRKCD	up_ACOR_EC
GO:2000753	0.027648686	1	1	1	positive regulation of glucosylceramide catabolic process	BP	0.96436359	PRKCD	up_ACOR_EC
GO:2000754	0.027648686	1	1	1	regulation of sphingomyelin catabolic	BP	0.96436359	PRKCD	up_ACOR_EC
GO:2000755	0.027648686	1	1	1	positive regulation of sphingomyelin catabolic	BP	0.96436359	PRKCD	up_ACOR_EC
GO:0021884	0.027693558	0.99805	2	10	forebrain neuron development	BP	0.96436359	DCLK2,NRP1	up_ACOR_EC
GO:0010810	0.0277	0.991	7	60	regulation of cell-substrate adhesion	BP	1	FBLN2,RHOD,THY1,EDIL3,GREM1,RAC2,ECM2	down_VCAV_EC
GO:0048524	0.0277	0.993	5	30	positive regulation of viral process	BP	0.791	P4HB,SMARCA4,CNOT7,APOE,RAD23A	down_VSAP_EC
GO:0001937	0.0277	0.995	4	15	negative regulation of endothelial cell	BP	0.718	MEF2C,DLL4,CAV2,VASH1	up_VCAV_EC
GO:0030033	0.0277	0.997	3	7	microvillus assembly	BP	0.718	PODXL,RAPGEF2,FSCN1	up_VCAV_EC
GO:0050857	0.0277	0.997	3	9	positive regulation of antigen receptor-mediated signaling	BP	0.718	PRKCH,NECTIN2,PRKD2	up_VCAV_EC
GO:0007596	0.0277	0.998	2	47	blood coagulation	BP	1	LYN,PDPN	down_ACOR_EC
GO:2001234	0.0277	0.998	2	75	negative regulation of apoptotic signaling	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0006656	0.0277	1	1	7	phosphatidylcholine biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0090398	0.0277	1	1	24	cellular senescence	BP	1	ARG2	up_AORT_VSMC
GO:0071225	0.0277	1	1	8	cellular response to muramyl dipeptide	BP	1	ARHGEF2	up_VPUL_EC
GO:0035608	0.027791732	1	1	1	protein deglutamylation	BP	0.96436359	AGBL5	up_ACOR_EC
GO:0035611	0.027791732	1	1	1	protein branching point deglutamylation	BP	0.96436359	AGBL5	up_ACOR_EC
GO:0034121	0.0278	0.994	5	22	regulation of toll-like receptor signaling	BP	0.718	TNFAIP3,PELI1,TLR3,OTUD4,HMGB1	up_VCAV_EC

GO:0043488	0.0278	0.996	3	28	regulation of mRNA stability	BP	1	TENT5C,AXIN2,SAMD4B	up_AFEM_EC
GO:1990440	0.0278	0.998	2	5	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP	0.792	DDIT3,ATF3	down_VSAP_EC
GO:0070848	0.0278	1	1	193	response to growth factor	BP	1	GATA5	down_AFEM_VSMC
GO:0007164	0.0278	1	1	23	establishment of tissue polarity	BP	1	WNT7A	up_AORT_VSMC
GO:0001736	0.0278	1	1	23	establishment of planar polarity	BP	1	WNT7A	up_AORT_VSMC
GO:0070227	0.0278	1	1	25	lymphocyte apoptotic process	BP	1	ARG2	up_AORT_VSMC
GO:0035051	0.0278	1	1	41	cardiocyte differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0045907	0.0278	1	1	6	positive regulation of vasoconstriction	BP	1	AVPR1A	up_VFEM_EC
GO:0046621	0.0278	1	1	8	negative regulation of organ growth	BP	1	TBX5	up_VPUL_EC
GO:0003209	0.0278	1	1	14	cardiac atrium morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0003230	0.0278	1	1	14	cardiac atrium development	BP	1	TBX5	up_VPUL_VSMC
GO:0032771	0.027888604	1	1	1	regulation of monophenol monooxygenase activity	BP	0.96436359	CDH3	up_ACOR_EC
GO:0032773	0.027888604	1	1	1	positive regulation of monophenol monooxygenase activity	BP	0.96436359	CDH3	up_ACOR_EC
GO:0032912	0.027888604	1	1	1	negative regulation of transforming growth factor beta2 production	BP	0.96436359	CDH3	up_ACOR_EC
GO:0048023	0.027888604	1	1	1	positive regulation of melanin biosynthetic	BP	0.96436359	CDH3	up_ACOR_EC
GO:0051796	0.027888604	1	1	1	negative regulation of timing of catagen	BP	0.96436359	CDH3	up_ACOR_EC
GO:0060901	0.027888604	1	1	1	regulation of hair cycle by canonical Wnt signaling	BP	0.96436359	CDH3	up_ACOR_EC
GO:1900378	0.027888604	1	1	1	positive regulation of secondary metabolite	BP	0.96436359	CDH3	up_ACOR_EC
GO:1902908	0.027888604	1	1	1	regulation of melanosome transport	BP	0.96436359	CDH3	up_ACOR_EC
GO:1902910	0.027888604	1	1	1	positive regulation of melanosome transport	BP	0.96436359	CDH3	up_ACOR_EC
GO:0051128	0.0279	0.979	81	790	regulation of cellular component organization	BP	0.719	EPHB1,PLK2,TEK,HCLS1,GBP5,SELP,KIT,SELE,PRKCH,ARHGEF15,IFRD1,CDA,ATP8A1,PDGFB,PODXL,BAIAP2L1,RELN,IWS1,MEF2C,RAPGEF1,TLR4,GATA3,EDN1,RAB11A,RALB,ARAP3,RAB27A,SNCAIP,NEDD9,IRF8,ARHGAP28,TMOD1,PPP3CA,MTOR,SLK,BMP2K,CNOT6,PDZD8,NCKAP1,RIOK3,PROX1,UHRF2,IQGAP2,STMN1,HMBOX1,PRKD2,SH3GLB1,SWAP70,SMARCA4,APOD,NCK1,FES,NSD1,HIST1H1A,RAPGEF2,PLCG2,SENP6,PAN3,TAOK1,FMNL3,HMGB1,TBC1D1,PMAIP1,ARPC5L,SMC5,RAD21,ARHGDIB,ZW10,KDM5A,HIF1A,KDM3A,ATRX,ENSCAFG00000002015,DCP2,TMOD3,RABGAP1,ARHGEF2,FSCN1,FBXO5,USP6NL,ZMYM2	up_VCAV_EC
GO:0051239	0.0279	0.981	55	859	regulation of multicellular organismal process	BP	1	GPAM,NOTCH2,HSPB6,LRP1,DCN,PRNP,LUM,VASN,FBN1,GLIPR2,BMPR1A,TRPV2,NUMBL,CHID1,LCAT,TFE3,SYDE1,LAMA3,CLSTN1,PLCL1,SEMA3C,ASPN,LRPAP1,THY1,RNF216,PEX5,TLX2,B4GALT1,GLI3,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,BPI,CYBA,MAVS,CDH2,LOXL3,SPRED1,RAB7B,IRX5,TSC22D3,UST,TWIST2,PRKCSH,DDR2,OMD,GREM1,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC
GO:0072359	0.0279	0.986	15	368	circulatory system development	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,RECK,TBXA2R,BVES,PTPRB,AXIN2,ACACB,CLIC4	up_AFEM_EC
GO:0009060	0.0279	0.991	7	31	aerobic respiration	BP	1	DLST,ENSCAFG00000004260,FXN,MTFR1L,IDH1,IDH3A,ENSCAFG00000006639	up_VSAP_EC
GO:0006942	0.0279	0.992	6	26	regulation of striated muscle contraction	BP	1	FGF13,ADRA1B,KCNE3,PDE5A,DMPK,JUP	up_ACOR_VSMC
GO:0051153	0.0279	0.996	3	28	regulation of striated muscle cell differentiation	BP	1	DLL1,GREM1,DMPK	up_AFEM_EC

GO:0070848	0.0279	0.996	3	193	response to growth factor	BP	1	FLRT3,NEO1,MXRA5	up_VPUL_EC
GO:0070848	0.0279	1	1	193	response to growth factor	BP	1	MXRA5	down_AORT_VSMC
GO:0008593	0.0279	1	1	33	regulation of Notch signaling pathway	BP	1	GATA5	down_VSAP_VSMC
GO:0030837	0.0279	1	1	14	negative regulation of actin filament	BP	1	SLIT2	up_VPUL_VSMC
GO:1901862	0.0279	1	1	14	negative regulation of muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0032060	0.0279	1	1	6	bleb assembly	BP	1	EMP1	up_VSAP_VSMC
GO:0050804	0.027920086	0.9918	6	87	modulation of chemical synaptic transmission	BP	0.96436359	CNTNAP4,BRSK1,PLCL1,KCNB1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0099177	0.027920086	0.9918	6	87	regulation of trans-synaptic signaling	BP	0.96436359	CNTNAP4,BRSK1,PLCL1,KCNB1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0055006	0.028	0.994	5	18	cardiac cell development	BP	1	ACTN2,BMP4,NEBL,EDN1,BVES	up_ACOR_VSMC
GO:0045823	0.028	0.999	2	4	positive regulation of heart contraction	BP	0.72	EDN1,GCH1	up_VCAV_EC
GO:0002507	0.028	1	1	7	tolerance induction	BP	1	LYN	down_ACOR_EC
GO:0098693	0.028	1	1	25	regulation of synaptic vesicle cycle	BP	1	WNT7A	up_AORT_VSMC
GO:0021825	0.028	1	1	4	substrate-dependent cerebral cortex tangential	BP	1	SEMA3A	up_VPOR_EC
GO:0016101	0.028	1	1	13	diterpenoid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0042698	0.028	1	1	14	ovulation cycle	BP	1	SLIT2	up_VPUL_VSMC
GO:0048635	0.028	1	1	14	negative regulation of muscle organ	BP	1	TBX5	up_VPUL_VSMC
GO:0046958	0.028063966	1	1	1	nonassociative learning	BP	0.96436359	MAPK8IP2	up_ACOR_EC
GO:1901576	0.0281	0.995	6	1877	organic substance biosynthetic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0051291	0.0281	0.993	5	21	protein heterooligomerization	BP	0.929	RRM1,C1QTNF6,RCC1,FARSA,PDSS1	down_ACOR_VSMC
GO:0030279	0.0281	0.994	5	19	negative regulation of ossification	BP	1	TWIST2,AXIN2,HDAC7,LRP4,LIMD1	up_VSAP_EC
GO:0045744	0.0281	0.995	4	15	negative regulation of G protein-coupled receptor signaling pathway	BP	0.72	CXCL8,APLNR,STMN1,RGS2	up_VCAV_EC
GO:0060536	0.0281	0.999	2	3	cartilage morphogenesis	BP	0.72	MEF2C,STC1	up_VCAV_EC
GO:0044090	0.0281	0.999	2	4	positive regulation of vacuole organization	BP	0.72	RALB,SH3GLB1	up_VCAV_EC
GO:2000786	0.0281	0.999	2	4	positive regulation of autophagosome assembly	BP	0.72	RALB,SH3GLB1	up_VCAV_EC
GO:0010977	0.0281	0.998	2	33	negative regulation of neuron projection	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0007266	0.0281	0.998	2	64	Rho protein signal transduction	BP	1	TIAM1,CDC42EP5	up_VFEM_EC
GO:0010720	0.0281	0.998	2	110	positive regulation of cell development	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0000028	0.0281	1	1	9	ribosomal small subunit assembly	BP	1	RPSA	down_ACOR_EC
GO:0043162	0.0281	1	1	7	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	BP	1	NEDD4	down_ACOR_EC
GO:0031076	0.0281	1	1	14	embryonic camera-type eye development	BP	1	CITED2	down_VPOR_EC
GO:0048645	0.0281	1	1	33	animal organ formation	BP	1	GATA5	down_VSAP_VSMC
GO:0048747	0.0281	1	1	20	muscle fiber development	BP	1	BEND2	up_AFEM_VSMC
GO:0016079	0.0281	1	1	27	synaptic vesicle exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0048634	0.0281	1	1	40	regulation of muscle organ development	BP	1	TBX5	up_APUL_VSMC
GO:0048841	0.0281	1	1	4	regulation of axon extension involved in	BP	1	SEMA3A	up_VPOR_EC
GO:0048643	0.0281	1	1	7	positive regulation of skeletal muscle tissue	BP	1	CYP26B1	up_VFEM_EC
GO:0038060	0.028101498	1	1	1	nitric oxide-cGMP-mediated signaling	BP	0.96436359	GUCY1B1	up_ACOR_EC
GO:1900454	0.028122114	1	1	1	positive regulation of long-term synaptic depression	BP	0.96436359	KCNB1	up_ACOR_EC

GO:0032498	0.028131274	1	1	1	detection of muramyl dipeptide	BP	0.96436359	NOD2	up_ACOR_EC
GO:0032499	0.028131274	1	1	1	detection of peptidoglycan	BP	0.96436359	NOD2	up_ACOR_EC
GO:0032889	0.028164414	1	1	1	regulation of vacuole fusion, non-autophagic	BP	0.96436359	VPS16	up_ACOR_EC
GO:0010803	0.028186101	0.99799	2	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	0.96436359	NR1H4,CCDC3	up_ACOR_EC
GO:0043069	0.0282	0.984	24	262	negative regulation of programmed cell death	BP	0.795	ARHGEF2,VEGFA,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,HYOU1,AARS,FHL2,PTGS2,HIF1A,ZPR1,MTDH,CTNNB1,CRYAB,BNIP3,GSK3B,HTT,GLO1,PAK2,SIX4,NRP1,ARF4	down_VSAP_EC
GO:0071345	0.0282	0.993	5	210	cellular response to cytokine stimulus	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ENSCAFG00000032731,GNPNAT1	up_VPOR_EC
GO:0051588	0.0282	0.996	3	28	regulation of neurotransmitter	BP	1	KCNC4,CHRM2,CAMK2A	up_AFEM_EC
GO:0007423	0.0282	0.996	3	155	sensory organ development	BP	1	SALL1,IRX5,MAB21L1	up_VSAP_VSMC
GO:0019219	0.0282	1	2	1151	regulation of nucleobase-containing compound metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0140059	0.0282	0.999	2	3	dendrite arborization	BP	1	ZNF365,NRP1	up_ACOR_VSMC
GO:0032496	0.0282	0.998	2	77	response to lipopolysaccharide	BP	1	NR1H4,MRC1	up_VPUL_EC
GO:0006189	0.0282	1	1	4	'de novo' IMP biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0031629	0.0282	1	1	8	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	STX4	down_ACOR_EC
GO:0099500	0.0282	1	1	8	vesicle fusion to plasma membrane	BP	1	STX4	down_ACOR_EC
GO:0007507	0.0282	1	1	194	heart development	BP	1	GATA5	down_AFEM_VSMC
GO:0051271	0.0282	1	1	98	negative regulation of cellular component	BP	1	JUP	down_VFEM_VSMC
GO:0051452	0.0282	1	1	20	intracellular pH reduction	BP	1	CA2	up_VCAV_VSMC
GO:0009190	0.0282	1	1	8	cyclic nucleotide biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0052652	0.0282	1	1	8	cyclic purine nucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0071379	0.0282	1	1	8	cellular response to prostaglandin stimulus	BP	1	PTGER2	up_VPUL_EC
GO:0060043	0.0282	1	1	14	regulation of cardiac muscle cell proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:1901052	0.028206196	1	1	1	sarcosine metabolic process	BP	0.96436359	SARDH	up_ACOR_EC
GO:1901053	0.028206196	1	1	1	sarcosine catabolic process	BP	0.96436359	SARDH	up_ACOR_EC
GO:0038190	0.028214623	1	1	1	VEGF-activated neuropilin signaling pathway	BP	0.96436359	NRP1	up_ACOR_EC
GO:0048842	0.028214623	1	1	1	positive regulation of axon extension involved in axon guidance	BP	0.96436359	NRP1	up_ACOR_EC
GO:0061441	0.028214623	1	1	1	renal artery morphogenesis	BP	0.96436359	NRP1	up_ACOR_EC
GO:1902336	0.028214623	1	1	1	positive regulation of retinal ganglion cell axon	BP	0.96436359	NRP1	up_ACOR_EC
GO:1902378	0.028214623	1	1	1	VEGF-activated neuropilin signaling pathway involved in axon guidance	BP	0.96436359	NRP1	up_ACOR_EC
GO:1902669	0.028214623	1	1	1	positive regulation of axon guidance	BP	0.96436359	NRP1	up_ACOR_EC
GO:1905040	0.028214623	1	1	1	otic placode development	BP	0.96436359	NRP1	up_ACOR_EC
GO:2000821	0.028214778	1	1	1	regulation of grooming behavior	BP	0.96436359	CNTNAP4	up_ACOR_EC
GO:0051695	0.028217394	1	1	1	actin filament uncapping	BP	0.96436359	ACTN2	up_ACOR_EC
GO:0086097	0.028217394	1	1	1	phospholipase C-activating angiotensin-activated signaling	BP	0.96436359	ACTN2	up_ACOR_EC
GO:2001137	0.028217394	1	1	1	positive regulation of endocytic recycling	BP	0.96436359	ACTN2	up_ACOR_EC
GO:0033624	0.028268997	1	1	1	negative regulation of integrin activation	BP	0.96436359	PTGER4	up_ACOR_EC
GO:0072682	0.028268997	1	1	1	eosinophil extravasation	BP	0.96436359	PTGER4	up_ACOR_EC

GO:2000417	0.028268997	1	1	1	negative regulation of eosinophil migration	BP	0.96436359	PTGER4	up_ACOR_EC
GO:2000419	0.028268997	1	1	1	regulation of eosinophil extravasation	BP	0.96436359	PTGER4	up_ACOR_EC
GO:2000420	0.028268997	1	1	1	negative regulation of eosinophil extravasation	BP	0.96436359	PTGER4	up_ACOR_EC
GO:0042221	0.0283	0.987	14	1012	response to chemical	BP	1	C3AR1,ARHGEF2,ENSCAFG00000002015,SLC7A11,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,SEMA3D,SRP54,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0007186	0.0283	0.991	7	124	G protein-coupled receptor signaling	BP	1	GPR1,CHRM2,HTR1D,CAMK2A,PTHLH,LGR6,CCL5	up_AFEM_EC
GO:0035967	0.0283	0.992	6	42	cellular response to topologically incorrect	BP	0.795	HSPA5,ERO1A,PTPN2,DDIT3,ATF3,CREB3L2	down_VSAP_EC
GO:0048675	0.0283	0.992	6	26	axon extension	BP	1	SLIT2,ABL1,PLXNA4,DPYSL2,TTL,ULK1	up_VSAP_EC
GO:0051353	0.0283	0.995	4	13	positive regulation of oxidoreductase activity	BP	1	HTR2B,ATP7A,EDN1,PARK7	up_ACOR_VSMC
GO:0045935	0.0283	0.995	4	491	positive regulation of nucleobase-containing compound metabolic	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0031498	0.0283	0.997	3	8	chromatin disassembly	BP	0.933	SMARCC1,SMARCB1,GRWD1	down_ACOR_VSMC
GO:0045824	0.0283	0.996	3	11	negative regulation of innate immune response	BP	0.795	PTPN2,CNOT7,A2M	down_VSAP_EC
GO:0050922	0.0283	0.996	3	11	negative regulation of chemotaxis	BP	0.795	PTPN2,MMP28,NRP1	down_VSAP_EC
GO:0070432	0.0283	0.999	2	3	regulation of nucleotide-binding oligomerization domain containing 2	BP	0.722	TNFAIP3,TLR4	up_VCAV_EC
GO:0070424	0.0283	0.999	2	3	regulation of nucleotide-binding oligomerization domain containing	BP	0.722	TNFAIP3,TLR4	up_VCAV_EC
GO:0051146	0.0283	0.998	2	76	striated muscle cell differentiation	BP	1	TBX5,MYBPC2	up_VPUL_EC
GO:0003015	0.0283	0.998	2	58	heart process	BP	1	IRX5,CAV1	up_VSAP_VSMC
GO:0031958	0.0283	1	1	5	corticosteroid receptor signaling pathway	BP	1	NEDD4	down_ACOR_EC
GO:0042921	0.0283	1	1	5	glucocorticoid receptor signaling pathway	BP	1	NEDD4	down_ACOR_EC
GO:0051293	0.0283	1	1	13	establishment of spindle localization	BP	1	GPSM2	down_AFEM_EC
GO:0015698	0.0283	1	1	24	inorganic anion transport	BP	1	SLC20A2	up_AORT_VSMC
GO:0106027	0.0283	1	1	24	neuron projection organization	BP	1	WNT7A	up_AORT_VSMC
GO:0032814	0.0283	1	1	7	regulation of natural killer cell activation	BP	1	TOX	up_VFEM_EC
GO:0071310	0.028326535	0.98369	25	634	cellular response to organic substance	BP	0.96436359	NR1H4,SOX9,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,CCDC3,AGRN,NOD2,RGMA,SMAD6,ACTN2,PAK3,PTGER4,ADAMTSL2,MAVS,FOXC2,LRRC15,IFIT2,LRP4,LRRC4,RARRES2,PRKACA,NRP1,PRKCD	up_ACOR_EC
GO:1903756	0.028326724	1	1	1	regulation of transcription from RNA polymerase II promoter by histone	BP	0.96436359	ZMYND8	up_ACOR_EC
GO:1903758	0.028326724	1	1	1	negative regulation of transcription from RNA polymerase II promoter by histone modification	BP	0.96436359	ZMYND8	up_ACOR_EC
GO:0010557	0.0284	0.98	54	492	positive regulation of macromolecule biosynthetic process	BP	0.722	HCLS1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,TCF4,FOXN2,ENSCAFG00000017103,IRF8,PPP3CA,YES1,MTOR,BMP2,HHEX,CREM,CNOT6,PROX1,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,LDB2,JAG1,NSD1,BCL10,CNOT7,HMGB1,AHR,BLM,RIPK1,ITGA6,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0006366	0.0284	0.991	7	583	transcription by RNA polymerase II	BP	1	ACVRL1,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0060688	0.0284	0.993	5	29	regulation of morphogenesis of a	BP	0.795	SULF1,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0019511	0.0284	0.998	2	5	peptidyl-proline hydroxylation	BP	0.795	P4HB,P4HA1	down_VSAP_EC
GO:0021825	0.0284	1	1	4	substrate-dependent cerebral cortex tangential	BP	1	NRP2	down_ACOR_EC

GO:0051642	0.0284	1	1	13	centrosome localization	BP	1	GPSM2	down_AFEM_EC
GO:0061842	0.0284	1	1	13	microtubule organizing center localization	BP	1	GPSM2	down_AFEM_EC
GO:0002027	0.0284	1	1	20	regulation of heart rate	BP	1	IRX5	up_AFEM_VSMC
GO:0060421	0.0284	1	1	14	positive regulation of heart growth	BP	1	TBX5	up_VPUL_VSMC
GO:0006139	0.0285	0.994	6	1909	nucleobase-containing compound metabolic	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0045669	0.0285	0.994	4	24	positive regulation of osteoblast differentiation	BP	1	BMPR1A,CLSTN1,GLI3,DDR2	down_VCAV_EC
GO:0007599	0.0285	0.998	2	48	hemostasis	BP	1	LYN,PDPN	down_ACOR_EC
GO:0048265	0.0285	0.999	2	3	response to pain	BP	0.725	RELN,P2RX2	up_VCAV_EC
GO:0032836	0.0285	1	1	4	glomerular basement membrane development	BP	1	SULF1	down_ACOR_EC
GO:0060601	0.0285	1	1	6	lateral sprouting from an epithelium	BP	1	SULF1	down_ACOR_EC
GO:0034695	0.0285	1	1	8	response to prostaglandin E	BP	1	PTGER2	up_VPUL_EC
GO:0072359	0.0286	0.981	47	368	circulatory system development	BP	1	TNNT2,PDLIM3,VEGFD,SMAD6,ACTN2,LEP,GATA5,GATA4,ANGPT1,HTR2B,RECK,BMP4,FGFR2,GJA1,TLR3,SEC24B,XIRP1,CITED2,SPINT1,SASH1,LMO4,FGF18,NEBL,ANKRD1,EGLN1,NRP1,SMARCD3,SLITRK5,TBX20,TBX5,FRS2,PSEN1,TGFBR1,SYNJ2BP,CHD7,JUP,PSKH1,EDN1,HPGD,JAM3,AP2B1,GAA,ERAP1,BVES,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0007050	0.0286	0.989	9	53	cell cycle arrest	BP	0.94	SLC29A1,PPM1G,CASP2,CDKN2C,MAP3K20,CDK4,BRCA1,PRR11,CDKN3	down_ACOR_VSMC
GO:0019935	0.0286	0.99	8	38	cyclic-nucleotide-mediated signaling	BP	1	ADRA1B,ADGRD1,HTR2B,ABCA1,PTGIR,ADCY6,APLP1,GNAQ	up_ACOR_VSMC
GO:0071900	0.0286	0.996	3	131	regulation of protein serine/threonine kinase	BP	1	LYN,IGF1R,PRKAR2A	down_ACOR_EC
GO:0016101	0.0286	0.996	3	13	diterpenoid metabolic process	BP	1	CYP1B1,RETSAT,RDH10	down_VCAV_EC
GO:0002376	0.0286	0.997	3	622	immune system process	BP	1	HOXA9,ARG2,ESR1	up_AORT_VSMC
GO:1990138	0.0286	0.998	2	35	neuron projection extension	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0001938	0.0286	1	1	34	positive regulation of endothelial cell	BP	1	TGFBR1	down_VSAP_VSMC
GO:0009308	0.0286	1	1	20	amine metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0003156	0.0286	1	1	20	regulation of animal organ formation	BP	1	GATA5	up_VCAV_VSMC
GO:0010646	0.0287	0.978	108	945	regulation of cell communication	BP	1	SH3TC2,ADRA1B,TLR1,SMAD6,LGR6,LEP,PLCL1,LBH,MID1,GATA5,HTR2B,RASSF2,ZRANB1,FBXL20,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,ELF1,HRH1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,ZNRF3,AR,PTGIR,SASH1,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ITPR1,LIMS2,ANKRD1,F2RL1,DAPK1,BNIP3,EGLN1,CRLF3,ENSCAFG00000006238,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,DMPK,NPNT,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,FRS2,RNF19A,SCG5,RGS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,CHD7,SIPA1L1,CCL5,WWC2,DUSP22,SIAH1,EDN1,SESN1,KCNC4,DUSP26,NOD2,LRRC4,FAM107A,DDIT4,DISC1,SH3RF3,SERINC3,USP20,HERPUD1,MAP3K7,INPP5K,PREPL,BMT2,PFKL,WFS1,SH3BP4,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0051094	0.0287	0.982	33	388	positive regulation of developmental process	BP	0.798	ARHGEF2,VEGFA,CELF1,NR1H4,SERPINE1,SOCS5,JCAD,DPYSL3,ILK,PTGS2,PIK3C2A,HOXB7,HIF1A,EVI2B,MTDH,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,APOE,KLF5,LYN,BNIP3,MMD,VLDLR,REST,PRMT1,DISC1,LRRTM2,INHBA,HIF1AN,SIX4,NRP1	down_VSAP_EC
GO:0032412	0.0287	0.989	9	46	regulation of ion transmembrane	BP	1	ACTN2,PLCG2,KCNE3,TCAF1,PTPN3,DAPK1,CACNB3,AKAP6,FXYD1	up_ACOR_VSMC
GO:0002761	0.0287	0.991	7	36	regulation of myeloid leukocyte differentiation	BP	0.727	HCLS1,CASP8,MTOR,CREB1,RIPK1,CUL4A,TJP2	up_VCAV_EC
GO:0071346	0.0287	0.992	6	41	cellular response to interferon-gamma	BP	0.798	FLNB,MYO1C,KIF5B,PTPN2,CDC37,GBP5	down_VSAP_EC

GO:0030239	0.0287	0.993	5	21	myofibril assembly	BP	0.727	MEF2C,EDN1,TMOD1,PROX1,TMOD3	up_VCAV_EC
GO:0019233	0.0287	0.995	4	16	sensory perception of pain	BP	0.727	EPHB1,HOXB8,ACPP,MMP24	up_VCAV_EC
GO:0042023	0.0287	0.997	3	8	DNA endoreduplication	BP	0.94	SMC1A,E2F8,SMC3	down_ACOR_VSMC
GO:0098801	0.0287	0.997	3	8	regulation of renal system process	BP	1	F2RL1,EDN1,INPP5K	up_ACOR_VSMC
GO:0035437	0.0287	0.998	2	5	maintenance of protein localization in endoplasmic reticulum	BP	0.798	HSPA5,KDELR2	down_VSAP_EC
GO:0050686	0.0287	1	1	13	negative regulation of mRNA processing	BP	1	SRSF6	down_AFEM_EC
GO:0035107	0.0288	0.991	7	60	appendage morphogenesis	BP	1	BMPR1A,RECK,SEMA3C,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0035108	0.0288	0.991	7	60	limb morphogenesis	BP	1	BMPR1A,RECK,SEMA3C,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0072527	0.0288	0.993	5	23	pyrimidine-containing compound metabolic	BP	0.727	CDA,MTOR,ACPP,DCK,TET2	up_VCAV_EC
GO:0046638	0.0288	0.995	4	13	positive regulation of alpha-beta T cell	BP	1	ZBTB16,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0048048	0.0288	0.995	4	13	embryonic eye morphogenesis	BP	1	RARG,ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:0009583	0.0288	0.998	2	5	detection of light stimulus	BP	0.799	GNAQ,RDH11	down_VSAP_EC
GO:0016311	0.0288	0.998	2	106	dephosphorylation	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0040013	0.0288	1	1	100	negative regulation of locomotion	BP	1	JUP	down_VFEM_VSMC
GO:0110110	0.0288	1	1	34	positive regulation of animal organ	BP	1	GATA5	down_VSAP_VSMC
GO:0065009	0.028829351	0.98288	28	735	regulation of molecular function	BP	0.97940892	CDH3,NR1H4,PLCL1,PKIB,PCSK1N,ENSCAFG00000004331,FZD5,IFI6,DUSP26,NOD2,DYNC1I1,ACTN2,ARHGAP28,PAK3,CST3,MAPK8IP2,MAVS,LRRC15,IFIT2,CLSTN1,LRRC4,CLU,PRKCD,PPP1R26,PM20D1,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0055088	0.0289	0.991	7	37	lipid homeostasis	BP	0.946	SREBF2,RALY,INSIG1,CAV1,LIPC,NUS1,THADA	down_ACOR_VSMC
GO:0001570	0.0289	0.991	7	37	vasculogenesis	BP	0.727	AMOT,CD34,TIPARP,APLNR,SOX18,HHEX,RAPGEF2	up_VCAV_EC
GO:0003208	0.0289	0.992	6	24	cardiac ventricle morphogenesis	BP	1	TNNT2,FGFR2,SMARCD3,TBX20,TBX5,CHD7	up_ACOR_VSMC
GO:0060042	0.0289	0.996	3	14	retina morphogenesis in camera-type eye	BP	1	THY1,IRX5,THRB	down_VCAV_EC
GO:0017157	0.0289	0.998	2	58	regulation of exocytosis	BP	1	LYN,STX4	down_ACOR_EC
GO:0015813	0.0289	0.999	2	3	L-glutamate transmembrane transport	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0051938	0.0289	0.999	2	3	L-glutamate import	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0098712	0.0289	0.999	2	3	L-glutamate import across plasma membrane	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0061209	0.0289	0.999	2	4	cell proliferation involved in mesonephros	BP	0.727	GATA3,BMP2	up_VCAV_EC
GO:1903409	0.0289	1	1	24	reactive oxygen species biosynthetic process	BP	1	ARG2	up_AORT_VSMC
GO:1901861	0.0289	1	1	41	regulation of muscle tissue development	BP	1	TBX5	up_APUL_VSMC
GO:0002682	0.029	0.996	3	343	regulation of immune system process	BP	1	TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0032836	0.029	0.999	2	4	glomerular basement membrane development	BP	0.803	SULF1,MYO1E	down_VSAP_EC
GO:0042692	0.029	0.998	2	105	muscle cell differentiation	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0002902	0.029	1	1	6	regulation of B cell apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0032233	0.029	1	1	21	positive regulation of actin filament bundle	BP	1	LIMK1	up_VCAV_VSMC
GO:1900027	0.029	1	1	6	regulation of ruffle assembly	BP	1	CAV1	up_VSAP_VSMC
GO:2000026	0.0291	0.981	38	560	regulation of multicellular organismal development	BP	1	NOTCH2,HSPB6,DCN,VASN,FBN1,GLIPR2,BMPR1A,TRPV2,NUMBL,TFE3,SYDE1,LAMA3,CLSTN1,SEMA3C,ASPN,THY1,TLX2,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,CDH2,LOXL3,SPRED1,RAB7B,TSC22D3,UST,PRKCSH,DDR2,OMD,GREM1,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC

GO:0030154	0.0291	0.982	34	1040	cell differentiation	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXC10,LEP,LBH,GAS1,HOXA7,DLL1,VXN,PLXNA4,NEFH,TWIST2,THRB,LGI4,HCK,TMEM100,GREM1,NFE2L1,CAMK2A,CYLD,MYBL1,PTHLH,EVI2B,BVES,AXIN2,NAPEPLD,PPARGC1A,DMPK,LRRN2,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0031346	0.0291	0.989	9	73	positive regulation of cell projection organization	BP	0.803	FSCN1,DPYSL3,DYNLL1,ANLN,APOE,LYN,VLDLR,HTT,NRP1	down_VSAP_EC
GO:0055007	0.0291	0.991	7	31	cardiac muscle cell differentiation	BP	1	ACTN2,BMP4,NEBL,TBX5,FRS2,EDN1,BVES	up_ACOR_VSMC
GO:1902895	0.0291	0.995	4	15	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	0.731	PDGFB,BMP2,SMARCA4,HIF1A	up_VCAV_EC
GO:0072079	0.0291	0.996	3	12	nephron tubule formation	BP	0.803	ENSCAFG00000032470,CTNNB1,SIX4	down_VSAP_EC
GO:0001845	0.0291	1	1	5	phagolysosome assembly	BP	1	SPG11	down_ACOR_EC
GO:0021854	0.0291	1	1	6	hypothalamus development	BP	1	NRP2	down_ACOR_EC
GO:0060968	0.0291	1	1	23	regulation of gene silencing	BP	1	ESR1	up_AORT_VSMC
GO:0044706	0.0291	1	1	27	multi-multicellular organism process	BP	1	ESR1	up_AORT_VSMC
GO:1902668	0.0291	1	1	4	negative regulation of axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:2000144	0.0291	1	1	12	positive regulation of DNA-templated transcription,	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060546	0.0291	1	1	7	negative regulation of necroptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:0060547	0.0291	1	1	7	negative regulation of necrotic cell death	BP	1	CAV1	up_VSAP_VSMC
GO:1901631	0.02912899	1	1	1	positive regulation of presynaptic membrane	BP	0.98132464	LRP4	up_ACOR_EC
GO:1903911	0.02912899	1	1	1	positive regulation of receptor clustering	BP	0.98132464	LRP4	up_ACOR_EC
GO:1904395	0.02912899	1	1	1	positive regulation of skeletal muscle acetylcholine-gated	BP	0.98132464	LRP4	up_ACOR_EC
GO:1904398	0.02912899	1	1	1	positive regulation of neuromuscular junction development	BP	0.98132464	LRP4	up_ACOR_EC
GO:0009063	0.0292	0.992	6	25	cellular amino acid catabolic process	BP	1	GOT1,ADHFE1,ALDH6A1,BCKDHB,ENSCAFG00000002977,IDO2	up_VSAP_EC
GO:0002792	0.0292	0.993	5	29	negative regulation of peptide secretion	BP	0.804	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0010499	0.0292	0.999	2	3	proteasomal ubiquitin-independent protein catabolic process	BP	0.731	PSME4,ENC1	up_VCAV_EC
GO:0050891	0.0292	1	1	12	multicellular organismal water homeostasis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0060260	0.0292	1	1	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035265	0.0293	0.988	10	54	organ growth	BP	1	ACACB,SLC6A4,FGF7,DLL1,SAV1,RARG,DDR2,FXN,TGFBR2,LATS2	up_VSAP_EC
GO:0090050	0.0293	0.995	4	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	0.731	PLK2,PIK3C2A,MAP3K3,JCAD	up_VCAV_EC
GO:0010557	0.0293	0.994	4	492	positive regulation of macromolecule biosynthetic process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0046456	0.0293	0.997	3	8	icosanoid biosynthetic process	BP	0.731	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:0007178	0.0293	0.998	2	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0007019	0.0293	1	1	13	microtubule depolymerization	BP	1	TAOK1	up_AORT_EC
GO:0032386	0.029333462	0.98941	8	137	regulation of intracellular transport	BP	0.98615433	SH3TC2,CDH3,KCNB1,EDEM2,ACTN2,PREB,MAVS,PRKCD	up_ACOR_EC
GO:0001503	0.0294	0.985	17	109	ossification	BP	1	FZD1,PEX7,TWIST2,WNT11,AXIN2,OSR2,PPARGC1B,ZHX3,HDAC7,OSR1,ZBTB16,DDR2,OMD,SHOX2,LRP4,LIMD1,BGLAP	up_VSAP_EC
GO:0050731	0.0294	0.99	8	44	positive regulation of peptidyl-tyrosine	BP	0.731	HCLS1,KIT,PDGFB,RELN,NEDD9,YES1,MTOR,ARHGEF2	up_VCAV_EC
GO:0045778	0.0294	0.993	5	35	positive regulation of ossification	BP	1	BMPR1A,CLSTN1,GLI3,DDR2,ZBTB16	down_VCAV_EC
GO:0002720	0.0294	0.995	4	13	positive regulation of cytokine production involved in immune	BP	1	F2RL1,B2M,MAP3K7,IL18R1	up_ACOR_VSMC

GO:0097150	0.0294	0.995	4	13	neuronal stem cell population maintenance	BP	0.731	HOOK3,PROX1,MMP24,JAG1	up_VCAV_EC
GO:0071498	0.0294	0.997	3	8	cellular response to fluid shear stress	BP	0.731	MEF2C,MTSS1,PTGS2	up_VCAV_EC
GO:0031326	0.0294	1	2	1176	regulation of cellular biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0007155	0.0294	0.998	2	324	cell adhesion	BP	1	TGFBI,GATA5	down_VSAP_VSMC
GO:0061438	0.0294	0.999	2	3	renal system vasculature morphogenesis	BP	1	BMP4,NRP1	up_ACOR_VSMC
GO:0061439	0.0294	0.999	2	3	kidney vasculature morphogenesis	BP	1	BMP4,NRP1	up_ACOR_VSMC
GO:0061551	0.0294	1	1	5	trigeminal ganglion development	BP	1	NRP2	down_ACOR_EC
GO:0090050	0.0294	1	1	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0003156	0.0294	1	1	20	regulation of animal organ formation	BP	1	EYA1	up_AFEM_VSMC
GO:0050806	0.0294	1	1	25	positive regulation of synaptic transmission	BP	1	WNT7A	up_AORT_VSMC
GO:0106049	0.0294	1	1	4	regulation of cellular response to osmotic	BP	1	ARHGEF2	up_VPOR_EC
GO:1902218	0.0294	1	1	4	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	ARHGEF2	up_VPOR_EC
GO:1902219	0.0294	1	1	4	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	ARHGEF2	up_VPOR_EC
GO:0032940	0.0295	0.982	31	231	secretion by cell	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FBXL20,FERMT1,SYT16,TM7SF3,ABCA1,CD274,STX11,ANKRD1,F2RL1,PTPN22,PRKCE,SCG5,PSEN1,PCSK6,CHD7,CCL5,RAB11B,EDN1,KCNC4,NOD2,SCAMP5,SCRN2,PREPL,PFKL,PARK7,LMF1	up_ACOR_VSMC
GO:0010605	0.0295	0.99	8	745	negative regulation of macromolecule metabolic	BP	1	ACVRL1,LYN,IGF1R,HOXA7,PRKAR2A,ELK3,ASPN,NEDD4	down_ACOR_EC
GO:0002376	0.0295	0.991	7	622	immune system process	BP	1	LYN,HOXA3,IGF1R,PDPN,HOXA7,IPO7,STX4	down_ACOR_EC
GO:0002042	0.0295	0.993	5	29	cell migration involved in sprouting angiogenesis	BP	0.81	VEGFA,JCAD,PIK3C2A,STARD13,NRP1	down_VSAP_EC
GO:1902043	0.0295	0.996	3	9	positive regulation of extrinsic apoptotic signaling pathway via	BP	0.731	ATF3,PMAIP1,SKIL	up_VCAV_EC
GO:0060836	0.0295	0.998	2	4	lymphatic endothelial cell differentiation	BP	0.731	SOX18,PROX1	up_VCAV_EC
GO:0050905	0.0295	1	1	26	neuromuscular process	BP	1	HOXC10	up_AORT_VSMC
GO:0051148	0.0295	1	1	12	negative regulation of muscle cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0000045	0.02955579	0.99386	4	46	autophagosome assembly	BP	0.98664651	ATG16L2,CHMP4B,TP53INP2,ENSCAFG00000010493	up_ACOR_EC
GO:0060249	0.029584643	0.99018	7	110	anatomical structure homeostasis	BP	0.98664651	CDH3,PKIB,SOX9,PTH1R,NOD2,CHMP4B,TP53INP2	up_ACOR_EC
GO:0071326	0.02959267	0.99565	3	26	cellular response to monosaccharide stimulus	BP	0.98664651	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0071331	0.02959267	0.99565	3	26	cellular response to hexose stimulus	BP	0.98664651	NR1H4,KCNB1,PRKACA	up_ACOR_EC

GO:0032501	0.0296	0.976	194	1782	multicellular organismal process	BP	1	EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,PLCL1,LBH,AFF3,SLC26A7,KCNE3,GATA5,GATA4,CD83,ANGPT1,EPYC,HTR2B,RASSF2,MBP,FBXL20,PRDX4,RECK,SHROOM3,FEZ1,COCH,MLLT3,ITM2C,FERMT1,BMP4,LCAT,LNPK,TBX18,NPPB,FGFR2,TP53BP1,ABCA1,GJA1,ELF1,ATRX,MED14,HRH1,TLR3,LRRN4,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,SPINT1,GLRB,ISG15,ACSL6,ZNRF3,CD274,ZNF365,SASH1,SLC2A5,GPR155,LMO4,TMEM108,FGF18,FAM210B,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,ADCY6,USP53,EBF4,ZMYM2,ITPR1,PLAC8B,LIMS2,ANKRD1,F2RL1,HRH2,CAMK2D,ENPP4,CTSB,RBM4B,EGLN1,ENSCAFG00000006238,CLSTN1,CREBRF,ABCA4,NRP1,PTPN22,GPM6A,CHD2,LRPAP1,ULK2,DMPK,NPNT,UNC5B,SMARCD3,EVL,SPINT2,SLITRK5,PTGDR,TBX20,BBX,TBX5,PRKCE,MARF1,FZD3,AFF4,DKKL1,FRS2,CPAMD8,RND1,RNLS,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,TGFBR1,PCSK6,SYNJ2BP,CHD7,JUP,SPINK2,SIPA1L1,DDR2,CLN8,WWC2,FOSL2,PERP,PSKH1,RTKN2,SIAH1,SSH3,C10H2orf49,EDN1,OXR1,NID1,HPGD,NOD2,ARID5B,ASAP1,FAM107A,DMC1,INSYN1,SERPINB5,JAM3,	up_ACOR_VSMC
GO:0051489	0.0296	1	1	14	regulation of filopodium assembly	BP	1	FSCN1	down_AFEM_EC
GO:0003283	0.0296	1	1	8	atrial septum development	BP	1	TBX5	up_APUL_EC
GO:0060413	0.0296	1	1	8	atrial septum morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0043500	0.0296	1	1	21	muscle adaptation	BP	1	GATA5	up_VCAV_VSMC
GO:0006357	0.0297	0.979	59	547	regulation of transcription by RNA polymerase II	BP	0.733	EDNRB,HCLS1,FLI1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,DLL4,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,ENSCAFG00000017103,IRF8,SOX18,PPP3CA,YES1,ELF4,BMP2,HMG20A,HHEX,CREM,PROX1,ARID4B,HMBOX1,PRKD2,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,JAG1,TCERG1,CTDSPL2,CNOT7,HMGB1,AHR,RIPK1,ITGA6,SKIL,MTA2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ARID5A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:1901566	0.0297	0.98	41	598	organonitrogen compound biosynthetic process	BP	1	GPAM,UBA52,ADCY6,LARP6,COA1,KRTCAP2,CLIP3,LCAT,SAMD4B,RPL23,RPL13,DDOST,UROS,ATP5MC1,GFPT2,PIGS,EIF3K,NECAB3,ADK,WDR45,MRPL37,B4GALT1,PARK7,RPL27A,EEF2,ZFP36L1,RPL27,AMPD2,MRPS11,ORMDL3,RPS27,FUT8,ACSS2,ENSCAFG00000015122,PYM1,RPN2,GLS2,FOXO3,SOAT1,EIF4EBP1,ACAT1	down_VCAV_EC
GO:0031345	0.0297	0.989	9	46	negative regulation of cell projection organization	BP	1	ITM2C,EVI5L,ZNF365,NRP1,ULK2,EVL,PSEN1,ASAP1,B2M	up_ACOR_VSMC
GO:0016485	0.0297	0.989	8	73	protein processing	BP	1	ADAMTS2,RHBDL1,PCSK7,GLI3,SEC11C,A2M,PCSK6,LONP2	down_VCAV_EC
GO:0007275	0.0297	0.992	7	1370	multicellular organism development	BP	1	HOXC10,DKK2,HOXA9,HOXC6,SGCD,TAOK1,DUSP2	up_AORT_EC
GO:0030182	0.0297	0.993	5	327	neuron differentiation	BP	1	LYN,ACSL4,SPG11,NRP2,NEDD4	down_ACOR_EC
GO:0042100	0.0297	0.994	4	19	B cell proliferation	BP	0.811	TFRC,LYN,BTK,CDKN1A	down_VSAP_EC
GO:1903672	0.0297	0.994	4	20	positive regulation of sprouting angiogenesis	BP	0.811	VEGFA,JCAD,PIK3C2A,NRP1	down_VSAP_EC
GO:0022610	0.0297	0.998	2	326	biological adhesion	BP	1	TGFBI,GATA5	down_VSAP_VSMC
GO:0034380	0.0297	0.999	2	3	high-density lipoprotein particle assembly	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0021563	0.0297	1	1	4	glossopharyngeal nerve development	BP	1	HOXA3	down_ACOR_EC
GO:0051963	0.0297	1	1	26	regulation of synapse assembly	BP	1	WNT7A	up_AORT_VSMC
GO:0006959	0.0297	1	1	21	humoral immune response	BP	1	C6	up_VCAV_VSMC
GO:0045851	0.0297	1	1	21	pH reduction	BP	1	CA2	up_VCAV_VSMC
GO:0001960	0.0297	1	1	15	negative regulation of cytokine-mediated	BP	1	SLIT2	up_VPUL_VSMC

GO:0031960	0.0297	1	1	15	response to corticosteroid	BP	1	SLIT2	up_VPUL_VSMC
GO:0051384	0.0297	1	1	15	response to glucocorticoid	BP	1	SLIT2	up_VPUL_VSMC
GO:0060761	0.0297	1	1	15	negative regulation of response to cytokine	BP	1	SLIT2	up_VPUL_VSMC
GO:0031128	0.0297	1	1	15	developmental induction	BP	1	GATA5	up_VPUL_VSMC
GO:0060707	0.0297	1	1	7	trophoblast giant cell differentiation	BP	1	GJB5	up_VSAP_VSMC
GO:0032870	0.029728892	0.98848	9	162	cellular response to hormone stimulus	BP	0.98710931	NR1H4,AQP1,ENSCAFG00000004331,AGRN,ACTN2,PTGER4,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0007204	0.0298	0.99	8	46	positive regulation of cytosolic calcium ion	BP	0.735	PDE4D,CHD7,GPR4,EDN1,APLNR,SWAP70,PLCG2,HMGB1	up_VCAV_EC
GO:0050793	0.0298	0.993	5	731	regulation of developmental process	BP	1	NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0034394	0.0298	0.993	5	19	protein localization to cell surface	BP	1	WNT11,FGF7,EMP2,RAB11B,STX4	up_VSAP_EC
GO:0009411	0.0298	0.998	2	56	response to UV	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0021537	0.0298	0.998	2	73	telencephalon development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0051099	0.0298	0.998	2	70	positive regulation of binding	BP	1	HOXA3,PLCL1	up_APUL_EC
GO:0051099	0.0298	1	1	70	positive regulation of binding	BP	1	PLCL1	down_VFEM_EC
GO:0048771	0.0298	1	1	43	tissue remodeling	BP	1	HOXA3	up_APUL_VSMC
GO:2000649	0.0298	1	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	NETO1	up_VFEM_VSMC
GO:0034139	0.0298	1	1	7	regulation of toll-like receptor 3 signaling	BP	1	CAV1	up_VSAP_VSMC
GO:1901576	0.0299	0.991	9	1877	organic substance biosynthetic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006487	0.0299	0.993	5	34	protein N-linked glycosylation	BP	1	DDOST,GFPT2,B4GALT1,FUT8,RPN2	down_VCAV_EC
GO:0050865	0.0299	0.996	3	135	regulation of cell activation	BP	1	LYN,PDPN,STX4	down_ACOR_EC
GO:1905953	0.0299	0.996	3	12	negative regulation of lipid localization	BP	0.813	PTPN11,PTPN2,ABHD5	down_VSAP_EC
GO:0045944	0.0299	0.996	3	287	positive regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9,SHOX2	up_VFEM_VSMC
GO:0050817	0.0299	0.998	2	50	coagulation	BP	1	LYN,PDPN	down_ACOR_EC
GO:0002756	0.0299	0.999	2	3	MyD88-independent toll-like receptor signaling	BP	1	TLR3,PRKCE	up_ACOR_VSMC
GO:0085020	0.0299	1	1	4	protein K6-linked ubiquitination	BP	1	RNF6	up_VPOR_EC
GO:0030278	0.029970569	0.99227	5	66	regulation of ossification	BP	0.9930905	SOX9,SMAD6,PTGER4,LRP4,CLSTN1	up_ACOR_EC
GO:0003170	0.03	0.992	6	25	heart valve development	BP	1	SMAD6,GATA5,GATA4,BMP4,TBX20,TBX5	up_ACOR_VSMC
GO:0050773	0.03	0.993	5	29	regulation of dendrite development	BP	0.813	SIPA1L1,TNIK,APOE,VLDLR,YWHAH	down_VSAP_EC
GO:0051208	0.03	0.993	5	29	sequestering of calcium ion	BP	0.813	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0051282	0.03	0.993	5	29	regulation of sequestering of calcium ion	BP	0.813	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0051240	0.03	0.994	4	489	positive regulation of multicellular organismal	BP	1	NKX2-5,BAMBI,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0009889	0.03	1	2	1190	regulation of biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071361	0.03	0.999	2	3	cellular response to ethanol	BP	1	TP53INP1,PRKCE	up_ACOR_VSMC
GO:1901381	0.03	0.999	2	3	positive regulation of potassium ion	BP	1	ACTN2,AKAP6	up_ACOR_VSMC
GO:1902523	0.03	0.999	2	3	positive regulation of protein K63-linked	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0045765	0.03	1	1	105	regulation of angiogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0061036	0.03	1	1	11	positive regulation of cartilage development	BP	1	HOXA11	up_VFEM_VSMC
GO:0048869	0.0301	0.99	8	1119	cellular developmental process	BP	1	TBX5,EVI2B,MYBPC2,WIF1,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0006612	0.0301	0.992	5	35	protein targeting to membrane	BP	1	PRNP,AKT2,SSR2,SSR3,SEC61B	down_VCAV_EC
GO:0086003	0.0301	0.996	3	10	cardiac muscle cell contraction	BP	0.739	PDE4D,STC1,KCNJ2	up_VCAV_EC

GO:0006906	0.0301	0.998	2	55	vesicle fusion	BP	1	SPG11,STX4	down_ACOR_EC
GO:0015849	0.0301	0.998	2	56	organic acid transport	BP	1	PDPN,ACSL3	down_ACOR_EC
GO:0046942	0.0301	0.998	2	56	carboxylic acid transport	BP	1	PDPN,ACSL3	down_ACOR_EC
GO:0002673	0.0301	0.998	2	6	regulation of acute inflammatory response	BP	1	PARK7,A2M	down_VCAV_EC
GO:0007213	0.0301	0.998	2	5	G protein-coupled acetylcholine receptor	BP	0.813	AGRN,GNAQ	down_VSAP_EC
GO:1903525	0.0301	0.999	2	3	regulation of membrane tubulation	BP	1	ASAP1,WASL	up_ACOR_VSMC
GO:0021602	0.0301	1	1	16	cranial nerve morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0035115	0.0301	1	1	12	embryonic forelimb morphogenesis	BP	1	HOXA9	up_AORT_EC
GO:0051588	0.0301	1	1	28	regulation of neurotransmitter	BP	1	WNT7A	up_AORT_VSMC
GO:0042474	0.0301	1	1	11	middle ear morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0010894	0.0301	1	1	9	negative regulation of steroid biosynthetic	BP	1	NR1H4	up_VPUL_EC
GO:0045939	0.0301	1	1	9	negative regulation of steroid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0007254	0.0302	0.987	12	67	JNK cascade	BP	1	RASSF2,TLR3,SH3RF2,SASH1,F2RL1,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0051240	0.0302	0.994	4	489	positive regulation of multicellular organismal	BP	1	GATM,NETO1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0050710	0.0302	0.995	4	13	negative regulation of cytokine secretion	BP	1	C5AR2,ANXA4,F2RL1,MAPKBP1	up_VSAP_EC
GO:0007167	0.0302	0.996	3	274	enzyme linked receptor protein signaling pathway	BP	1	FGF5,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0051222	0.0302	1	1	103	positive regulation of protein transport	BP	1	JUP	down_VFEM_VSMC
GO:0032677	0.0302	1	1	22	regulation of interleukin-8 production	BP	1	TLR2	up_AFEM_VSMC
GO:0021879	0.0302	1	1	15	forebrain neuron differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0055021	0.0302	1	1	15	regulation of cardiac muscle tissue growth	BP	1	TBX5	up_VPUL_VSMC
GO:0045907	0.0302	1	1	6	positive regulation of vasoconstriction	BP	1	CAV1	up_VSAP_VSMC
GO:0040012	0.030214797	0.98553	14	303	regulation of locomotion	BP	0.99913151	SOX9,AQP1,SEMA6D,ZMYND8,MMP28,TRIM8,PTGER4,ARHGDIB,FOXC2,LRRC15,TBX5,CHMP4B,RARRES2,NRP1	up_ACOR_EC
GO:0010927	0.0303	0.991	6	28	cellular component assembly involved in	BP	0.742	MEF2C,EDN1,TMOD1,NECTIN2,PROX1,TMOD3	up_VCAV_EC
GO:0001922	0.0303	0.999	2	3	B-1 B cell homeostasis	BP	0.742	TNFAIP3,HIF1A	up_VCAV_EC
GO:0035773	0.0303	1	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0060996	0.0303	1	1	26	dendritic spine development	BP	1	WNT7A	up_AORT_VSMC
GO:0046621	0.0303	1	1	8	negative regulation of organ growth	BP	1	TBX5	up_APUL_EC
GO:0060079	0.0303	1	1	15	excitatory postsynaptic potential	BP	1	NETO1	up_VFEM_VSMC
GO:2000738	0.0303	1	1	9	positive regulation of stem cell differentiation	BP	1	TBX5	up_VPUL_EC
GO:0014909	0.0303	1	1	15	smooth muscle cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0034134	0.0303	1	1	7	toll-like receptor 2 signaling pathway	BP	1	TLR2	up_VSAP_VSMC
GO:0048557	0.0303	1	1	7	embryonic digestive tract morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0048534	0.0304	0.982	24	262	hematopoietic or lymphoid organ development	BP	0.813	VEGFA,MYH9,ACTN1,SOCS5,ETV6,CASP3,PTPN11,WDR1,HOXB7,HIF1A,PTPN2,EVI2B,CTNNB1,ANLN,TFRC,LYN,MYO1E,REST,PRMT1,SH2B3,GLO1,INHBA,BTK,SIX4	down_VSAP_EC
GO:0051493	0.0304	0.983	24	188	regulation of cytoskeleton organization	BP	0.742	PLK2,TEK,HCLS1,ARHGEF15,BAIAP2L1,MEF2C,EDN1,ARHGAP28,TMOD1,MTOR,NCKAP1,PROX1,IQGAP2,STMN1,SWAP70,NCK1,FES,SENP6,TAOK1,ARPC5L,ARHGDIB,TMOD3,ARHGEF2,FSCN1	up_VCAV_EC
GO:0001525	0.0304	0.984	17	173	angiogenesis	BP	0.813	VEGFA,SULF1,MYH9,SERPINE1,SPARC,JCAD,PGK1,PRCP,PIK3C2A,HIF1A,THBS2,MTDH,ESM1,CTNNB1,STARD13,KLF5,NRP1	down_VSAP_EC

GO:0050708	0.0304	0.985	16	101	regulation of protein secretion	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,CCL5,NOD2,SCAMP5,PFKL	up_ACOR_VSMC
GO:1904062	0.0304	0.987	11	62	regulation of cation transmembrane transport	BP	1	ACTN2,PLCG2,KCNE3,PTPN3,DAPK1,CACNB3,AKAP6,PRKCE,CHD7,FXYD1,PARK7	up_ACOR_VSMC
GO:0032436	0.0304	0.991	6	40	positive regulation of proteasomal ubiquitin-dependent protein	BP	0.813	PRICKLE1,PLK3,SOCS5,TRIB3,GSK3B,RAD23A	down_VSAP_EC
GO:0010812	0.0304	0.993	5	19	negative regulation of cell-substrate adhesion	BP	1	HOXA7,FAM107A,PIK3R1,FBLN1,ACVRL1	up_VSAP_EC
GO:0030166	0.0304	0.994	4	19	proteoglycan biosynthetic process	BP	0.813	ENSCAFG00000032470,CHSY1,CTNNB1,EXT1	down_VSAP_EC
GO:0050801	0.0304	0.996	3	200	ion homeostasis	BP	1	HOXA3,NR1H4,NEO1	up_VPUL_EC
GO:0055083	0.0304	1	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:1902204	0.0304	1	1	1	positive regulation of hepatocyte growth factor receptor signaling	BP	0.813	ESM1	down_VSAP_EC
GO:0021544	0.0304	1	1	8	subpallium development	BP	1	SLITRK5	up_APUL_EC
GO:0001710	0.0304	1	1	7	mesodermal cell fate commitment	BP	1	EYA1	up_VFEM_EC
GO:0021955	0.0304	1	1	15	central nervous system neuron axonogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0046622	0.0304	1	1	15	positive regulation of organ growth	BP	1	TBX5	up_VPUL_VSMC
GO:0002374	0.0304	1	1	7	cytokine secretion involved in immune	BP	1	TLR2	up_VSAP_VSMC
GO:1903779	0.0304	1	1	6	regulation of cardiac conduction	BP	1	CAV1	up_VSAP_VSMC
GO:0007212	0.030423479	0.9977	2	11	dopamine receptor signaling pathway	BP	1	CALY,GNAO1	up_ACOR_EC
GO:0060538	0.0305	0.99	7	51	skeletal muscle organ development	BP	0.814	ACTN1,FLNB,CTNNB1,KLF5,ATF3,SIX4,HOMER1	down_VSAP_EC
GO:0042221	0.0305	0.992	6	1012	response to chemical	BP	1	CHL1,FGF5,NKX2-5,BAMBI,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0038180	0.0305	0.999	2	3	nerve growth factor signaling pathway	BP	0.743	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:0014816	0.0305	0.999	2	3	skeletal muscle satellite cell differentiation	BP	0.743	EPHB1,CDON	up_VCAV_EC
GO:0090025	0.0305	1	1	7	regulation of monocyte chemotaxis	BP	1	LYN	down_ACOR_EC
GO:0048729	0.0305	1	1	209	tissue morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0038034	0.0305	1	1	21	signal transduction in absence of ligand	BP	1	EYA1	up_AFEM_VSMC
GO:0097192	0.0305	1	1	21	extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_AFEM_VSMC
GO:0032228	0.0305	1	1	8	regulation of synaptic transmission, GABAergic	BP	1	PLCL1	up_APUL_EC
GO:1904467	0.0305	1	1	8	regulation of tumor necrosis factor secretion	BP	1	NR1H4	up_APUL_EC
GO:0071675	0.0305	1	1	13	regulation of mononuclear cell	BP	1	C3AR1	up_VPOR_VSMC
GO:0009058	0.0306	0.994	6	1910	biosynthetic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0051055	0.0306	0.994	4	21	negative regulation of lipid biosynthetic process	BP	0.814	NR1H4,TRIB3,APOE,REST	down_VSAP_EC
GO:0048646	0.0306	0.994	4	349	anatomical structure formation involved in	BP	1	TBX5,HOXA3,MYBPC2,CCL24	up_VPUL_EC
GO:0072337	0.0306	1	1	7	modified amino acid transport	BP	1	PDPN	down_ACOR_EC
GO:1902285	0.0306	1	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	NRP2	down_ACOR_EC
GO:0060359	0.0306	1	1	14	response to ammonium ion	BP	1	GABPA	down_AFEM_EC
GO:0006721	0.0306	1	1	14	terpenoid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0040012	0.0307	0.98	39	303	regulation of locomotion	BP	1	HOXA7,TWIST2,WNT11,FAM107A,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,CHRM1,FUZ,PDGFD,PLXNA4,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,FBXO7,PC,FBLN1,ZNF580,STX4,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0002376	0.0307	0.994	4	622	immune system process	BP	1	HOXA3,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC

GO:0032733	0.0307	0.996	3	9	positive regulation of interleukin-10 production	BP	0.744	CD34,TLR4,HMGB1	up_VCAV_EC
GO:0071478	0.0307	0.997	2	58	cellular response to radiation	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0046903	0.0307	0.998	2	255	secretion	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0006826	0.0307	1	1	15	iron ion transport	BP	1	RAB11B	down_VPOR_EC
GO:0030730	0.0307	1	1	4	sequestering of triglyceride	BP	1	ABHD5	up_VPOR_EC
GO:0007215	0.0307	1	1	13	glutamate receptor signaling pathway	BP	1	NETO1	up_VFEM_VSMC
GO:0010002	0.0307	1	1	9	cardioblast differentiation	BP	1	TBX5	up_VPUL_EC
GO:0010939	0.0307	1	1	9	regulation of necrotic cell death	BP	1	ARHGEF2	up_VPUL_EC
GO:0043648	0.030707469	0.99542	3	26	dicarboxylic acid metabolic process	BP	1	NR1H4,NMNAT2,NIT2	up_ACOR_EC
GO:0043122	0.0308	0.988	10	62	regulation of I-kappaB kinase/NF-kappaB	BP	0.744	TNFAIP3,TNIP1,TLR4,PELI1,CASP8,MAP3K3,RIOK3,TLR3,BCL10,RIPK1	up_VCAV_EC
GO:0090659	0.0308	0.995	4	12	walking behavior	BP	1	GLRB,CHD7,CLN8,OXR1	up_ACOR_VSMC
GO:0014829	0.0308	0.996	3	8	vascular smooth muscle contraction	BP	0.744	EDNRB,DOCK4,EDN1	up_VCAV_EC
GO:0090174	0.0308	0.997	2	56	organelle membrane fusion	BP	1	SPG11,STX4	down_ACOR_EC
GO:1900221	0.0308	0.998	2	6	regulation of amyloid-beta clearance	BP	1	LRP1,LRPAP1	down_VCAV_EC
GO:0034616	0.0308	0.999	2	3	response to laminar fluid shear stress	BP	1	SMAD6,ABCA1	up_ACOR_VSMC
GO:0060412	0.0308	1	1	15	ventricular septum morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0071071	0.0308	1	1	8	regulation of phospholipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0006541	0.0308	1	1	9	glutamine metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0001710	0.0308	1	1	7	mesodermal cell fate commitment	BP	1	HOXA11	up_VSAP_VSMC
GO:0001823	0.030880334	0.99351	4	45	mesonephros development	BP	1	SOX9,SMAD6,FOXC2,CLSTN1	up_ACOR_EC
GO:0048514	0.0309	0.987	10	214	blood vessel morphogenesis	BP	1	LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0072175	0.0309	0.989	8	60	epithelial tube formation	BP	0.818	PRICKLE1,PRKACB,ENSCAFG00000032470,TMED2,HIF1A,CTNNB1,SDC4,SIX4	down_VSAP_EC
GO:0001843	0.0309	0.989	8	38	neural tube closure	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0043242	0.0309	0.993	5	21	negative regulation of protein complex	BP	0.744	TMOD1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0009314	0.0309	0.995	3	143	response to radiation	BP	1	USP28,HOXA1,NEDD4	down_ACOR_EC
GO:1904646	0.0309	0.998	2	6	cellular response to amyloid-beta	BP	1	LRP1,PRNP	down_VCAV_EC
GO:0045723	0.0309	0.998	2	5	positive regulation of fatty acid biosynthetic process	BP	0.818	PTGS2,SLC45A3	down_VSAP_EC
GO:1905906	0.0309	0.998	2	5	regulation of amyloid fibril formation	BP	0.818	CRYAB,APOE	down_VSAP_EC
GO:0048511	0.0309	0.997	2	72	rhythmic process	BP	1	HTR7,NTRK2	up_APUL_EC
GO:0014706	0.0309	0.998	2	112	striated muscle tissue development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0045785	0.0309	1	1	107	positive regulation of cell adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0021855	0.0309	1	1	4	hypothalamus cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0071300	0.0309	1	1	12	cellular response to retinoic acid	BP	1	CYP26B1	up_VPOR_VSMC
GO:0043113	0.0309	1	1	12	receptor clustering	BP	1	LHFPL4	up_VPOR_VSMC
GO:1990774	0.0309	1	1	9	tumor necrosis factor secretion	BP	1	NR1H4	up_VPUL_EC
GO:0120035	0.031	0.984	16	160	regulation of plasma membrane bounded cell projection organization	BP	0.819	SIPA1L1,FSCN1,DPYSL3,IFRD1,DYNLL1,TNIK,UST,ANLN,APOE,KLF5,LYN,VLDLR,HTT,DISC1,NRP1,YWHAH	down_VSAP_EC
GO:0008361	0.031	0.988	9	50	regulation of cell size	BP	0.744	IL7R,IFRD1,LRRC8D,EDN1,RAB11A,MTOR,LRRC8C,SLC12A7,CREB1	up_VCAV_EC
GO:0006986	0.031	0.991	6	42	response to unfolded protein	BP	0.819	HSPA5,ERO1A,PTPN2,DDIT3,ATF3,CREB3L2	down_VSAP_EC
GO:1903055	0.031	1	1	6	positive regulation of extracellular matrix	BP	1	PDPN	down_ACOR_EC

GO:0034121	0.031	1	1	22	regulation of toll-like receptor signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0032720	0.031	1	1	13	negative regulation of tumor necrosis factor	BP	1	BPI	up_AORT_EC
GO:0050777	0.031	1	1	28	negative regulation of immune response	BP	1	ARG2	up_AORT_VSMC
GO:0045933	0.031	1	1	8	positive regulation of muscle contraction	BP	1	NPNT	up_APUL_EC
GO:0090103	0.031	1	1	8	cochlea morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0051926	0.031	1	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_VPOR_VSMC
GO:0060065	0.031	1	1	7	uterus development	BP	1	HOXA9	up_VFEM_EC
GO:1901379	0.031	1	1	12	regulation of potassium ion transmembrane	BP	1	NETO1	up_VFEM_VSMC
GO:0019222	0.0311	0.994	6	1934	regulation of metabolic process	BP	1	HOXC10,TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0051084	0.0311	0.998	2	5	'de novo' posttranslational protein	BP	0.819	ERO1A,SH3GLB1	down_VSAP_EC
GO:0032656	0.0311	0.998	2	4	regulation of interleukin-13 production	BP	0.744	GATA3,ARG2	up_VCAV_EC
GO:0032616	0.0311	0.998	2	4	interleukin-13 production	BP	0.744	GATA3,ARG2	up_VCAV_EC
GO:0042733	0.0311	1	1	27	embryonic digit morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0031114	0.0311	1	1	9	regulation of microtubule depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0042981	0.0312	0.98	38	471	regulation of apoptotic process	BP	0.819	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,CASP3,HYOU1,AARS,FHL2,PTGS2,HIF1A,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,GLO1,PAK2,INHBA,SIX4,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0002573	0.0312	0.987	11	71	myeloid leukocyte differentiation	BP	0.744	HCLS1,KIT,MEF2C,GATA3,CASP8,MTOR,HHEX,CREB1,RIPK1,CUL4A,TJP2	up_VCAV_EC
GO:0032602	0.0312	0.992	5	23	chemokine production	BP	0.744	ACKR1,TLR4,ARG2,TLR3,APOD	up_VCAV_EC
GO:0019220	0.0312	0.992	5	525	regulation of phosphate metabolic process	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0051174	0.0312	0.992	5	525	regulation of phosphorus metabolic process	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0051966	0.0312	0.996	3	8	regulation of synaptic transmission,	BP	0.744	RELN,MEF2C,GRM8	up_VCAV_EC
GO:0050877	0.0312	0.995	3	164	nervous system process	BP	1	HOXC10,MME,SIX1	up_VFEM_EC
GO:0032703	0.0312	1	1	8	negative regulation of interleukin-2 production	BP	1	NR1H4	up_APUL_EC
GO:0044703	0.0313	0.982	22	172	multi-organism reproductive process	BP	1	ACSL4,NDC1,TRIP13,CTDNEP1,FBXO5,AAAS,NCAPH,POC1A,B4GALT1,PPARD,HIST1H1A,EMP2,FOSL1,HMGB2,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,CCT4,TTLL1	down_ACOR_VSMC
GO:0001649	0.0313	0.988	10	54	osteoblast differentiation	BP	1	FZD1,TWIST2,WNT11,AXIN2,ZHX3,HDAC7,DDR2,SHOX2,LIMD1,BGLAP	up_VSAP_EC
GO:0006139	0.0313	0.991	8	1909	nucleobase-containing compound metabolic	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,SRSF6,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0034440	0.0313	0.992	5	35	lipid oxidation	BP	1	AKT2,ACAA1,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:1902931	0.0313	0.998	2	5	negative regulation of alcohol biosynthetic	BP	0.819	APOE,REST	down_VSAP_EC
GO:1903961	0.0313	0.999	2	3	positive regulation of anion transmembrane	BP	1	TCAF1,PSEN1	up_ACOR_VSMC
GO:0048871	0.0313	0.997	2	120	multicellular organismal homeostasis	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0050709	0.0313	1	1	28	negative regulation of protein secretion	BP	1	ARG2	up_AORT_VSMC
GO:0032620	0.0313	1	1	8	interleukin-17 production	BP	1	NR1H4	up_APUL_EC
GO:0044070	0.0313	1	1	22	regulation of anion transport	BP	1	CA2	up_VCAV_VSMC
GO:0072172	0.0313	1	1	7	mesonephric tubule formation	BP	1	SIX1	up_VFEM_EC
GO:1990868	0.0313	1	1	16	response to chemokine	BP	1	SLIT2	up_VPUL_VSMC
GO:1990869	0.0313	1	1	16	cellular response to chemokine	BP	1	SLIT2	up_VPUL_VSMC
GO:0046323	0.031320192	0.9953	3	26	glucose import	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC

GO:0051348	0.031329055	0.99054	6	90	negative regulation of transferase activity	BP	1	PKIB,DUSP26,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0050768	0.031376335	0.99181	5	66	negative regulation of neurogenesis	BP	1	SOX9,DIXDC1,RGMA,LRP4,NRP1	up_ACOR_EC
GO:0016477	0.0314	0.981	30	426	cell migration	BP	1	PDGFRB,DCN,NDN,SDC4,GLIPR2,KANK2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,HSD3B7,LAMA3,CSPG4,SEMA3C,THY1,PEX5,B4GALT1,GLI3,SASH1,CDH2,FUT8,SPRED1,TWIST2,DDR2,GREM1,RAC2,FOXO3	down_VCAV_EC
GO:0002449	0.0314	0.988	9	53	lymphocyte mediated immunity	BP	0.746	IL7R,GATA3,RAB27A,NECTIN2,THOC1,SWAP70,JAG1,BCL10,HMGB1	up_VCAV_EC
GO:0001510	0.0314	0.992	5	22	RNA methylation	BP	1	FBL,THUMPD2,METTL1,WTAP,EMG1	down_ACOR_VSMC
GO:1901570	0.0314	0.994	4	16	fatty acid derivative biosynthetic process	BP	0.746	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0045047	0.0314	0.996	3	14	protein targeting to ER	BP	1	SSR3,SEC61B,SEC61A1	down_VCAV_EC
GO:0072599	0.0314	0.996	3	14	establishment of protein localization to endoplasmic reticulum	BP	1	SSR3,SEC61B,SEC61A1	down_VCAV_EC
GO:0032689	0.0314	1	1	8	negative regulation of interferon-gamma	BP	1	NR1H4	up_APUL_EC
GO:0050829	0.0314	1	1	8	defense response to Gram-negative bacterium	BP	1	BPI	up_APUL_EC
GO:0021561	0.0314	1	1	8	facial nerve development	BP	1	SIX1	up_VFEM_EC
GO:0021610	0.0314	1	1	8	facial nerve morphogenesis	BP	1	SIX1	up_VFEM_EC
GO:0035909	0.0314	1	1	14	aorta morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0001934	0.0315	0.98	32	274	positive regulation of protein phosphorylation	BP	0.746	TEK,HCLS1,KIT,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,APLNR,NEDD9,YES1,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,TLR3,PTGS2,MMD,RAPGEF2,TAOK1,HMGB1,RIPK1,PDGFD,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0035690	0.0315	0.985	15	91	cellular response to drug	BP	1	PRKAA2,ATRX,CASTOR1,TP53INP1,ADCY6,ANKRD1,PTPN22,PRKCE,AGRN,JUP,NR3C1,NOD2,DDIT4,GNAQ,PARK7	up_ACOR_VSMC
GO:0002761	0.0315	0.992	5	36	regulation of myeloid leukocyte differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,ZFP36L1	down_VCAV_EC
GO:1905332	0.0315	0.994	4	20	positive regulation of morphogenesis of an	BP	0.819	HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0080111	0.0315	0.996	3	9	DNA demethylation	BP	0.747	GATA3,OTUD4,TET2	up_VCAV_EC
GO:0007420	0.0315	0.995	3	169	brain development	BP	1	PITX1,EMX2,SALL1	up_VSAP_VSMC
GO:0034103	0.0315	0.998	2	12	regulation of tissue remodeling	BP	1	LEP,GREM1	up_AFEM_EC
GO:0032642	0.0315	1	1	22	regulation of chemokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0060972	0.0315	1	1	13	left/right pattern formation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0016579	0.0316	0.988	9	49	protein deubiquitination	BP	0.747	TNFAIP3,TNIP1,USP33,ENSCAFG00000010893,OTUD4,USP28,USP13,USP38,USP37	up_VCAV_EC
GO:0046483	0.0316	0.994	6	1948	heterocycle metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:1901976	0.0316	0.992	5	21	regulation of cell cycle checkpoint	BP	1	WDR76,RNASEH2B,NDC80,DDX39B,GEN1	down_ACOR_VSMC
GO:0033692	0.0316	0.994	4	20	cellular polysaccharide biosynthetic process	BP	0.819	ENPP1,ENSCAFG00000032470,PPP1R3C,EXT1	down_VSAP_EC
GO:0009100	0.0316	0.997	2	139	glycoprotein metabolic process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:1902373	0.0316	0.998	2	12	negative regulation of mRNA catabolic process	BP	1	TENT5C,AXIN2	up_AFEM_EC
GO:0034134	0.0316	1	1	7	toll-like receptor 2 signaling pathway	BP	1	LYN	down_ACOR_EC
GO:1904951	0.0316	1	1	108	positive regulation of establishment of protein localization	BP	1	JUP	down_VFEM_VSMC
GO:0021549	0.0316	1	1	26	cerebellum development	BP	1	WNT7A	up_AORT_VSMC
GO:0048566	0.0316	1	1	13	embryonic digestive tract development	BP	1	SHOX2	up_VFEM_VSMC
GO:0023061	0.0317	0.985	15	95	signal release	BP	1	LEP,FBXL20,TM7SF3,STX11,PRKCE,SCG5,PSEN1,CHD7,CCL5,RAB11B,EDN1,KCNC4,PREPL,PFKL,PARK7	up_ACOR_VSMC
GO:0002696	0.0317	0.986	12	80	positive regulation of leukocyte activation	BP	0.749	IL7R,MEF2C,TLR4,GATA3,PELI1,NECTIN2,ITPKB,NCK1,CD200,BCL10,HMGB1,ATP11C	up_VCAV_EC

GO:0050727	0.0317	0.988	9	74	regulation of inflammatory response	BP	0.819	NR1H4,SERPINE1,SOCS5,PTGS2,PTPN2,APOE,LYN,GBP5,A2M	down_VSAP_EC
GO:0051310	0.0317	0.992	5	22	metaphase plate congression	BP	1	ZW10,KIF22,CDCA8,NDC80,NUP62	down_ACOR_VSMC
GO:0007043	0.0317	0.992	5	28	cell-cell junction assembly	BP	0.819	NR1H4,FSCN1,WDR1,MYO1C,CTNNB1	down_VSAP_EC
GO:0071709	0.0317	0.996	3	8	membrane assembly	BP	1	EMP2,LRP4,FLOT1	up_VSAP_EC
GO:0019229	0.0317	0.998	2	12	regulation of vasoconstriction	BP	1	AVPR1A,TBXA2R	up_AFEM_EC
GO:0030514	0.0317	0.998	2	12	negative regulation of BMP signaling pathway	BP	1	GREM1,GREM2	up_AFEM_EC
GO:0043066	0.0317	0.998	2	253	negative regulation of apoptotic process	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0097530	0.0317	0.997	2	33	granulocyte migration	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0002065	0.0317	1	1	37	columnar/cuboidal epithelial cell	BP	1	GATA5	down_VSAP_VSMC
GO:0060688	0.0317	1	1	29	regulation of morphogenesis of a	BP	1	ESR1	up_AORT_VSMC
GO:0030104	0.0317	1	1	13	water homeostasis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0061384	0.0317	1	1	12	heart trabecula morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0034694	0.0317	1	1	9	response to prostaglandin	BP	1	PTGER2	up_VPUL_EC
GO:0035136	0.0317	1	1	16	forelimb morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0032868	0.031742494	0.99169	5	66	response to insulin	BP	1	NR1H4,ENSCAFG00000004331,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0045596	0.0318	0.983	18	186	negative regulation of cell differentiation	BP	0.819	PRICKLE1,SOCS5,ENPP1,DPYSL3,HOOK3,TRIB3,IFRD1,PTPN2,CTNNB1,APOE,LYN,STRAP,DDIT3,REST,PRMT1,SIX4,NRP1,YWHAH	down_VSAP_EC
GO:0062012	0.0318	0.986	11	100	regulation of small molecule metabolic	BP	0.819	NR1H4,ENPP1,TRIB3,PGAM1,SESN2,PTGS2,HIF1A,SLC45A3,PTPN2,APOE,REST	down_VSAP_EC
GO:0060576	0.0318	0.998	2	5	intestinal epithelial cell development	BP	0.819	HIF1A,KLF5	down_VSAP_EC
GO:0014706	0.0318	0.997	2	112	striated muscle tissue development	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0030857	0.0318	1	1	15	negative regulation of epithelial cell	BP	1	SRSF6	down_AFEM_EC
GO:0060236	0.0318	1	1	15	regulation of mitotic spindle organization	BP	1	GPSM2	down_AFEM_EC
GO:0031214	0.0318	1	1	45	biomineral tissue development	BP	1	HOXA3	up_APUL_VSMC
GO:0140058	0.0318	1	1	4	neuron projection arborization	BP	1	SEMA3A	up_VPOR_EC
GO:0061548	0.0318	1	1	8	ganglion development	BP	1	SIX1	up_VFEM_EC
GO:1903427	0.0318	1	1	7	negative regulation of reactive oxygen species biosynthetic process	BP	1	CAV1	up_VSAP_VSMC
GO:1905037	0.031807644	0.99323	4	47	autophagosome organization	BP	1	ATG16L2,CHMP4B,TP53INP2,ENSCAFG00000010493	up_ACOR_EC
GO:1903670	0.0319	0.992	5	30	regulation of sprouting angiogenesis	BP	0.819	VEGFA,JCAD,PIK3C2A,STARD13,NRP1	down_VSAP_EC
GO:0010092	0.0319	0.992	5	19	specification of animal organ identity	BP	1	GATA5,BMP4,FGFR2,SMARCD3,FRS2	up_ACOR_VSMC
GO:1905475	0.0319	0.997	2	52	regulation of protein localization to membrane	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0010559	0.0319	0.998	2	6	regulation of glycoprotein biosynthetic process	BP	1	NECAB3,SOAT1	down_VCAV_EC
GO:1903018	0.0319	0.998	2	6	regulation of glycoprotein metabolic process	BP	1	NECAB3,SOAT1	down_VCAV_EC
GO:0033006	0.0319	1	1	7	regulation of mast cell activation involved in	BP	1	LYN	down_ACOR_EC
GO:0043304	0.0319	1	1	7	regulation of mast cell degranulation	BP	1	LYN	down_ACOR_EC
GO:0048663	0.0319	1	1	13	neuron fate commitment	BP	1	HOXC10	up_AORT_EC
GO:0001738	0.0319	1	1	27	morphogenesis of a polarized epithelium	BP	1	WNT7A	up_AORT_VSMC
GO:0050868	0.0319	1	1	28	negative regulation of T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0042398	0.0319	1	1	12	cellular modified amino acid biosynthetic process	BP	1	GATM	up_VFEM_VSMC
GO:0031579	0.0319	1	1	6	membrane raft organization	BP	1	CAV1	up_VSAP_VSMC
GO:0002026	0.0319	1	1	8	regulation of the force of heart contraction	BP	1	CAV1	up_VSAP_VSMC

GO:0007249	0.032	0.986	11	71	I-kappaB kinase/NF-kappaB signaling	BP	0.751	TNFAIP3,TNIP1,TLR4,PELI1,CASP8,MAP3K3,ERC1,RIOK3,TLR3,BCL10,RIPK1	up_VCAV_EC
GO:0060236	0.032	0.994	4	15	regulation of mitotic spindle organization	BP	1	SMC1A,NUP62,SMC3,STAG1	down_ACOR_VSMC
GO:0045185	0.032	0.993	4	25	maintenance of protein location	BP	1	FBN1,TLN2,PARK7,ARL2BP	down_VCAV_EC
GO:0035924	0.032	0.994	4	21	cellular response to vascular endothelial growth factor stimulus	BP	0.819	VEGFA,JCAD,MYO1C,NRP1	down_VSAP_EC
GO:1990845	0.032	0.993	4	51	adaptive thermogenesis	BP	1	CMKLR1,HOXC10,LEP,PPARGC1A	up_AFEM_EC
GO:1902916	0.032	0.996	3	8	positive regulation of protein polyubiquitination	BP	1	SKP2,PTPN22,NOD2	up_ACOR_VSMC
GO:0048070	0.032	0.998	2	4	regulation of developmental	BP	0.751	KIT,ADAMTS9	up_VCAV_EC
GO:0014904	0.032	1	1	12	myotube cell development	BP	1	SHOX2	up_VFEM_VSMC
GO:0048741	0.032	1	1	12	skeletal muscle fiber development	BP	1	SHOX2	up_VFEM_VSMC
GO:0043502	0.032	1	1	16	regulation of muscle adaptation	BP	1	GATA5	up_VPUL_VSMC
GO:1902743	0.032	1	1	16	regulation of lamellipodium	BP	1	SLIT2	up_VPUL_VSMC
GO:0072006	0.0321	0.987	10	59	nephron development	BP	0.751	HOXB7,PDGFB,PODXL,MEF2C,GPR4,GATA3,MTSS1,BMP2,JAG1,BASP1	up_VCAV_EC
GO:0035710	0.0321	0.992	5	22	CD4-positive, alpha-beta T cell activation	BP	0.751	IL6,GATA3,ARG2,MTOR,HMGB1	up_VCAV_EC
GO:0090183	0.0321	0.994	4	21	regulation of kidney development	BP	0.819	HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0042592	0.0321	0.994	4	522	homeostatic process	BP	1	HOXC10,ENSCAFG00000005494,LNPEP,TAOK1	up_AORT_EC
GO:0010628	0.0321	0.996	3	527	positive regulation of gene expression	BP	1	TLR2,EYA1,HOXA9	up_AFEM_VSMC
GO:0002279	0.0321	0.996	3	10	mast cell activation involved in immune	BP	0.751	KIT,SNAP23,FES	up_VCAV_EC
GO:0010939	0.0321	0.996	3	9	regulation of necrotic cell death	BP	0.751	PELI1,RIPK1,ARHGEF2	up_VCAV_EC
GO:0002448	0.0321	0.996	3	10	mast cell mediated immunity	BP	0.751	KIT,SNAP23,FES	up_VCAV_EC
GO:0043303	0.0321	0.996	3	10	mast cell degranulation	BP	0.751	KIT,SNAP23,FES	up_VCAV_EC
GO:0035115	0.0321	0.997	2	12	embryonic forelimb morphogenesis	BP	1	HOXA9,RECK	up_AFEM_EC
GO:0072079	0.0321	0.997	2	12	nephron tubule formation	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0021510	0.0321	1	1	23	spinal cord development	BP	1	HOXC10	up_AFEM_VSMC
GO:1905941	0.0321	1	1	4	positive regulation of gonad development	BP	1	SEMA3A	up_VPOR_EC
GO:2000018	0.0321	1	1	4	regulation of male gonad development	BP	1	SEMA3A	up_VPOR_EC
GO:2000020	0.0321	1	1	4	positive regulation of male gonad development	BP	1	SEMA3A	up_VPOR_EC
GO:0045880	0.0321	1	1	14	positive regulation of smoothened signaling	BP	1	SHOX2	up_VFEM_VSMC
GO:0021602	0.0321	1	1	16	cranial nerve morphogenesis	BP	1	HOXA3	up_VPUL_VSMC
GO:0002040	0.032129687	0.99315	4	46	sprouting angiogenesis	BP	1	ENSCAFG00000004331,ESM1,FOXC2,NRP1	up_ACOR_EC
GO:0080090	0.0322	0.986	14	1734	regulation of primary metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,SULF1,ELK3,HOXA1,ACSL3,ASPN,NEDD4	down_ACOR_EC
GO:0030326	0.0322	0.993	4	51	embryonic limb morphogenesis	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0035113	0.0322	0.993	4	51	embryonic appendage morphogenesis	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0048015	0.0322	0.997	2	48	phosphatidylinositol-mediated signaling	BP	1	IGF1R,NEDD4	down_ACOR_EC
GO:0048017	0.0322	0.997	2	48	inositol lipid-mediated signaling	BP	1	IGF1R,NEDD4	down_ACOR_EC
GO:0032488	0.0322	0.998	2	5	Cdc42 protein signal transduction	BP	0.819	APOE,NRP1	down_VSAP_EC
GO:0032489	0.0322	0.998	2	5	regulation of Cdc42 protein signal	BP	0.819	APOE,NRP1	down_VSAP_EC
GO:0051036	0.0322	0.998	2	4	regulation of endosome size	BP	0.751	RAB11A,ALS2	up_VCAV_EC
GO:0006725	0.0323	0.994	6	1956	cellular aromatic compound metabolic	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0061647	0.0323	0.994	4	13	histone H3-K9 modification	BP	0.751	GATA3,ARID4B,KDM3A,ATRX	up_VCAV_EC

GO:0007179	0.0323	0.997	2	57	transforming growth factor beta receptor	BP	1	ACVRL1,ASPN	down_ACOR_EC
GO:0034654	0.0323	1	2	1236	nucleobase-containing compound biosynthetic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1903307	0.0323	1	1	8	positive regulation of regulated secretory	BP	1	STX4	down_ACOR_EC
GO:0033194	0.0323	1	1	7	response to hydroperoxide	BP	1	STX4	down_ACOR_EC
GO:0021522	0.0323	1	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_VFEM_EC
GO:0010647	0.0324	0.977	56	460	positive regulation of cell communication	BP	1	ADRA1B,TLR1,LGR6,LEP,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,SKP2,NACC2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,TLR3,SH3RF2,PDE5A,CITED2,TP53INP1,SASH1,TMEM108,FGF18,CDKN2B,LIMS2,ANKRD1,F2RL1,BNIP3,CRLF3,CREBRF,NRP1,PTPN22,NPNT,UNC5B,PRKCE,FRS2,PARP9,APP,PSEN1,CCL5,DUSP22,SIAH1,EDN1,NOD2,FAM107A,DISC1,SH3RF3,SERINC3,MAP3K7,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0022603	0.0324	0.99	6	301	regulation of anatomical structure morphogenesis	BP	1	C3AR1,ENSCAFG00000002015,SEMA3A,ASPN,MTDH,RNF6	up_VPOR_EC
GO:0032634	0.0324	0.998	2	4	interleukin-5 production	BP	0.751	PDE4D,GATA3	up_VCAV_EC
GO:0032674	0.0324	0.998	2	4	regulation of interleukin-5 production	BP	0.751	PDE4D,GATA3	up_VCAV_EC
GO:0034504	0.0324	1	1	111	protein localization to nucleus	BP	1	JUP	down_VFEM_VSMC
GO:0034505	0.0324	1	1	4	tooth mineralization	BP	1	ASPN	up_VPOR_EC
GO:0071498	0.0324	1	1	8	cellular response to fluid shear stress	BP	1	MTSS1	up_VFEM_EC
GO:0006575	0.0325	0.989	7	53	cellular modified amino acid metabolic process	BP	0.825	P4HB,PLOD2,ERO1A,P4HA1,ENSCAFG00000028814,ALDH1L2,PLOD3	down_VSAP_EC
GO:0010960	0.0325	1	1	6	magnesium ion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:0061549	0.0325	1	1	5	sympathetic ganglion development	BP	1	NRP2	down_ACOR_EC
GO:0003197	0.0325	1	1	16	endocardial cushion development	BP	1	CITED2	down_VPOR_EC
GO:1901342	0.0325	1	1	114	regulation of vasculature development	BP	1	JUP	down_VFEM_VSMC
GO:0050772	0.0325	1	1	13	positive regulation of axonogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:1902305	0.0325	1	1	12	regulation of sodium ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0008584	0.0326	0.989	8	39	male gonad development	BP	1	GATA4,PRDX4,ATRX,CITED2,SPINK2,ARID5B,LHX9,WDR48	up_ACOR_VSMC
GO:0046546	0.0326	0.989	8	39	development of primary male sexual	BP	1	GATA4,PRDX4,ATRX,CITED2,SPINK2,ARID5B,LHX9,WDR48	up_ACOR_VSMC
GO:0032465	0.0326	0.991	6	29	regulation of cytokinesis	BP	1	AURKB,PLK3,E2F8,CDC6,NUP62,PDXP	down_ACOR_VSMC
GO:0070266	0.0326	0.994	4	14	necroptotic process	BP	0.756	PELI1,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:0009056	0.0326	0.999	2	755	catabolic process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0086002	0.0326	1	1	7	cardiac muscle cell action potential involved in	BP	1	CAV1	up_VSAP_VSMC
GO:0072657	0.032613916	0.98797	8	144	protein localization to membrane	BP	1	KCNB1,AGRN,PLS1,ACTN2,LRRC15,LRP4,LRRC4,CHMP4B	up_ACOR_EC
GO:0032103	0.032677836	0.99137	5	69	positive regulation of response to external	BP	1	NOD2,IL33,PTGER4,RARRES2,NRP1	up_ACOR_EC
GO:0031344	0.0327	0.983	16	161	regulation of cell projection organization	BP	0.827	SIPA1L1,FSCN1,DPYSL3,IFRD1,DYNLL1,TNIK,UST,ANLN,APOE,KLF5,LYN,VLDLR,HTT,DISC1,NRP1,YWHAH	down_VSAP_EC
GO:0019933	0.0327	0.99	7	32	cAMP-mediated signaling	BP	1	ADRA1B,ADGRD1,ABCA1,PTGIR,ADCY6,APLP1,GNAQ	up_ACOR_VSMC
GO:0043524	0.0327	0.99	6	39	negative regulation of neuron apoptotic process	BP	0.827	HYOU1,AARS,HIF1A,ZPR1,SIX4,NRP1	down_VSAP_EC
GO:0032637	0.0327	0.991	6	26	interleukin-8 production	BP	1	C5AR2,ANXA4,F2RL1,MAPKBP1,ZNF580,MAVS	up_VSAP_EC
GO:0070168	0.0327	0.998	2	6	negative regulation of biomineral tissue	BP	1	ASPN,GREM1	down_VCAV_EC
GO:0006099	0.0327	1	1	15	tricarboxylic acid cycle	BP	1	SUCLG2	down_AFEM_EC
GO:0051653	0.0327	1	1	15	spindle localization	BP	1	GPSM2	down_AFEM_EC
GO:0043393	0.0327	1	1	77	regulation of protein binding	BP	1	PLCL1	down_VFEM_EC

GO:0048565	0.0327	1	1	38	digestive tract development	BP	1	GATA5	down_VSAP_VSMC
GO:0002792	0.0327	1	1	29	negative regulation of peptide secretion	BP	1	ARG2	up_AORT_VSMC
GO:0060544	0.0327	1	1	8	regulation of necroptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:0060561	0.032780476	0.99742	2	11	apoptotic process involved in	BP	1	FZD5,FOXC2	up_ACOR_EC
GO:0048513	0.0328	0.975	104	906	animal organ development	BP	1	EXPH5,TNNT2,PDLIM3,FGF13,TMEM176B,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,LBH,GATA5,GATA4,CD83,HTR2B,RASSF2,PRDX4,MLLT3,FERMT1,BMP4,LNPK,FGFR2,GJA1,ATRX,SEC24B,XIRP1,PPARGC1A,LATS2,CITED2,SPINT1,ISG15,ZNRF3,ZNF365,LMO4,TMEM108,FGF18,FAM210B,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,LIMS2,ANKRD1,F2RL1,CTSB,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,GPM6A,CHD2,NPNT,SMARCD3,SPINT2,SLITRK5,TBX20,BBX,TBX5,FZD3,FRS2,CPAMD8,DAG1,POMK,APP,PSEN1,SEMA6D,TGFBR1,CHD7,JUP,SPINK2,DDR2,CLN8,FOSL2,PERP,PSKH1,RTKN2,EDN1,NID1,ARID5B,DMC1,SERPINB5,JAM3,B2M,DISC1,AP2B1,TNFRSF11B,TACC1,GAA,SUN1,CNOT4,LHX9,WFS1,WDR48,ID3,SLC8A1,TEAD1,ENSCAFG00000003530,IL18R1,BVES,RREB1,ZDHHC21,CRKL	up_ACOR_VSMC
GO:1900076	0.0328	0.992	5	29	regulation of cellular response to insulin	BP	0.827	NR1H4,ENPP1,PTPN11,MYO1C,PTPN2	down_VSAP_EC
GO:0061014	0.0328	0.996	3	8	positive regulation of mRNA catabolic process	BP	1	ZFP36L1,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0062009	0.0328	0.996	3	8	secondary palate development	BP	1	FZD1,WNT11,TGFBR2	up_VSAP_EC
GO:0035929	0.0328	0.998	2	5	steroid hormone secretion	BP	0.827	PTPN11,INHBA	down_VSAP_EC
GO:0008015	0.0328	0.997	2	120	blood circulation	BP	1	LNPEP,SGCD	up_AORT_EC
GO:1902743	0.0328	1	1	16	regulation of lamellipodium	BP	1	FSCN1	down_AFEM_EC
GO:0031572	0.0328	1	1	15	G2 DNA damage checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0042592	0.0329	0.976	63	522	homeostatic process	BP	1	RHOT1,ADRA1B,PLCG2,LEP,PLCL1,SLC26A7,HTR2B,RASSF2,PRDX4,PRKAA2,BMP4,LCAT,CNNM2,ABCA1,GJA1,ATRX,PPARGC1A,CITED2,ISG15,ZNF365,PTPN3,CLCN3,FAM210B,P4HTM,MICU2,TMX3,ITPR1,PLAC8B,F2RL1,STN1,ERO1B,EGLN1,SLC12A7,LRRC8C,DMPK,ATP7A,ORMDL3,SESN3,PRKCE,APP,PSEN1,CHD7,LAMP2,DMXL1,CLN8,RAB11B,EDN1,NOD2,JAM3,B2M,DISC1,HERPUD1,TXNDC5,GAA,INPP5K,WFS1,WDR48,ATP2C1,PARK7,SLC8A1,STC2,IL18R1,HMBOX1	up_ACOR_VSMC
GO:1904951	0.0329	0.983	17	108	positive regulation of establishment of protein localization	BP	1	EXPH5,TLR1,LEP,HTR2B,TCAF1,MBP,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,PSEN1,JUP,NOD2,SCAMP5	up_ACOR_VSMC
GO:0019222	0.0329	0.99	9	1934	regulation of metabolic process	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0034138	0.0329	0.996	3	9	toll-like receptor 3 signaling pathway	BP	0.762	TNFAIP3,PELI1,TLR3	up_VCAV_EC
GO:0006936	0.0329	0.997	2	74	muscle contraction	BP	1	HTR7,NPNT	up_APUL_EC
GO:0032602	0.0329	1	1	23	chemokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0032755	0.0329	1	1	24	positive regulation of interleukin-6 production	BP	1	TLR2	up_AFEM_VSMC
GO:0048864	0.0329	1	1	29	stem cell development	BP	1	WNT7A	up_AORT_VSMC
GO:2000145	0.033	0.985	12	279	regulation of cell motility	BP	1	CMKLR1,ANGPT4,HOXA7,TWIST2,CAMK2A,LRRC15,RECK,TBXA2R,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0048731	0.033	1	2	1247	system development	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0060339	0.033	0.998	2	5	negative regulation of type I interferon-mediated signaling	BP	0.83	PTPN2,CNOT7	down_VSAP_EC
GO:2000106	0.033	1	1	29	regulation of leukocyte apoptotic process	BP	1	ARG2	up_AORT_VSMC
GO:0003231	0.033	1	1	48	cardiac ventricle development	BP	1	TBX5	up_APUL_VSMC

GO:0006520	0.033039386	0.98876	7	114	cellular amino acid metabolic process	BP	1	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,AZIN2,PM20D1	up_ACOR_EC
GO:0001816	0.033048463	0.98621	10	194	cytokine production	BP	1	CDH3,NR1H4,NDRG2,FZD5,NOD2,IL33,PTGER4,MAVS,AGPAT2,PRKCD	up_ACOR_EC
GO:0031345	0.033081653	0.99288	4	46	negative regulation of cell projection organization	BP	1	RGMA,LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0120036	0.0331	0.979	32	373	plasma membrane bounded cell projection organization	BP	0.832	SIPA1L1,SGK1,PTPN11,EXOC5,FSCN1,DPYSL3,IFRD1,RPGR,KIF5B,DYNLL1,TNIK,UBA6,ZPR1,NEO1,UST,CDH11,CTNNB1,ANLN,APOE,KLF5,LYN,GSK3B,VLDLR,SDC4,HTT,PRMT1,EXT1,DISC1,PAK2,NRP1,ARF4,YWHAH	down_VSAP_EC
GO:0031109	0.0331	0.997	2	36	microtubule polymerization or	BP	1	MZT1,ARHGEF2	up_VPOR_EC
GO:0046660	0.0331	1	1	28	female sex differentiation	BP	1	ESR1	up_AORT_VSMC
GO:0072132	0.0331	1	1	23	mesenchyme morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:1905209	0.0331	1	1	13	positive regulation of cardiocyte differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060306	0.0331	1	1	7	regulation of membrane repolarization	BP	1	CAV1	up_VSAP_VSMC
GO:0086009	0.0331	1	1	7	membrane repolarization	BP	1	CAV1	up_VSAP_VSMC
GO:0051704	0.0332	0.982	18	476	multi-organism process	BP	1	HOXA9,LEP,CD40,BPI,GPAM,CHRM2,SLC17A5,THRB,OVOL1,LRRC15,RECK,TBXA2R,RAB7A,NAPEPLD,SPATA6,CCL5,ADAM17,GCNT4	up_AFEM_EC
GO:0046621	0.0332	0.996	3	8	negative regulation of organ growth	BP	1	SLC6A4,SAV1,FXN	up_VSAP_EC
GO:0050877	0.0332	0.995	3	164	nervous system process	BP	1	NETO1,GATM,HOXC10	up_VSAP_VSMC
GO:0022037	0.0332	1	1	27	metencephalon development	BP	1	WNT7A	up_AORT_VSMC
GO:0003279	0.0332	1	1	48	cardiac septum development	BP	1	TBX5	up_APUL_VSMC
GO:0030388	0.0332	1	1	4	fructose 1,6-bisphosphate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0003171	0.0332	1	1	10	atrioventricular valve development	BP	1	TBX5	up_VPUL_EC
GO:0050769	0.0333	0.986	11	95	positive regulation of neurogenesis	BP	0.834	ARHGEF2,DPYSL3,HIF1A,CTNNB1,APOE,LYN,MMD,VLDLR,REST,DISC1,NRP1	down_VSAP_EC
GO:0002367	0.0333	0.991	6	26	cytokine production involved in immune	BP	1	TLR3,F2RL1,NOD2,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0071326	0.0333	0.991	6	26	cellular response to monosaccharide stimulus	BP	1	RAB11B,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0071331	0.0333	0.991	6	26	cellular response to hexose stimulus	BP	1	RAB11B,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0048010	0.0333	0.993	4	20	vascular endothelial growth factor receptor	BP	0.834	VEGFA,SULF1,HIF1A,NRP1	down_VSAP_EC
GO:0031328	0.0333	0.993	4	512	positive regulation of cellular biosynthetic	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0061469	0.0333	0.998	2	4	regulation of type B pancreatic cell	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0048646	0.0333	0.998	2	349	anatomical structure formation involved in	BP	1	TGFBI,GATA5	down_VSAP_VSMC
GO:0003013	0.0333	0.997	2	121	circulatory system process	BP	1	LNPEP,SGCD	up_AORT_EC
GO:0014819	0.0333	0.998	2	4	regulation of skeletal muscle contraction	BP	0.766	KCNJ2,ATP2A1	up_VCAV_EC
GO:1901889	0.0333	1	1	8	negative regulation of cell junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0035904	0.0333	1	1	25	aorta development	BP	1	EYA1	up_AFEM_VSMC
GO:0010888	0.0333	1	1	4	negative regulation of lipid storage	BP	1	ABHD5	up_VPOR_EC
GO:0070887	0.033363611	0.97976	29	775	cellular response to chemical stimulus	BP	1	NR1H4,SOX9,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,CCDC3,AGRN,NOD2,RGMA,PDE4A,SMAD6,ACTN2,PAK3,MMP28,GUCY1B1,PTGER4,ELMO2,ADAMTSL2,MAVS,FOXC2,LRRC15,IFIT2,LRP4,LRRC4,RARRES2,PRKACA,NRP1,PRKCD	up_ACOR_EC

GO:0048523	0.0334	0.974	133	1399	negative regulation of cellular process	BP	0.766	EPHB1,PLK2,EDNRB,HCLS1,IL7R,ADGRF5,KIT, PPP2R5A,CXCL8,PRKCH,ARHGEF15,IFRD1,TIE 1,CDA,TNFAIP3,ADAMTS9,TNIP1,PDGFB,POD XL,CD34,PDE4D,MEF2C,FERMT1,ATF3,CHD7, DLL4,RAPGEF1,WWP1,TLR4,NLRC5,STC1,GAT A3,MMP28,EDN1,HOXB8,APLNR,ARAP3,HO MER3,ARHGAP28,SOX18,TMOD1,EGFL7,FIG NL1,PELI1,PPP3CA,FAM3C,MTSS1,ARG2,CAS P8,MTOR,TENT2,HOOK3,MAP3K3,BMP2,CDY L,HMG20A,HHEX,CREM,CAV2,PREX2,SH3BP5 ,RSC1A1,ENC1,ITPKB,GDPD5,RIOK3,ANGPT2, PROX1,UHRF2,ENSCAFG00000010224,MDFI, ENSCAFG00000010596,STMN1,HMBOX1,PA K2,MCC,THOC1,SWAP70,SMARCA4,APOD,NC K1,TIMELESS,OTUD4,CD200,JAG1,PTGS2,ETA A1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1, BCL10,BASP1,USP28,TAOK1,CTNNA1,CNOT7, ENSCAFG00000002897,HMGB1,BLM,RIPK1,I TGA6,RAD21,RAD17,RGS2,SKIL,MTA2,ARHG DIB,CUL4A,ZW10,KDM5A,HIF1A,KDM3A,ATR X,NR4A1,HIST2H2AC,ARID5A,TOPBP1,ENSCA FG00000002015,VASH1,DCP2,TNFAIP1,IVNS 1ABP,FKBP15,RGL2,TMOD3,ZEB1,ARHGEF2,P EAR1,FBXO5,ELK3,TJP2	up_VCAV_EC
GO:0003002	0.0334	0.982	18	118	regionalization	BP	1	HOXA11,EMX2,HOXA7,HOXA9,CDON,AXIN2, HOXD3,DLL1,HOXA6,OSR1,ZBTB16,RARG,HO XC4,IRX3,HOXC10,LRP4,KDM2B,CITED2	up_VSAP_EC
GO:0023052	0.0334	0.988	10	1602	signaling	BP	1	TBX5,NR1H4,RGS1,STK32B,CCL24,HTR7,PTGE R2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0009058	0.0334	0.99	9	1910	biosynthetic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EM X2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0010033	0.0334	0.988	8	772	response to organic substance	BP	1	ACVRL1,LYN,IGF1R,NRP2,SULF1,STX4,ASPN, NEDD4	down_ACOR_EC
GO:0048645	0.0334	0.989	7	33	animal organ formation	BP	1	GATA5,BMP4,FGFR2,CITED2,SMARCD3,TBX5, FRS2	up_ACOR_VSMC
GO:0035282	0.0334	0.995	3	30	segmentation	BP	1	IRX3,DLL1,AXIN2	up_AFEM_EC
GO:0010575	0.0334	0.996	3	8	positive regulation of vascular endothelial growth factor production	BP	1	HPSE,CCBE1,SULF2	up_VSAP_EC
GO:0019438	0.0334	1	2	1258	aromatic compound biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048729	0.0334	0.997	2	209	tissue morphogenesis	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0000470	0.0334	1	1	9	maturation of LSU-rRNA	BP	1	WDR12	down_ACOR_EC
GO:0048247	0.0334	1	1	16	lymphocyte chemotaxis	BP	1	HSD3B7	down_VPOR_EC
GO:0003002	0.0334	1	1	118	regionalization	BP	1	GATA5	down_VFEM_VSMC
GO:0051196	0.0334	1	1	13	regulation of coenzyme metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0098901	0.0334	1	1	7	regulation of cardiac muscle cell action	BP	1	CAV1	up_VSAP_VSMC
GO:0003008	0.033471567	0.98331	15	336	system process	BP	1	TMOD1,BRSK1,SOX9,AQP1,GNAO1,NOD2,PD E4A,INSYN1,PLS1,ACTN2,RNLS,USP53,MAPK 8IP2,FOXC2,CLSTN1	up_ACOR_EC
GO:0009792	0.0335	0.98	28	231	embryo development ending in birth or egg hatching	BP	1	ACSL4,EIF4A3,HINFP,HOXA3,GINS4,PRMT1,X YLT1,MMP14,SLC30A1,NEK2,RNASEH2B,HOX A7,HOXB7,BRCA1,E2F8,FOSL1,PLK4,HOXC6,S MARCB1,HOXB5,RBBP8,NOLC1,PHACTR4,TB X15,HOXA9,EMG1,RTCB,SIX4	down_ACOR_VSMC
GO:0045005	0.0335	0.992	5	21	DNA-dependent DNA replication maintenance	BP	1	POLE,RAD51,TONSL,SMARCAL1,GEN1	down_ACOR_VSMC
GO:0050848	0.0335	0.995	3	30	regulation of calcium-mediated signaling	BP	1	CMKLR1,LMCD1,TMEM100	up_AFEM_EC
GO:0018130	0.0335	1	2	1261	heterocycle biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1904590	0.0335	0.998	2	5	negative regulation of protein import	BP	0.766	FERMT1,APOD	up_VCAV_EC
GO:0042308	0.0335	0.998	2	5	negative regulation of protein import into	BP	0.766	FERMT1,APOD	up_VCAV_EC
GO:0030219	0.0335	1	1	16	megakaryocyte differentiation	BP	1	GABPA	down_AFEM_EC
GO:0044818	0.0335	0.999	1	15	mitotic G2/M transition checkpoint	BP	1	TAOK1	up_AORT_EC
GO:1903409	0.0335	1	1	24	reactive oxygen species biosynthetic process	BP	1	CYP1A1	up_VCAV_VSMC

GO:0060562	0.0336	0.984	13	120	epithelial tube morphogenesis	BP	0.84	PRICKLE1,PRKACB,ENSCAFG00000032470,TMED2,ILK,HOXB7,HIF1A,MAGED1,CTNNB1,STARD13,SDC4,SIX4,NRP1	down_VSAP_EC
GO:0002237	0.0336	0.985	12	85	response to molecule of bacterial origin	BP	0.766	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,TLR4,IRF8,PELI1,ABCA1,PLCG2,BCL10,GCH1	up_VCAV_EC
GO:0048704	0.0336	0.988	8	46	embryonic skeletal system morphogenesis	BP	1	EIF4A3,HOXA3,MMP14,HOXA7,HOXB7,HOXB5,TBX15,SIX4	down_ACOR_VSMC
GO:0008344	0.0336	0.991	6	25	adult locomotory behavior	BP	1	GLRB,APP,CHD7,CLN8,OXR1,PARK7	up_ACOR_VSMC
GO:0048598	0.0336	0.995	3	207	embryonic morphogenesis	BP	1	TBX5,HOXA3,FLRT3	up_VPUL_EC
GO:0060900	0.0336	0.998	2	4	embryonic camera-type eye formation	BP	0.766	PROX1,ALDH1A3	up_VCAV_EC
GO:0034381	0.0336	1	1	10	plasma lipoprotein particle clearance	BP	1	NR1H4	up_VPUL_EC
GO:0023014	0.0337	0.979	29	248	signal transduction by protein phosphorylation	BP	0.766	EPHB1,TEK,KIT,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,MEF2C,ATF3,RAPGEF1,TLR4,EDN1,MAP3K3,BMP2,SLK,MAPK13,ITPKB,MADD,PAK2,PRKD2,TLR3,RAPGEF2,TAOK1,HMGB1,RIPK1,PDGFD,JCAD,CDON	up_VCAV_EC
GO:1903706	0.0337	0.985	11	119	regulation of hemopoiesis	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,GLI3,ZFP36L1,LOXL3,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0032635	0.0337	0.989	7	37	interleukin-6 production	BP	0.766	TNFAIP3,TLR4,MAPK13,TLR3,HMGB1,NOS2,ARHGEF2	up_VCAV_EC
GO:0060537	0.0337	0.997	2	117	muscle tissue development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0006367	0.0337	1	1	32	transcription initiation from RNA polymerase II	BP	1	ESR1	up_AORT_VSMC
GO:0017156	0.0337	1	1	32	calcium ion regulated exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0015698	0.0337	1	1	24	inorganic anion transport	BP	1	CA2	up_VCAV_VSMC
GO:0003205	0.033742723	0.99102	5	67	cardiac chamber development	BP	1	GATA4,SMAD6,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0050890	0.0338	0.997	2	67	cognition	BP	1	NETO1,GATM	up_VSAP_VSMC
GO:0048752	0.0338	1	1	5	semicircular canal morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0042462	0.0338	1	1	9	eye photoreceptor cell development	BP	1	NTRK2	up_APUL_EC
GO:0032925	0.0338	1	1	4	regulation of activin receptor signaling	BP	1	ACVR2A	up_VPOR_EC
GO:0006047	0.0338	1	1	4	UDP-N-acetylglucosamine metabolic process	BP	1	GNPNAT1	up_VPOR_EC
GO:0051645	0.0338	1	1	4	Golgi localization	BP	1	HOOK3	up_VPOR_EC
GO:1902742	0.0338	0.999	1	14	apoptotic process involved in development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010803	0.0338	1	1	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0021522	0.0338	1	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_VSAP_VSMC
GO:0046434	0.0339	0.989	7	52	organophosphate catabolic process	BP	0.84	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC	down_VSAP_EC
GO:0034341	0.0339	0.99	6	43	response to interferon-gamma	BP	0.84	FLNB,MYO1C,KIF5B,PTPN2,CDC37,GBP5	down_VSAP_EC
GO:0060337	0.0339	0.995	3	12	type I interferon signaling pathway	BP	0.84	PTPN2,CNOT7,CDC37	down_VSAP_EC
GO:0071357	0.0339	0.995	3	12	cellular response to type I interferon	BP	0.84	PTPN2,CNOT7,CDC37	down_VSAP_EC
GO:0002726	0.0339	0.996	3	8	positive regulation of T cell cytokine production	BP	1	B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0006091	0.0339	0.997	2	139	generation of precursor metabolites and energy	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0007417	0.0339	0.997	2	235	central nervous system development	BP	1	HOXC10,WNT7A	up_AORT_VSMC
GO:0002237	0.0339	0.997	2	85	response to molecule of bacterial origin	BP	1	NR1H4,MRC1	up_VPUL_EC
GO:0090224	0.0339	0.999	1	16	regulation of spindle organization	BP	1	GPSM2	down_AFEM_EC
GO:0001658	0.0339	0.999	1	24	branching involved in ureteric bud	BP	1	EYA1	up_AFEM_VSMC
GO:1903556	0.0339	0.999	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	BPI	up_AORT_EC
GO:1902667	0.0339	1	1	5	regulation of axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:1905207	0.0339	0.999	1	17	regulation of cardiocyte differentiation	BP	1	TBX5	up_VPUL_VSMC

GO:1901800	0.033940422	0.99264	4	46	positive regulation of proteasomal protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0022008	0.034	0.977	46	406	neurogenesis	BP	0.766	EPHB1,EDNRB,PRKCH,IFRD1,RELN,MEF2C,CHD7,DLL4,RAPGEF1,TLR4,EIF2B2,GATA3,RAB11A,TCF4,NTN4,PPP3CA,MTOR,NAV2,HOOK3,BMP2,HMG20A,PREX2,GDPD5,PROX1,ENSCAFG00000010224,STMN1,MMP24,PAK2,APOD,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,NUP133,SPTBN4,SKIL,HIF1A,ALS2,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:1902905	0.034	0.985	11	72	positive regulation of supramolecular fiber	BP	0.766	ARHGEF15,BAIAP2L1,EDN1,MTOR,NCKAP1,PROX1,IQGAP2,SWAP70,NCK1,FES,ARPC5L	up_VCAV_EC
GO:0007275	0.034	0.988	9	1370	multicellular organism development	BP	1	TBX5,HOXA3,NR1H4,EVI2B,HOXA2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0070887	0.034	0.988	8	775	cellular response to chemical stimulus	BP	1	ACVRL1,LYN,IGF1R,NRP2,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:2001235	0.034	0.988	8	69	positive regulation of apoptotic signaling	BP	0.84	PTPN2,MAGED1,BNIP3,FAM162A,ATF3,SH3GLB1,PAK2,INHBA	down_VSAP_EC
GO:0019751	0.034	0.99	6	33	polyol metabolic process	BP	0.766	GK5,SPTLC2,ITPKB,PLCG2,GCH1,IMPA1	up_VCAV_EC
GO:0035024	0.034	0.996	3	8	negative regulation of Rho protein signal	BP	0.766	ARAP3,STMN1,TNFAIP1	up_VCAV_EC
GO:0048596	0.034	0.996	3	9	embryonic camera-type eye morphogenesis	BP	0.766	PROX1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0061318	0.034	0.996	3	8	renal filtration cell differentiation	BP	0.766	PODXL,JAG1,BASP1	up_VCAV_EC
GO:0072010	0.034	0.996	3	8	glomerular epithelium development	BP	0.766	PODXL,JAG1,BASP1	up_VCAV_EC
GO:0072112	0.034	0.996	3	8	glomerular visceral epithelial cell	BP	0.766	PODXL,JAG1,BASP1	up_VCAV_EC
GO:0072311	0.034	0.996	3	8	glomerular epithelial cell differentiation	BP	0.766	PODXL,JAG1,BASP1	up_VCAV_EC
GO:0010572	0.034	0.998	2	4	positive regulation of platelet activation	BP	0.766	SELP,TLR4	up_VCAV_EC
GO:0021783	0.034	0.999	1	9	preganglionic parasympathetic fiber	BP	1	SIX1	up_VFEM_EC
GO:0003044	0.034	1	1	8	regulation of systemic arterial blood pressure mediated by a chemical	BP	1	AVPR1A	up_VFEM_EC
GO:0072074	0.034	1	1	8	kidney mesenchyme development	BP	1	SIX1	up_VFEM_EC
GO:0008542	0.034	0.999	1	13	visual learning	BP	1	NETO1	up_VFEM_VSMC
GO:0055081	0.034	0.999	1	17	anion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0007044	0.034008766	0.99471	3	27	cell-substrate junction assembly	BP	1	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0000578	0.034089891	0.99726	2	11	embryonic axis specification	BP	1	FZD5,SMAD6	up_ACOR_EC
GO:0019081	0.0341	0.996	3	8	viral translation	BP	1	EIF3G,EIF3L,EIF3D	up_VSAP_EC
GO:0006729	0.0341	0.998	2	4	tetrahydrobiopterin biosynthetic process	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0046146	0.0341	0.998	2	4	tetrahydrobiopterin metabolic process	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0043069	0.0341	0.997	2	262	negative regulation of programmed cell death	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:1901653	0.0341	0.997	2	84	cellular response to peptide	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0002183	0.0341	0.999	1	16	cytoplasmic translational initiation	BP	1	EIF3M	down_AFEM_EC
GO:0016042	0.0341	1	1	80	lipid catabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0010631	0.0341	1	1	118	epithelial cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0090132	0.0341	1	1	118	epithelium migration	BP	1	JUP	down_VFEM_VSMC
GO:0055025	0.0341	0.999	1	17	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0098815	0.0341	0.999	1	9	modulation of excitatory postsynaptic potential	BP	1	NETO1	up_VSAP_VSMC
GO:0022613	0.0342	0.98	25	208	ribonucleoprotein complex biogenesis	BP	1	USP4,EDC3,SLC29A1,NOP56,RAN,FBL,DIS3,NOC4L,NOC2L,DDX28,RSL1D1,RRP1,DDX39B,SF3A2,ENSCAFG00000019620,NOP14,PRMT5,NOP58,ENSCAFG00000015189,EMG1,EXOSC5,GEMIN7,SF3A1,EIF3M,NOB1	down_ACOR_VSMC
GO:0010468	0.0342	1	2	1270	regulation of gene expression	BP	1	JUP,GATA5	down_VFEM_VSMC

GO:0048871	0.0342	0.997	2	120	multicellular organismal homeostasis	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0060562	0.0342	0.997	2	120	epithelial tube morphogenesis	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0051438	0.0342	0.999	1	24	regulation of ubiquitin-protein transferase	BP	1	LIMK1	up_VCAV_VSMC
GO:0003229	0.0342	0.999	1	17	ventricular cardiac muscle tissue development	BP	1	TBX5	up_VPUL_VSMC
GO:0051129	0.0343	0.979	30	221	negative regulation of cellular component organization	BP	1	FGF13,SMAD6,ARHGAP28,MID1,FEZ1,ITM2C,BMP4,EVI5L,TUBB4A,ATRX,ATXN2,ZNF365,AR,LMO4,BNIP3,CLSTN1,NRP1,LRPAP1,ULK2,EVL,TBX20,PSEN1,DUSP22,ASAP1,FAM107A,B2M,SCAMP5,FEZ2,INPP5K,WASL	up_ACOR_VSMC
GO:1902531	0.0343	0.991	5	536	regulation of intracellular signal transduction	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0051457	0.0343	0.996	3	8	maintenance of protein location in nucleus	BP	1	MORC3,CIZ1,TAF8	up_VSAP_EC
GO:1904668	0.0343	0.998	2	4	positive regulation of ubiquitin protein ligase	BP	1	UBE2S,CDC20	down_ACOR_VSMC
GO:0048568	0.0343	0.997	2	148	embryonic organ development	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0060537	0.0343	0.997	2	117	muscle tissue development	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0008015	0.0343	1	1	120	blood circulation	BP	1	JUP	down_VFEM_VSMC
GO:0055123	0.0343	1	1	40	digestive system development	BP	1	GATA5	down_VSAP_VSMC
GO:0048745	0.0343	0.999	1	8	smooth muscle tissue development	BP	1	SIX1	up_VFEM_EC
GO:0001759	0.0343	0.999	1	13	organ induction	BP	1	HOXA11	up_VFEM_VSMC
GO:0043266	0.0343	0.999	1	14	regulation of potassium ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0050704	0.03430161	0.99724	2	11	regulation of interleukin-1 secretion	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0050922	0.034302473	0.99724	2	11	negative regulation of chemotaxis	BP	1	MMP28,NRP1	up_ACOR_EC
GO:0012501	0.0344	0.977	44	561	programmed cell death	BP	0.846	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,ETV6,ERO1A,CASP3,HYOU1,EXOC5,AARS,FHL2,PTGS2,UACA,HIF1A,DNAJC10,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,GLO1,PAK2,INHBA,SIX4,CDKN1A,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0006874	0.0344	0.984	13	91	cellular calcium ion homeostasis	BP	0.771	ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,PDZD8,SWAP70,PLCG2,HMGB1,MCU,ATP2A1	up_VCAV_EC
GO:0009725	0.0344	0.986	9	188	response to hormone	BP	1	LEP,LBH,CRY2,FIBIN,CHRM2,AVPR1A,CAMK2A,NR3C1,KANK1	up_AFEM_EC
GO:0061217	0.0344	0.995	3	13	regulation of mesonephros	BP	0.846	HOXB7,MAGED1,SIX4	down_VSAP_EC
GO:0035295	0.0344	0.998	2	356	tube development	BP	1	TGFBI,GATA5	down_VSAP_VSMC
GO:0071071	0.0344	0.999	1	8	regulation of phospholipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0051932	0.0344	0.999	1	9	synaptic transmission, GABAergic	BP	1	PLCL1	up_APUL_EC
GO:1990774	0.0344	0.999	1	9	tumor necrosis factor secretion	BP	1	NR1H4	up_APUL_EC
GO:0007254	0.034464514	0.99077	5	67	JNK cascade	BP	1	FZD5,NOD2,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC
GO:0030072	0.0345	0.987	9	48	peptide hormone secretion	BP	1	LEP,TM7SF3,PRKCE,CHD7,CCL5,RAB11B,EDN1,PFKL,PARK7	up_ACOR_VSMC
GO:0045638	0.0345	0.989	7	33	negative regulation of myeloid cell	BP	1	HOXA7,HOXA9,DLL1,ZBTB16,ZFP36L1,PIK3R1,MYC	up_VSAP_EC
GO:0019221	0.0345	0.989	6	102	cytokine-mediated signaling pathway	BP	1	LEP,GREM2,CYLD,LRRC15,CCL5,ADAM17	up_AFEM_EC
GO:0090257	0.0345	0.992	4	52	regulation of muscle system process	BP	1	LMCD1,CHRM2,TBXA2R,DMPK	up_AFEM_EC
GO:2000772	0.0345	0.993	4	15	regulation of cellular senescence	BP	0.771	PLK2,ARG2,MAP3K3,VASH1	up_VCAV_EC
GO:0032332	0.0345	0.998	2	6	positive regulation of chondrocyte	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:1903038	0.0345	0.999	1	30	negative regulation of leukocyte cell-cell	BP	1	ARG2	up_AORT_VSMC
GO:0006541	0.0345	0.999	1	9	glutamine metabolic process	BP	1	NR1H4	up_APUL_EC

GO:0019216	0.0346	0.983	14	101	regulation of lipid metabolic process	BP	0.771	TEK,ADGRF5,PPP2R5A,PDGFB,MTOR,SAMD8,BMP2,PROX1,ENSCAFG00000010596,SH3GLB1,APOD,PTGS2,CREB1,NR1D2	up_VCAV_EC
GO:0031175	0.0346	0.993	4	224	neuron projection development	BP	1	LYN,SPG11,NRP2,NEDD4	down_ACOR_EC
GO:0071604	0.0346	0.995	3	10	transforming growth factor beta production	BP	0.771	CD34,CD200,HIF1A	up_VCAV_EC
GO:0071634	0.0346	0.995	3	10	regulation of transforming growth factor beta	BP	0.771	CD34,CD200,HIF1A	up_VCAV_EC
GO:0048568	0.0346	0.997	2	148	embryonic organ development	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0003013	0.0346	1	1	121	circulatory system process	BP	1	JUP	down_VFEM_VSMC
GO:0009566	0.0346	0.999	1	24	fertilization	BP	1	HOXA9	up_AFEM_VSMC
GO:0001974	0.0346	0.999	1	13	blood vessel remodeling	BP	1	HOXA3	up_VPOR_VSMC
GO:0003209	0.0346	0.999	1	14	cardiac atrium morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003230	0.0346	0.999	1	14	cardiac atrium development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010677	0.0346	0.999	1	14	negative regulation of cellular carbohydrate	BP	1	FBP1	up_VFEM_VSMC
GO:0048103	0.0346	0.999	1	10	somatic stem cell division	BP	1	ARHGEF2	up_VPUL_EC
GO:0008202	0.0347	0.984	12	80	steroid metabolic process	BP	1	SQLE,LSS,SREBF1,HMGCR,SF1,INSIG1,ENSCAFG00000018572,DHCR24,MVD,FDFT1,SGPL1,LIPC	down_ACOR_VSMC
GO:0007268	0.0347	0.988	7	130	chemical synaptic transmission	BP	1	KCNC4,GPR1,CHRM2,SLC6A6,HTR1D,CAMK2A,DMPK	up_AFEM_EC
GO:0098916	0.0347	0.988	7	130	anterograde trans-synaptic signaling	BP	1	KCNC4,GPR1,CHRM2,SLC6A6,HTR1D,CAMK2A,DMPK	up_AFEM_EC
GO:0072160	0.0347	0.999	1	9	nephron tubule epithelial cell differentiation	BP	1	MTSS1	up_VFEM_EC
GO:0042092	0.034704212	0.99719	2	11	type 2 immune response	BP	1	NOD2,IL33	up_ACOR_EC
GO:1901700	0.034732295	0.98219	16	364	response to oxygen-containing compound	BP	1	NR1H4,SOX9,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,AGRN,PTGIR,NOD2,ACTN2,GUCY1B1,PTGER4,FOXC2,RARRES2,PRKACA,PRKCD	up_ACOR_EC
GO:0030218	0.0348	0.99	6	42	erythrocyte differentiation	BP	0.853	CASP3,HIF1A,PTPN2,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0006721	0.0348	0.995	3	14	terpenoid metabolic process	BP	1	CYP1B1,RETSAT,RDH10	down_VCAV_EC
GO:0043101	0.0348	0.998	2	6	purine-containing compound salvage	BP	1	ADK,AMPD2	down_VCAV_EC
GO:0048732	0.0348	0.997	2	116	gland development	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0040037	0.0348	1	1	6	negative regulation of fibroblast growth factor receptor signaling	BP	1	SULF1	down_ACOR_EC
GO:1900120	0.0348	0.999	1	7	regulation of receptor binding	BP	1	HOXA3	down_ACOR_EC
GO:0007422	0.0348	0.999	1	18	peripheral nervous system development	BP	1	CITED2	down_VPOR_EC
GO:0032637	0.0348	0.999	1	26	interleukin-8 production	BP	1	TLR2	up_AFEM_VSMC
GO:0003170	0.0348	0.999	1	25	heart valve development	BP	1	GATA5	up_VCAV_VSMC
GO:0006536	0.0348	0.999	1	10	glutamate metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0043207	0.0349	0.979	29	216	response to external biotic stimulus	BP	1	VEGFD,TLR1,PLCG2,TMEM255A,COCH,MX1,ABCA1,TLR3,ISG15,PTGIR,SASH1,PLAC8B,ANKRD1,F2RL1,BNIP3,SLC17A5,PTPN22,GPM6A,PRKCE,PARP9,CHD7,CCL5,NOD2,DDIT4,NAALADL2,B2M,SERINC3,TNFRSF11B,WASL	up_ACOR_VSMC
GO:0051707	0.0349	0.979	29	216	response to other organism	BP	1	VEGFD,TLR1,PLCG2,TMEM255A,COCH,MX1,ABCA1,TLR3,ISG15,PTGIR,SASH1,PLAC8B,ANKRD1,F2RL1,BNIP3,SLC17A5,PTPN22,GPM6A,PRKCE,PARP9,CHD7,CCL5,NOD2,DDIT4,NAALADL2,B2M,SERINC3,TNFRSF11B,WASL	up_ACOR_VSMC
GO:0003073	0.0349	0.991	5	20	regulation of systemic arterial blood pressure	BP	1	ADRA1B,SLC2A5,F2RL1,EDN1,NCALD	up_ACOR_VSMC
GO:1903426	0.0349	0.993	4	17	regulation of reactive oxygen species	BP	0.771	CD34,TLR4,RAB27A,ARG2	up_VCAV_EC
GO:0060479	0.0349	0.996	3	8	lung cell differentiation	BP	1	THRB,SAV1,NFIB	up_VSAP_EC

GO:0046006	0.0349	0.998	2	6	regulation of activated T cell proliferation	BP	1	GPAM,PRNP	down_VCAV_EC
GO:0097152	0.0349	0.998	2	5	mesenchymal cell apoptotic process	BP	0.853	ETV6,HIF1A	down_VSAP_EC
GO:0006101	0.0349	0.999	1	16	citrate metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0090130	0.0349	1	1	121	tissue migration	BP	1	JUP	down_VFEM_VSMC
GO:0010002	0.0349	0.999	1	9	cardioblast differentiation	BP	1	TBX5	up_APUL_EC
GO:0003206	0.0349	1	1	51	cardiac chamber morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0060078	0.0349	0.999	1	17	regulation of postsynaptic membrane potential	BP	1	NETO1	up_VFEM_VSMC
GO:0099565	0.0349	0.999	1	17	chemical synaptic transmission, postsynaptic	BP	1	NETO1	up_VFEM_VSMC
GO:2001239	0.0349	0.999	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	EYA1	up_VFEM_VSMC
GO:2000146	0.034987276	0.98915	6	92	negative regulation of cell motility	BP	1	SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,TBX5	up_ACOR_EC
GO:0030334	0.035	0.98	24	267	regulation of cell migration	BP	0.853	ARHGEF2,VEGFA,SULF1,HSPA5,SERPINE1,SPARC,JCAD,DPYSL3,PRCP,MYO1C,PIK3C2A,MSN,HIF1A,ADAM17,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,NEXN,SDC4,ZMYND8,NRP1	down_VSAP_EC
GO:0006793	0.035	0.987	9	948	phosphorus metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,CSGALNACT1,ACSL3,MYO1D,TNRC6B,ASPN	down_ACOR_EC
GO:0032680	0.035	0.989	7	36	regulation of tumor necrosis factor production	BP	0.771	TNFAIP3,CD34,TLR4,ARG2,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:0042060	0.035	0.989	6	103	wound healing	BP	1	F5,F3,TFPI2,LGR6,ADAM17,KANK1	up_AFEM_EC
GO:0002027	0.035	0.991	5	20	regulation of heart rate	BP	1	KCNE3,RNLS,JUP,EDN1,BVES	up_ACOR_VSMC
GO:0043549	0.035	0.992	4	244	regulation of kinase activity	BP	1	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0018279	0.035	0.993	4	14	protein N-linked glycosylation via	BP	1	ST3GAL5,MAGT1,STT3B,FUT8	up_ACOR_VSMC
GO:0070233	0.035	0.995	3	9	negative regulation of T cell apoptotic process	BP	0.771	IL7R,ARG2,HIF1A	up_VCAV_EC
GO:0006817	0.035	0.998	2	5	phosphate ion transport	BP	0.853	SLC20A1,SLC20A2	down_VSAP_EC
GO:0000466	0.035	0.999	1	8	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	WDR12	down_ACOR_EC
GO:0050729	0.035	0.999	1	25	positive regulation of inflammatory response	BP	1	TLR2	up_AFEM_VSMC
GO:0010894	0.035	0.999	1	9	negative regulation of steroid biosynthetic	BP	1	NR1H4	up_APUL_EC
GO:0045939	0.035	0.999	1	9	negative regulation of steroid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0071709	0.035	0.999	1	8	membrane assembly	BP	1	CAV1	up_VSAP_VSMC
GO:1900449	0.035	0.999	1	9	regulation of glutamate receptor signaling	BP	1	NETO1	up_VSAP_VSMC
GO:0046483	0.0351	0.99	8	1948	heterocycle metabolic process	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,SRSF6,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0065009	0.0351	0.99	6	735	regulation of molecular function	BP	1	HOXA3,NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0003156	0.0351	0.991	5	20	regulation of animal organ formation	BP	1	GATA5,BMP4,CITED2,TBX5,FRS2	up_ACOR_VSMC
GO:0030500	0.0351	0.993	4	25	regulation of bone mineralization	BP	1	BMPR1A,DDR2,OMD,GREM1	down_VCAV_EC
GO:0046189	0.0351	0.995	3	9	phenol-containing compound biosynthetic	BP	0.771	GATA3,RAPGEF2,GCH1	up_VCAV_EC
GO:0031018	0.0351	0.996	3	8	endocrine pancreas development	BP	1	HNF4A,IL6R,DLL1	up_VSAP_EC
GO:0042532	0.0351	0.998	2	4	negative regulation of tyrosine phosphorylation	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0050770	0.0351	0.997	2	39	regulation of axonogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0002021	0.0351	0.999	1	9	response to dietary excess	BP	1	PCSK1N	up_APUL_EC
GO:0050806	0.0351	0.999	1	25	positive regulation of synaptic transmission	BP	1	CA2	up_VCAV_VSMC
GO:0098657	0.0352	0.979	25	181	import into cell	BP	1	DNAJC6,PLCG2,LEP,CDC7,HTR2B,ABCA1,ATXN2,SLC2A5,TMEM108,F2RL1,LRPAP1,APP,PSEN1,SYNJ2BP,PIK3C3,CLN8,GTF2A1L,B2M,AP2B1,SCAMP5,TXNDC5,RAB5C,PARK7,SLC8A1,PIK3C2A	up_ACOR_VSMC

GO:0032091	0.0352	0.989	7	34	negative regulation of protein binding	BP	1	XIRP1,CLSTN1,LRPAP1,MITD1,B2M,DISC1,PARK7	up_ACOR_VSMC
GO:1901700	0.0352	0.993	4	364	response to oxygen-containing compound	BP	1	NR1H4,MRC1,PTGER2,ARHGEF2	up_VPUL_EC
GO:1901362	0.0352	1	2	1293	organic cyclic compound biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0001916	0.0352	0.998	2	6	positive regulation of T cell mediated cytotoxicity	BP	0.856	FAM49B,PVR	down_VSAP_EC
GO:0043393	0.0352	0.997	2	77	regulation of protein binding	BP	1	HOXA3,PLCL1	up_APUL_EC
GO:0002418	0.0352	0.998	2	5	immune response to tumor cell	BP	0.771	NECTIN2,HMGB1	up_VCAV_EC
GO:0002834	0.0352	0.998	2	5	regulation of response to tumor cell	BP	0.771	NECTIN2,HMGB1	up_VCAV_EC
GO:0002837	0.0352	0.998	2	5	regulation of immune response to tumor cell	BP	0.771	NECTIN2,HMGB1	up_VCAV_EC
GO:0032352	0.0352	0.998	2	4	positive regulation of hormone metabolic	BP	0.771	GATA3,HIF1A	up_VCAV_EC
GO:0072007	0.0352	0.998	2	5	mesangial cell differentiation	BP	0.771	PDGFB,GPR4	up_VCAV_EC
GO:0072143	0.0352	0.998	2	5	mesangial cell development	BP	0.771	PDGFB,GPR4	up_VCAV_EC
GO:1904238	0.0352	0.998	2	5	pericyte cell differentiation	BP	0.771	PDGFB,GPR4	up_VCAV_EC
GO:0021537	0.0352	0.997	2	73	telencephalon development	BP	1	EMX2,SALL1	up_VSAP_VSMC
GO:0001707	0.0352	0.999	1	25	mesoderm formation	BP	1	EYA1	up_AFEM_VSMC
GO:0031099	0.0352	0.999	1	30	regeneration	BP	1	WNT7A	up_AORT_VSMC
GO:0006880	0.0352	1	1	4	intracellular sequestering of iron ion	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0097577	0.0352	1	1	4	sequestering of iron ion	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:2000826	0.0352	0.999	1	14	regulation of heart morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0002068	0.0353	0.996	3	8	glandular epithelial cell development	BP	1	HNF4A,DLL1,RARG	up_VSAP_EC
GO:1901857	0.0353	0.998	2	4	positive regulation of cellular respiration	BP	1	PRELID1,CDK1	down_ACOR_VSMC
GO:0030279	0.0353	0.999	1	19	negative regulation of ossification	BP	1	HDAC7	down_VPOR_EC
GO:2000738	0.0353	0.999	1	9	positive regulation of stem cell differentiation	BP	1	TBX5	up_APUL_EC
GO:0006805	0.0353	0.999	1	8	xenobiotic metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0060606	0.0354	0.987	8	39	tube closure	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0060021	0.0354	0.988	7	34	roof of mouth development	BP	1	FZD1,WNT11,OSR2,INSIG2,OSR1,TGFBR2,NPRL3	up_VSAP_EC
GO:0045648	0.0354	0.995	3	13	positive regulation of erythrocyte	BP	0.857	HIF1A,PRMT1,INHBA	down_VSAP_EC
GO:0048254	0.0354	0.998	2	4	snoRNA localization	BP	1	FBL,NOP58	down_ACOR_VSMC
GO:0002521	0.0354	0.997	2	149	leukocyte differentiation	BP	1	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0001783	0.0354	0.999	1	8	B cell apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0070613	0.0354	0.999	1	25	regulation of protein processing	BP	1	C6	up_VCAV_VSMC
GO:1903317	0.0354	0.999	1	25	regulation of protein maturation	BP	1	C6	up_VCAV_VSMC
GO:0048675	0.0354	0.999	1	26	axon extension	BP	1	LIMK1	up_VCAV_VSMC
GO:0047484	0.0354	1	1	5	regulation of response to osmotic stress	BP	1	ARHGEF2	up_VPOR_EC
GO:0045992	0.0355	0.995	3	12	negative regulation of embryonic development	BP	0.857	SULF1,PRKACB,CTNNB1	down_VSAP_EC
GO:0050858	0.0355	0.997	2	6	negative regulation of antigen receptor-mediated signaling	BP	1	PRNP,THY1	down_VCAV_EC
GO:0050860	0.0355	0.997	2	6	negative regulation of T cell receptor signaling	BP	1	PRNP,THY1	down_VCAV_EC
GO:0007028	0.0355	0.998	2	5	cytoplasm organization	BP	0.857	ETV6,KIF5B	down_VSAP_EC
GO:0001775	0.0355	0.997	2	219	cell activation	BP	1	TLR2,HOXA9	up_AFEM_VSMC
GO:0051960	0.0355	0.997	2	216	regulation of nervous system development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC

GO:0051961	0.0356	0.986	9	73	negative regulation of nervous system	BP	0.857	PRKACB,DPYSL3,HOOK3,IFRD1,CTNNB1,APOE,REST,NRP1,YWHAH	down_VSAP_EC
GO:0009891	0.0356	0.993	4	521	positive regulation of biosynthetic process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048468	0.0356	0.995	3	553	cell development	BP	1	EYA1,BEND2,IRX5	up_AFEM_VSMC
GO:0060412	0.0356	0.999	1	15	ventricular septum morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002115	0.0356	0.999	1	8	store-operated calcium entry	BP	1	STIM1	up_VSAP_VSMC
GO:0048729	0.0357	0.978	29	209	tissue morphogenesis	BP	1	TNNT2,GATA5,SHROOM3,MLLT3,BMP4,FGFR2,GJA1,SEC24B,CITED2,SPINT1,ZNRF3,LMO4,ANKRD1,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,NPNT,SPINT2,TBX20,TBX5,FZD3,FRS2,DAG1,PSEN1,CHD7,EDN1,SERPINB5,RREB1	up_ACOR_VSMC
GO:0006935	0.0357	0.994	3	143	chemotaxis	BP	1	LYN,NRP2,STX4	down_ACOR_EC
GO:0042330	0.0357	0.994	3	143	taxis	BP	1	LYN,NRP2,STX4	down_ACOR_EC
GO:0035239	0.0357	0.995	3	299	tube morphogenesis	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0080009	0.0357	0.998	2	4	mRNA methylation	BP	0.779	WTAP,ZC3H13	up_VCAV_EC
GO:0048514	0.0357	0.997	2	214	blood vessel morphogenesis	BP	1	C6,TGFBI	up_VCAV_VSMC
GO:0045747	0.0357	0.999	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	up_VPUL_VSMC
GO:0032272	0.0357	0.999	1	18	negative regulation of protein polymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0031667	0.0358	0.982	16	102	response to nutrient levels	BP	1	LEP,PRKAA2,CASTOR1,PPARGC1A,CDKN2B,GABARAPL1,CDKN1A,P2RX7,ULK2,SESN3,PIK3C3,LAMP2,SESN1,FAM107A,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0006338	0.0358	0.987	8	45	chromatin remodeling	BP	1	HMGA1,SMARCC1,OIP5,DMAP1,SMARCB1,CENPP,TADA2A,MIS18A	down_ACOR_VSMC
GO:0007266	0.0358	0.987	8	64	Rho protein signal transduction	BP	0.861	ARHGEF2,FARP1,APOE,PLEKHG2,TAX1BP3,PAK2,NRP1,TNFAIP1	down_VSAP_EC
GO:0099537	0.0358	0.988	7	131	trans-synaptic signaling	BP	1	KCNC4,GPR1,CHRM2,SLC6A6,HTR1D,CAMK2A,DMPK	up_AFEM_EC
GO:0018193	0.0358	0.992	4	368	peptidyl-amino acid modification	BP	1	NR1H4,STK32B,PTGER2,ARHGEF2	up_VPUL_EC
GO:0007160	0.0358	0.997	2	56	cell-matrix adhesion	BP	1	ACVRL1,HOXA7	down_ACOR_EC
GO:0046601	0.0358	0.998	2	4	positive regulation of centriole replication	BP	1	NUP62,PLK4	down_ACOR_VSMC
GO:0006335	0.0358	0.998	2	4	DNA replication-dependent nucleosome	BP	0.779	NASP,ASF1A	up_VCAV_EC
GO:0034723	0.0358	0.998	2	4	DNA replication-dependent nucleosome	BP	0.779	NASP,ASF1A	up_VCAV_EC
GO:0002707	0.0358	0.998	2	4	negative regulation of lymphocyte mediated	BP	0.779	IL7R,THOC1	up_VCAV_EC
GO:0072529	0.0358	0.998	2	4	pyrimidine-containing compound catabolic	BP	0.779	CDA,TET2	up_VCAV_EC
GO:0050435	0.0358	0.999	1	8	amyloid-beta metabolic process	BP	1	MME	up_VFEM_EC
GO:0009612	0.035867914	0.99208	4	47	response to mechanical stimulus	BP	1	SOX9,AQP1,PTGER4,USP53	up_ACOR_EC
GO:0006725	0.0359	0.99	8	1956	cellular aromatic compound metabolic	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,SRSF6,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0006986	0.0359	0.987	8	42	response to unfolded protein	BP	1	TM7SF3,CREBRF,STT3B,JKAMP,HERPUD1,WFS1,DZIP3,STC2	up_ACOR_VSMC
GO:0007032	0.0359	0.991	5	22	endosome organization	BP	0.779	RAB11A,RAB27A,HOOK3,DNAJC13,ALS2	up_VCAV_EC
GO:0006468	0.0359	0.991	5	544	protein phosphorylation	BP	1	STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0022603	0.0359	0.992	4	301	regulation of anatomical structure morphogenesis	BP	1	EYA1,HOXB7,SIX1,CDC42EP5	up_VFEM_EC
GO:0055007	0.0359	0.994	3	31	cardiac muscle cell differentiation	BP	1	DLL1,GREM1,BVES	up_AFEM_EC
GO:0022603	0.0359	0.994	3	301	regulation of anatomical structure morphogenesis	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0045214	0.0359	0.999	1	13	sarcomere organization	BP	1	NKX2-5	up_VPOR_VSMC
GO:0001666	0.036	0.985	10	67	response to hypoxia	BP	0.779	CXCR4,CD34,EDN1,MTOR,BMP2,PTGS2,PMAIP1,HIF1A,HP1BP3,P2RX2	up_VCAV_EC
GO:0036293	0.036	0.985	10	67	response to decreased oxygen levels	BP	0.779	CXCR4,CD34,EDN1,MTOR,BMP2,PTGS2,PMAIP1,HIF1A,HP1BP3,P2RX2	up_VCAV_EC
GO:0072359	0.036	0.992	4	368	circulatory system development	BP	1	TBX5,HOXA3,CCL24,FLRT3	up_VPUL_EC

GO:0120162	0.036	0.994	3	31	positive regulation of cold-induced thermogenesis	BP	1	CMKLR1,LEP,PPARGC1A	up_AFEM_EC
GO:0033003	0.036	0.999	1	8	regulation of mast cell activation	BP	1	LYN	down_ACOR_EC
GO:0045604	0.036	0.999	1	17	regulation of epidermal cell differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0050905	0.036	0.999	1	26	neuromuscular process	BP	1	HOXC10	up_AFEM_VSMC
GO:0007269	0.036	0.999	1	34	neurotransmitter secretion	BP	1	WNT7A	up_AORT_VSMC
GO:0099643	0.036	0.999	1	34	signal release from synapse	BP	1	WNT7A	up_AORT_VSMC
GO:0030326	0.036	0.999	1	51	embryonic limb morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0035113	0.036	0.999	1	51	embryonic appendage morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0009187	0.036	0.999	1	10	cyclic nucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0050771	0.036089422	0.99701	2	11	negative regulation of axonogenesis	BP	1	LRP4,NRP1	up_ACOR_EC
GO:0051495	0.0361	0.984	12	82	positive regulation of cytoskeleton organization	BP	0.78	TEK,ARHGEF15,BAIAP2L1,EDN1,MTOR,NCKAP1,PROX1,IQGAP2,SWAP70,NCK1,FES,ARPC5L	up_VCAV_EC
GO:0007154	0.0361	0.987	10	1622	cell communication	BP	1	TBX5,NR1H4,RGS1,STK32B,CCL24,HTR7,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0061326	0.0361	0.989	6	41	renal tubule development	BP	0.865	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0072080	0.0361	0.989	6	41	nephron tubule development	BP	0.865	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0032501	0.0361	0.994	5	1782	multicellular organismal process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0051653	0.0361	0.993	4	15	spindle localization	BP	1	ZW10,CENPA,NDC80,ASPM	down_ACOR_VSMC
GO:0048592	0.0361	0.992	4	53	eye morphogenesis	BP	1	IRX5,COL8A2,DLL1,THRB	up_AFEM_EC
GO:2000401	0.0361	0.997	2	13	regulation of lymphocyte migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0001976	0.0361	0.998	2	4	neurological system process involved in regulation of systemic	BP	0.78	NAV2,P2RX2	up_VCAV_EC
GO:1902904	0.0361	0.997	2	38	negative regulation of supramolecular fiber	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0046847	0.0361	0.999	1	17	filopodium assembly	BP	1	FSCN1	down_AFEM_EC
GO:0048332	0.0361	0.999	1	26	mesoderm morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0034502	0.0361	0.999	1	30	protein localization to chromosome	BP	1	ESR1	up_AORT_VSMC
GO:0014896	0.0361	0.999	1	18	muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0014897	0.0361	0.999	1	18	striated muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0003300	0.0361	0.999	1	18	cardiac muscle hypertrophy	BP	1	GATA5	up_VPUL_VSMC
GO:0060038	0.0361	0.999	1	18	cardiac muscle cell proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0000187	0.0362	0.989	6	28	activation of MAPK activity	BP	0.78	KIT,MAP3K11,TLR4,BMP2,MADD,RIPK1	up_VCAV_EC
GO:0006029	0.0362	0.991	5	29	proteoglycan metabolic process	BP	0.866	SULF1,ENSCAFG00000032470,CHSY1,CTNNB1,EXT1	down_VSAP_EC
GO:0006493	0.0362	0.991	5	20	protein O-linked glycosylation	BP	1	GALNT3,GALNT10,B3GALNT2,POMK,EOGT	up_ACOR_VSMC
GO:1903428	0.0362	0.995	3	8	positive regulation of reactive oxygen species biosynthetic process	BP	1	CYBA,ZNF205,ASS1	up_VSAP_EC
GO:0045739	0.0362	0.999	1	26	positive regulation of DNA repair	BP	1	EYA1	up_AFEM_VSMC
GO:0006766	0.0362	0.999	1	16	vitamin metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003209	0.0362	0.999	1	14	cardiac atrium morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0003230	0.0362	0.999	1	14	cardiac atrium development	BP	1	SHOX2	up_VFEM_VSMC
GO:0060420	0.0362	0.999	1	18	regulation of heart growth	BP	1	TBX5	up_VPUL_VSMC
GO:0043066	0.036219561	0.9833	12	253	negative regulation of apoptotic process	BP	1	NR1H4,SOX9,AQP1,IFI6,SMAD6,BCL2,MAPK8IP2,FOXC2,FIGNL1,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0071902	0.0363	0.984	12	79	positive regulation of protein serine/threonine	BP	0.781	KIT,MAP3K11,PDGFB,TLR4,EDN1,RALB,BMP2,PROX1,MADD,RAPGEF2,RIPK1,PDGFD	up_VCAV_EC

GO:0016202	0.0363	0.988	7	39	regulation of striated muscle tissue	BP	0.78	EPHB1,MEF2C,EDN1,BMP2,CREB1,NR1D2,CDON	up_VCAV_EC
GO:0010646	0.0363	0.989	7	945	regulation of cell communication	BP	1	NR1H4,RGS1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0009889	0.0363	0.994	4	1190	regulation of biosynthetic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0007507	0.0363	0.994	3	194	heart development	BP	1	TBX5,ZDHHC16,PDLIM3	up_APUL_EC
GO:0002903	0.0363	0.998	2	4	negative regulation of B cell apoptotic process	BP	1	AURKB,NOC2L	down_ACOR_VSMC
GO:0071495	0.0363	0.997	2	365	cellular response to endogenous stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0055119	0.0363	0.998	2	4	relaxation of cardiac muscle	BP	0.78	PDE4D,KCNJ2	up_VCAV_EC
GO:0045089	0.0363	0.997	2	70	positive regulation of innate immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0002367	0.0363	0.999	1	26	cytokine production involved in immune	BP	1	TLR2	up_AFEM_VSMC
GO:0009798	0.0363	0.999	1	31	axis specification	BP	1	WNT7A	up_AORT_VSMC
GO:0021515	0.0363	0.999	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_VFEM_EC
GO:0044257	0.0364	0.978	28	327	cellular protein catabolic process	BP	0.868	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,TRIB3,MSN,SEL1L,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0034764	0.0364	0.989	6	50	positive regulation of transmembrane transport	BP	1	FXYD1,CLIP3,ENSCAFG00000014978,AKT2,THY1,PARK7	down_VCAV_EC
GO:0051240	0.0364	0.991	5	489	positive regulation of multicellular organismal	BP	1	NR1H4,TBX5,SLITRK5,NPNT,NTRK2	up_APUL_EC
GO:1902692	0.0364	0.995	3	11	regulation of neuroblast proliferation	BP	0.868	HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0061550	0.0364	0.999	1	6	cranial ganglion development	BP	1	NRP2	down_ACOR_EC
GO:0035265	0.0364	0.999	1	54	organ growth	BP	1	TBX5	up_APUL_VSMC
GO:0086091	0.0364	0.999	1	8	regulation of heart rate by cardiac conduction	BP	1	CAV1	up_VSAP_VSMC
GO:0010647	0.0365	0.976	37	460	positive regulation of cell communication	BP	0.868	VEGFA,SULF1,NR1H4,JCAD,PTPN11,ILK,SMARCA4,MYO1C,CHSY1,KIF5B,HIF1A,TNIK,PTPN2,NEO1,MTDH,ESM1,ADAM17,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,LYN,BNIP3,FAM162A,ATF3,SH3GLB1,HTT,CALM1,DISC1,PAK2,LRRTM2,INHBA,NRP1,SH3RF3,MADD,SEC13,MID1	down_VSAP_EC
GO:1901615	0.0365	0.98	19	128	organic hydroxy compound metabolic process	BP	1	NAPEPLD,LIPC,INSIG2,ACAA1,SULT1A1,GOT1,INPP5E,LMF1,PPIP5K1,GALK1,RETSAT,LCAT,PCBD1,TKFC,MVK,LIPE,PNPO,CYB5R3,SOAT1	up_VSAP_EC
GO:0051179	0.0365	0.984	14	1747	localization	BP	1	ACVRL1,LYN,HOXA3,IGF1R,SPG11,PDPN,NRP2,HOXA7,IPO7,SULF1,ACSL3,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0051650	0.0365	0.986	8	65	establishment of vesicle localization	BP	0.868	MYH9,SHROOM2,MYO1C,KIF5B,CTNNB1,GSK3B,HTT,AP3S1	down_VSAP_EC
GO:0065003	0.0365	0.993	4	616	protein-containing complex assembly	BP	1	EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:0042592	0.0365	0.993	4	522	homeostatic process	BP	1	HOXA3,TRPC4,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0033120	0.0365	0.995	3	9	positive regulation of RNA splicing	BP	1	U2AF2,THRAP3,SF3B4	down_ACOR_VSMC
GO:0060413	0.0365	0.995	3	8	atrial septum morphogenesis	BP	1	GATA4,TBX20,TBX5	up_ACOR_VSMC
GO:0003283	0.0365	0.995	3	8	atrial septum development	BP	1	GATA4,TBX20,TBX5	up_ACOR_VSMC
GO:0045597	0.0365	1	1	253	positive regulation of cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0006913	0.0365	1	1	124	nucleocytoplasmic transport	BP	1	JUP	down_VFEM_VSMC
GO:0051169	0.0365	1	1	124	nuclear transport	BP	1	JUP	down_VFEM_VSMC
GO:0042472	0.0365	0.999	1	27	inner ear morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0003148	0.0365	0.999	1	13	outflow tract septum morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0097120	0.0365	0.999	1	9	receptor localization to synapse	BP	1	NETO1	up_VSAP_VSMC
GO:0032271	0.0366	0.984	11	73	regulation of protein polymerization	BP	0.784	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,STMN1,NCK1,FES,ARPC5L,TMOD3	up_VCAV_EC

GO:0010595	0.0366	0.988	7	52	positive regulation of endothelial cell migration	BP	0.868	VEGFA,SPARC,JCAD,PIK3C2A,HIF1A,ADAM17,NRP1	down_VSAP_EC
GO:1904589	0.0366	0.988	7	33	regulation of protein import	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,J UP	up_ACOR_VSMC
GO:0030282	0.0366	0.99	5	37	bone mineralization	BP	1	BMPR1A,ASPN,DDR2,OMD,GREM1	down_VCAV_EC
GO:0070887	0.0366	0.991	5	775	cellular response to chemical stimulus	BP	1	FGF5,NKX2-5,BAMBI,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0044818	0.0366	0.993	4	15	mitotic G2/M transition checkpoint	BP	1	CDK1,FANCI,TOPBP1,CLSPN	down_ACOR_VSMC
GO:0043207	0.0366	0.994	3	216	response to external biotic stimulus	BP	1	NR1H4,RGS1,MRC1	up_VPUL_EC
GO:0051707	0.0366	0.994	3	216	response to other organism	BP	1	NR1H4,RGS1,MRC1	up_VPUL_EC
GO:0002683	0.0366	0.997	2	126	negative regulation of immune system process	BP	1	HOXA9,BPI	up_AORT_EC
GO:0060059	0.0366	0.998	2	3	embryonic retina morphogenesis in camera-	BP	0.784	PROX1,CDON	up_VCAV_EC
GO:0061549	0.0366	0.999	1	5	sympathetic ganglion development	BP	1	SEMA3A	up_VPOR_EC
GO:0030593	0.0366	0.999	1	19	neutrophil chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0030154	0.0367	0.99	6	1040	cell differentiation	BP	1	CHL1,BARX1,NKX2-5,BAMBI,TRPC4,CYP26B1	up_VPOR_VSMC
GO:0010628	0.0367	0.992	4	527	positive regulation of gene expression	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0010543	0.0367	0.995	3	10	regulation of platelet activation	BP	0.784	SELP,PDGFB,TLR4	up_VCAV_EC
GO:0032989	0.0367	0.994	3	292	cellular component morphogenesis	BP	1	CHL1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0060982	0.0367	0.998	2	3	coronary artery morphogenesis	BP	1	SEC24B,NRP1	up_ACOR_VSMC
GO:0042127	0.0367	0.998	2	452	regulation of cell proliferation	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0071636	0.0367	0.998	2	5	positive regulation of transforming growth factor beta production	BP	0.784	CD34,CD200	up_VCAV_EC
GO:0002011	0.0367	0.999	1	28	morphogenesis of an epithelial sheet	BP	1	WNT7A	up_AORT_VSMC
GO:0045638	0.0367	0.999	1	33	negative regulation of myeloid cell	BP	1	HOXA9	up_AORT_VSMC
GO:0051963	0.0367	0.999	1	26	regulation of synapse assembly	BP	1	SLITRK5	up_VCAV_VSMC
GO:0097435	0.0368	0.978	28	230	supramolecular fiber organization	BP	0.784	HCLS1,ARHGEF15,BAIAP2L1,MEF2C,EDN1,RA B11A,ARHGAP28,TMOD1,MTOR,HOOK3,SLK, NCKAP1,MZT1,PROX1,IQGAP2,STMN1,SWAP 70,NCK1,FES,TAOK1,CTNNA1,ARPC5L,RIPK1, TNFAIP1,TMOD3,ARHGEF2,FSCN1,FBXO5	up_VCAV_EC
GO:0031272	0.0368	0.995	3	8	regulation of pseudopodium assembly	BP	1	CDC42EP5,CDC42EP2,F2RL1	up_VSAP_EC
GO:0031274	0.0368	0.995	3	8	positive regulation of pseudopodium assembly	BP	1	CDC42EP5,CDC42EP2,F2RL1	up_VSAP_EC
GO:0043489	0.0368	0.997	2	13	RNA stabilization	BP	1	TENT5C,AXIN2	up_AFEM_EC
GO:0060428	0.0368	0.999	1	17	lung epithelium development	BP	1	SRSF6	down_AFEM_EC
GO:0002224	0.0368	0.999	1	34	toll-like receptor signaling pathway	BP	1	ESR1	up_AORT_VSMC
GO:0015893	0.0368	0.999	1	26	drug transport	BP	1	CA2	up_VCAV_VSMC
GO:0030808	0.0368	0.999	1	15	regulation of nucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:1900371	0.0368	0.999	1	15	regulation of purine nucleotide biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0070372	0.0369	0.983	12	85	regulation of ERK1 and ERK2 cascade	BP	0.784	EPHB1,TEK,TNIP1,PDGFB,ATF3,RAPGEF1,TLR 4,BMP2,PRKD2,RAPGEF2,HMGB1,PDGFD	up_VCAV_EC
GO:0010977	0.0369	0.988	7	33	negative regulation of neuron projection	BP	1	ITM2C,ZNF365,NRP1,ULK2,PSEN1,ASAP1,B2 M	up_ACOR_VSMC
GO:0002763	0.0369	0.992	4	17	positive regulation of myeloid leukocyte	BP	0.784	HCLS1,CASP8,CREB1,RIPK1	up_VCAV_EC
GO:0009888	0.0369	0.995	3	545	tissue development	BP	1	GATA5,CA2,LRRC17	up_VCAV_VSMC
GO:0045351	0.0369	0.998	2	4	type I interferon biosynthetic process	BP	0.784	TLR4,TLR3	up_VCAV_EC
GO:0010831	0.0369	0.999	1	9	positive regulation of myotube differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:1905276	0.0369	0.999	1	9	regulation of epithelial tube formation	BP	1	SIX1	up_VFEM_EC

GO:0050709	0.036983733	0.99404	3	28	negative regulation of protein secretion	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:0048514	0.037	0.98	17	214	blood vessel morphogenesis	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,BMPR1A,LOX,ANPEP,THY1,B4GALT1,ZFP36L1,MYDGF,SASH1,CDH2,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC
GO:0030900	0.037	0.982	15	101	forebrain development	BP	0.786	PTCHD1,RELN,CHD7,HOOK3,BMP2,HHEX,GDPD5,PROX1,ENSCAFG00000010224,RAPGEF2,CREB1,HIF1A,ATRX,ALDH1A3,CDON	up_VCAV_EC
GO:0048646	0.037	0.982	14	349	anatomical structure formation involved in morphogenesis	BP	1	IRX3,LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,TBXA2R,CNNM4,PTPRB,AXIN2,CLIC4	up_AFEM_EC
GO:0030072	0.037	0.986	9	48	peptide hormone secretion	BP	1	HNF4A,SLC8B1,RAB11B,PASK,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0008211	0.037	0.998	2	5	glucocorticoid metabolic process	BP	0.871	REST,YWHAH	down_VSAP_EC
GO:0007193	0.037	0.997	2	13	adenylate cyclase-inhibiting G protein-coupled receptor signaling	BP	1	CHRM2,HTR1D	up_AFEM_EC
GO:0050804	0.037	1	1	87	modulation of chemical synaptic transmission	BP	1	PLCL1	down_VFEM_EC
GO:0099177	0.037	1	1	87	regulation of trans-synaptic signaling	BP	1	PLCL1	down_VFEM_EC
GO:1900003	0.037	1	1	1	regulation of serine-type endopeptidase activity	BP	0.871	SPINK2	down_VSAP_EC
GO:1900004	0.037	1	1	1	negative regulation of serine-type	BP	0.871	SPINK2	down_VSAP_EC
GO:1902571	0.037	1	1	1	regulation of serine-type peptidase activity	BP	0.871	SPINK2	down_VSAP_EC
GO:1902572	0.037	1	1	1	negative regulation of serine-type peptidase	BP	0.871	SPINK2	down_VSAP_EC
GO:0045446	0.037	0.999	1	32	endothelial cell differentiation	BP	1	WNT7A	up_AORT_VSMC
GO:0007413	0.037	0.999	1	5	axonal fasciculation	BP	1	SEMA3A	up_VPOR_EC
GO:0106030	0.037	0.999	1	5	neuron projection fasciculation	BP	1	SEMA3A	up_VPOR_EC
GO:0006111	0.037	0.999	1	15	regulation of gluconeogenesis	BP	1	FBP1	up_VFEM_VSMC
GO:0007632	0.037	0.999	1	14	visual behavior	BP	1	NETO1	up_VFEM_VSMC
GO:0043627	0.037	0.999	1	8	response to estrogen	BP	1	CAV1	up_VSAP_VSMC
GO:0043412	0.0371	0.972	88	1225	macromolecule modification	BP	0.871	ARHGEF2,PRICKLE1,VEGFA,P4HB,PLOD2,NR1H4,HSPA5,SOCS5,SGK1,ERO1A,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,WSB1,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PUM3,ILK,PPP1R12A,SESN2,PTGS2,PPIB,USP12,MRPL1,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,PLCL1,TTLL7,ADAM17,CNOT7,MAGED1,CTNNB1,CDK8,APOE,PLOD3,USP48,UBA5,LYN,STRAP,BACH1,ASPH,CCNYL1,STT3A,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,CUL2,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,EXT1,CALM1,CDYL,PAK2,INHBA,CAMK2D,HIF1AN,BTK,CDKN1A,NRP1,SH3RF3,USP14,ARF4,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:0016125	0.0371	0.987	8	41	sterol metabolic process	BP	1	LIPC,INSIG2,LMF1,LCAT,MVK,LIPE,CYB5R3,SOAT1	up_VSAP_EC
GO:0051252	0.0371	0.99	6	1051	regulation of RNA metabolic process	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0050920	0.0371	0.992	4	53	regulation of chemotaxis	BP	1	CMKLR1,PLXNA4,CCL5,ADAM17	up_AFEM_EC
GO:0045721	0.0371	0.998	2	4	negative regulation of gluconeogenesis	BP	0.786	FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0010660	0.0371	0.999	1	14	regulation of muscle cell apoptotic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002053	0.0371	0.999	1	15	positive regulation of mesenchymal cell	BP	1	SHOX2	up_VFEM_VSMC
GO:0006644	0.037172504	0.98702	7	118	phospholipid metabolic process	BP	1	NR1H4,ENSCAFG00000004331,CFI,CHPT1,PIGS,AGPAT2,PRKCD	up_ACOR_EC

GO:1901576	0.0372	0.97	176	1877	organic substance biosynthetic process	BP	1	ELK3,SCD,ACSL3,PRPSAP1,SQLE,HMGB1,MCM6,LSS,SREBF1,ACLY,MCM4,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,RRM1,MED17,POLA1,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,SF1,POLA2,MPDU1,SRRT,GINS4,CTDNEP1,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,RAD51,XYLT1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,CDK4,SMARCC1,PLK3,PCNA,DHX33,HOXA7,TONSL,ARG2,MCM10,UHRF1,CKS2,TKT,GMNN,DHCR24,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,ELOVL1,FARSA,PPARD,CDC6,POLH,YBX3,NCL,NUP62,UGDH,MRPL37,DTL,VAC14,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,FDFT1,RBM14,CYC1,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,ATP5F1A,PUM3,CDC45,MAST2,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,GRWD1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GL	down_ACOR_VSMC
GO:0019725	0.0372	0.979	22	245	cellular homeostasis	BP	0.872	P4HB,SLC39A7,NR1H4,ENSCAFG00000013214,ERO1A,ENPP1,ENSCAFG00000003477,ATP2B1,LRRC8A,SMARCA4,HIF1A,DNAJC10,NXN,PDIA4,TFRC,APOE,LYN,DDIT3,CLCN3,HTT,CALM1,DISC1	down_VSAP_EC
GO:2000576	0.0372	0.998	2	4	positive regulation of microtubule motor	BP	1	DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:2000580	0.0372	0.998	2	4	regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:2000582	0.0372	0.998	2	4	positive regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:0048663	0.0372	0.997	2	13	neuron fate commitment	BP	1	HOXC10,DLL1	up_AFEM_EC
GO:0021545	0.0372	0.999	1	21	cranial nerve development	BP	1	CITED2	down_VPOR_EC
GO:0035195	0.0372	0.999	1	28	gene silencing by miRNA	BP	1	ESR1	up_AORT_VSMC
GO:0070201	0.0373	0.978	26	187	regulation of establishment of protein localization	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,MBP,FERMT1,BMP4,TM7SF3,CD274,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,PSEN1,JUP,CCL5,NOD2,SCAMP5,INPP5K,PFKL,PARK7,PTPN14	up_ACOR_VSMC
GO:0019222	0.0373	0.984	15	1934	regulation of metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,SULF1,ELK3,HOXA1,ACSL3,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0043523	0.0373	0.987	7	52	regulation of neuron apoptotic process	BP	0.872	HYOU1,AARS,HIF1A,ZPR1,DDIT3,SIX4,NRP1	down_VSAP_EC
GO:0016241	0.0373	0.989	6	41	regulation of macroautophagy	BP	0.872	SESN2,HIF1A,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0021522	0.0373	0.995	3	8	spinal cord motor neuron differentiation	BP	1	LMO4,TBX20,CLN8	up_ACOR_VSMC
GO:0035239	0.0373	0.994	3	299	tube morphogenesis	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0034377	0.0373	0.999	1	7	plasma lipoprotein particle assembly	BP	1	ACSL3	down_ACOR_EC
GO:0065005	0.0373	0.999	1	7	protein-lipid complex assembly	BP	1	ACSL3	down_ACOR_EC
GO:0034394	0.0373	0.999	1	19	protein localization to cell surface	BP	1	RAB11B	down_VPOR_EC
GO:0010224	0.0373	0.999	1	9	response to UV-B	BP	1	MME	up_VFEM_EC
GO:0031272	0.0373	0.999	1	8	regulation of pseudopodium assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0031274	0.0373	0.999	1	8	positive regulation of pseudopodium assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0034138	0.0373	0.999	1	9	toll-like receptor 3 signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0046330	0.037309666	0.99166	4	47	positive regulation of JNK cascade	BP	1	FZD5,NOD2,TNFRSF19,SH3RF3	up_ACOR_EC

GO:0050793	0.0374	0.972	85	731	regulation of developmental process	BP	1	VEGFD,TMEM176B,TMEM176A,SMAD6,LEP,LBH,GATA5,CD83,CDC7,RASSF2,FNDC5,MBP,ZRANB1,MLLT3,ITM2C,FERMT1,BMP4,LNPK,FGFR2,TP53BP1,GJA1,TLR3,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,ISG15,ZNRF3,CD274,ZNF365,SASH1,LMO4,FGF18,FAM210B,ATRN,P4HTM,ZMYM2,PLAC8B,LIMS2,PLEKHB2,MARCH5,BNIP3,EGLN1,CLSTN1,NRP1,ULK2,DMPK,NPNT,SMARCD3,SLITRK5,TBX20,TBX5,CCDC3,FZD3,DKKL1,FRS2,DAG1,APP,LAMA3,PSEN1,TGFBR1,SYNJ2BP,CHD7,JUP,SIPA1L1,DDR2,WWC2,SSH3,EDN1,ASAP1,B2M,DISC1,TNFRSF11B,CNOT4,DOCK5,ERAP1,SLC8A1,STC2,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0045595	0.0374	0.975	38	469	regulation of cell differentiation	BP	0.874	ARHGEF2,PRICKLE1,SIPA1L1,SERPINE1,SOCS5,ENPP1,ERRFI1,DPYSL3,HOOK3,TRIB3,IFRD1,ILK,TGFBR1,PTGS2,HIF1A,SLC45A3,TNIK,PTPN2,EVI2B,UST,CTNNB1,ENSCAFG00000002015,APOE,KLF5,LYN,STRAP,DDIT3,MMD,VLDLR,REST,PRMT1,DISC1,INHBA,HIF1AN,SIX4,NRP1,YWHAH,KDM3A	down_VSAP_EC
GO:1901360	0.0374	0.992	6	2016	organic cyclic compound metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0060042	0.0374	0.993	4	14	retina morphogenesis in camera-type eye	BP	1	THRB,CDON,IRX5,DLL1	up_VSAP_EC
GO:0043588	0.0374	0.997	2	74	skin development	BP	1	HOXA7,CYP26B1	up_VFEM_EC
GO:0061448	0.0374	0.997	2	89	connective tissue development	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:0032663	0.0374	0.999	1	19	regulation of interleukin-2 production	BP	1	HDAC7	down_VPOR_EC
GO:0006826	0.0374	0.999	1	15	iron ion transport	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0042129	0.0374	0.999	1	35	regulation of T cell proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0021515	0.0374	0.999	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_VSAP_VSMC
GO:0055117	0.0375	0.991	5	21	regulation of cardiac muscle contraction	BP	1	FGF13,ADRA1B,KCNE3,PDE5A,JUP	up_ACOR_VSMC
GO:0042118	0.0375	0.998	2	4	endothelial cell activation	BP	1	PRMT5,HOXA9	down_ACOR_VSMC
GO:0007600	0.0375	0.997	2	73	sensory perception	BP	1	MME,SIX1	up_VFEM_EC
GO:0032970	0.0375	1	1	130	regulation of actin filament-based process	BP	1	JUP	down_VFEM_VSMC
GO:0045912	0.0375	0.999	1	15	negative regulation of carbohydrate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0030513	0.0375	0.999	1	11	positive regulation of BMP signaling pathway	BP	1	NEO1	up_VPUL_EC
GO:0070670	0.0375	0.999	1	11	response to interleukin-4	BP	1	MRC1	up_VPUL_EC
GO:0071353	0.0375	0.999	1	11	cellular response to interleukin-4	BP	1	MRC1	up_VPUL_EC
GO:1902042	0.0375	0.999	1	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	ARHGEF2	up_VPUL_EC
GO:0060070	0.0376	0.988	6	105	canonical Wnt signaling pathway	BP	1	GREM1,FAM53B,CYLD,RECK,AXIN2,KANK1	up_AFEM_EC
GO:0032330	0.0376	0.991	5	20	regulation of chondrocyte differentiation	BP	1	HOXA11,AXIN2,ZBTB16,RARG,SHOX2	up_VSAP_EC
GO:0002551	0.0376	0.997	2	5	mast cell chemotaxis	BP	0.793	KIT,SWAP70	up_VCAV_EC
GO:0097531	0.0376	0.997	2	5	mast cell migration	BP	0.793	KIT,SWAP70	up_VCAV_EC
GO:0032456	0.0376	0.999	1	19	endocytic recycling	BP	1	RAB11B	down_VPOR_EC
GO:0030593	0.0376	0.999	1	19	neutrophil chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0031111	0.0376	0.999	1	11	negative regulation of microtubule polymerization or	BP	1	ARHGEF2	up_VPUL_EC
GO:2001275	0.0376	0.999	1	11	positive regulation of glucose import in response to insulin	BP	1	NR1H4	up_VPUL_EC
GO:0030032	0.0376	0.999	1	19	lamellipodium assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0050767	0.0377	0.98	18	184	regulation of neurogenesis	BP	0.874	ARHGEF2,SIPA1L1,DPYSL3,HOOK3,IFRD1,HIF1A,SLC45A3,TNIK,UST,CTNNB1,APOE,LYN,MMD,VLDLR,REST,DISC1,NRP1,YWHAH	down_VSAP_EC

GO:1903050	0.0377	0.984	10	88	regulation of proteolysis involved in cellular protein catabolic process	BP	0.874	PRICKLE1,PLK3,SOCS5,TRIB3,UCHL5,GSK3B,DISC1,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0048593	0.0377	0.986	8	41	camera-type eye morphogenesis	BP	1	THRB,CDON,IRX5,DLL1,MFN2,ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:1900180	0.0377	0.988	6	50	regulation of protein localization to nucleus	BP	1	ENSCAFG00000014978,TRIM8,GLI3,PARK7,MAVS,GLIS2	down_VCAV_EC
GO:0031175	0.0377	0.997	2	224	neuron projection development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0071407	0.0377	1	1	129	cellular response to organic cyclic compound	BP	1	JUP	down_VFEM_VSMC
GO:0030206	0.0377	0.999	1	9	chondroitin sulfate biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:0032715	0.0377	0.999	1	11	negative regulation of interleukin-6 production	BP	1	NR1H4	up_VPUL_EC
GO:0010827	0.037765516	0.99386	3	28	regulation of glucose transmembrane transport	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0051402	0.0378	0.986	8	64	neuron apoptotic process	BP	0.874	HYOU1,AARS,HIF1A,ZPR1,DDIT3,FAM162A,SIX4,NRP1	down_VSAP_EC
GO:0007399	0.0378	0.995	3	564	nervous system development	BP	1	HOXC10,EYA1,IRX5	up_AFEM_VSMC
GO:0090382	0.0378	0.999	1	8	phagosome maturation	BP	1	SPG11	down_ACOR_EC
GO:0021604	0.0378	0.999	1	6	cranial nerve structural organization	BP	1	NRP2	down_ACOR_EC
GO:0021612	0.0378	0.999	1	6	facial nerve structural organization	BP	1	NRP2	down_ACOR_EC
GO:0008627	0.0378	0.999	1	5	intrinsic apoptotic signaling pathway in response to osmotic	BP	1	ARHGEF2	up_VPOR_EC
GO:0060043	0.0378	0.999	1	14	regulation of cardiac muscle cell proliferation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0061337	0.0378	0.999	1	16	cardiac conduction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0009954	0.0378	0.999	1	16	proximal/distal pattern formation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0060914	0.0378	0.999	1	11	heart formation	BP	1	TBX5	up_VPUL_EC
GO:2000482	0.0378	0.999	1	9	regulation of interleukin-8 secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0001944	0.0379	0.979	20	263	vasculature development	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,BMPR1A,LOX,RECK,ANPEP,SEMA3C,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,CDH2,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC
GO:0044282	0.0379	0.985	9	89	small molecule catabolic process	BP	1	AKT2,ACAA1,THNSL2,PEX5,ENSCAFG00000002977,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:1903555	0.0379	0.987	7	37	regulation of tumor necrosis factor superfamily cytokine	BP	0.795	TNFAIP3,CD34,TLR4,ARG2,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:0021675	0.0379	0.99	5	29	nerve development	BP	0.874	SULF1,ILK,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0032655	0.0379	0.992	4	16	regulation of interleukin-12 production	BP	0.795	TLR4,IRF8,TLR3,HMGB1	up_VCAV_EC
GO:0022603	0.0379	0.994	3	301	regulation of anatomical structure morphogenesis	BP	1	BAMBI,ANKRD6,C3AR1	up_VPOR_VSMC
GO:0060788	0.0379	0.997	2	5	ectodermal placode formation	BP	0.874	CTNNB1,SIX4	down_VSAP_EC
GO:0071697	0.0379	0.997	2	5	ectodermal placode morphogenesis	BP	0.874	CTNNB1,SIX4	down_VSAP_EC
GO:0030517	0.0379	0.997	2	5	negative regulation of axon extension	BP	0.874	IFRD1,NRP1	down_VSAP_EC
GO:0061551	0.0379	0.999	1	5	trigeminal ganglion development	BP	1	SEMA3A	up_VPOR_EC
GO:1905331	0.0379	0.999	1	9	negative regulation of morphogenesis of an	BP	1	SIX1	up_VFEM_EC
GO:0010092	0.0379	0.999	1	19	specification of animal organ identity	BP	1	GATA5	up_VPUL_VSMC
GO:0010562	0.037997047	0.98122	14	312	positive regulation of phosphorus metabolic process	BP	1	NR1H4,SOX9,ENSCAFG00000004331,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,MAVS,LRP4,SH3RF3,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0045937	0.037997047	0.98122	14	312	positive regulation of phosphate metabolic process	BP	1	NR1H4,SOX9,ENSCAFG00000004331,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,MAVS,LRP4,SH3RF3,RARRES2,NRP1,PRKCD	up_ACOR_EC

GO:0071310	0.038	0.972	65	634	cellular response to organic substance	BP	0.797	ACKR1,HCLS1,GBP5,KIT,PRCP,CXCL8,LAPTM5,CXCR4,CALCRL,TNFAIP3,PPARG,TNIP1,PDGFB,BAIAP2L1,TMEM173,PDE4D,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,NLRC5,GATA3,RALB,SMAD1,TFPI,IRF8,YES1,MTOR,BMP2,HHEX,ST3GAL6,ABCA1,MAPK13,IFNGR1,RIOK3,ENSCAFG00000010596,FLNB,PAK2,PRKD2,SMARCA4,NCK1,TIMELESS,OTUD4,RAPGEF2,CTDSPL2,CREB1,CTNNA1,CNOT7,ADIPOR2,BLM,RIPK1,LSM14A,SKIL,PDGFD,UFSP2,HIF1A,KDM3A,NR4A1,ENSCAFG00000002015,JCAD,ZEB1,ARHGEF2,TJP2	up_VCAV_EC
GO:0023051	0.038	0.988	7	954	regulation of signaling	BP	1	NR1H4,RGS1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0034332	0.038	0.99	5	32	adherens junction organization	BP	0.874	VEGFA,ACTN1,CTNNB1,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:1904062	0.038	0.996	2	62	regulation of cation transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0008584	0.038	0.996	2	39	male gonad development	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0046546	0.038	0.996	2	39	development of primary male sexual	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0031349	0.038	0.997	2	90	positive regulation of defense response	BP	1	NR1H4,CCL24	up_VPUL_EC
GO:0003012	0.038	0.997	2	90	muscle system process	BP	1	MYBPC2,HTR7	up_VPUL_EC
GO:0036230	0.038	0.999	1	9	granulocyte activation	BP	1	STX4	down_ACOR_EC
GO:0006536	0.038	0.999	1	10	glutamate metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0033002	0.038	0.999	1	55	muscle cell proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0051924	0.038	0.999	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0008206	0.038	0.999	1	11	bile acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0060045	0.038	0.999	1	11	positive regulation of cardiac muscle cell	BP	1	TBX5	up_VPUL_EC
GO:0021591	0.038067282	0.99671	2	12	ventricular system development	BP	1	AQP1,SEMA6D	up_ACOR_EC
GO:0030856	0.0381	0.986	8	41	regulation of epithelial cell differentiation	BP	1	HOXA7,BTG1,DLL1,OSR1,ZFP36L1,ZEB1,ACVRL1,KEAP1	up_VSAP_EC
GO:2000177	0.0381	0.989	6	26	regulation of neural precursor cell	BP	0.797	DLL4,RAPGEF1,PROX1,CTNNA1,HIF1A,CDON	up_VCAV_EC
GO:0003407	0.0381	0.994	3	15	neural retina development	BP	1	THY1,IRX5,THRB	down_VCAV_EC
GO:0045637	0.0381	0.996	2	73	regulation of myeloid cell differentiation	BP	1	HOXA9,HOXA7	up_VFEM_EC
GO:0035136	0.0381	0.999	1	16	forelimb morphogenesis	BP	1	HOXA9	up_AORT_EC
GO:0045683	0.0381	0.999	1	9	negative regulation of epidermis development	BP	1	HOXA7	up_VFEM_EC
GO:0055017	0.0381	0.999	1	19	cardiac muscle tissue growth	BP	1	TBX5	up_VPUL_VSMC
GO:0010498	0.0382	0.979	18	194	proteasomal protein catabolic process	BP	0.874	PRICKLE1,PLK3,SOCS5,HM13,HSP90B1,TRIB3,SEL1L,DNAJC10,UCHL5,SPOPL,DNAJB9,DDIT3,GSK3B,SPOP,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0006486	0.0382	0.981	14	91	protein glycosylation	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,B3GNT7,CCDC126,MAGT1,STT3B,FUT11,FUT8,POMK,PSEN1,EOGT,LMF1	up_ACOR_VSMC
GO:0043413	0.0382	0.981	14	91	macromolecule glycosylation	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,B3GNT7,CCDC126,MAGT1,STT3B,FUT11,FUT8,POMK,PSEN1,EOGT,LMF1	up_ACOR_VSMC
GO:0036035	0.0382	0.997	2	7	osteoclast development	BP	1	NOTCH2,FBN1	down_VCAV_EC
GO:0051093	0.0382	0.997	2	273	negative regulation of developmental process	BP	1	HOXA9,WNT7A	up_AORT_VSMC
GO:0050869	0.0382	0.999	1	8	negative regulation of B cell activation	BP	1	LYN	down_ACOR_EC
GO:0048486	0.0382	0.999	1	10	parasympathetic nervous system development	BP	1	SIX1	up_VFEM_EC
GO:0046580	0.0382	0.999	1	18	negative regulation of Ras protein signal	BP	1	FBP1	up_VFEM_VSMC
GO:0048641	0.0382	0.999	1	16	regulation of skeletal muscle tissue	BP	1	SHOX2	up_VFEM_VSMC
GO:1901888	0.038211713	0.99375	3	29	regulation of cell junction assembly	BP	1	ARHGAP6,FZD5,NRP1	up_ACOR_EC
GO:0002686	0.038245924	0.99669	2	12	negative regulation of leukocyte migration	BP	1	MMP28,PTGER4	up_ACOR_EC

GO:2000249	0.038294772	0.99668	2	12	regulation of actin cytoskeleton	BP	1	ARHGDIB,NRP1	up_ACOR_EC
GO:0045785	0.0383	0.984	10	107	positive regulation of cell adhesion	BP	1	GPAM,FBLN2,RHOD,ENSCAFG00000014978,TFE3,THY1,GLI3,EDIL3,ZBTB16,ECM2	down_VCAV_EC
GO:0097529	0.0383	0.986	8	52	myeloid leukocyte migration	BP	0.799	EDNRB,KIT,CXCL8,PDGFB,PDE4D,MMP28,SWAP70,HMGB1	up_VCAV_EC
GO:0010824	0.0383	0.99	5	23	regulation of centrosome duplication	BP	1	POC1A,NUP62,PLK4,RBM14,GEN1	down_ACOR_VSMC
GO:0007031	0.0383	0.99	5	20	peroxisome organization	BP	1	PEX7,PEX2,LONP2,PEX6,MAVS	up_VSAP_EC
GO:0050688	0.0383	0.99	5	20	regulation of defense response to virus	BP	1	NLRX1,TKFC,RNF216,PQBP1,MAVS	up_VSAP_EC
GO:0090343	0.0383	0.998	2	4	positive regulation of cell aging	BP	1	HMGA1,ARG2	down_ACOR_VSMC
GO:2000774	0.0383	0.998	2	4	positive regulation of cellular senescence	BP	1	HMGA1,ARG2	down_ACOR_VSMC
GO:0002265	0.0383	0.998	2	3	astrocyte activation involved in immune	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0098742	0.0383	0.999	1	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5	down_VSAP_VSMC
GO:0007140	0.0383	0.999	1	10	male meiotic nuclear division	BP	1	CYP26B1	up_VFEM_EC
GO:0021872	0.0383	0.999	1	19	forebrain generation of neurons	BP	1	SLIT2	up_VPUL_VSMC
GO:0010939	0.0383	0.999	1	9	regulation of necrotic cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0051302	0.0384	0.986	8	47	regulation of cell division	BP	1	AURKB,PLK3,E2F8,CDC6,NUP62,PDXP,FGF5,ASPM	down_ACOR_VSMC
GO:0032870	0.0384	0.985	8	162	cellular response to hormone stimulus	BP	1	LEP,LBH,CRY2,CHRM2,AVPR1A,CAMK2A,NR3C1,KANK1	up_AFEM_EC
GO:0099536	0.0384	0.986	7	133	synaptic signaling	BP	1	KCNC4,GPR1,CHRM2,SLC6A6,HTR1D,CAMK2A,DMPK	up_AFEM_EC
GO:0010389	0.0384	0.989	6	30	regulation of G2/M transition of mitotic cell	BP	0.799	RAB11A,TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0009967	0.0384	0.99	5	435	positive regulation of signal transduction	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0051241	0.0384	0.992	4	336	negative regulation of multicellular organismal	BP	1	NR1H4,TBX5,BPI,PLCL1	up_APUL_EC
GO:0045670	0.0384	0.994	3	16	regulation of osteoclast differentiation	BP	1	NOTCH2,FBN1,TFE3	down_VCAV_EC
GO:0060338	0.0384	0.995	3	10	regulation of type I interferon-mediated	BP	0.799	NLRC5,CNOT7,LSM14A	up_VCAV_EC
GO:0060340	0.0384	0.998	2	4	positive regulation of type I interferon-mediated signaling pathway	BP	0.799	NLRC5,LSM14A	up_VCAV_EC
GO:0007350	0.0384	0.999	1	7	blastoderm segmentation	BP	1	NRP2	down_ACOR_EC
GO:1903305	0.0384	0.999	1	36	regulation of regulated secretory pathway	BP	1	WNT7A	up_AORT_VSMC
GO:0015800	0.0384	0.999	1	10	acidic amino acid transport	BP	1	NTRK2	up_APUL_EC
GO:0043010	0.0385	0.981	15	96	camera-type eye development	BP	1	THRB,CDON,OSR2,MAB21L1,IRX5,DLL1,RARG,MFN2,ZEB1,CTNS,CLCN2,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0043087	0.0385	0.982	13	83	regulation of GTPase activity	BP	0.799	AMOT,FGD6,RAPGEF1,MTOR,CHN2,IQGAP2,RAPGEF2,TBC1D1,ITGA6,ALS2,ENSCAFG00000002015,RABGAP1,USP6NL	up_VCAV_EC
GO:0003008	0.0385	0.992	4	336	system process	BP	1	HTR7,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0070988	0.0385	0.992	4	14	demethylation	BP	0.799	GATA3,OTUD4,KDM3A,TET2	up_VCAV_EC
GO:0003433	0.0385	0.998	2	4	chondrocyte development involved in endochondral bone morphogenesis	BP	1	POC1A,SERPINH1	down_ACOR_VSMC
GO:0042987	0.0385	0.999	1	10	amyloid precursor protein catabolic process	BP	1	LYN	down_ACOR_EC
GO:0071887	0.0385	0.999	1	34	leukocyte apoptotic process	BP	1	ARG2	up_AORT_VSMC
GO:0030511	0.0385	0.999	1	10	positive regulation of transforming growth factor beta receptor	BP	1	NPNT	up_APUL_EC
GO:1903846	0.0385	0.999	1	10	positive regulation of cellular response to transforming growth	BP	1	NPNT	up_APUL_EC
GO:0060071	0.0385	0.999	1	14	Wnt signaling pathway, planar cell polarity	BP	1	ANKRD6	up_VPOR_VSMC

GO:0023056	0.0386	0.975	37	462	positive regulation of signaling	BP	0.874	VEGFA,SULF1,NR1H4,JCAD,PTPN11,ILK,SMARCA4,MYO1C,CHSY1,KIF5B,HIF1A,TNIK,PTPN2,NEO1,MTDH,ESM1,ADAM17,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,LYN,BNIP3,FAM162A,ATF3,SH3GLB1,HTT,CALM1,DISC1,PAK2,LRRTM2,INHBA,NRP1,SH3RF3,MADD,SEC13,MID1	down_VSAP_EC
GO:1901890	0.0386	0.994	3	13	positive regulation of cell junction assembly	BP	0.874	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0009142	0.0386	0.999	1	46	nucleoside triphosphate biosynthetic process	BP	1	AK5	down_VSAP_VSMC
GO:0009410	0.0386	0.999	1	27	response to xenobiotic stimulus	BP	1	SLITRK5	up_VCAV_VSMC
GO:0051193	0.0386	0.999	1	15	regulation of cofactor metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0042127	0.0387	0.973	55	452	regulation of cell proliferation	BP	1	CDON,WNT11,HNF4A,CD274,AXIN2,C5AR2,OSR2,PTGFR,MAB21L1,LIMS2,IL6R,CRIP2,FGF7,ABL1,PEX2,BTG1,EMP2,DLL1,OSR1,PDGFD,SAV1,HPSE,ZBTB16,RARG,STAT5A,STAT6,AMBRA1,MORC3,DDR2,MFN2,ZFP36L1,TIAM1,MYC,PTGES,ZEB1,FBXW4,SULF2,SHOX2,FBXO4,MYD88,E2F4,KDM2B,FBLN1,RAF1,PNP,NFIB,ZNF580,STX4,SMARCA2,ACVRL1,NCK1,HMOX1,TGFBR2,LBH,DPT	up_VSAP_EC
GO:0045765	0.0387	0.988	6	105	regulation of angiogenesis	BP	1	LEP,ANGPT4,DLL1,F3,GREM1,TBXA2R	up_AFEM_EC
GO:1900227	0.0387	0.998	2	4	positive regulation of NLRP3 inflammasome	BP	0.802	GBP5,TLR4	up_VCAV_EC
GO:0042147	0.0387	0.996	2	38	retrograde transport, endosome to Golgi	BP	1	GCC2,TMEM87B	up_VPOR_EC
GO:0051098	0.0387	0.996	2	129	regulation of binding	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0072009	0.038788876	0.99121	4	48	nephron epithelium development	BP	1	SOX9,AQP1,FOXC2,CLSTN1	up_ACOR_EC
GO:0030178	0.0388	0.988	6	52	negative regulation of Wnt signaling pathway	BP	1	CLSTN1,GLI3,CDH2,GREM1,NPHP4,FOXO3	down_VCAV_EC
GO:0007492	0.0388	0.991	4	27	endoderm development	BP	1	BMPR1A,COL6A1,LAMA3,ZFP36L1	down_VCAV_EC
GO:0006875	0.0388	0.996	2	129	cellular metal ion homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0008544	0.0388	0.996	2	75	epidermis development	BP	1	HOXA7,CYP26B1	up_VFEM_EC
GO:0007389	0.0388	1	1	137	pattern specification process	BP	1	GATA5	down_VFEM_VSMC
GO:0090102	0.0388	0.999	1	10	cochlea development	BP	1	HOXA1	up_APUL_EC
GO:0051492	0.0388	0.999	1	28	regulation of stress fiber assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0001657	0.0389	0.988	6	42	ureteric bud development	BP	0.874	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0072163	0.0389	0.988	6	42	mesonephric epithelium development	BP	0.874	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0072164	0.0389	0.988	6	42	mesonephric tubule development	BP	0.874	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0001649	0.0389	0.991	4	54	osteoblast differentiation	BP	1	TWIST2,GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:0010107	0.0389	0.997	2	5	potassium ion import	BP	0.803	KCNJ3,KCNJ2	up_VCAV_EC
GO:0051090	0.0389	1	1	134	regulation of DNA-binding transcription factor	BP	1	JUP	down_VFEM_VSMC
GO:0010803	0.0389	0.999	1	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0034381	0.0389	0.999	1	10	plasma lipoprotein particle clearance	BP	1	NR1H4	up_APUL_EC
GO:0048546	0.0389	0.999	1	16	digestive tract morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0044766	0.0389	0.999	1	9	multi-organism transport	BP	1	CAV1	up_VSAP_VSMC
GO:1902579	0.0389	0.999	1	9	multi-organism localization	BP	1	CAV1	up_VSAP_VSMC
GO:0001953	0.039	0.992	4	14	negative regulation of cell-matrix adhesion	BP	1	HOXA7,FAM107A,PIK3R1,ACVRL1	up_VSAP_EC
GO:0060394	0.039	0.997	2	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	0.874	SNX25,STRAP	down_VSAP_EC
GO:0090103	0.039	0.999	1	8	cochlea morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0072350	0.039	0.999	1	18	tricarboxylic acid metabolic process	BP	1	SUCLG2	down_AFEM_EC

GO:0045655	0.039	0.999	1	9	regulation of monocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0010927	0.039085368	0.99356	3	28	cellular component assembly involved in	BP	1	MYOZ2,TMOD1,ACTN2	up_ACOR_EC
GO:2001057	0.0391	0.992	4	16	reactive nitrogen species metabolic process	BP	0.807	CD34,TLR4,NOS3,NOS2	up_VCAV_EC
GO:0030238	0.0391	0.998	2	4	male sex determination	BP	1	SF1,SIX4	down_ACOR_VSMC
GO:0006607	0.0391	0.997	2	5	NLS-bearing protein import into nucleus	BP	0.874	KPNB1,KPNA1	down_VSAP_EC
GO:1903672	0.0391	0.999	1	20	positive regulation of sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0050715	0.0391	0.999	1	29	positive regulation of cytokine secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0016441	0.0391	0.999	1	30	posttranscriptional gene silencing	BP	1	ESR1	up_AORT_VSMC
GO:0035194	0.0391	0.999	1	30	posttranscriptional gene silencing by RNA	BP	1	ESR1	up_AORT_VSMC
GO:0003171	0.0391	0.999	1	10	atrioventricular valve development	BP	1	TBX5	up_APUL_EC
GO:0055062	0.0391	0.999	1	5	phosphate ion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0072505	0.0391	0.999	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0072506	0.0391	0.999	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0045616	0.0391	0.999	1	9	regulation of keratinocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0016055	0.0392	0.986	7	134	Wnt signaling pathway	BP	1	GREM1,FAM53B,CYLD,RECK,LGR6,AXIN2,KANK1	up_AFEM_EC
GO:0198738	0.0392	0.986	7	134	cell-cell signaling by wnt	BP	1	GREM1,FAM53B,CYLD,RECK,LGR6,AXIN2,KANK1	up_AFEM_EC
GO:0009954	0.0392	0.992	4	16	proximal/distal pattern formation	BP	1	GREM1,HOXC10,HOXA9,GLI1	down_ACOR_VSMC
GO:0003177	0.0392	0.995	3	8	pulmonary valve development	BP	1	SMAD6,BMP4,TBX20	up_ACOR_VSMC
GO:1901564	0.0393	0.97	119	2053	organonitrogen compound metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,MAOA,CFD,PRNP,UBA52,ADCY6,GLIPR2,BGN,LARP6,COA1,BMPR1A,KRTCAP2,VKORC1,RECK,CLIP3,NUMBL,CHID1,AKT1S1,TIMP2,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,H6PD,HR,RPL23,RPL13,PCSK7,PLCL1,DDOST,CSPG4,PRMT6,UROS,NT5C2,THNSL2,PGLS,ATP5MC1,GFPT2,UQCR10,ASPN,PIGS,HS3ST3B1,EIF3K,THY1,NECAB3,RNF216,ADK,WDR45,MRPL37,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RNPEP,RPL27,COPS7A,ARL2BP,AMPD2,IFT57,MAVS,MRPS11,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,A2M,SEC61B,ACSS2,MAPRE3,CDKL2,HM13,PRKCSH,DDR2,SHC1,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,FBH1,GREM1,RPN2,KLHL29,ATOX1,LONP2,NAPEPLD,GLS2,FOXO3,SOAT1,PACSIN3,EIF4EBP1,BCKDHB,ACAT1,BRSK1,CDK14	down_VCAV_EC
GO:0010562	0.0393	0.974	40	312	positive regulation of phosphorus metabolic process	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PPARGC1A,PDE5A,AR,SASH1,LMO4,FGF18,F2RL1,FAM129A,NRP1,PTPN22,NPNT,SMPD1,PRKCE,CCNT1,FRS2,PARP9,APP,PSEN1,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,SH3RF3,MAP3K7,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0045937	0.0393	0.974	40	312	positive regulation of phosphate metabolic process	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PPARGC1A,PDE5A,AR,SASH1,LMO4,FGF18,F2RL1,FAM129A,NRP1,PTPN22,NPNT,SMPD1,PRKCE,CCNT1,FRS2,PARP9,APP,PSEN1,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,SH3RF3,MAP3K7,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0007389	0.0393	0.978	20	137	pattern specification process	BP	1	HOXA11,EMX2,HOXA7,HOXA9,CDON,AXIN2,HOXD3,DLL1,HOXA6,OSR1,ZBTB16,RARG,HOXC4,IRX3,ZEB1,HOXC10,LRP4,KDM2B,TGFBR2,CITED2	up_VSAP_EC
GO:0010720	0.0393	0.982	12	110	positive regulation of cell development	BP	0.874	ARHGEF2,DPYSL3,HIF1A,CTNNB1,ENSCAFG00000002015,APOE,LYN,MMD,VLDLR,REST,DISC1,NRP1	down_VSAP_EC

GO:0006939	0.0393	0.993	3	32	smooth muscle contraction	BP	1	CHRM2,HTR1D,TBXA2R	up_AFEM_EC
GO:0061013	0.0393	0.993	3	32	regulation of mRNA catabolic process	BP	1	TENT5C,AXIN2,SAMD4B	up_AFEM_EC
GO:0001933	0.039329639	0.98495	8	146	negative regulation of protein phosphorylation	BP	1	PKIB,NDRG2,DUSP26,SMAD6,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0071322	0.039393046	0.99348	3	29	cellular response to carbohydrate stimulus	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0010629	0.0394	0.972	54	502	negative regulation of gene expression	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,EIF4A3,EDC3,HNRNPD,SREBF2,NEDD4,U2AF2,MTDH,SRRT,NAB2,SLC35C2,RAN,BIRC5,CAV1,TIMELESS,THRAP3,FAM129B,EDC4,AURKB,EZH2,GREM1,RNASEH2B,PLK3,HOXA7,SMG9,UHRF1,GMNN,FASTKD3,NOC2L,PPARD,NCL,SUV39H1,HMGB2,DMAP1,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,ENSCAFG00000015189,HAT1,HIST2H2AC,H2AFX,EXOSC5,SIX4,ANXA7	down_ACOR_VSMC
GO:0030308	0.0394	0.985	9	49	negative regulation of cell growth	BP	1	DCBLD2,GJA1,RERG,CDKN1A,CRLF3,NRP1,ULK2,NAIF1,SH3BP4	up_ACOR_VSMC
GO:0051239	0.0394	0.987	7	859	regulation of multicellular organismal process	BP	1	NR1H4,TBX5,BPI,PLCL1,SLITRK5,NPNT,NTRK2	up_APUL_EC
GO:0060993	0.0394	0.988	6	42	kidney morphogenesis	BP	0.874	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0086001	0.0394	0.995	3	9	cardiac muscle cell action potential	BP	1	FGF13,KCNE3,JUP	up_ACOR_VSMC
GO:0030032	0.0394	0.999	1	19	lamellipodium assembly	BP	1	FSCN1	down_AFEM_EC
GO:0007200	0.0394	0.999	1	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	C3AR1	up_VPOR_VSMC
GO:0031128	0.0394	0.999	1	15	developmental induction	BP	1	HOXA11	up_VFEM_VSMC
GO:0048538	0.0394	0.999	1	20	thymus development	BP	1	HOXA3	up_VPUL_VSMC
GO:1905314	0.039471593	0.99652	2	12	semi-lunar valve development	BP	1	GATA4,SMAD6	up_ACOR_EC
GO:2000379	0.0395	0.99	5	20	positive regulation of reactive oxygen species	BP	1	F2RL1,CYBA,ZNF205,ASS1,TGFBR2	up_VSAP_EC
GO:0009892	0.0395	0.998	2	835	negative regulation of metabolic process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0006002	0.0395	0.999	1	5	fructose 6-phosphate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:2001222	0.0395	0.999	1	11	regulation of neuron migration	BP	1	ARHGEF2	up_VPUL_EC
GO:0010831	0.0395	0.999	1	9	positive regulation of myotube differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0010942	0.0396	0.978	18	200	positive regulation of cell death	BP	0.874	CASP3,PTPN2,MAGED1,CTNNB1,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,EIF2S1,PAK2,INHBA,CDKN1A,SPINK2	down_VSAP_EC
GO:0031076	0.0396	0.992	4	14	embryonic camera-type eye development	BP	1	RARG,ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:0035296	0.0396	0.993	3	32	regulation of tube diameter	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0097746	0.0396	0.993	3	32	regulation of blood vessel diameter	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0030001	0.0396	0.993	3	172	metal ion transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0045616	0.0396	0.999	1	9	regulation of keratinocyte differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0032386	0.0396	1	1	137	regulation of intracellular transport	BP	1	JUP	down_VFEM_VSMC
GO:0055010	0.0396	0.999	1	15	ventricular cardiac muscle tissue morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC

GO:0006807	0.0397	0.967	290	3221	nitrogen compound metabolic process	BP	1	ELK3,ACSL3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,ENSCAFG00000016095,PPRC1,USP4,SF3B2,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,THOP1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,PFAS,EDC4,AURKB,NONO,MMP14,HNRNPL,TK1,CDKN2C,TOPBP1,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,RNF152,DIS3,GMNN,DHCR24,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,PRCP,ELOVL1,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPA	down_ACOR_VSMC
GO:1901861	0.0397	0.986	8	41	regulation of muscle tissue development	BP	1	BMP4,FGFR2,GJA1,PPARGC1A,TBX20,TBX5,FRS2,EDN1	up_ACOR_VSMC
GO:0006928	0.0397	0.99	5	557	movement of cell or subcellular component	BP	1	TBX5,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043009	0.0397	0.997	2	227	chordate embryonic development	BP	1	HOXC6,C6	up_VCAV_VSMC
GO:0007041	0.0397	0.996	2	41	lysosomal transport	BP	1	HOOK3,GCC2	up_VPOR_EC
GO:0007618	0.0397	0.999	1	5	mating	BP	1	ACVR2A	up_VPOR_EC
GO:0007613	0.0397	0.999	1	20	memory	BP	1	LRRN4	up_VPUL_VSMC
GO:0050999	0.0397	0.999	1	9	regulation of nitric-oxide synthase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0099601	0.0397	0.999	1	10	regulation of neurotransmitter	BP	1	NETO1	up_VSAP_VSMC
GO:0090316	0.039739463	0.99093	4	48	positive regulation of intracellular protein	BP	1	KCNB1,EDEM2,MAVS,PRKCD	up_ACOR_EC
GO:0006066	0.0398	0.981	14	89	alcohol metabolic process	BP	1	PLCG2,LEP,LCAT,PCBD1,ABCA1,PPIP5K1,LIPE,MOXD1,APP,CLN8,INPP5K,PTS,PARK7,LMF1	up_ACOR_VSMC
GO:0016070	0.0398	0.984	11	1479	RNA metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0030239	0.0398	0.991	4	21	myofibril assembly	BP	0.874	ACTN1,WDR1,SIX4,MYBPC2	down_VSAP_EC
GO:0090066	0.0398	0.991	4	162	regulation of anatomical structure size	BP	1	HTR7,SEMA3A,TWF1,RNF6	up_VPOR_EC
GO:0007275	0.0398	1	2	1370	multicellular organism development	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0051781	0.0398	0.999	1	18	positive regulation of cell division	BP	1	FGF5	up_VPOR_VSMC
GO:0003279	0.039812668	0.99091	4	48	cardiac septum development	BP	1	GATA4,SMAD6,TBX5,NRP1	up_ACOR_EC
GO:0043113	0.039878561	0.99647	2	12	receptor clustering	BP	1	AGRN,LRP4	up_ACOR_EC
GO:0072001	0.0399	0.98	15	104	renal system development	BP	0.822	HOXB7,PDGFB,PODXL,MEF2C,TIPARP,GPR4,GATA3,MTSS1,ODC1,ARG2,BMP2,PROX1,JAG1,BASP1,ITGA6	up_VCAV_EC
GO:0097194	0.0399	0.99	5	23	execution phase of apoptosis	BP	0.822	CASP8,MADD,PAK2,ENSCAFG00000005099,TAOK1	up_VCAV_EC
GO:0006355	0.0399	0.995	3	974	regulation of transcription, DNA-	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0006335	0.0399	0.998	2	4	DNA replication-dependent nucleosome	BP	1	IPO4,HAT1	down_ACOR_VSMC
GO:0034723	0.0399	0.998	2	4	DNA replication-dependent nucleosome	BP	1	IPO4,HAT1	down_ACOR_VSMC
GO:0001678	0.039952582	0.99335	3	29	cellular glucose homeostasis	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC

GO:1902531	0.04	0.973	43	536	regulation of intracellular signal transduction	BP	0.874	ARHGEF2,VEGFA,P4HB,SIPA1L1,NR1H4,SOCS5,JCAD,HYOU1,PTPN11,TRIB3,FARP1,ILK,FHL2,SESN2,PTGS2,UACA,HIF1A,TNIK,PTPN2,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,LYN,DDIT3,PLEKHG2,CBLC,ATF3,GSK3B,HTT,ARFGEF3,CALM1,PAK2,INHBA,NRP1,SH3RF3,TNFAIP1,MADD,SEC13,MID1	down_VSAP_EC
GO:0098660	0.04	0.978	20	141	inorganic ion transmembrane transport	BP	1	ACTN2,PLCG2,SLC26A7,KCNE3,HTR2B,PTPN3,CLCN3,MICU2,ITPR1,CACNB3,AKAP6,KCNJ4,PRKCE,CHD7,ATP6V0E1,KCNC4,FXYD1,NDUFA4L2,PARK7,SLC8A1	up_ACOR_VSMC
GO:0043603	0.04	0.994	3	372	cellular amide metabolic process	BP	1	DARS,SUCLG2,EIF3M	down_AFEM_EC
GO:0001706	0.04	0.999	1	20	endoderm formation	BP	1	DUSP2	up_AORT_EC
GO:0009953	0.04	0.999	1	34	dorsal/ventral pattern formation	BP	1	WNT7A	up_AORT_VSMC
GO:0010657	0.04	0.999	1	15	muscle cell apoptotic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0065008	0.0401	0.97	77	1056	regulation of biological quality	BP	0.874	VEGFA,P4HB,MYH9,SLC39A7,NR1H4,FMNL3,ENSCAFG00000013214,HSPA5,SERPINE1,ERO1A,ENPP1,CASP3,ENSCAFG00000003477,AKAP2,PTPN11,EXOC5,ATP2B1,AARS,LRRC8A,IFRD1,PRCP,SMARCA4,SESN2,PTGS2,WDR1,TMTC2,MSN,KIF5B,HIF1A,HTR7,TUBB,DNAJC10,NXN,PTPN2,NEO1,PLCL1,SMG7,ACTA2,PDIA4,ACTR3,GNAQ,CTNNB1,CRYAB,TFRC,APOE,PLOD3,LYN,BNIP3,STRAP,DDIT3,TWF1,PLEKHG2,TLN1,CLCN3,SLC7A11,GSK3B,CDC37,ITGB3,SH3GLB1,HTT,REST,ABHD5,PRMT1,CALM1,RAB11FIP1,DISC1,RAD23A,KDELR2,LRRTM2,CAPG,INHBA,SIX4,NRP1,ARF4,YWHAH,KDM3A,HOMER1	down_VSAP_EC
GO:0003006	0.0401	0.976	25	180	developmental process involved in reproduction	BP	1	LEP,GATA4,PRDX4,BMP4,FGFR2,ATRX,PDE5A,CITED2,SPINT1,CTSB,EGLN1,ENSCAFG00000006238,SPINT2,PTGDR,MARF1,AFF4,FRS2,CHD7,SPINK2,ARID5B,DMC1,SERPINB5,JAM3,LHX9,WDR48	up_ACOR_VSMC
GO:0010959	0.0401	0.984	9	79	regulation of metal ion transport	BP	0.874	REM1,KIF5B,CTNNB1,LYN,NKAIN1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0061311	0.0401	0.994	3	9	cell surface receptor signaling pathway involved in heart	BP	0.824	DLL4,BMP2,JAG1	up_VCAV_EC
GO:0048284	0.0401	0.996	2	66	organelle fusion	BP	1	SPG11,STX4	down_ACOR_EC
GO:0036010	0.0401	0.997	2	6	protein localization to endosome	BP	0.874	MSN,NRP1	down_VSAP_EC
GO:0006941	0.0401	0.999	1	36	striated muscle contraction	BP	1	ARG2	up_AORT_VSMC
GO:0003382	0.0401	0.999	1	11	epithelial cell morphogenesis	BP	1	ARHGEF26	up_APUL_EC
GO:0010770	0.0401	0.999	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	LIMK1	up_VCAV_VSMC
GO:0071466	0.0401	0.999	1	17	cellular response to xenobiotic stimulus	BP	1	CYP26B1	up_VPOR_VSMC
GO:0032024	0.0401	0.999	1	12	positive regulation of insulin secretion	BP	1	NR1H4	up_VPUL_EC
GO:0035115	0.0401	0.999	1	12	embryonic forelimb morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0061178	0.0401	0.999	1	12	regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_VPUL_EC
GO:0090277	0.0401	0.999	1	12	positive regulation of peptide hormone	BP	1	NR1H4	up_VPUL_EC
GO:0021795	0.0401	0.999	1	20	cerebral cortex cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0071560	0.0402	0.982	12	72	cellular response to transforming growth factor beta stimulus	BP	1	SMAD6,FERMT1,CITED2,CDKN2B,ANKRD1,NPNT,FUT8,TGFBR1,NR3C1,DUSP22,HPGD,CRKL	up_ACOR_VSMC
GO:0050866	0.0402	0.985	8	48	negative regulation of cell activation	BP	0.824	ADGRF5,TNFAIP3,PDGFB,PELI1,ARG2,THOC1,CD200,HMGB1	up_VCAV_EC
GO:0030324	0.0402	0.986	7	64	lung development	BP	1	ADAMTS2,BMPR1A,LOX,GLI3,LOXL3,RDH10,THRB	down_VCAV_EC
GO:0044818	0.0402	0.992	4	15	mitotic G2/M transition checkpoint	BP	0.824	TAOK1,BLM,RAD17,TOPBP1	up_VCAV_EC
GO:0032613	0.0402	0.992	4	14	interleukin-10 production	BP	1	CD274,DLL1,F2RL1,CD83	up_VSAP_EC

GO:1903506	0.0402	0.995	3	977	regulation of nucleic acid-templated transcription	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0045822	0.0402	0.995	3	8	negative regulation of heart contraction	BP	1	KCNE3,PDE5A,RNLS	up_ACOR_VSMC
GO:0048731	0.0402	0.996	3	1247	system development	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0051482	0.0402	0.997	2	5	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-	BP	0.824	GPR4,EDN1	up_VCAV_EC
GO:0021563	0.0402	0.998	2	4	glossopharyngeal nerve development	BP	1	HOXD3,PLXNA4	up_VSAP_EC
GO:0045840	0.0403	0.994	3	12	positive regulation of mitotic nuclear division	BP	0.824	PDGFB,EDN1,SMC5	up_VCAV_EC
GO:0071214	0.0403	0.996	2	93	cellular response to abiotic stimulus	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0104004	0.0403	0.996	2	93	cellular response to environmental stimulus	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0060039	0.0403	0.999	1	11	pericardium development	BP	1	TBX5	up_APUL_EC
GO:0090161	0.0403	0.999	1	5	Golgi ribbon formation	BP	1	GCC2	up_VPOR_EC
GO:0010830	0.0403	0.999	1	16	regulation of myotube differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0002042	0.040311793	0.99326	3	29	cell migration involved in sprouting angiogenesis	BP	1	ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC
GO:0023051	0.0404	0.975	31	954	regulation of signaling	BP	1	CMKLR1,LEP,KCNC4,LBH,CRY2,GAS1,DLL1,F3,MLLT11,LMCD1,CHRM2,TMEM100,SLC6A6,PLAGL2,GREM1,FAM53B,CAMK2A,GREM2,CLEC16A,CYLD,POSTN,LRRC15,RECK,BVES,LGR6,RAB7A,AXIN2,CCL5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0046632	0.0404	0.988	6	29	alpha-beta T cell differentiation	BP	0.825	IL6,GATA3,MTOR,ITPKB,HMGB1,BMX	up_VCAV_EC
GO:0002688	0.0404	0.989	5	34	regulation of leukocyte chemotaxis	BP	0.874	VEGFA,SERPINE1,ADAM17,MMP28,LYN	down_VSAP_EC
GO:0034123	0.0404	0.994	3	10	positive regulation of toll-like receptor signaling	BP	0.824	PELI1,TLR3,HMGB1	up_VCAV_EC
GO:0033327	0.0404	0.998	2	4	Leydig cell differentiation	BP	1	SF1,SGPL1	down_ACOR_VSMC
GO:0097242	0.0404	0.997	2	7	amyloid-beta clearance	BP	1	LRP1,LRPAP1	down_VCAV_EC
GO:0009225	0.0404	0.999	1	10	nucleotide-sugar metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0050857	0.0404	0.999	1	9	positive regulation of antigen receptor-mediated signaling	BP	1	LYN	down_ACOR_EC
GO:0045655	0.0404	0.999	1	9	regulation of monocyte differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0003156	0.0404	0.999	1	20	regulation of animal organ formation	BP	1	CITED2	down_VPOR_EC
GO:0048844	0.0404	0.999	1	30	artery morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0060675	0.0404	0.999	1	29	ureteric bud morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0007338	0.0404	0.999	1	16	single fertilization	BP	1	HOXA9	up_AORT_EC
GO:0042116	0.0404	0.999	1	18	macrophage activation	BP	1	BPI	up_AORT_EC
GO:1905939	0.0404	0.999	1	5	regulation of gonad development	BP	1	SEMA3A	up_VPOR_EC
GO:0051094	0.0405	0.972	48	388	positive regulation of developmental process	BP	1	VEGFD,LEP,LBH,GATA5,CD83,FNDC5,BMP4,FGFR2,TP53BP1,GJA1,TLR3,WASF3,PPARGC1A,PDE5A,CITED2,ISG15,CD274,ZNF365,SASH1,FGF18,FAM210B,MARCH5,BNIP3,CLSTN1,NRP1,NPNT,SMARCD3,SLITRK5,TBX20,TBX5,CCDC3,FZD3,DKKL1,FRS2,DAG1,APP,PSEN1,CHD7,JUP,DDR2,EDN1,DISC1,DOCK5,ERAP1,SLC8A1,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0090224	0.0405	0.992	4	16	regulation of spindle organization	BP	1	SMC1A,NUP62,SMC3,STAG1	down_ACOR_VSMC
GO:0045665	0.0405	0.991	4	55	negative regulation of neuron differentiation	BP	1	IRX3,DLL1,THRB,KANK1	up_AFEM_EC
GO:2001141	0.0405	0.995	3	979	regulation of RNA biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0090596	0.0405	0.996	2	84	sensory organ morphogenesis	BP	1	NTRK2,HOXA1	up_APUL_EC

GO:0070427	0.0405	0.998	2	4	nucleotide-binding oligomerization domain containing 1 signaling	BP	0.826	TNFAIP3,TLR4	up_VCAV_EC
GO:0048538	0.0405	0.999	1	20	thymus development	BP	1	CITED2	down_VPOR_EC
GO:0072657	0.0405	1	1	144	protein localization to membrane	BP	1	JUP	down_VFEM_VSMC
GO:0030155	0.0406	0.976	25	180	regulation of cell adhesion	BP	1	LEP,CD83,MBP,FERMT1,BMP4,PDE5A,CITED2,CD274,NRP1,PTPN22,NPNT,SPINT2,PRKCE,RND1,ECM2,LAMA3,JUP,DUSP22,NID1,DUSP26,FAM107A,DOCK5,RREB1,PAG1,CRKL	up_ACOR_VSMC
GO:0002532	0.0406	0.989	5	25	production of molecular mediator involved in inflammatory response	BP	0.826	GBP5,TLR4,SNAP23,APOD,NOS2	up_VCAV_EC
GO:0090049	0.0406	0.999	1	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0002792	0.040696596	0.99317	3	29	negative regulation of peptide secretion	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:0060322	0.0407	0.975	26	193	head development	BP	1	EMX2,PCDH19,SEZ6L,CDON,OSR2,SLIT2,SLC6A4,ABL1,DLL1,PLXNA4,RARG,CTNS,RTN4RL1,DPYSL2,GDPD5,SMG9,MCPH1,KIF27,KDM2B,RAF1,NFIB,ZFAND5,QARS,HTRA2,MAP2K2,TGFBR2	up_VSAP_EC
GO:0030217	0.0407	0.982	11	65	T cell differentiation	BP	1	ABL1,ZBTB16,STAT6,PATZ1,ZFP36L1,ZEB1,CD83,ZFP36L2,PNP,PPP3CB,TGFBR2	up_VSAP_EC
GO:0021537	0.0407	0.984	9	73	telencephalon development	BP	0.874	HIF1A,UBA6,UCHL5,CTNNB1,GSK3B,EXT1,DISC1,INHBA,NRP1	down_VSAP_EC
GO:0060307	0.0407	0.998	2	4	regulation of ventricular cardiac muscle cell membrane repolarization	BP	1	KCNE3,GJA1	up_ACOR_VSMC
GO:0099622	0.0407	0.998	2	4	cardiac muscle cell membrane repolarization	BP	1	KCNE3,GJA1	up_ACOR_VSMC
GO:0099623	0.0407	0.998	2	4	regulation of cardiac muscle cell membrane	BP	1	KCNE3,GJA1	up_ACOR_VSMC
GO:0099625	0.0407	0.998	2	4	ventricular cardiac muscle cell membrane	BP	1	KCNE3,GJA1	up_ACOR_VSMC
GO:0007276	0.0407	0.996	2	130	gamete generation	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0010972	0.0407	0.999	1	18	negative regulation of G2/M transition of mitotic	BP	1	TAOK1	up_AORT_EC
GO:0055021	0.0407	0.999	1	15	regulation of cardiac muscle tissue growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0018105	0.0408	0.979	16	116	peptidyl-serine phosphorylation	BP	0.83	PLK2,HCLS1,PRKCH,PDGFB,PDE4D,MTOR,MAPK13,PAK2,PRKD2,NCK1,NSD1,PTGS2,TOP1,SPTBN4,RIPK1,LMTK2	up_VCAV_EC
GO:0071495	0.0408	0.989	5	365	cellular response to endogenous stimulus	BP	1	ACVRL1,IGF1R,SULF1,ASPN,NEDD4	down_ACOR_EC
GO:0001837	0.0408	0.999	1	48	epithelial to mesenchymal transition	BP	1	TGFBR1	down_VSAP_VSMC
GO:0045927	0.0408	0.999	1	61	positive regulation of growth	BP	1	TBX5	up_APUL_VSMC
GO:0042088	0.0408	0.999	1	12	T-helper 1 type immune response	BP	1	IL18BP	up_VPUL_EC
GO:0036295	0.0408	0.999	1	9	cellular response to increased oxygen levels	BP	1	CAV1	up_VSAP_VSMC
GO:0036296	0.0408	0.999	1	9	response to increased oxygen levels	BP	1	CAV1	up_VSAP_VSMC
GO:0010941	0.0409	0.972	41	524	regulation of cell death	BP	0.874	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,CASP3,HYOU1,AARS,FHL2,PTGS2,HIF1A,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,APOE,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,EIF2S1,GLO1,PAK2,INHBA,SIX4,CDKN1A,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0030334	0.0409	0.977	20	267	regulation of cell migration	BP	1	PDGFRB,DCN,SDC4,GLIPR2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,LAMA3,SEMA3C,THY1,SASH1,SPRED1,TWIST2,DDR2,RAC2,FOXO3	down_VCAV_EC
GO:0010833	0.0409	0.988	6	30	telomere maintenance via telomere lengthening	BP	1	SLC29A1,RAD51,AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0032410	0.0409	0.991	4	17	negative regulation of transporter activity	BP	1	NEDD4,CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0042982	0.0409	0.994	3	15	amyloid precursor protein metabolic process	BP	1	PRNP,NECAB3,SOAT1	down_VCAV_EC
GO:0030036	0.0409	0.993	3	223	actin cytoskeleton organization	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0000077	0.0409	0.996	2	60	DNA damage checkpoint	BP	1	USP28,ATRIP	down_ACOR_EC

GO:0031579	0.0409	0.997	2	6	membrane raft organization	BP	0.83	MALL,CAV2	up_VCAV_EC
GO:0006188	0.0409	0.999	1	7	IMP biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0021602	0.0409	0.999	1	16	cranial nerve morphogenesis	BP	1	HOXA3	up_VPOR_VSMC
GO:2001273	0.0409	0.999	1	12	regulation of glucose import in response to	BP	1	NR1H4	up_VPUL_EC
GO:0001932	0.041	0.974	29	416	regulation of protein phosphorylation	BP	1	NOTCH2,PDGFRB,KIRREL1,DCN,PRNP,GLIPR2,BGN,BMPR1A,CLIP3,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,ASPN,THY1,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,SPRED1,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0009792	0.041	0.996	2	231	embryo development ending in birth or egg	BP	1	HOXC6,C6	up_VCAV_VSMC
GO:0050878	0.041	0.996	2	75	regulation of body fluid levels	BP	1	CAV1,F5	up_VSAP_VSMC
GO:0043001	0.041	0.999	1	11	Golgi to plasma membrane protein	BP	1	ACSL3	down_ACOR_EC
GO:0000381	0.041	0.999	1	19	regulation of alternative mRNA splicing, via	BP	1	SRSF6	down_AFEM_EC
GO:0030812	0.041	0.999	1	5	negative regulation of nucleotide catabolic	BP	1	FBP1	up_VPOR_EC
GO:0045820	0.041	0.999	1	5	negative regulation of glycolytic process	BP	1	FBP1	up_VPOR_EC
GO:0048846	0.041	0.999	1	6	axon extension involved in axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0051195	0.041	0.999	1	5	negative regulation of cofactor metabolic	BP	1	FBP1	up_VPOR_EC
GO:0051198	0.041	0.999	1	5	negative regulation of coenzyme metabolic	BP	1	FBP1	up_VPOR_EC
GO:1902284	0.041	0.999	1	6	neuron projection extension involved in neuron projection	BP	1	SEMA3A	up_VPOR_EC
GO:0003007	0.041011962	0.98679	6	94	heart morphogenesis	BP	1	GATA4,SOX9,SMAD6,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0046887	0.0411	0.991	4	18	positive regulation of hormone secretion	BP	0.833	EDN1,CREB1,MCU,HIF1A	up_VCAV_EC
GO:0001936	0.0411	0.999	1	49	regulation of endothelial cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0002931	0.0411	0.999	1	9	response to ischemia	BP	1	CAV1	up_VSAP_VSMC
GO:0060415	0.0412	0.988	6	27	muscle tissue morphogenesis	BP	1	TNNT2,FGFR2,ANKRD1,EGLN1,TBX20,CHD7	up_ACOR_VSMC
GO:0045682	0.0412	0.988	6	27	regulation of epidermis development	BP	1	HOXA7,DLL1,HPSE,ZFP36L1,TRADD,KEAP1	up_VSAP_EC
GO:0000271	0.0412	0.991	4	22	polysaccharide biosynthetic process	BP	0.874	ENPP1,ENSCAFG00000032470,PPP1R3C,EXT1	down_VSAP_EC
GO:0032623	0.0412	0.999	1	21	interleukin-2 production	BP	1	HDAC7	down_VPOR_EC
GO:0070227	0.0413	0.989	5	25	lymphocyte apoptotic process	BP	0.833	IL7R,ARG2,BCL10,RIPK1,HIF1A	up_VCAV_EC
GO:0019915	0.0413	0.991	4	22	lipid storage	BP	0.874	ENPP1,PTPN2,APOE,ABHD5	down_VSAP_EC
GO:0043299	0.0413	0.991	4	18	leukocyte degranulation	BP	0.833	KIT,RAB27A,SNAP23,FES	up_VCAV_EC
GO:0061551	0.0413	0.997	2	5	trigeminal ganglion development	BP	0.874	SIX4,NRP1	down_VSAP_EC
GO:0048608	0.0413	0.996	2	129	reproductive structure development	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0006044	0.0413	0.999	1	5	N-acetylglucosamine metabolic process	BP	1	OGA	up_VPOR_EC
GO:2000142	0.0413	0.999	1	17	regulation of DNA-templated transcription,	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006620	0.041373906	0.99957	1	2	posttranslational protein targeting to endoplasmic reticulum membrane	BP	1	CHMP4B	up_ACOR_EC
GO:0050801	0.0414	0.975	27	200	ion homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,CNNM2,ABCA1,GJA1,PTPN3,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,DMXL1,EDN1,B2M,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:1902904	0.0414	0.986	7	38	negative regulation of supramolecular fiber	BP	0.833	ARHGAP28,TMOD1,STMN1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0048522	0.0414	0.991	5	1484	positive regulation of cellular process	BP	1	SLITRK5,LIMK1,GATA5,CA2,C6	up_VCAV_VSMC
GO:0030890	0.0414	0.994	3	9	positive regulation of B cell proliferation	BP	0.833	MEF2C,TLR4,PELI1	up_VCAV_EC
GO:0072567	0.0414	0.997	2	4	chemokine (C-X-C motif) ligand 2 production	BP	1	MBP,F2RL1	up_ACOR_VSMC

GO:0001782	0.0414	0.999	1	8	B cell homeostasis	BP	1	LYN	down_ACOR_EC
GO:0001947	0.0414	0.999	1	21	heart looping	BP	1	CITED2	down_VPOR_EC
GO:0061371	0.0414	0.999	1	21	determination of heart left/right asymmetry	BP	1	CITED2	down_VPOR_EC
GO:0008206	0.0414	0.999	1	11	bile acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0036445	0.0414	0.999	1	6	neuronal stem cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:0055057	0.0414	0.999	1	6	neuroblast division	BP	1	ARHGEF2	up_VPOR_EC
GO:0090175	0.0414	0.999	1	15	regulation of establishment of planar	BP	1	ANKRD6	up_VPOR_VSMC
GO:0055023	0.0414	0.999	1	12	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0044262	0.0415	0.982	10	89	cellular carbohydrate metabolic process	BP	0.874	ENPP1,TPI1,ENSCAFG00000032470,PGAM1,SESN2,SLC45A3,PTPN2,PPP1R3C,GSK3B,EXT1	down_VSAP_EC
GO:0007263	0.0415	0.994	3	8	nitric oxide mediated signal transduction	BP	0.833	GUCY1A1,GUCY1B1,NOS2	up_VCAV_EC
GO:0071863	0.0415	0.997	2	4	regulation of cell proliferation in bone	BP	0.833	MEF2C,MAP3K3	up_VCAV_EC
GO:0071864	0.0415	0.997	2	4	positive regulation of cell proliferation in bone	BP	0.833	MEF2C,MAP3K3	up_VCAV_EC
GO:0051146	0.0415	0.996	2	76	striated muscle cell differentiation	BP	1	STIM1,SHOX2	up_VSAP_VSMC
GO:0008306	0.0415	0.999	1	21	associative learning	BP	1	LRRN4	up_VPUL_VSMC
GO:0010596	0.0415	0.999	1	21	negative regulation of endothelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:2000027	0.0416	0.981	12	72	regulation of animal organ morphogenesis	BP	1	GATA5,MLLT3,BMP4,FGFR2,SEC24B,CITED2,ZNRF3,LIMS2,TBX5,FZD3,FRS2,TNFRSF11B	up_ACOR_VSMC
GO:0030326	0.0416	0.987	6	51	embryonic limb morphogenesis	BP	1	BMPR1A,RECK,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0035113	0.0416	0.987	6	51	embryonic appendage morphogenesis	BP	1	BMPR1A,RECK,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0002685	0.0416	0.99	4	55	regulation of leukocyte migration	BP	1	CMKLR1,HOXA7,CCL5,ADAM17	up_AFEM_EC
GO:0050853	0.0416	0.994	3	10	B cell receptor signaling pathway	BP	0.834	PRKCH,MEF2C,PLCG2	up_VCAV_EC
GO:0022417	0.0416	0.997	2	4	protein maturation by protein folding	BP	1	PRDX4,ERO1B	up_ACOR_VSMC
GO:0060548	0.0416	0.996	2	294	negative regulation of cell death	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0060291	0.0416	0.999	1	11	long-term synaptic potentiation	BP	1	NTRK2	up_APUL_EC
GO:0035107	0.0416	0.999	1	60	appendage morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0035108	0.0416	0.999	1	60	limb morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0031268	0.0416	0.999	1	9	pseudopodium organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0031269	0.0416	0.999	1	9	pseudopodium assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0035725	0.0416	0.999	1	16	sodium ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0071360	0.0416	0.999	1	9	cellular response to exogenous dsRNA	BP	1	CAV1	up_VSAP_VSMC
GO:0032501	0.0417	0.968	103	1782	multicellular organismal process	BP	1	ADAMTS2,GPAM,NOTCH2,HSPB6,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,NDN,ANGPT1,PRNP,LUM,SDC4,VASN,FBN1,ADCY6,GLIPR2,KANK2,THBS3,BMPR1A,LOX,VKORC1,LMO4,EVC,RECK,TRPV2,ANPEP,COL6A1,NUMBL,CHID1,NAGLU,CHRDL1,TBX15,AKT2,LCAT,TFE3,ENSCAFG00000018277,SYDE1,HOXC4,LAMA3,CLSTN1,PLCL1,CSPG4,TRIM8,PKD1,ENSCAFG00000013404,SEMA3C,ASPN,LRPAP1,THY1,RNF216,TEAD1,MEA1,HAPLN3,PEX5,TLX2,VCAN,B4GALT1,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,NCDN,BPI,RNPEP,CYBA,IFT57,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,IRX5,TSC22D3,UST,GLIS2,TWIST2,PRKCSH,DDR2,SHC1,RDH10,PCSK6,OMD,GREM1,NAPEPLD,CLIC4,FOXO3,SOAT1,THRB,ZBTB16,ANKRD54,RGMA,SEC61A1,BRSK1	down_VCAV_EC

GO:0032870	0.0417	0.976	23	162	cellular response to hormone stimulus	BP	1	ACTN2,LEP,LBH,SKP2,PRKAA2,BMP4,MED14,LATS2,AR,FAM210B,ADCY6,CTSB,CREBRF,PTGDR,SESN3,PRKCE,AGRN,NR3C1,FAM107A,DDIT4,GNAQ,INPP5K,PARK7	up_ACOR_VSMC
GO:2000027	0.0417	0.981	12	72	regulation of animal organ morphogenesis	BP	1	HOXA11,FZD1,THRB,WNT11,LIMS2,FGF7,ABL1,SULF2,NTN4,NFIB,TGFBR2,CITED2	up_VSAP_EC
GO:0048738	0.0417	0.982	10	64	cardiac muscle tissue development	BP	0.834	ADAMTS9,MEF2C,CHD7,DLL4,EDN1,MTOR,BMP2,PROX1,ENSCAFG00000010596,CREB1	up_VCAV_EC
GO:0042982	0.0417	0.991	4	15	amyloid precursor protein metabolic process	BP	1	ITM2C,PSEN2,APP,PSEN1	up_ACOR_VSMC
GO:0006396	0.0417	0.993	3	368	RNA processing	BP	1	IVNS1ABP,SRSF6,TSEN15	down_AFEM_EC
GO:0060676	0.0417	0.997	2	6	ureteric bud formation	BP	0.874	ENSCAFG00000032470,SIX4	down_VSAP_EC
GO:0061162	0.0417	0.997	2	6	establishment of monopolar cell polarity	BP	0.874	FSCN1,MSN	down_VSAP_EC
GO:0061339	0.0417	0.997	2	6	establishment or maintenance of	BP	0.874	FSCN1,MSN	down_VSAP_EC
GO:0034122	0.0417	0.999	1	9	negative regulation of toll-like receptor signaling	BP	1	LYN	down_ACOR_EC
GO:2000279	0.0417	0.999	1	9	negative regulation of DNA biosynthetic process	BP	1	ACVRL1	down_ACOR_EC
GO:0021800	0.0417	0.999	1	6	cerebral cortex tangential migration	BP	1	NRP2	down_ACOR_EC
GO:0015718	0.0417	0.999	1	30	monocarboxylic acid transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0007569	0.0417	0.999	1	36	cell aging	BP	1	ARG2	up_AORT_VSMC
GO:0042742	0.0417	0.999	1	39	defense response to bacterium	BP	1	ARG2	up_AORT_VSMC
GO:0006616	0.0417	0.999	1	5	SRP-dependent cotranslational protein targeting to membrane,	BP	1	SRP54	up_VPOR_EC
GO:0046461	0.0417	0.999	1	5	neutral lipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0046464	0.0417	0.999	1	5	acylglycerol catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:1903034	0.0418	0.986	7	40	regulation of response to wounding	BP	0.834	SELP,PDGFB,CD34,KLKB1,TLR4,TFPI,MTOR	up_VCAV_EC
GO:0090184	0.0418	0.993	3	14	positive regulation of kidney development	BP	0.874	HOXB7,MAGED1,SIX4	down_VSAP_EC
GO:0090306	0.0418	0.997	2	4	spindle assembly involved in meiosis	BP	1	FBXO5,ASPM	down_ACOR_VSMC
GO:0006940	0.0418	0.996	2	14	regulation of smooth muscle contraction	BP	1	CHRM2,TBXA2R	up_AFEM_EC
GO:0043269	0.0418	0.996	2	135	regulation of ion transport	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0043500	0.0418	0.999	1	21	muscle adaptation	BP	1	GATA5	up_VPUL_VSMC
GO:2000736	0.0418	0.999	1	21	regulation of stem cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0002528	0.04185417	0.99956	1	2	regulation of vascular permeability involved in acute inflammatory	BP	1	CLSTN1	up_ACOR_EC
GO:0065008	0.041889943	0.97273	37	1056	regulation of biological quality	BP	1	CNTNAP4,CDH3,NR1H4,TMOD1,BRSK1,PLCL1,PKIB,CALY,SOX9,RHOU,PTH1R,PCSK1N,AQP1,PORCN,KCNB1,IFI6,NOD2,INSYN1,PLS1,ACTN2,RNLS,PAK3,USP53,MAPK8IP2,FOXC2,LRP4,CLSTN1,LRRC4,CLU,SLC9A9,CHMP4B,TP53INP2,TMTC2,PRKACA,NRP1,PRKCD,PM20D1	up_ACOR_EC
GO:0016072	0.0419	0.979	14	102	rRNA metabolic process	BP	1	NOP56,FBL,DIS3,NOC4L,NCL,RSL1D1,RRP1,ENSCAFG00000019620,NOP14,NOP58,ENSCAFG00000015189,EMG1,EXOSC5,NOB1	down_ACOR_VSMC
GO:0050678	0.0419	0.98	12	117	regulation of epithelial cell proliferation	BP	0.874	VEGFA,SULF1,SPARC,JCAD,TGFBR1,ADAM17,MAGED1,CTNNB1,APOE,STRAP,NR4A1,SIX4	down_VSAP_EC
GO:1902905	0.0419	0.981	12	72	positive regulation of supramolecular fiber	BP	1	SYNPO2L,ACTN2,SYNPO2,F2RL1,JMY,NRP1,EVL,PRKCE,APP,PSEN1,EDN1,WASL	up_ACOR_VSMC
GO:0000723	0.0419	0.983	9	54	telomere maintenance	BP	1	RPA1,HNRNPD,SLC29A1,RAD51,AURKB,NEK2,SMC6,TINF2,CCT4	down_ACOR_VSMC
GO:0032200	0.0419	0.983	9	54	telomere organization	BP	1	RPA1,HNRNPD,SLC29A1,RAD51,AURKB,NEK2,SMC6,TINF2,CCT4	down_ACOR_VSMC
GO:2001237	0.0419	0.986	7	33	negative regulation of extrinsic apoptotic	BP	1	BMP4,AR,DAPK1,NRP1,UNC5B,SH3RF1,PARK7	up_ACOR_VSMC
GO:0048534	0.0419	0.99	4	262	hematopoietic or lymphoid organ	BP	1	LYN,HOXA3,PDPN,HOXA7	down_ACOR_EC
GO:0050879	0.0419	0.991	4	16	multicellular organismal movement	BP	0.834	MTOR,KCNJ2,VPS54,ATP2A1	up_VCAV_EC

GO:0050881	0.0419	0.991	4	16	musculoskeletal movement	BP	0.834	MTOR,KCNJ2,VPS54,ATP2A1	up_VCAV_EC
GO:0080134	0.0419	0.991	4	386	regulation of response to stress	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:1902745	0.0419	0.994	3	9	positive regulation of lamellipodium	BP	0.834	MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0060612	0.0419	0.996	2	14	adipose tissue development	BP	1	LEP,PPARGC1A	up_AFEM_EC
GO:0045944	0.0419	1	1	287	positive regulation of transcription by RNA polymerase II	BP	1	GATA5	down_AFEM_VSMC
GO:0001889	0.0419	0.999	1	22	liver development	BP	1	CITED2	down_VPOR_EC
GO:0071417	0.0419	1	1	142	cellular response to organonitrogen	BP	1	JUP	down_VFEM_VSMC
GO:0001935	0.0419	0.999	1	50	endothelial cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0072171	0.0419	0.999	1	30	mesonephric tubule morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0021800	0.0419	0.999	1	6	cerebral cortex tangential migration	BP	1	SEMA3A	up_VPOR_EC
GO:0016925	0.0419	0.999	1	16	protein sumoylation	BP	1	EYA1	up_VFEM_VSMC
GO:0014812	0.0419	0.999	1	21	muscle cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0007178	0.042	0.982	10	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD9,VASN,FBN1,BMPR1A,CHRDL1,ASPN,FUT8,ENSCAFG00000017708,GREM1,RGMA	down_VCAV_EC
GO:0042127	0.042	0.989	5	452	regulation of cell proliferation	BP	1	EYA1,SIX1,MAB21L1,TIAM1,MTSS1	up_VFEM_EC
GO:0051851	0.042	0.991	4	23	modification by host of symbiont morphology or	BP	0.874	SMARCA4,APOE,REST,CALM1	down_VSAP_EC
GO:0031570	0.042	0.996	2	61	DNA integrity checkpoint	BP	1	USP28,ATRIP	down_ACOR_EC
GO:0021563	0.042	0.997	2	4	glossopharyngeal nerve development	BP	1	HOXA3,NAV2	down_ACOR_VSMC
GO:0009719	0.042	0.997	2	395	response to endogenous stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0098911	0.042	0.997	2	4	regulation of ventricular cardiac muscle cell action	BP	1	KCNE3,JUP	up_ACOR_VSMC
GO:0001667	0.042	1	1	146	ameboidal-type cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0031111	0.042	0.999	1	11	negative regulation of microtubule polymerization or	BP	1	TUBB4A	up_APUL_EC
GO:0055013	0.042	0.999	1	17	cardiac muscle cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:1901099	0.042	0.999	1	10	negative regulation of signal transduction in	BP	1	EYA1	up_VFEM_EC
GO:2001240	0.042	0.999	1	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_VFEM_EC
GO:0010771	0.042	0.999	1	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0048640	0.042	0.999	1	21	negative regulation of developmental growth	BP	1	TBX5	up_VPUL_VSMC
GO:0072507	0.0421	0.979	14	103	divalent inorganic cation homeostasis	BP	0.836	ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,ATP2A1	up_VCAV_EC
GO:0060512	0.0421	0.991	4	14	prostate gland morphogenesis	BP	1	BMP4,FGFR2,FRS2,SERPINB5	up_ACOR_VSMC
GO:0018195	0.0421	0.997	2	6	peptidyl-arginine modification	BP	0.874	NR1H4,PRMT1	down_VSAP_EC
GO:0046888	0.0421	0.996	2	14	negative regulation of hormone secretion	BP	1	LEP,CRY2	up_AFEM_EC
GO:0060872	0.0421	0.999	1	6	semicircular canal development	BP	1	HOXA1	down_ACOR_EC
GO:0001570	0.0421	0.999	1	37	vasculogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0060045	0.0421	0.999	1	11	positive regulation of cardiac muscle cell	BP	1	TBX5	up_APUL_EC
GO:0048641	0.0421	0.999	1	16	regulation of skeletal muscle tissue	BP	1	CYP26B1	up_VPOR_VSMC
GO:0042157	0.0422	0.983	9	51	lipoprotein metabolic process	BP	1	LCAT,ABCA1,PIGN,PIGS,PIGG,APOL6,LYPLAL1,PIK3C3,ZDHHC21	up_ACOR_VSMC
GO:0034968	0.0422	0.986	7	34	histone lysine methylation	BP	0.836	IWS1,GATA3,ARID4B,NSD1,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0033198	0.0422	0.994	3	10	response to ATP	BP	0.836	P2RX7,SELL,P2RX2	up_VCAV_EC

GO:0010452	0.0422	0.998	2	3	histone H3-K36 methylation	BP	0.836	IWS1,NSD1	up_VCAV_EC
GO:0010575	0.0422	0.999	1	8	positive regulation of vascular endothelial growth factor production	BP	1	SULF1	down_ACOR_EC
GO:0035914	0.0422	0.999	1	22	skeletal muscle cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:0071772	0.0422	0.999	1	50	response to BMP	BP	1	GATA5	down_VSAP_VSMC
GO:0071773	0.0422	0.999	1	50	cellular response to BMP stimulus	BP	1	GATA5	down_VSAP_VSMC
GO:2001275	0.0422	0.999	1	11	positive regulation of glucose import in response to insulin	BP	1	NR1H4	up_APUL_EC
GO:0031397	0.0422	0.999	1	30	negative regulation of protein ubiquitination	BP	1	LIMK1	up_VCAV_VSMC
GO:0002703	0.0423	0.984	8	47	regulation of leukocyte mediated immunity	BP	0.836	IL7R,TLR4,GATA3,NECTIN2,THOC1,TLR3,FES, HMGB1	up_VCAV_EC
GO:0009888	0.0423	0.991	4	545	tissue development	BP	1	EYA1,SPINK5,HOXA11,SHOX2	up_VFEM_VSMC
GO:0043487	0.0423	0.993	3	33	regulation of RNA stability	BP	1	TENT5C,AXIN2,SAMD4B	up_AFEM_EC
GO:0047497	0.0423	0.997	2	5	mitochondrion transport along microtubule	BP	0.874	HIF1A,TRAK1	down_VSAP_EC
GO:0034643	0.0423	0.997	2	5	establishment of mitochondrion localization, microtubule-	BP	0.874	HIF1A,TRAK1	down_VSAP_EC
GO:1901857	0.0423	0.997	2	4	positive regulation of cellular respiration	BP	1	PPARGC1A,PARK7	up_ACOR_VSMC
GO:0061458	0.0423	0.996	2	131	reproductive system development	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0022012	0.0423	1	1	1	subpallium cell proliferation in forebrain	BP	1	GLI3	down_VCAV_EC
GO:0022018	0.0423	1	1	1	lateral ganglionic eminence cell	BP	1	GLI3	down_VCAV_EC
GO:0001869	0.0423	1	1	1	negative regulation of complement activation, lectin pathway	BP	1	A2M	down_VCAV_EC
GO:0035582	0.0423	1	1	1	sequestering of BMP in extracellular matrix	BP	1	FBN1	down_VCAV_EC
GO:0035583	0.0423	1	1	1	sequestering of TGFbeta in extracellular matrix	BP	1	FBN1	down_VCAV_EC
GO:0040009	0.0423	1	1	1	regulation of growth rate	BP	1	NOTCH2	down_VCAV_EC
GO:0045967	0.0423	1	1	1	negative regulation of growth rate	BP	1	NOTCH2	down_VCAV_EC
GO:0002921	0.0423	1	1	1	negative regulation of humoral immune	BP	1	A2M	down_VCAV_EC
GO:0060366	0.0423	1	1	1	lambdoid suture morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0060367	0.0423	1	1	1	sagittal suture morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0060981	0.0423	1	1	1	cell migration involved in coronary angiogenesis	BP	1	PDGFRB	down_VCAV_EC
GO:0071692	0.0423	1	1	1	protein localization to extracellular region	BP	1	FBN1	down_VCAV_EC
GO:0071694	0.0423	1	1	1	maintenance of protein location in extracellular	BP	1	FBN1	down_VCAV_EC
GO:0097118	0.0423	1	1	1	neuroligin clustering involved in postsynaptic	BP	1	CDH2	down_VCAV_EC
GO:0001868	0.0423	1	1	1	regulation of complement activation, lectin pathway	BP	1	A2M	down_VCAV_EC
GO:0045916	0.0423	1	1	1	negative regulation of complement activation	BP	1	A2M	down_VCAV_EC
GO:0060873	0.0423	1	1	1	anterior semicircular canal development	BP	1	GLI3	down_VCAV_EC
GO:0060875	0.0423	1	1	1	lateral semicircular canal development	BP	1	GLI3	down_VCAV_EC
GO:0070444	0.0423	1	1	1	oligodendrocyte progenitor proliferation	BP	1	CDH2	down_VCAV_EC
GO:0070445	0.0423	1	1	1	regulation of oligodendrocyte	BP	1	CDH2	down_VCAV_EC
GO:2000258	0.0423	1	1	1	negative regulation of protein activation cascade	BP	1	A2M	down_VCAV_EC
GO:0048489	0.0423	0.999	1	38	synaptic vesicle transport	BP	1	WNT7A	up_AORT_VSMC
GO:0097480	0.0423	0.999	1	38	establishment of synaptic vesicle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0042481	0.0423	0.999	1	5	regulation of odontogenesis	BP	1	ASPN	up_VPOR_EC

GO:0021545	0.0423	0.999	1	21	cranial nerve development	BP	1	HOXA3	up_VPUL_VSMC
GO:0003337	0.0423	0.999	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	SALL1	up_VSAP_VSMC
GO:0007155	0.0424	0.979	13	324	cell adhesion	BP	1	LEP,CDH18,HOXA7,DLL1,GPAM,GREM1,CYLD,POSTN,ICAM5,BVES,ADAM17,KANK1,TNC	up_AFEM_EC
GO:0050768	0.0424	0.985	7	66	negative regulation of neurogenesis	BP	1	BMPR1A,THY1,TLX2,GLI3,PRKCSH,THRB,RGMA	down_VCAV_EC
GO:0042481	0.0424	0.997	2	5	regulation of odontogenesis	BP	0.838	CD34,BMP2	up_VCAV_EC
GO:0046631	0.0424	0.999	1	35	alpha-beta T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0007416	0.0424	0.999	1	36	synapse assembly	BP	1	WNT7A	up_AORT_VSMC
GO:0016999	0.0424	0.999	1	30	antibiotic metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0030316	0.0424	0.999	1	31	osteoclast differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0048709	0.0424	0.999	1	17	oligodendrocyte differentiation	BP	1	TRPC4	up_VPOR_VSMC
GO:0086001	0.0424	0.999	1	9	cardiac muscle cell action potential	BP	1	CAV1	up_VSAP_VSMC
GO:0071772	0.042431914	0.99009	4	50	response to BMP	BP	1	SOX9,RGMA,SMAD6,LRP4	up_ACOR_EC
GO:0071773	0.042431914	0.99009	4	50	cellular response to BMP stimulus	BP	1	SOX9,RGMA,SMAD6,LRP4	up_ACOR_EC
GO:0002376	0.0425	0.97	48	622	immune system process	BP	0.874	ARHGEF2,VEGFA,MYH9,NR1H4,SERPINE1,ACTN1,SOCS5,ETV6,ENPP1,CASP3,FAM49B,PTPN11,FLNB,WDR1,MYO1C,MSN,HOXB7,KIF5B,HIF1A,CX3CL1,PTPN2,EIF2B1,EVI2B,PVR,ADAM17,SKAP2,CNOT7,CTNNB1,ANLN,TFRC,MMP28,LYN,BNIP3,CDC37,GBP5,MYO1E,SDC4,REST,PRMT1,SH2B3,GLO1,A2M,INHBA,BTK,SIX4,CDKN1A,TNFAIP1,DEFB124	down_VSAP_EC
GO:0051656	0.0425	0.979	13	129	establishment of organelle localization	BP	0.874	MYH9,SHROOM2,HOOK3,MYO1C,KIF5B,HIF1A,TRAK1,CTNNB1,KPNB1,LYN,GSK3B,HTT,AP3S1	down_VSAP_EC
GO:0042886	0.0425	0.987	6	527	amide transport	BP	1	LYN,PDPN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0031047	0.0425	0.999	1	33	gene silencing by RNA	BP	1	ESR1	up_AORT_VSMC
GO:0060914	0.0425	0.999	1	11	heart formation	BP	1	TBX5	up_APUL_EC
GO:0051058	0.0425	0.999	1	21	negative regulation of small GTPase mediated signal transduction	BP	1	SLIT2	up_VPUL_VSMC
GO:1901360	0.0426	0.987	8	2016	organic cyclic compound metabolic process	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,SRSF6,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0048634	0.0426	0.985	7	40	regulation of muscle organ development	BP	0.838	EPHB1,MEF2C,EDN1,BMP2,CREB1,NR1D2,CDON	up_VCAV_EC
GO:0090190	0.0426	0.994	3	10	positive regulation of branching involved in ureteric bud	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0051453	0.0426	0.993	3	33	regulation of intracellular pH	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:1905952	0.0426	0.993	3	33	regulation of lipid localization	BP	1	LEP,CRY2,ACACB	up_AFEM_EC
GO:0010869	0.0426	0.997	2	4	regulation of receptor biosynthetic process	BP	0.838	EDN1,HIF1A	up_VCAV_EC
GO:0032800	0.0426	0.997	2	4	receptor biosynthetic process	BP	0.838	EDN1,HIF1A	up_VCAV_EC
GO:0051482	0.0426	0.999	1	5	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-	BP	1	C3AR1	up_VPOR_EC
GO:0002063	0.0426	0.999	1	18	chondrocyte development	BP	1	SHOX2	up_VFEM_VSMC
GO:0061061	0.0427	0.977	17	179	muscle structure development	BP	0.874	PRICKLE1,ACTN1,FLNB,IFRD1,FHL2,WDR1,CTNNB1,CRYAB,KLF5,DDIT3,ATF3,NEXN,REST,HIF1AN,SIX4,MYBPC2,HOMER1	down_VSAP_EC
GO:0032870	0.0427	0.978	16	162	cellular response to hormone stimulus	BP	0.874	NR1H4,ENPP1,PTPN11,TRIB3,PRCP,SMARCA4,MYO1C,MSN,PTPN2,AGRN,GNAQ,UBA5,REST,NR4A1,YWHAH,KDM3A	down_VSAP_EC
GO:0035136	0.0427	0.993	3	16	forelimb morphogenesis	BP	1	RECK,RDH10,ZBTB16	down_VCAV_EC
GO:1904645	0.0427	0.996	2	7	response to amyloid-beta	BP	1	LRP1,PRNP	down_VCAV_EC

GO:0060348	0.0427	0.996	2	78	bone development	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0002279	0.0427	0.999	1	10	mast cell activation involved in immune	BP	1	LYN	down_ACOR_EC
GO:0002448	0.0427	0.999	1	10	mast cell mediated immunity	BP	1	LYN	down_ACOR_EC
GO:0043303	0.0427	0.999	1	10	mast cell degranulation	BP	1	LYN	down_ACOR_EC
GO:0006000	0.0427	0.999	1	5	fructose metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0042551	0.0427	0.999	1	10	neuron maturation	BP	1	IRX5	up_VSAP_VSMC
GO:0007399	0.0428	0.969	60	564	nervous system development	BP	0.841	EPHB1,EDNRB,PCDH12,PTCHD1,PRKCH,ARHGEF15,IFRD1,MALL,RELN,MEF2C,CHD7,DLL4,RAPGEF1,TLR4,EIF2B2,GATA3,HOXB8,RAB11A,TCF4,NTN4,PPP3CA,SERINC5,B3GNT5,MTOR,NAV2,HOOK3,BMP2,HMG20A,HHEX,PREX2,ENC1,GDPD5,PROX1,ENSCAFG00000010224,STMN1,MMP24,PAK2,APOD,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,BCL10,ZC4H2,TAOK1,CTNNA1,NUP133,SPTBN4,SKIL,HIF1A,ALS2,ATRX,ALDH1A3,LUZP1,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:1903708	0.0428	0.985	7	65	positive regulation of hemopoiesis	BP	1	CLSTN1,GLI3,ZFP36L1,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0018212	0.0428	0.988	5	81	peptidyl-tyrosine modification	BP	1	LEP,HCK,GREM1,TPST2,ADAM17	up_AFEM_EC
GO:0016322	0.0428	0.997	2	4	neuron remodeling	BP	1	RND1,APP	up_ACOR_VSMC
GO:1902902	0.0428	0.997	2	4	negative regulation of autophagosome assembly	BP	1	FEZ1,FEZ2	up_ACOR_VSMC
GO:0040007	0.0428	0.996	2	276	growth	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0032680	0.0428	0.999	1	36	regulation of tumor necrosis factor production	BP	1	ARG2	up_AORT_VSMC
GO:0046717	0.0428	0.999	1	17	acid secretion	BP	1	TRPC4	up_VPOR_VSMC
GO:1903530	0.0429	0.983	8	165	regulation of secretion by cell	BP	1	LEP,KCNC4,CRY2,GPAM,CHRM2,CAMK2A,RAB7A,CCL5	up_AFEM_EC
GO:0097553	0.0429	0.988	5	32	calcium ion transmembrane import	BP	0.874	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0048641	0.0429	0.991	4	16	regulation of skeletal muscle tissue	BP	0.842	EPHB1,MEF2C,NR1D2,CDON	up_VCAV_EC
GO:0045638	0.0429	0.993	3	33	negative regulation of myeloid cell	BP	1	HOXA9,HOXA7,DLL1	up_AFEM_EC
GO:0045683	0.0429	0.999	1	9	negative regulation of epidermis development	BP	1	HOXA7	down_ACOR_EC
GO:0071960	0.0429	1	1	1	maintenance of mitotic sister chromatid cohesion,	BP	0.874	NAA10	down_VSAP_EC
GO:1903570	0.0429	1	1	1	regulation of protein kinase D signaling	BP	0.874	VEGFA	down_VSAP_EC
GO:1903572	0.0429	1	1	1	positive regulation of protein kinase D signaling	BP	0.874	VEGFA	down_VSAP_EC
GO:2000718	0.0429	1	1	1	regulation of maintenance of mitotic sister chromatid cohesion, centromeric	BP	0.874	NAA10	down_VSAP_EC
GO:2000719	0.0429	1	1	1	negative regulation of maintenance of mitotic sister chromatid cohesion,	BP	0.874	NAA10	down_VSAP_EC
GO:0051250	0.0429	0.999	1	38	negative regulation of lymphocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0110020	0.0429	0.999	1	31	regulation of actomyosin structure organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0010759	0.0429	0.999	1	5	positive regulation of macrophage chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0032386	0.043	0.976	20	137	regulation of intracellular transport	BP	1	SH3TC2,ACTN2,LEP,TCAF1,FBXL20,FERMT1,BMP4,SEC24B,CDKN1A,PTPN22,OS9,SCP2,PSEN1,JUP,RAB11B,INPP5K,PREPL,PARK7,BVES,PTPN14	up_ACOR_VSMC
GO:0048844	0.043	0.987	6	30	artery morphogenesis	BP	0.842	ADGRF5,ADAMTS9,CHD7,DLL4,PROX1,JAG1	up_VCAV_EC
GO:0045947	0.043	0.997	2	6	negative regulation of translational initiation	BP	0.874	EIF4EBP1,EIF2S1	down_VSAP_EC
GO:0030038	0.043	0.999	1	31	contractile actin filament bundle assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0043149	0.043	0.999	1	31	stress fiber assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0021772	0.043	0.999	1	11	olfactory bulb development	BP	1	SALL1	up_VSAP_VSMC

GO:0021988	0.043	0.999	1	11	olfactory lobe development	BP	1	SALL1	up_VSAP_VSMC
GO:0030335	0.0431	0.99	4	165	positive regulation of cell migration	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0019395	0.0431	0.993	3	33	fatty acid oxidation	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC
GO:0047484	0.0431	0.997	2	5	regulation of response to osmotic stress	BP	0.874	ARHGEF2,PTGS2	down_VSAP_EC
GO:0018401	0.0431	0.997	2	4	peptidyl-proline hydroxylation to 4-	BP	1	EGLN1,P4HA1	up_ACOR_VSMC
GO:0001763	0.0431	0.996	2	78	morphogenesis of a branching structure	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:1901222	0.0431	0.999	1	32	regulation of NIK/NF-kappaB signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0034405	0.0431	0.999	1	11	response to fluid shear stress	BP	1	MTSS1	up_VFEM_EC
GO:0090185	0.0431	0.999	1	10	negative regulation of kidney development	BP	1	SIX1	up_VFEM_EC
GO:0060627	0.0432	0.983	8	165	regulation of vesicle-mediated transport	BP	1	RAB20,GAS1,DLL1,CHRM2,GREM1,CAMK2A,BVES,RAB7A	up_AFEM_EC
GO:0007045	0.0432	0.99	4	23	cell-substrate adherens junction assembly	BP	0.874	VEGFA,ACTN1,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0048041	0.0432	0.99	4	23	focal adhesion assembly	BP	0.874	VEGFA,ACTN1,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0072698	0.0432	0.993	3	13	protein localization to microtubule cytoskeleton	BP	0.874	HOOK3,GSK3B,MID1	down_VSAP_EC
GO:0051489	0.0432	0.993	3	14	regulation of filopodium assembly	BP	0.874	FSCN1,DPYSL3,NRP1	down_VSAP_EC
GO:1905331	0.0432	0.999	1	9	negative regulation of morphogenesis of an	BP	1	SULF1	down_ACOR_EC
GO:1901016	0.0432	0.999	1	9	regulation of potassium ion transmembrane transporter activity	BP	1	NEDD4	down_ACOR_EC
GO:1902106	0.0432	0.999	1	31	negative regulation of leukocyte differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0030878	0.0432	0.999	1	13	thyroid gland development	BP	1	HOXA3	up_VPUL_EC
GO:0048518	0.0433	0.982	12	1676	positive regulation of biological process	BP	1	HOXA11,HOXA9,NETO1,GATM,SALL1,MAB21L1,PRR16,STIM1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0045778	0.0433	0.985	7	35	positive regulation of ossification	BP	1	BMP4,GJA1,ISG15,CLSTN1,NPNT,DDR2,SLC8A1	up_ACOR_VSMC
GO:0003151	0.0433	0.985	7	34	outflow tract morphogenesis	BP	1	SMAD6,BMP4,FGFR2,SEC24B,CITED2,NRP1,TBX20	up_ACOR_VSMC
GO:0044786	0.0433	0.989	5	23	cell cycle DNA replication	BP	1	SMC1A,RAD51,GMNN,E2F8,SMC3	down_ACOR_VSMC
GO:0021795	0.0433	0.989	5	20	cerebral cortex cell migration	BP	1	FGF13,NRP1,PSEN1,DISC1,SUN1	up_ACOR_VSMC
GO:0051289	0.0433	0.988	5	25	protein homotetramerization	BP	0.847	GBP5,CDA,ACPP,KCNJ2,ALDH1A3	up_VCAV_EC
GO:0048598	0.0433	0.993	3	207	embryonic morphogenesis	BP	1	TBX5,HOXA3,HOXA1	up_APUL_EC
GO:0048846	0.0433	0.999	1	6	axon extension involved in axon guidance	BP	1	NRP2	down_ACOR_EC
GO:1902284	0.0433	0.999	1	6	neuron projection extension involved in neuron projection	BP	1	NRP2	down_ACOR_EC
GO:1904377	0.0433	0.999	1	21	positive regulation of protein localization to cell	BP	1	GPSM2	down_AFEM_EC
GO:0048469	0.0433	0.999	1	31	cell maturation	BP	1	IRX5	up_AFEM_VSMC
GO:0120163	0.0433	0.999	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_VFEM_VSMC
GO:0001817	0.0434	0.974	25	182	regulation of cytokine production	BP	1	WNT11,CD274,C5AR2,IL6R,ABL1,HDAC7,DLL1,IL17RC,ANXA4,HPSE,CCBE1,F2RL1,PIK3R1,SULF2,MYD88,NLRX1,TKFC,CD83,RNF216,MAPKBP1,ZNF580,CYBA,PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0043009	0.0434	0.981	10	227	chordate embryonic development	BP	1	TBX15,HOXA9,IRX5,XYLT1,HOXA7,DLL1,TMEM100,HOXA6,LUZP1,AXIN2	up_AFEM_EC
GO:0007159	0.0434	0.983	8	79	leukocyte cell-cell adhesion	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0030323	0.0434	0.985	7	65	respiratory tube development	BP	1	ADAMTS2,BMPR1A,LOX,GLI3,LOXL3,RDH10,THRB	down_VCAV_EC
GO:1905475	0.0434	0.986	6	52	regulation of protein localization to membrane	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,CDH2	down_VCAV_EC
GO:0071398	0.0434	0.991	4	14	cellular response to fatty acid	BP	1	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0060571	0.0434	0.993	3	13	morphogenesis of an epithelial fold	BP	0.874	SULF1,HIF1A,CTNNB1	down_VSAP_EC

GO:0035520	0.0434	0.997	2	4	monoubiquitinated protein deubiquitination	BP	1	USP1,BAP1	down_ACOR_VSMC
GO:0031953	0.0434	0.997	2	6	negative regulation of protein	BP	0.874	ENPP1,ERRFI1	down_VSAP_EC
GO:0003143	0.0434	0.999	1	22	embryonic heart tube morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0030307	0.0434	0.999	1	31	positive regulation of cell growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0045428	0.0434	0.999	1	10	regulation of nitric oxide biosynthetic process	BP	1	CAV1	up_VSAP_VSMC
GO:0061136	0.0435	0.982	9	78	regulation of proteasomal protein catabolic process	BP	0.874	PRICKLE1,PLK3,SOCS5,TRIB3,UCHL5,GSK3B,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0046631	0.0435	0.985	7	35	alpha-beta T cell activation	BP	1	CD274,ABL1,ZBTB16,STAT6,CD83,PNP,TGFBR2	up_VSAP_EC
GO:1901673	0.0435	0.994	3	10	regulation of mitotic spindle assembly	BP	1	SMC1A,SMC3,STAG1	down_ACOR_VSMC
GO:0010804	0.0435	0.997	2	6	negative regulation of tumor necrosis factor-mediated signaling	BP	0.874	NR1H4,PTPN2	down_VSAP_EC
GO:0034135	0.0435	0.997	2	4	regulation of toll-like receptor 2 signaling	BP	1	TLR1,F2RL1	up_ACOR_VSMC
GO:0030206	0.0435	0.999	1	9	chondroitin sulfate biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0003158	0.0435	0.999	1	38	endothelium development	BP	1	WNT7A	up_AORT_VSMC
GO:0051058	0.0435	0.999	1	21	negative regulation of small GTPase mediated signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0006950	0.0436	0.967	80	1102	response to stress	BP	0.874	ARHGEF2,VEGFA,P4HB,ASNS,PLOD2,NR1H4,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,SOCS5,HM13,SGK1,ERO1A,HSP90B1,CBX5,CASP3,ENSCAFG00000003477,HYOU1,PGK1,NUAK1,PTPN11,FLNB,COTL1,DPYSL3,LRRC8A,IFRD1,PRCP,SESN2,PTGS2,MYO1C,SEL1L,KIF5B,HIF1A,DNAJC10,TNIK,UBA6,PTPN2,PVR,DDX39B,ADAM17,PDIA4,CNOT7,DNAJB9,CTNNB1,CRYAB,APOE,KPNA4,UBA5,LYN,BNIP3,DDIT3,PDS5B,FAM162A,BACH1,SLC7A11,ATF3,GSK3B,CDC37,GTF2H1,ITGB3,GBP5,SDC4,REST,RBBP8,MAPK10,EIF2S1,RAD23A,PAK2,CREB3L2,A2M,HIF1AN,BTK,MSRB3,CDKN1A,TMTC3,SH3RF3,USP14,DEFB124,MID1	down_VSAP_EC
GO:0035051	0.0436	0.984	8	41	cardiocyte differentiation	BP	1	ACTN2,BMP4,CITED2,NEBL,TBX5,FRS2,EDN1,BVES	up_ACOR_VSMC
GO:1903037	0.0436	0.984	7	65	regulation of leukocyte cell-cell adhesion	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0060341	0.0436	0.99	4	255	regulation of cellular localization	BP	1	LYN,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0007162	0.0436	0.996	2	66	negative regulation of cell adhesion	BP	1	ACVRL1,HOXA7	down_ACOR_EC
GO:0046639	0.0436	0.996	2	7	negative regulation of alpha-beta T cell	BP	1	GLI3,LOXL3	down_VCAV_EC
GO:0022603	0.0436	1	1	301	regulation of anatomical structure morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:2001237	0.0436	0.999	1	33	negative regulation of extrinsic apoptotic	BP	1	EYA1	up_AFEM_VSMC
GO:1903555	0.0436	0.999	1	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	ARG2	up_AORT_VSMC
GO:0031669	0.0437	0.98	12	72	cellular response to nutrient levels	BP	1	PRKAA2,CASTOR1,CDKN2B,GABARAPL1,CDKN1A,SESN3,PIK3C3,LAMP2,SESN1,FAM107A,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0048518	0.0437	0.984	10	1676	positive regulation of biological process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,WIF1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043624	0.0437	0.985	7	39	cellular protein complex disassembly	BP	1	CAPG,LIMA1,STMN1,EIF5A,PDXP,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0032386	0.0437	0.984	7	137	regulation of intracellular transport	BP	1	LEP,GAS1,CRYAB,CHRM2,CAMK2A,REEP2,BVES	up_AFEM_EC
GO:0098900	0.0437	0.991	4	15	regulation of action potential	BP	1	FGF13,KCNE3,PTPN3,JUP	up_ACOR_VSMC
GO:0009968	0.0437	0.99	4	392	negative regulation of signal transduction	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0097028	0.0437	0.999	1	11	dendritic cell differentiation	BP	1	LYN	down_ACOR_EC

GO:0071495	0.0438	0.972	31	365	cellular response to endogenous stimulus	BP	0.874	ARHGEF2,SULF1,NR1H4,HSPA5,ENPP1,SNX25,PTPN11,TRIB3,ILK,PRCP,SMARCA4,SESN2,TGFBR1,MYO1C,MSN,ZPR1,PTPN2,YES1,NEO1,ADAM17,AGRN,GNAQ,CTNNB1,ENSCAFG00000002015,UBA5,STRAP,REST,NR4A1,ENSCAFG00000018360,YWHAH,KDM3A	down_VSAP_EC
GO:0048638	0.0438	0.987	5	82	regulation of developmental growth	BP	1	LEP,DLL1,PLXNA4,GPAM,ACACB	up_AFEM_EC
GO:0060627	0.0438	0.992	3	165	regulation of vesicle-mediated transport	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0095500	0.0438	0.997	2	6	acetylcholine receptor signaling pathway	BP	0.874	AGRN,GNAQ	down_VSAP_EC
GO:1903831	0.0438	0.997	2	6	signal transduction involved in cellular response to ammonium	BP	0.874	AGRN,GNAQ	down_VSAP_EC
GO:1905144	0.0438	0.997	2	6	response to acetylcholine	BP	0.874	AGRN,GNAQ	down_VSAP_EC
GO:1905145	0.0438	0.997	2	6	cellular response to acetylcholine	BP	0.874	AGRN,GNAQ	down_VSAP_EC
GO:0061008	0.0438	0.999	1	23	hepaticobiliary system development	BP	1	CITED2	down_VPOR_EC
GO:1901880	0.0438	0.999	1	19	negative regulation of protein depolymerization	BP	1	TAOK1	up_AORT_EC
GO:0045843	0.0438	0.999	1	13	negative regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0055024	0.0438	0.999	1	22	regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0048568	0.0439	0.975	21	148	embryonic organ development	BP	1	TBX15,HOXA11,HOXA7,WNT11,OSR2,INSIG2,GJB5,LRIG3,IRX5,HOXD3,DLL1,HOXA6,OSR1,RARG,HOXC4,ZFP36L1,ZEB1,SHOX2,KDM2B,TGFBR2,CITED2	up_VSAP_EC
GO:0006950	0.0439	0.982	10	1102	response to stress	BP	1	ACVRL1,LYN,IGF1R,PDPN,USP28,IPO7,ATRIP,ELK3,STX4,NEDD4	down_ACOR_EC
GO:0009411	0.0439	0.982	9	56	response to UV	BP	1	USP1,NEDD4,AURKB,PCNA,NOC2L,POLH,DTL,CDC25A,HMGN1	down_ACOR_VSMC
GO:0002718	0.0439	0.988	5	21	regulation of cytokine production involved in	BP	1	TLR3,F2RL1,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:1900015	0.0439	0.991	4	17	regulation of cytokine production involved in inflammatory response	BP	0.855	GBP5,TLR4,APOD,NOS2	up_VCAV_EC
GO:0060560	0.0439	0.996	2	58	developmental growth involved in	BP	1	SPG11,NRP2	down_ACOR_EC
GO:2001198	0.0439	0.997	2	4	regulation of dendritic cell differentiation	BP	1	TMEM176B,TMEM176A	up_ACOR_VSMC
GO:0044070	0.0439	0.999	1	22	regulation of anion transport	BP	1	RAB11B	down_VPOR_EC
GO:0060021	0.0439	0.999	1	34	roof of mouth development	BP	1	WNT7A	up_AORT_VSMC
GO:0048738	0.0439	0.999	1	64	cardiac muscle tissue development	BP	1	TBX5	up_APUL_VSMC
GO:0021604	0.0439	0.999	1	6	cranial nerve structural organization	BP	1	SEMA3A	up_VPOR_EC
GO:0021612	0.0439	0.999	1	6	facial nerve structural organization	BP	1	SEMA3A	up_VPOR_EC
GO:1905209	0.0439	0.999	1	13	positive regulation of cardiocyte differentiation	BP	1	TBX5	up_VPUL_EC
GO:0006816	0.044	0.979	12	84	calcium ion transport	BP	0.856	CALCRL,PDGFB,ATP2B1,PDE4D,CHD7,STC1,APLNR,PPP3CA,SLC25A25,PLCG2,MCU,ATP2A1	up_VCAV_EC
GO:0009607	0.044	0.992	3	232	response to biotic stimulus	BP	1	NR1H4,RGS1,MRC1	up_VPUL_EC
GO:0070563	0.044	1	1	1	negative regulation of vitamin D receptor	BP	1	KANK2	down_VCAV_EC
GO:0072594	0.044	1	1	155	establishment of protein localization to organelle	BP	1	JUP	down_VFEM_VSMC
GO:0090257	0.044	0.999	1	52	regulation of muscle system process	BP	1	GATA5	down_VSAP_VSMC
GO:0055081	0.044	0.999	1	17	anion homeostasis	BP	1	HOXA3	up_VPOR_VSMC
GO:1905207	0.044	0.999	1	17	regulation of cardiocyte differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032720	0.044	0.999	1	13	negative regulation of tumor necrosis factor	BP	1	NR1H4	up_VPUL_EC
GO:0050710	0.044	0.999	1	13	negative regulation of cytokine secretion	BP	1	NR1H4	up_VPUL_EC
GO:0014855	0.044	0.999	1	22	striated muscle cell proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0060419	0.044	0.999	1	22	heart growth	BP	1	TBX5	up_VPUL_VSMC

GO:2000416	0.044026705	0.99951	1	2	regulation of eosinophil migration	BP	1	PTGER4	up_ACOR_EC
GO:0001952	0.0441	0.988	5	34	regulation of cell-matrix adhesion	BP	0.874	VEGFA,SERPINE1,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:0016601	0.0441	0.999	1	11	Rac protein signal transduction	BP	1	TIAM1	up_VFEM_EC
GO:0065007	0.0442	0.98	23	3499	biological regulation	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,PDPN,NRP2,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,IPO7,ATRIP,SULF1,ELK3,HOXA1,ACSL3,WDR12,STX4,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0005975	0.0442	0.976	17	183	carbohydrate metabolic process	BP	0.874	ENSCAFG00000009211,ENPP1,PGK1,TPI1,ENSCAFG00000032470,PGAM1,SESN2,HIF1A,SLC45A3,PTPN2,MOGS,ALDOC,PPP1R3C,ATF3,GSK3B,GALE,EXT1	down_VSAP_EC
GO:0032755	0.0442	0.988	5	24	positive regulation of interleukin-6 production	BP	0.86	TLR4,MAPK13,TLR3,HMGB1,ARHGEF2	up_VCAV_EC
GO:0018196	0.0442	0.991	4	15	peptidyl-asparagine modification	BP	1	ST3GAL5,MAGT1,STT3B,FUT8	up_ACOR_VSMC
GO:0007399	0.0442	0.99	4	564	nervous system development	BP	1	HOXC10,EYA1,EMX2,SHOX2	up_VFEM_VSMC
GO:0021564	0.0442	1	1	2	vagus nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0032231	0.0442	0.999	1	32	regulation of actin filament bundle assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0044381	0.0442	0.999	1	13	glucose import in response to insulin	BP	1	NR1H4	up_VPUL_EC
GO:0044091	0.0442	0.999	1	10	membrane biogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:1903725	0.044243365	0.99231	3	30	regulation of phospholipid metabolic process	BP	1	NR1H4,ENSCAFG00000004331,PRKCD	up_ACOR_EC
GO:0071496	0.0443	0.977	15	97	cellular response to external stimulus	BP	1	PRKAA2,CASTOR1,TLR3,CDKN2B,ANKRD1,GABARAPL1,BNIP3,CDKN1A,SESN3,PIK3C3,LAMP2,SESN1,FAM107A,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0043062	0.0443	0.98	11	99	extracellular structure organization	BP	0.874	SULF1,SERPINH1,ERO1A,P4HA1,FSCN1,APOE,PLOD3,MYO1E,SDC4,P3H4,COL12A1	down_VSAP_EC
GO:0060412	0.0443	0.991	4	15	ventricular septum morphogenesis	BP	1	BMP4,FGFR2,CITED2,EGLN1	up_ACOR_VSMC
GO:0010828	0.0443	0.993	3	16	positive regulation of glucose transmembrane	BP	1	CLIP3,ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0060322	0.0443	0.992	3	193	head development	BP	1	PITX1,EMX2,SALL1	up_VSAP_VSMC
GO:0051155	0.0443	0.999	1	18	positive regulation of striated muscle cell	BP	1	SHOX2	up_VFEM_VSMC
GO:0048592	0.0444	0.986	6	53	eye morphogenesis	BP	1	FBN1,NAGLU,THY1,GLI3,IRX5,THRB	down_VCAV_EC
GO:0042221	0.0444	0.992	4	1012	response to chemical	BP	1	SLITRK5,CYP1A1,GATA5,CA2	up_VCAV_VSMC
GO:0045932	0.0444	0.994	3	8	negative regulation of muscle contraction	BP	1	KCNE3,PDE5A,DOCK5	up_ACOR_VSMC
GO:0071359	0.0444	0.993	3	11	cellular response to dsRNA	BP	0.861	TMEM173,RALB,RIOK3	up_VCAV_EC
GO:0097435	0.0444	0.992	3	230	supramolecular fiber organization	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0060973	0.0444	0.996	2	7	cell migration involved in heart development	BP	1	PDGFRB,SEMA3C	down_VCAV_EC
GO:0006575	0.0444	0.999	1	53	cellular modified amino acid metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC
GO:0017145	0.0444	0.999	1	13	stem cell division	BP	1	ARHGEF2	up_VPUL_EC

GO:0009058	0.0445	0.964	178	1910	biosynthetic process	BP	1	ELK3,SCD,ACSL3,PRPSAP1,SQLE,HMGB1,MCM6,LSS,SREBF1,ACLY,MCM4,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,RRM1,MED17,POLA1,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,SF1,POLA2,MPDU1,SRRT,GINS4,CTDNEP1,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,RAD51,XYLT1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,CDK4,SMARCC1,PLK3,PCNA,DHX33,HOXA7,TONSL,ARG2,MCM10,UHRF1,CKS2,TKT,GMNN,DHCR24,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,ELOVL1,FARSA,PPARD,CDC6,POLH,YBX3,NCL,NUP62,UGDH,MRPL37,DTL,VAC14,FOSL1,SUV39H1,AADAT,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,FDFT1,RBM14,CYC1,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,ATP5F1A,PUM3,CDC45,MAST2,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,GRWD1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HO	down_ACOR_VSMC
GO:0048878	0.0445	0.971	36	283	chemical homeostasis	BP	1	ADRA1B,PLCG2,LEP,SLC26A7,HTR2B,PRKAA2,LCAT,CNNM2,ABCA1,GJA1,PTPN3,MICU2,ITPR1,F2RL1,ERO1B,EGLN1,DMPK,ATP7A,ORMDL3,SESN3,PRKCE,APP,PSEN1,CHD7,DMXL1,RAB11B,EDN1,B2M,DISC1,HERPUD1,INPP5K,WFS1,ATP2C1,PARK7,SLC8A1,STC2	up_ACOR_VSMC
GO:0055085	0.0445	0.973	24	284	transmembrane transport	BP	0.874	SLC39A7,NR1H4,TRAM1,ERO1A,ENPP1,PTPN11,LRRC8A,SLC38A1,TRIB3,SESN2,SRP54,REM1,WDR1,NDUFA4L2,YES1,SRP72,LYN,DDIT3,SLC2A3,CLCN3,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0072358	0.0445	0.975	20	268	cardiovascular system development	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,BMPR1A,LOX,RECK,ANPEP,SEMA3C,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,CDH2,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC
GO:1902105	0.0445	0.983	8	80	regulation of leukocyte differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0061549	0.0445	0.997	2	5	sympathetic ganglion development	BP	0.874	CTNNB1,NRP1	down_VSAP_EC
GO:0003159	0.0445	0.999	1	9	morphogenesis of an endothelium	BP	1	ACVRL1	down_ACOR_EC
GO:0061154	0.0445	0.999	1	9	endothelial tube morphogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0007354	0.0445	1	1	1	zygotic determination of anterior/posterior axis,	BP	1	PCSK6	down_VCAV_EC
GO:0032898	0.0445	1	1	1	neurotrophin production	BP	1	PCSK6	down_VCAV_EC
GO:0032902	0.0445	1	1	1	nerve growth factor production	BP	1	PCSK6	down_VCAV_EC
GO:0050923	0.0445	0.999	1	2	regulation of negative chemotaxis	BP	1	PLXNA4	up_AFEM_EC
GO:0071674	0.0445	0.999	1	23	mononuclear cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:1902186	0.044539597	0.99576	2	13	regulation of viral release from host cell	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0048736	0.0446	0.984	7	66	appendage development	BP	1	BMPR1A,RECK,SEMA3C,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0060173	0.0446	0.984	7	66	limb development	BP	1	BMPR1A,RECK,SEMA3C,GLI3,RDH10,GREM1,ZBTB16	down_VCAV_EC
GO:0071542	0.0446	0.996	2	6	dopaminergic neuron differentiation	BP	0.874	HIF1A,CTNNB1	down_VSAP_EC
GO:0051138	0.0446	0.997	2	4	positive regulation of NK T cell differentiation	BP	1	ZBTB16,TGFBR2	up_VSAP_EC
GO:1900078	0.0446	0.999	1	13	positive regulation of cellular response to	BP	1	NR1H4	up_VPUL_EC
GO:0043009	0.0447	0.972	27	227	chordate embryonic development	BP	1	EIF4A3,HINFP,HOXA3,GINS4,PRMT1,XYLT1,MMP14,SLC30A1,NEK2,RNASEH2B,HOXA7,HOXB7,BRCA1,E2F8,FOSL1,PLK4,HOXC6,SMARCB1,HOXB5,RBBP8,NOLC1,PHACTR4,TBX15,HOXA9,EMG1,RTCB,SIX4	down_ACOR_VSMC
GO:0048583	0.0447	0.987	6	1095	regulation of response to stimulus	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0006084	0.0447	0.99	4	15	acetyl-CoA metabolic process	BP	1	ACACB,PDK2,ACSS2,MVK	up_VSAP_EC

GO:1902236	0.0447	0.993	3	9	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0042551	0.0447	0.993	3	10	neuron maturation	BP	0.867	EDNRB,NTN4,SPTBN4	up_VCAV_EC
GO:0006811	0.0447	0.993	3	330	ion transport	BP	1	HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0009150	0.0447	0.996	2	161	purine ribonucleotide metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0050804	0.0447	0.995	2	87	modulation of chemical synaptic transmission	BP	1	PLCL1,NTRK2	up_APUL_EC
GO:0099177	0.0447	0.995	2	87	regulation of trans-synaptic signaling	BP	1	PLCL1,NTRK2	up_APUL_EC
GO:0061515	0.0447	0.999	1	24	myeloid cell development	BP	1	CITED2	down_VPOR_EC
GO:0001974	0.0447	0.999	1	13	blood vessel remodeling	BP	1	HOXA3	up_VPUL_EC
GO:0035282	0.044760611	0.99219	3	30	segmentation	BP	1	FZD5,FOXC2,NRP1	up_ACOR_EC
GO:0016477	0.0448	0.976	16	426	cell migration	BP	1	CMKLR1,ANGPT4,HOXA7,TWIST2,HCK,GREM1,CAMK2A,LRRC15,RECK,TBXA2R,BVES,LGR6,CCL5,FAP,ADAM17,KANK1	up_AFEM_EC
GO:0043368	0.0448	0.993	3	9	positive T cell selection	BP	0.867	IL6,MTOR,ITPKB	up_VCAV_EC
GO:0048011	0.0448	0.996	2	7	neurotrophin TRK receptor signaling	BP	1	NDN,AKT1S1	down_VCAV_EC
GO:0030194	0.0448	0.999	1	9	positive regulation of blood coagulation	BP	1	PDPN	down_ACOR_EC
GO:1900048	0.0448	0.999	1	9	positive regulation of hemostasis	BP	1	PDPN	down_ACOR_EC
GO:2000377	0.0448	0.999	1	41	regulation of reactive oxygen species metabolic	BP	1	ARG2	up_AORT_VSMC
GO:0030324	0.0448	0.999	1	64	lung development	BP	1	TBX5	up_APUL_VSMC
GO:0061550	0.0448	0.999	1	6	cranial ganglion development	BP	1	SEMA3A	up_VPOR_EC
GO:0007019	0.0448	0.999	1	13	microtubule depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0045214	0.0448	0.999	1	13	sarcomere organization	BP	1	MYBPC2	up_VPUL_EC
GO:0030003	0.0449	0.974	22	157	cellular cation homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,DMXL1,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0002376	0.0449	0.986	6	622	immune system process	BP	1	HOXA9,TOX,HOXB7,HOXA7,SIX1,CYP26B1	up_VFEM_EC
GO:0034097	0.0449	0.987	5	238	response to cytokine	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ENSCAFG00000032731,GNPNAT1	up_VPOR_EC
GO:0031100	0.0449	0.997	2	4	animal organ regeneration	BP	1	EZH2,GLI1	down_ACOR_VSMC
GO:0035774	0.0449	0.996	2	6	positive regulation of insulin secretion involved in cellular response to	BP	0.874	NR1H4,HIF1A	down_VSAP_EC
GO:0048588	0.0449	0.995	2	44	developmental cell growth	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0009247	0.0449	0.999	1	22	glycolipid biosynthetic process	BP	1	GBGT1	down_VPOR_EC
GO:0002028	0.0449	0.999	1	19	regulation of sodium ion transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:0055006	0.0449	0.999	1	18	cardiac cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:1900180	0.044922604	0.98932	4	50	regulation of protein localization to nucleus	BP	1	TRIM8,DCLK2,MAVS,PRKCD	up_ACOR_EC
GO:0016053	0.045	0.977	15	97	organic acid biosynthetic process	BP	1	ACSM3,LIPC,INSIG2,ACACB,GOT1,GLUL,ENSCAFG00000013986,HSD17B8,GALK1,PTGES,HACD4,ENSCAFG00000016140,DHRS9,ASS1,DDIT4	up_VSAP_EC
GO:0046394	0.045	0.977	15	97	carboxylic acid biosynthetic process	BP	1	ACSM3,LIPC,INSIG2,ACACB,GOT1,GLUL,ENSCAFG00000013986,HSD17B8,GALK1,PTGES,HACD4,ENSCAFG00000016140,DHRS9,ASS1,DDIT4	up_VSAP_EC
GO:0001906	0.045	0.99	4	20	cell killing	BP	0.867	IL7R,LYZ,RAB27A,NECTIN2	up_VCAV_EC
GO:0033628	0.045	0.993	3	14	regulation of cell adhesion mediated by integrin	BP	0.874	SERPINE1,PTPN11,LYN	down_VSAP_EC
GO:0043031	0.045	0.997	2	4	negative regulation of macrophage activation	BP	0.867	ADGRF5,CD200	up_VCAV_EC
GO:2000647	0.045	0.997	2	4	negative regulation of stem cell proliferation	BP	0.867	FERMT1,CTNNA1	up_VCAV_EC

GO:2000241	0.045	0.999	1	40	regulation of reproductive process	BP	1	ESR1	up_AORT_VSMC
GO:0003229	0.045	0.999	1	17	ventricular cardiac muscle tissue development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0072132	0.045	0.999	1	23	mesenchyme morphogenesis	BP	1	GATA5	up_VPUL_VSMC
GO:0050727	0.04505981	0.98699	5	74	regulation of inflammatory response	BP	1	NR1H4,FNDC4,NOD2,IL33,PTGER4	up_ACOR_EC
GO:2000725	0.0451	0.993	3	10	regulation of cardiac muscle cell differentiation	BP	0.867	MEF2C,EDN1,BMP2	up_VCAV_EC
GO:0046653	0.0451	0.997	2	5	tetrahydrofolate metabolic process	BP	0.867	PIPOX,GCH1	up_VCAV_EC
GO:2000649	0.0451	0.999	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	NEDD4	down_ACOR_EC
GO:1903531	0.0451	0.999	1	41	negative regulation of secretion by cell	BP	1	ARG2	up_AORT_VSMC
GO:0001754	0.0451	0.999	1	12	eye photoreceptor cell differentiation	BP	1	NTRK2	up_APUL_EC
GO:0006959	0.0452	0.988	5	21	humoral immune response	BP	1	PLA2G6,TFE3,CFD,CD83,JCHAIN	up_VSAP_EC
GO:0045087	0.0452	0.992	3	161	innate immune response	BP	1	LYN,IPO7,STX4	down_ACOR_EC
GO:1903115	0.0452	0.999	1	12	regulation of actin filament-based movement	BP	1	PDPN	down_ACOR_EC
GO:0038061	0.0452	0.999	1	34	NIK/NF-kappaB signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0042461	0.0452	0.999	1	12	photoreceptor cell development	BP	1	NTRK2	up_APUL_EC
GO:0051155	0.0452	0.999	1	18	positive regulation of striated muscle cell	BP	1	CYP26B1	up_VPOR_VSMC
GO:0021846	0.0452	0.999	1	11	cell proliferation in forebrain	BP	1	EMX2	up_VSAP_VSMC
GO:0051962	0.0453	0.979	12	112	positive regulation of nervous system	BP	0.874	ARHGEF2,DPYSL3,HIF1A,CTNNB1,APOE,LYN,MMD,VLDLR,REST,DISC1,LRRTM2,NRP1	down_VSAP_EC
GO:2001258	0.0453	0.993	3	11	negative regulation of cation channel activity	BP	1	CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0002757	0.0453	0.995	2	78	immune response-activating signal	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0061298	0.0453	0.999	1	8	retina vasculature development in camera-	BP	1	ACVRL1	down_ACOR_EC
GO:1901098	0.0453	1	1	1	positive regulation of autophagosome	BP	1	CLEC16A	down_VCAV_EC
GO:1904766	0.0453	1	1	1	negative regulation of macroautophagy by TORC1 signaling	BP	1	CLEC16A	down_VCAV_EC
GO:0072673	0.0454	0.999	1	8	lamellipodium morphogenesis	BP	1	PDPN	down_ACOR_EC
GO:0009887	0.0454	1	1	314	animal organ morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0043030	0.0454	0.999	1	12	regulation of macrophage activation	BP	1	BPI	up_APUL_EC
GO:0010721	0.045447501	0.98685	5	73	negative regulation of cell development	BP	1	SOX9,DIXDC1,RGMA,LRP4,NRP1	up_ACOR_EC
GO:0061138	0.04547428	0.98684	5	73	morphogenesis of a branching epithelium	BP	1	SOX9,FZD5,FOXC2,CLSTN1,NRP1	up_ACOR_EC
GO:0014033	0.045490839	0.99201	3	30	neural crest cell differentiation	BP	1	SOX9,FOXC2,NRP1	up_ACOR_EC
GO:0032409	0.045493626	0.98912	4	52	regulation of transporter activity	BP	1	ACTN2,MAPK8IP2,PRKCD,PM20D1	up_ACOR_EC
GO:0045859	0.0455	0.974	20	219	regulation of protein kinase activity	BP	0.874	VEGFA,SOCS5,ERRFI1,PTPN11,TRIB3,SESN2,TNIK,PTPN2,ADAM17,MAGED1,APOE,LYN,CCNYL1,MMD,CBLC,VLDLR,HTT,PAK2,CDKN1A,MADD	down_VSAP_EC
GO:1902041	0.0455	0.99	4	23	regulation of extrinsic apoptotic signaling pathway via death	BP	0.874	ARHGEF2,SERPINE1,ATF3,MADD	down_VSAP_EC
GO:1900272	0.0455	0.997	2	4	negative regulation of long-term synaptic	BP	1	APP,FAM107A	up_ACOR_VSMC
GO:0007565	0.0455	0.999	1	23	female pregnancy	BP	1	CITED2	down_VPOR_EC
GO:0030323	0.0455	0.999	1	65	respiratory tube development	BP	1	TBX5	up_APUL_VSMC
GO:0048736	0.0455	0.999	1	66	appendage development	BP	1	TBX5	up_APUL_VSMC
GO:0060173	0.0455	0.999	1	66	limb development	BP	1	TBX5	up_APUL_VSMC
GO:0006216	0.0455	1	1	1	cytidine catabolic process	BP	0.871	CDA	up_VCAV_EC

GO:0009972	0.0455	1	1	1	cytidine deamination	BP	0.871	CDA	up_VCAV_EC
GO:0046087	0.0455	1	1	1	cytidine metabolic process	BP	0.871	CDA	up_VCAV_EC
GO:0051961	0.045581227	0.98681	5	73	negative regulation of nervous system	BP	1	SOX9,DIXDC1,RGMA,LRP4,NRP1	up_ACOR_EC
GO:0006468	0.0456	0.97	36	544	protein phosphorylation	BP	1	NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,GLIPR2,BGN,BMPR1A,CLIP3,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,ASPN,THY1,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,CAMK2D,SPRED1,MAPRE3,CDKL2,DDR2,SHC1,FBH1,GREM1,BRSK1,CDK14	down_VCAV_EC
GO:0031098	0.0456	0.977	15	109	stress-activated protein kinase signaling cascade	BP	0.873	EPHB1,MAP3K11,STK10,SH2D3C,TLR4,EDN1,MAP3K3,BMP2,SLK,MAPK13,PAK2,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0019222	0.0456	0.992	5	1934	regulation of metabolic process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0071470	0.0456	0.993	3	13	cellular response to osmotic stress	BP	0.874	ARHGEF2,CASP3,PTGS2	down_VSAP_EC
GO:1900078	0.0456	0.993	3	13	positive regulation of cellular response to	BP	0.874	NR1H4,PTPN11,MYO1C	down_VSAP_EC
GO:0061025	0.0456	0.995	2	69	membrane fusion	BP	1	SPG11,STX4	down_ACOR_EC
GO:1901722	0.0456	0.997	2	5	regulation of cell proliferation involved in	BP	0.873	PDGFB,GATA3	up_VCAV_EC
GO:0010573	0.0456	0.999	1	9	vascular endothelial growth factor production	BP	1	SULF1	down_ACOR_EC
GO:0010574	0.0456	0.999	1	9	regulation of vascular endothelial growth factor	BP	1	SULF1	down_ACOR_EC
GO:0015734	0.0456	0.999	1	2	taurine transport	BP	1	SLC6A6	up_AFEM_EC
GO:0031999	0.0456	0.999	1	2	negative regulation of fatty acid beta-oxidation	BP	1	ACACB	up_AFEM_EC
GO:0070091	0.0456	0.999	1	2	glucagon secretion	BP	1	LEP	up_AFEM_EC
GO:0070092	0.0456	0.999	1	2	regulation of glucagon secretion	BP	1	LEP	up_AFEM_EC
GO:1902744	0.0456	0.999	1	2	negative regulation of lamellipodium	BP	1	KANK1	up_AFEM_EC
GO:0030534	0.0456	0.999	1	33	adult behavior	BP	1	SLITRK5	up_VCAV_VSMC
GO:0051262	0.0457	0.984	7	40	protein tetramerization	BP	1	HMGCR,RRM1,TK1,RCC1,FARSA,CTH,PDSS1	down_ACOR_VSMC
GO:0031960	0.0457	0.99	4	15	response to corticosteroid	BP	1	CREBRF,NR3C1,FAM107A,DDIT4	up_ACOR_VSMC
GO:0051384	0.0457	0.99	4	15	response to glucocorticoid	BP	1	CREBRF,NR3C1,FAM107A,DDIT4	up_ACOR_VSMC
GO:0072160	0.0457	0.993	3	9	nephron tubule epithelial cell differentiation	BP	0.874	MEF2C,GATA3,MTSS1	up_VCAV_EC
GO:0045602	0.0457	0.997	2	4	negative regulation of endothelial cell	BP	1	ZEB1,ACVRL1	up_VSAP_EC
GO:0021784	0.0457	0.999	1	2	postganglionic parasympathetic fiber	BP	1	PLXNA4	up_AFEM_EC
GO:0061643	0.0457	0.999	1	2	chemorepulsion of axon	BP	1	PLXNA4	up_AFEM_EC
GO:0003205	0.0457	0.999	1	67	cardiac chamber development	BP	1	TBX5	up_APUL_VSMC
GO:0043069	0.045745039	0.97814	12	262	negative regulation of programmed cell death	BP	1	NR1H4,SOX9,AQP1,IFI6,SMAD6,BCL2,MAPK8IP2,FOXC2,FIGNL1,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0030073	0.0458	0.983	8	42	insulin secretion	BP	1	HNF4A,SLC8B1,RAB11B,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0006733	0.0458	0.985	6	45	oxidoreduction coenzyme metabolic process	BP	0.874	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:2000026	0.0458	0.99	4	560	regulation of multicellular organismal development	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051984	0.0458	0.993	3	10	positive regulation of chromosome segregation	BP	1	FEN1,CDC6,SMC6	down_ACOR_VSMC
GO:0045893	0.0458	0.996	2	413	positive regulation of transcription, DNA-	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0006543	0.0458	1	1	1	glutamine catabolic process	BP	1	GLS2	down_VCAV_EC
GO:0042478	0.0458	0.999	1	2	regulation of eye photoreceptor cell	BP	1	THRB	up_AFEM_EC
GO:0045741	0.0458	0.999	1	2	positive regulation of epidermal growth factor-activated receptor activity	BP	1	ADAM17	up_AFEM_EC
GO:0006749	0.0458	0.999	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	up_VPUL_EC

GO:1902235	0.0459	0.99	4	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	SERINC3,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0043534	0.0459	0.989	4	57	blood vessel endothelial cell migration	BP	1	ANGPT4,GREM1,TBXA2R,ADAM17	up_AFEM_EC
GO:0035239	0.0459	0.996	2	299	tube morphogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0061548	0.0459	0.999	1	8	ganglion development	BP	1	NRP2	down_ACOR_EC
GO:0014012	0.0459	0.999	1	2	peripheral nervous system axon regeneration	BP	1	TNC	up_AFEM_EC
GO:1990051	0.0459	0.999	1	2	activation of protein kinase C activity	BP	1	LEP	up_AFEM_EC
GO:0032640	0.0459	0.999	1	39	tumor necrosis factor production	BP	1	ARG2	up_AORT_VSMC
GO:0031644	0.0459	0.999	1	19	regulation of neurological system process	BP	1	NETO1	up_VFEM_VSMC
GO:0022029	0.0459	0.999	1	23	telencephalon cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0010737	0.045981809	0.99555	2	13	protein kinase A signaling	BP	1	PDE4A,PRKACA	up_ACOR_EC
GO:0031396	0.046	0.977	14	90	regulation of protein ubiquitination	BP	1	SKP2,SH3RF2,ISG15,SASH1,PTPN22,PRKCE,PSEN1,NOD2,FAM107A,DCUN1D4,HERPUD1,WFS1,WDR48,PARK7	up_ACOR_VSMC
GO:0030641	0.046	0.992	3	34	regulation of cellular pH	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0061448	0.046	0.995	2	89	connective tissue development	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0003203	0.046	0.999	1	11	endocardial cushion morphogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0072078	0.046	0.999	1	33	nephron tubule morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0001708	0.046	0.999	1	20	cell fate specification	BP	1	HOXC10	up_AORT_EC
GO:0055023	0.046	0.999	1	12	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_EC
GO:2001273	0.046	0.999	1	12	regulation of glucose import in response to	BP	1	NR1H4	up_APUL_EC
GO:0001766	0.046	1	1	1	membrane raft polarization	BP	0.877	MALL	up_VCAV_EC
GO:0031580	0.046	1	1	1	membrane raft distribution	BP	0.877	MALL	up_VCAV_EC
GO:0010960	0.046	0.999	1	6	magnesium ion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0051926	0.046	0.999	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0042417	0.0461	0.993	3	9	dopamine metabolic process	BP	1	MAOA,MOXD1,PARK7	up_ACOR_VSMC
GO:0090101	0.0461	0.992	3	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	GREM1,GREM2,ADAM17	up_AFEM_EC
GO:0034377	0.0461	0.996	2	7	plasma lipoprotein particle assembly	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0065005	0.0461	0.996	2	7	protein-lipid complex assembly	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0001525	0.0461	0.995	2	173	angiogenesis	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:2000483	0.0461	0.997	2	4	negative regulation of interleukin-8 secretion	BP	1	ANXA4,MAPKBP1	up_VSAP_EC
GO:0043570	0.0461	0.999	1	2	maintenance of DNA repeat elements	BP	1	AXIN2	up_AFEM_EC
GO:0018345	0.0461	0.999	1	12	protein palmitoylation	BP	1	ZDHHC16	up_APUL_EC
GO:0051453	0.0461	0.999	1	33	regulation of intracellular pH	BP	1	CA2	up_VCAV_VSMC
GO:0001709	0.0461	0.999	1	11	cell fate determination	BP	1	CYP26B1	up_VFEM_EC
GO:0035493	0.0461	0.999	1	11	SNARE complex assembly	BP	1	TRIM9	up_VFEM_EC
GO:0070098	0.0461	0.999	1	14	chemokine-mediated signaling pathway	BP	1	CCL24	up_VPUL_EC
GO:0033137	0.0461	0.999	1	10	negative regulation of peptidyl-serine	BP	1	CAV1	up_VSAP_VSMC
GO:0032651	0.046101946	0.99553	2	13	regulation of interleukin-1 beta production	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0001654	0.0462	0.985	6	110	eye development	BP	1	IRX5,COL8A2,DLL1,CRYAB,MAB21L1,THRB	up_AFEM_EC
GO:0150063	0.0462	0.985	6	110	visual system development	BP	1	IRX5,COL8A2,DLL1,CRYAB,MAB21L1,THRB	up_AFEM_EC

GO:0048880	0.0462	0.985	6	110	sensory system development	BP	1	IRX5,COL8A2,DLL1,CRYAB,MAB21L1,THRB	up_AFEM_EC
GO:1901016	0.0462	0.993	3	9	regulation of potassium ion transmembrane transporter activity	BP	1	ACTN2,KCNE3,AKAP6	up_ACOR_VSMC
GO:1902680	0.0462	0.996	2	415	positive regulation of RNA biosynthetic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:1903508	0.0462	0.996	2	415	positive regulation of nucleic acid-templated	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:1901097	0.0462	0.999	1	2	negative regulation of autophagosome	BP	1	CLEC16A	up_AFEM_EC
GO:0051606	0.0462	0.999	1	33	detection of stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0035115	0.0462	0.999	1	12	embryonic forelimb morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0010092	0.0462	0.999	1	19	specification of animal organ identity	BP	1	HOXA11	up_VFEM_VSMC
GO:1990266	0.0462	0.999	1	24	neutrophil migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0040011	0.046238292	0.97364	20	505	locomotion	BP	1	SOX9,AQP1,ENSCAFG00000004331,SEMA6D,DIXDC1,ZMYND8,PAK3,MMP28,TRIM8,PTGER4,ARHGDIB,ELMO2,FOXC2,LRRC15,TBX5,CHMP4B,RARRES2,NRP1,PRKCD,CCNYL1	up_ACOR_EC
GO:0055074	0.0463	0.977	13	95	calcium ion homeostasis	BP	0.88	ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,PDZD8,SWAP70,PLCG2,HMGB1,MCU,ATP2A1	up_VCAV_EC
GO:0016070	0.0463	1	2	1479	RNA metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0090102	0.0463	0.999	1	10	cochlea development	BP	1	HOXA1	down_ACOR_EC
GO:0001787	0.0463	0.999	1	2	natural killer cell proliferation	BP	1	LEP	up_AFEM_EC
GO:0003151	0.0463	0.999	1	34	outflow tract morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0045638	0.0463	0.999	1	33	negative regulation of myeloid cell	BP	1	HOXA9	up_AFEM_VSMC
GO:0051048	0.0463	0.999	1	42	negative regulation of secretion	BP	1	ARG2	up_AORT_VSMC
GO:0086003	0.0463	0.999	1	10	cardiac muscle cell contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0051480	0.0464	0.982	8	50	regulation of cytosolic calcium ion concentration	BP	0.881	PDE4D,CHD7,GPR4,EDN1,APLNR,SWAP70,PLCG2,HMGB1	up_VCAV_EC
GO:0035116	0.0464	0.99	4	15	embryonic hindlimb morphogenesis	BP	1	OSR2,OSR1,ZBTB16,RARG	up_VSAP_EC
GO:0014902	0.0464	0.999	1	34	myotube differentiation	BP	1	BEND2	up_AFEM_VSMC
GO:0042471	0.0464	0.999	1	34	ear morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0002831	0.0464	0.999	1	42	regulation of response to biotic stimulus	BP	1	ARG2	up_AORT_VSMC
GO:0097479	0.0464	0.999	1	41	synaptic vesicle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0061178	0.0464	0.999	1	12	regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_APUL_EC
GO:1903321	0.0464	0.999	1	33	negative regulation of protein modification by small protein conjugation	BP	1	LIMK1	up_VCAV_VSMC
GO:0050650	0.0464	0.999	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	CHST7	up_VFEM_EC
GO:0060713	0.0464	0.999	1	10	labyrinthine layer morphogenesis	BP	1	GJB5	up_VSAP_VSMC
GO:0071804	0.046453521	0.99176	3	31	cellular potassium ion transport	BP	1	KCNB1,ACTN2,SLC9A9	up_ACOR_EC
GO:0071805	0.046453521	0.99176	3	31	potassium ion transmembrane transport	BP	1	KCNB1,ACTN2,SLC9A9	up_ACOR_EC
GO:0022607	0.0465	0.988	5	969	cellular component assembly	BP	1	GPSM2,EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:0044249	0.0465	0.994	4	1851	cellular biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:1990000	0.0465	0.996	2	6	amyloid fibril formation	BP	0.874	CRYAB,APOE	down_VSAP_EC
GO:0032099	0.0465	0.999	1	2	negative regulation of appetite	BP	1	LEP	up_AFEM_EC
GO:0038108	0.0465	0.999	1	2	negative regulation of appetite by leptin-mediated signaling	BP	1	LEP	up_AFEM_EC
GO:0060242	0.0465	0.999	1	2	contact inhibition	BP	1	FAP	up_AFEM_EC

GO:0032095	0.0465	0.999	1	2	regulation of response to food	BP	1	LEP	up_AFEM_EC
GO:0032096	0.0465	0.999	1	2	negative regulation of response to food	BP	1	LEP	up_AFEM_EC
GO:0032098	0.0465	0.999	1	2	regulation of appetite	BP	1	LEP	up_AFEM_EC
GO:1904684	0.0465	0.999	1	2	negative regulation of metalloendopeptidase	BP	1	RECK	up_AFEM_EC
GO:1905049	0.0465	0.999	1	2	negative regulation of metallopeptidase activity	BP	1	RECK	up_AFEM_EC
GO:0045638	0.0465	0.999	1	33	negative regulation of myeloid cell	BP	1	LRRC17	up_VCAV_VSMC
GO:0006096	0.0465	0.999	1	18	glycolytic process	BP	1	FBP1	up_VFEM_VSMC
GO:0006165	0.0465	0.999	1	18	nucleoside diphosphate phosphorylation	BP	1	FBP1	up_VFEM_VSMC
GO:0006757	0.0465	0.999	1	18	ATP generation from ADP	BP	1	FBP1	up_VFEM_VSMC
GO:0042866	0.0465	0.999	1	18	pyruvate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0050710	0.046568864	0.99546	2	13	negative regulation of cytokine secretion	BP	1	NR1H4,PTGER4	up_ACOR_EC
GO:0002286	0.0466	0.987	5	24	T cell activation involved in immune response	BP	0.881	IL6,GATA3,RAB27A,MTOR,HMGB1	up_VCAV_EC
GO:2000147	0.0466	0.989	4	169	positive regulation of cell motility	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0010971	0.0466	0.993	3	10	positive regulation of G2/M transition of mitotic	BP	1	CDK1,CDK4,DTL	down_ACOR_VSMC
GO:0007269	0.0466	0.992	3	34	neurotransmitter secretion	BP	1	KCNC4,CHRM2,CAMK2A	up_AFEM_EC
GO:0099643	0.0466	0.992	3	34	signal release from synapse	BP	1	KCNC4,CHRM2,CAMK2A	up_AFEM_EC
GO:0000083	0.0466	0.996	2	6	regulation of transcription involved in G1/S transition of mitotic cell	BP	0.874	ZPR1,BACH1	down_VSAP_EC
GO:0010990	0.0466	0.997	2	4	regulation of SMAD protein complex assembly	BP	1	SMAD6,TBX20	up_ACOR_VSMC
GO:0010991	0.0466	0.997	2	4	negative regulation of SMAD protein complex	BP	1	SMAD6,TBX20	up_ACOR_VSMC
GO:1901858	0.0466	0.999	1	2	regulation of mitochondrial DNA	BP	1	PPARGC1A	up_AFEM_EC
GO:0032675	0.0466	0.999	1	34	regulation of interleukin-6 production	BP	1	TLR2	up_AFEM_VSMC
GO:0032024	0.0466	0.999	1	12	positive regulation of insulin secretion	BP	1	NR1H4	up_APUL_EC
GO:0090277	0.0466	0.999	1	12	positive regulation of peptide hormone	BP	1	NR1H4	up_APUL_EC
GO:0048048	0.046674953	0.99544	2	13	embryonic eye morphogenesis	BP	1	FZD5,EFEMP1	up_ACOR_EC
GO:0000079	0.0467	0.987	5	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	0.881	TNFAIP3,PDGFB,HHEX,PROX1,BLM	up_VCAV_EC
GO:0031952	0.0467	0.992	3	15	regulation of protein autophosphorylation	BP	0.874	VEGFA,ENPP1,ERRFI1	down_VSAP_EC
GO:0008284	0.0467	0.992	3	238	positive regulation of cell proliferation	BP	1	TBX5,HOXA3,CCL24	up_VPUL_EC
GO:0001501	0.0467	0.995	2	178	skeletal system development	BP	1	CITED2,TBX15	down_VPOR_EC
GO:1900409	0.0467	0.997	2	4	positive regulation of cellular response to	BP	0.881	TLR4,RIPK1	up_VCAV_EC
GO:1902884	0.0467	0.997	2	4	positive regulation of response to oxidative	BP	0.881	TLR4,RIPK1	up_VCAV_EC
GO:1903209	0.0467	0.997	2	4	positive regulation of oxidative stress-induced	BP	0.881	TLR4,RIPK1	up_VCAV_EC
GO:0045664	0.0467	0.995	2	144	regulation of neuron differentiation	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0070235	0.0467	0.999	1	2	regulation of activation-induced cell death of T	BP	1	GPAM	up_AFEM_EC
GO:0070236	0.0467	0.999	1	2	negative regulation of activation-induced cell	BP	1	GPAM	up_AFEM_EC
GO:1903265	0.0467	0.999	1	2	positive regulation of tumor necrosis factor-mediated signaling	BP	1	ADAM17	up_AFEM_EC
GO:0043901	0.0467	0.999	1	44	negative regulation of multi-organism process	BP	1	ARG2	up_AORT_VSMC
GO:0071706	0.0467	0.999	1	40	tumor necrosis factor superfamily cytokine	BP	1	ARG2	up_AORT_VSMC
GO:0048645	0.0467	0.999	1	33	animal organ formation	BP	1	GATA5	up_VCAV_VSMC

GO:0021517	0.0467	0.999	1	12	ventral spinal cord development	BP	1	HOXC10	up_VFEM_EC
GO:0042327	0.0468	0.969	37	289	positive regulation of phosphorylation	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,AR,SASH1,LMO4,FGF18,F2RL1,FAM129A,NRP1,PTPN22,NPNT,PRKCE,CCNT1,FRS2,PARP9,APP,PSEN1,CCL5,DDR2,DUSP22,EDN1,AKTIP,NOD2,SH3RF3,MAP3K7,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0050868	0.0468	0.985	6	28	negative regulation of T cell activation	BP	1	BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0044271	0.0468	1	2	1501	cellular nitrogen compound biosynthetic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0070365	0.0468	0.996	2	5	hepatocyte differentiation	BP	0.881	HHEX,PROX1	up_VCAV_EC
GO:0097325	0.0468	0.999	1	2	melanocyte proliferation	BP	1	FAP	up_AFEM_EC
GO:1990108	0.0468	0.999	1	2	protein linear deubiquitination	BP	1	CYLD	up_AFEM_EC
GO:0032571	0.0468	0.999	1	2	response to vitamin K	BP	1	POSTN	up_AFEM_EC
GO:0035581	0.0468	0.999	1	2	sequestering of extracellular ligand from	BP	1	GREM2	up_AFEM_EC
GO:0060844	0.0468	0.999	1	2	arterial endothelial cell fate commitment	BP	1	DLL1	up_AFEM_EC
GO:0060846	0.0468	0.999	1	2	blood vessel endothelial cell fate commitment	BP	1	DLL1	up_AFEM_EC
GO:0060847	0.0468	0.999	1	2	endothelial cell fate specification	BP	1	DLL1	up_AFEM_EC
GO:0097101	0.0468	0.999	1	2	blood vessel endothelial cell fate specification	BP	1	DLL1	up_AFEM_EC
GO:1900115	0.0468	0.999	1	2	extracellular regulation of signal transduction	BP	1	GREM2	up_AFEM_EC
GO:1900116	0.0468	0.999	1	2	extracellular negative regulation of signal	BP	1	GREM2	up_AFEM_EC
GO:1903054	0.0468	0.999	1	2	negative regulation of extracellular matrix	BP	1	FAP	up_AFEM_EC
GO:0008593	0.0468	0.999	1	33	regulation of Notch signaling pathway	BP	1	GATA5	up_VCAV_VSMC
GO:0048513	0.0469	0.963	101	906	animal organ development	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,PCDH19,HOXA9,SEZ6L,CDON,WNT11,HNF4A,AXIN2,OSR2,INSIG2,PPARGC1B,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,IL6R,IRX5,SLIT2,CRIP2,HOXD3,SLC6A4,FGF7,ABL1,EBF2,DLL1,HOXA6,OSR1,SAV1,KLF15,HPSE,PLXNA4,ANKRD54,CLDN1,ZBTB16,TOX,RARG,CCBE1,STAT6,HOXC4,PATZ1,GTF3C5,F2RL1,DLX3,GLIS2,DDR2,MFN2,ZFP36L1,PIK3R1,TIAM1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,SULF2,SHOX2,EEF2,RTN4RL1,HOXC10,LOX,TFE3,LRP4,DPYSL2,GDPD5,CLCN2,E2F4,SMG9,MCPH1,KIF27,FBXO7,NTN4,CD83,KDM2B,ZFP36L2,RAF1,PNP,NFIB,ZFAND5,QARS,ACVRL1,HTRA2,FLOT1,PPP3CB,BGLAP,MAP2K2,TGFBR2,NPRL3,CITED2,TRADD,PIR,LBH,LATS2	up_VSAP_EC
GO:0014020	0.0469	0.982	8	41	primary neural tube formation	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0003231	0.0469	0.982	8	48	cardiac ventricle development	BP	0.881	MEF2C,CHD7,DLL4,GATA3,PROX1,JAG1,HIF1A,LUZP1	up_VCAV_EC
GO:0006584	0.0469	0.993	3	11	catecholamine metabolic process	BP	0.881	GATA3,SNCAIP,GCH1	up_VCAV_EC
GO:0009712	0.0469	0.993	3	11	catechol-containing compound metabolic	BP	0.881	GATA3,SNCAIP,GCH1	up_VCAV_EC
GO:0003012	0.0469	0.995	2	90	muscle system process	BP	1	HTR7,NPNT	up_APUL_EC
GO:0001957	0.0469	0.999	1	2	intramembranous ossification	BP	1	AXIN2	up_AFEM_EC
GO:0032423	0.0469	0.999	1	2	regulation of mismatch repair	BP	1	AXIN2	up_AFEM_EC
GO:0036072	0.0469	0.999	1	2	direct ossification	BP	1	AXIN2	up_AFEM_EC
GO:0090208	0.0469	0.999	1	6	positive regulation of triglyceride metabolic	BP	1	ABHD5	up_VPOR_EC
GO:0060359	0.047	0.992	3	14	response to ammonium ion	BP	0.874	AGRN,GNAQ,HOMER1	down_VSAP_EC
GO:0002688	0.047	0.992	3	34	regulation of leukocyte chemotaxis	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:0022603	0.047	0.996	2	301	regulation of anatomical structure morphogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC

GO:0051494	0.047	0.995	2	44	negative regulation of cytoskeleton organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0021561	0.047	0.999	1	8	facial nerve development	BP	1	NRP2	down_ACOR_EC
GO:0021610	0.047	0.999	1	8	facial nerve morphogenesis	BP	1	NRP2	down_ACOR_EC
GO:0021692	0.047	0.999	1	2	cerebellar Purkinje cell layer morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:0042711	0.047	0.999	1	2	maternal behavior	BP	1	AVPR1A	up_AFEM_EC
GO:0060746	0.047	0.999	1	2	parental behavior	BP	1	AVPR1A	up_AFEM_EC
GO:1903556	0.047	0.999	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4	up_VPUL_EC
GO:0086004	0.047	0.999	1	10	regulation of cardiac muscle cell contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0050728	0.047031036	0.99161	3	31	negative regulation of inflammatory response	BP	1	NR1H4,FNDC4,PTGER4	up_ACOR_EC
GO:0033559	0.0471	0.987	5	21	unsaturated fatty acid metabolic process	BP	1	PTGES,DAGLB,ABHD16A,HPGD,ENSCAFG00000023820	up_VSAP_EC
GO:0010573	0.0471	0.993	3	9	vascular endothelial growth factor production	BP	1	HPSE,CCBE1,SULF2	up_VSAP_EC
GO:0010574	0.0471	0.993	3	9	regulation of vascular endothelial growth factor	BP	1	HPSE,CCBE1,SULF2	up_VSAP_EC
GO:0071560	0.0471	0.995	2	72	cellular response to transforming growth	BP	1	ACVRL1,ASPN	down_ACOR_EC
GO:0032402	0.0471	0.996	2	5	melanosome transport	BP	0.881	RAB11A,RAB27A	up_VCAV_EC
GO:0051904	0.0471	0.996	2	5	pigment granule transport	BP	0.881	RAB11A,RAB27A	up_VCAV_EC
GO:0036022	0.0471	0.997	2	4	limb joint morphogenesis	BP	1	OSR2,OSR1	up_VSAP_EC
GO:0002764	0.0471	0.995	2	80	immune response-regulating signaling	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0000380	0.0471	0.999	1	22	alternative mRNA splicing, via spliceosome	BP	1	SRSF6	down_AFEM_EC
GO:0044771	0.0471	0.999	1	2	meiotic cell cycle phase transition	BP	1	OVOL1	up_AFEM_EC
GO:1901993	0.0471	0.999	1	2	regulation of meiotic cell cycle phase transition	BP	1	OVOL1	up_AFEM_EC
GO:1901994	0.0471	0.999	1	2	negative regulation of meiotic cell cycle phase	BP	1	OVOL1	up_AFEM_EC
GO:2001171	0.0471	0.999	1	2	positive regulation of ATP biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0021679	0.0471	0.999	1	2	cerebellar molecular layer development	BP	1	DLL1	up_AFEM_EC
GO:0021687	0.0471	0.999	1	2	cerebellar molecular layer morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:0045607	0.0471	0.999	1	2	regulation of inner ear auditory receptor cell	BP	1	DLL1	up_AFEM_EC
GO:0045631	0.0471	0.999	1	2	regulation of mechanoreceptor	BP	1	DLL1	up_AFEM_EC
GO:0061181	0.0471	0.999	1	2	regulation of chondrocyte development	BP	1	AXIN2	up_AFEM_EC
GO:2000980	0.0471	0.999	1	2	regulation of inner ear receptor cell	BP	1	DLL1	up_AFEM_EC
GO:0002028	0.0471	0.999	1	19	regulation of sodium ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0034142	0.0471	0.999	1	14	toll-like receptor 4 signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0060706	0.0471	0.999	1	11	cell differentiation involved in embryonic	BP	1	GJB5	up_VSAP_VSMC
GO:0040012	0.0472	0.971	26	303	regulation of locomotion	BP	0.874	ARHGEF2,VEGFA,SULF1,HSPA5,SERPINE1,SPARC,JCAD,DPYSL3,PRCP,MYO1C,PIK3C2A,MSN,HIF1A,PTPN2,ADAM17,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,NEXN,SDC4,ZMYND8,NRP1,USP14	down_VSAP_EC
GO:0032652	0.0472	0.989	4	18	regulation of interleukin-1 production	BP	0.881	TNFAIP3,TLR4,ARG2,HMGB1	up_VCAV_EC
GO:0060687	0.0472	0.997	2	4	regulation of branching involved in prostate gland	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0046823	0.0472	0.996	2	6	negative regulation of nucleocytoplasmic	BP	0.881	FERMT1,APOD	up_VCAV_EC
GO:0006083	0.0472	1	1	1	acetate metabolic process	BP	1	ACSS2	down_VCAV_EC
GO:0019427	0.0472	1	1	1	acetyl-CoA biosynthetic process from acetate	BP	1	ACSS2	down_VCAV_EC
GO:0006477	0.0472	0.999	1	2	protein sulfation	BP	1	TPST2	up_AFEM_EC

GO:0010663	0.0472	0.999	1	2	positive regulation of striated muscle cell	BP	1	CAMK2A	up_AFEM_EC
GO:0010666	0.0472	0.999	1	2	positive regulation of cardiac muscle cell	BP	1	CAMK2A	up_AFEM_EC
GO:0042415	0.0472	0.999	1	2	norepinephrine metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0042421	0.0472	0.999	1	2	norepinephrine biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0046813	0.0472	0.999	1	2	receptor-mediated virion attachment to host cell	BP	1	LRRC15	up_AFEM_EC
GO:1905907	0.0472	0.999	1	2	negative regulation of amyloid fibril formation	BP	1	CRYAB	up_AFEM_EC
GO:0048645	0.0472	0.999	1	33	animal organ formation	BP	1	EYA1	up_AFEM_VSMC
GO:0099173	0.0472	0.999	1	40	postsynapse organization	BP	1	WNT7A	up_AORT_VSMC
GO:0055083	0.0472	0.999	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0003230	0.0472	0.999	1	14	cardiac atrium development	BP	1	TBX5	up_VPUL_EC
GO:0003209	0.0472	0.999	1	14	cardiac atrium morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:1901862	0.0472	0.999	1	14	negative regulation of muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:1903052	0.047291178	0.98856	4	51	positive regulation of proteolysis involved in cellular protein catabolic	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0007167	0.0473	0.989	4	274	enzyme linked receptor protein signaling pathway	BP	1	ACVRL1,LYN,SULF1,ASPN	down_ACOR_EC
GO:0030182	0.0473	0.989	4	327	neuron differentiation	BP	1	EMX2,HOXC10,IRX5,SHOX2	up_VSAP_VSMC
GO:0006954	0.0473	0.995	2	147	inflammatory response	BP	1	CYP26B1,C3AR1	up_VPOR_VSMC
GO:0007197	0.0473	0.999	1	2	adenylate cyclase-inhibiting G protein-coupled acetylcholine	BP	1	CHRM2	up_AFEM_EC
GO:0007207	0.0473	0.999	1	2	phospholipase C-activating G protein-coupled acetylcholine	BP	1	CHRM2	up_AFEM_EC
GO:0042670	0.0473	0.999	1	2	retinal cone cell differentiation	BP	1	THRB	up_AFEM_EC
GO:0046549	0.0473	0.999	1	2	retinal cone cell development	BP	1	THRB	up_AFEM_EC
GO:0072014	0.0473	0.999	1	2	proximal tubule development	BP	1	DLL1	up_AFEM_EC
GO:0072086	0.0473	0.999	1	2	specification of loop of Henle identity	BP	1	IRX3	up_AFEM_EC
GO:0030879	0.0473	0.999	1	34	mammary gland development	BP	1	HOXA9	up_AFEM_VSMC
GO:0048635	0.0473	0.999	1	14	negative regulation of muscle organ	BP	1	TBX5	up_VPUL_EC
GO:2000826	0.0473	0.999	1	14	regulation of heart morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0050778	0.0474	0.973	20	141	positive regulation of immune response	BP	1	TLR1,PLCG2,COCH,TP53BP1,ELF1,TLR3,CD274,F2RL1,C1S,PTPN22,C7,PRKCE,PARP9,PSEN1,DUSP22,NOD2,B2M,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0003012	0.0474	0.976	14	90	muscle system process	BP	1	TNNT2,ADRA1B,ACTN2,KCNE3,GATA5,HTR2B,PDE5A,DMPK,NPNT,TBX20,JUP,EDN1,GAA,DOCK5	up_ACOR_VSMC
GO:0006941	0.0474	0.983	7	36	striated muscle contraction	BP	1	TNNT2,ADRA1B,KCNE3,PDE5A,DMPK,JUP,GAA	up_ACOR_VSMC
GO:0006081	0.0474	0.989	4	27	cellular aldehyde metabolic process	BP	1	H6PD,PGLS,PARK7,RDH10	down_VCAV_EC
GO:0003416	0.0474	0.993	3	9	endochondral bone growth	BP	1	RARG,DDR2,TGFBR2	up_VSAP_EC
GO:0048596	0.0474	0.993	3	9	embryonic camera-type eye morphogenesis	BP	1	ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:0009259	0.0474	0.995	2	166	ribonucleotide metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:1990535	0.0474	0.997	2	4	neuron projection maintenance	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0015732	0.0474	0.997	2	4	prostaglandin transport	BP	0.883	SLCO3A1,NOS2	up_VCAV_EC
GO:0001764	0.0474	0.995	2	45	neuron migration	BP	1	ARHGEF2,SEMA3A	up_VPOR_EC
GO:0030035	0.0474	0.997	2	4	microspike assembly	BP	1	ABL1,FGD4	up_VSAP_EC
GO:0045088	0.0474	0.995	2	81	regulation of innate immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC

GO:1990009	0.0474	0.999	1	2	retinal cell apoptotic process	BP	1	THRB	up_AFEM_EC
GO:0042098	0.0474	0.999	1	43	T cell proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0036438	0.047470776	0.99943	1	2	maintenance of lens transparency	BP	1	CHMP4B	up_ACOR_EC
GO:0048869	0.0475	0.969	35	1119	cellular developmental process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXC10,LEP,LBH,GAS1,HOXA7,DLL1,VXN,PLXNA4,NEFH,TWIST2,THRB,LGI4,HCK,TMEM100,GREM1,NFE2L1,CAMK2A,CYLD,MYBL1,PTHLH,EVI2B,BVES,AXIN2,NAPEPLD,PPARGC1A,CDC42EP5,DMPK,LRRN2,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0034101	0.0475	0.985	6	45	erythrocyte homeostasis	BP	0.874	CASP3,HIF1A,PTPN2,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0051272	0.0475	0.988	4	170	positive regulation of cellular component	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0030516	0.0475	0.99	4	15	regulation of axon extension	BP	1	ABL1,PLXNA4,DPYSL2,TTL	up_VSAP_EC
GO:0002366	0.0475	0.995	2	65	leukocyte activation involved in immune	BP	1	LYN,STX4	down_ACOR_EC
GO:0043094	0.0475	0.996	2	7	cellular metabolic compound salvage	BP	1	ADK,AMPD2	down_VCAV_EC
GO:0007155	0.0475	1	1	324	cell adhesion	BP	1	GATA5	down_AFEM_VSMC
GO:0060926	0.0475	0.999	1	2	cardiac pacemaker cell development	BP	1	BVES	up_AFEM_EC
GO:0060920	0.0475	0.999	1	2	cardiac pacemaker cell differentiation	BP	1	BVES	up_AFEM_EC
GO:0021517	0.0475	0.999	1	12	ventral spinal cord development	BP	1	HOXC10	up_VSAP_VSMC
GO:1905475	0.047504543	0.98848	4	52	regulation of protein localization to membrane	BP	1	KCNB1,PLS1,LRRC15,LRP4	up_ACOR_EC
GO:0030154	0.0476	0.991	4	1040	cell differentiation	BP	1	SLITRK5,LIMK1,GATA5,LRRC17	up_VCAV_VSMC
GO:0002684	0.0476	0.992	3	239	positive regulation of immune system process	BP	1	NR1H4,EVI2B,CCL24	up_VPUL_EC
GO:0045988	0.0476	0.997	2	4	negative regulation of striated muscle	BP	1	KCNE3,PDE5A	up_ACOR_VSMC
GO:0006935	0.0476	0.995	2	143	chemotaxis	BP	1	CHL1,C3AR1	up_VPOR_VSMC
GO:0042330	0.0476	0.995	2	143	taxis	BP	1	CHL1,C3AR1	up_VPOR_VSMC
GO:1903827	0.0476	0.999	1	164	regulation of cellular protein localization	BP	1	JUP	down_VFEM_VSMC
GO:0045777	0.0476	0.999	1	2	positive regulation of blood pressure	BP	1	TBXA2R	up_AFEM_EC
GO:0030641	0.0476	0.999	1	34	regulation of cellular pH	BP	1	CA2	up_VCAV_VSMC
GO:1990138	0.0476	0.999	1	35	neuron projection extension	BP	1	LIMK1	up_VCAV_VSMC
GO:0055117	0.0476	0.999	1	21	regulation of cardiac muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048333	0.0476	0.999	1	12	mesodermal cell differentiation	BP	1	EYA1	up_VFEM_EC
GO:0008585	0.0476	0.999	1	24	female gonad development	BP	1	SLIT2	up_VPUL_VSMC
GO:0046545	0.0476	0.999	1	24	development of primary female sexual	BP	1	SLIT2	up_VPUL_VSMC
GO:0009593	0.0476	0.999	1	11	detection of chemical stimulus	BP	1	TLR2	up_VSAP_VSMC
GO:0010466	0.047635885	0.99144	3	32	negative regulation of peptidase activity	BP	1	PCSK1N,IFI6,CST3	up_ACOR_EC
GO:0010951	0.047635885	0.99144	3	32	negative regulation of endopeptidase activity	BP	1	PCSK1N,IFI6,CST3	up_ACOR_EC
GO:0046635	0.0477	0.99	4	15	positive regulation of alpha-beta T cell	BP	1	ZBTB16,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0010453	0.0477	0.993	3	9	regulation of cell fate commitment	BP	1	BMP4,FGFR2,LMO4	up_ACOR_VSMC
GO:0002483	0.0477	0.997	2	4	antigen processing and presentation of endogenous peptide	BP	1	B2M,ERAP1	up_ACOR_VSMC
GO:0019885	0.0477	0.997	2	4	antigen processing and presentation of endogenous peptide	BP	1	B2M,ERAP1	up_ACOR_VSMC
GO:0090196	0.0477	0.997	2	4	regulation of chemokine secretion	BP	1	MBP,F2RL1	up_ACOR_VSMC
GO:0098810	0.0477	0.997	2	4	neurotransmitter reuptake	BP	1	CLN8,PARK7	up_ACOR_VSMC
GO:0051181	0.0477	0.999	1	11	cofactor transport	BP	1	PDPN	down_ACOR_EC

GO:0010042	0.0477	0.999	1	2	response to manganese ion	BP	1	FIBIN	up_AFEM_EC
GO:0086036	0.0477	0.999	1	2	regulation of cardiac muscle cell membrane	BP	1	FXYD1	up_AFEM_EC
GO:1903542	0.0477	0.999	1	2	negative regulation of exosomal secretion	BP	1	RAB7A	up_AFEM_EC
GO:0009409	0.0477	0.999	1	13	response to cold	BP	1	PCSK1N	up_APUL_EC
GO:0007020	0.0477	0.999	1	6	microtubule nucleation	BP	1	MZT1	up_VPOR_EC
GO:0021885	0.0477	0.999	1	24	forebrain cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0048333	0.0477	0.999	1	12	mesodermal cell differentiation	BP	1	HOXA11	up_VSAP_VSMC
GO:1901861	0.0478	0.983	7	41	regulation of muscle tissue development	BP	0.884	EPHB1,MEF2C,EDN1,BMP2,CREB1,NR1D2,CDON	up_VCAV_EC
GO:0010977	0.0478	0.986	5	33	negative regulation of neuron projection	BP	0.874	DPYSL3,IFRD1,APOE,NRP1,YWHAH	down_VSAP_EC
GO:1901135	0.0478	0.992	3	390	carbohydrate derivative metabolic process	BP	1	EXTL2,SUCLG2,NDUFA10	down_AFEM_EC
GO:0033363	0.0478	0.993	3	10	secretory granule organization	BP	0.884	NECTIN2,ABCA1,CREB1	up_VCAV_EC
GO:0048863	0.0478	0.995	2	70	stem cell differentiation	BP	1	NRP2,HOXA7	down_ACOR_EC
GO:0010657	0.0478	0.995	2	15	muscle cell apoptotic process	BP	1	CAMK2A,DMPK	up_AFEM_EC
GO:1900744	0.0478	0.995	2	15	regulation of p38MAPK cascade	BP	1	LEP,CYLD	up_AFEM_EC
GO:1901725	0.0478	0.997	2	4	regulation of histone deacetylase activity	BP	0.884	PRKD2,KDM5A	up_VCAV_EC
GO:0010862	0.0478	0.999	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	ACVRL1	down_ACOR_EC
GO:0022610	0.0478	1	1	326	biological adhesion	BP	1	GATA5	down_AFEM_VSMC
GO:0043242	0.0478	0.999	1	21	negative regulation of protein complex	BP	1	TAOK1	up_AORT_EC
GO:0060038	0.0478	0.999	1	18	cardiac muscle cell proliferation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0045844	0.0478	0.999	1	24	positive regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0048636	0.0478	0.999	1	24	positive regulation of muscle organ	BP	1	TBX5	up_VPUL_VSMC
GO:0009792	0.0479	0.979	10	231	embryo development ending in birth or egg	BP	1	TBX15,HOXA9,IRX5,XYLT1,HOXA7,DLL1,TMEM100,HOXA6,LUZP1,AXIN2	up_AFEM_EC
GO:0050920	0.0479	0.981	8	53	regulation of chemotaxis	BP	0.884	CXCL8,CXCR4,PDGFB,MMP28,ANGPT2,PRKD2,SWAP70,HMGB1	up_VCAV_EC
GO:0010647	0.0479	0.987	5	460	positive regulation of cell communication	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0070306	0.0479	0.992	3	11	lens fiber cell differentiation	BP	0.884	TMOD1,PROX1,SKIL	up_VCAV_EC
GO:0045655	0.0479	0.993	3	9	regulation of monocyte differentiation	BP	1	HOXA7,ZFP36L1,MYC	up_VSAP_EC
GO:0051650	0.0479	0.995	2	65	establishment of vesicle localization	BP	1	SPG11,STX4	down_ACOR_EC
GO:2000027	0.0479	0.995	2	72	regulation of animal organ morphogenesis	BP	1	SULF1,ASPN	down_ACOR_EC
GO:0070601	0.0479	0.996	2	6	centromeric sister chromatid cohesion	BP	0.874	NAA10,CTNNB1	down_VSAP_EC
GO:0030857	0.0479	0.995	2	15	negative regulation of epithelial cell	BP	1	HOXA7,DLL1	up_AFEM_EC
GO:0034104	0.0479	0.999	1	2	negative regulation of tissue remodeling	BP	1	GREM1	up_AFEM_EC
GO:0048813	0.0479	0.999	1	39	dendrite morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0099504	0.0479	0.999	1	42	synaptic vesicle cycle	BP	1	WNT7A	up_AORT_VSMC
GO:0016242	0.0479	0.999	1	13	negative regulation of macroautophagy	BP	1	LZTS1	up_APUL_EC
GO:0060043	0.0479	0.999	1	14	regulation of cardiac muscle cell proliferation	BP	1	TBX5	up_VPUL_EC
GO:0046689	0.047916513	0.99942	1	2	response to mercury ion	BP	1	AQP1	up_ACOR_EC
GO:0009798	0.047945215	0.99138	3	31	axis specification	BP	1	FZD5,SMAD6,LRP4	up_ACOR_EC
GO:0055080	0.048	0.971	24	176	cation homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,CNNM2,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,DMXL1,EDN1,B2M,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC

GO:0050731	0.048	0.984	6	44	positive regulation of peptidyl-tyrosine	BP	0.874	ARHGEF2,VEGFA,YES1,ADAM17,LYN,NRP1	down_VSAP_EC
GO:0044264	0.048	0.986	5	32	cellular polysaccharide metabolic process	BP	0.874	ENPP1,ENSCAFG00000032470,PPP1R3C,GSK3B,EXT1	down_VSAP_EC
GO:0060421	0.048	0.99	4	14	positive regulation of heart growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0051043	0.048	0.996	2	7	regulation of membrane protein ectodomain	BP	1	TIMP2,PACSIN3	down_VCAV_EC
GO:0009713	0.048	0.996	2	5	catechol-containing compound biosynthetic	BP	0.884	GATA3,GCH1	up_VCAV_EC
GO:0042423	0.048	0.996	2	5	catecholamine biosynthetic process	BP	0.884	GATA3,GCH1	up_VCAV_EC
GO:1900154	0.048	0.999	1	2	regulation of bone trabecula formation	BP	1	GREM1	up_AFEM_EC
GO:1900155	0.048	0.999	1	2	negative regulation of bone trabecula formation	BP	1	GREM1	up_AFEM_EC
GO:0001656	0.048	0.999	1	35	metanephros development	BP	1	EYA1	up_AFEM_VSMC
GO:0002224	0.048	0.999	1	34	toll-like receptor signaling pathway	BP	1	TLR2	up_AFEM_VSMC
GO:0060612	0.048	0.999	1	14	adipose tissue development	BP	1	NR1H4	up_VPUL_EC
GO:0003208	0.048	0.999	1	24	cardiac ventricle morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0050702	0.048009948	0.99524	2	13	interleukin-1 beta secretion	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0007160	0.0481	0.98	9	56	cell-matrix adhesion	BP	0.884	TEK,ADAMTS9,CD34,FERMT1,SLK,APOD,JAG1,ITGA6,ENSCAFG00000002015	up_VCAV_EC
GO:0035966	0.0481	0.984	6	47	response to topologically incorrect protein	BP	0.874	HSPA5,ERO1A,PTPN2,DDIT3,ATF3,CREB3L2	down_VSAP_EC
GO:0006939	0.0481	0.985	6	32	smooth muscle contraction	BP	0.884	EDNRB,DOCK4,PDE4D,EDN1,GUCY1A1,P2RX2	up_VCAV_EC
GO:0071360	0.0481	0.993	3	9	cellular response to exogenous dsRNA	BP	1	PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0006952	0.0481	0.996	2	319	defense response	BP	1	ARG2,ESR1	up_AORT_VSMC
GO:0070970	0.0481	0.997	2	4	interleukin-2 secretion	BP	1	ABL1,PNP	up_VSAP_EC
GO:0099563	0.0481	0.997	2	4	modification of synaptic structure	BP	1	WASF3,ABL1	up_VSAP_EC
GO:0001974	0.0481	0.999	1	13	blood vessel remodeling	BP	1	HOXA3	up_APUL_EC
GO:0000165	0.0482	0.97	27	236	MAPK cascade	BP	0.884	EPHB1,TEK,KIT,MAP3K11,TNIP1,PDGFB,SH2D3C,MEF2C,ATF3,RAPGEF1,TLR4,EDN1,MAP3K3,BMP2,MAPK13,ITPKB,MADD,PAK2,PRKD2,TLR3,RAPGEF2,TAOK1,HMGB1,RIPK1,PDGFD,JCAD,CDON	up_VCAV_EC
GO:0006913	0.0482	0.976	13	124	nucleocytoplasmic transport	BP	0.874	PRICKLE1,PTPN14,PTPN11,PPP1R12A,IWS1,ZPR1,SMG7,DDX39B,KPNB1,KPNA4,GSK3B,KPNA1,CDKN1A	down_VSAP_EC
GO:0051169	0.0482	0.976	13	124	nuclear transport	BP	0.874	PRICKLE1,PTPN14,PTPN11,PPP1R12A,IWS1,ZPR1,SMG7,DDX39B,KPNB1,KPNA4,GSK3B,KPNA1,CDKN1A	down_VSAP_EC
GO:2000112	0.0482	0.986	6	1119	regulation of cellular macromolecule biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0048699	0.0482	0.986	5	371	generation of neurons	BP	1	LYN,ACSL4,SPG11,NRP2,NEDD4	down_ACOR_EC
GO:0120036	0.0482	0.986	5	373	plasma membrane bounded cell projection	BP	1	LYN,SPG11,PDPN,NRP2,NEDD4	down_ACOR_EC
GO:0050654	0.0482	0.995	2	15	chondroitin sulfate proteoglycan metabolic	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC
GO:0001568	0.0482	0.995	2	252	blood vessel development	BP	1	C6,TGFBI	up_VCAV_VSMC
GO:0050853	0.0482	0.999	1	10	B cell receptor signaling pathway	BP	1	LYN	down_ACOR_EC
GO:0010257	0.0482	0.999	1	25	NADH dehydrogenase complex assembly	BP	1	NDUFA10	down_AFEM_EC
GO:0032981	0.0482	0.999	1	25	mitochondrial respiratory chain complex I assembly	BP	1	NDUFA10	down_AFEM_EC
GO:0043086	0.0482	0.999	1	170	negative regulation of catalytic activity	BP	1	CST3	down_AORT_EC
GO:1901699	0.0482	0.999	1	164	cellular response to nitrogen compound	BP	1	JUP	down_VFEM_VSMC
GO:1900086	0.0482	0.999	1	2	positive regulation of peptidyl-tyrosine	BP	1	GREM1	up_AFEM_EC
GO:1900157	0.0482	0.999	1	2	regulation of bone mineralization involved in	BP	1	GREM1	up_AFEM_EC

GO:1900158	0.0482	0.999	1	2	negative regulation of bone mineralization involved in bone	BP	1	GREM1	up_AFEM_EC
GO:0031113	0.0482	0.999	1	13	regulation of microtubule polymerization	BP	1	TUBB4A	up_APUL_EC
GO:0032526	0.0482	0.999	1	19	response to retinoic acid	BP	1	CYP26B1	up_VPOR_VSMC
GO:0040019	0.0482	0.999	1	12	positive regulation of embryonic development	BP	1	SIX1	up_VFEM_EC
GO:0071300	0.0482	0.999	1	12	cellular response to retinoic acid	BP	1	CYP26B1	up_VFEM_EC
GO:0070266	0.0482	0.999	1	14	necroptotic process	BP	1	ARHGEF2	up_VPUL_EC
GO:0031077	0.048216136	0.99941	1	2	post-embryonic camera-type eye development	BP	1	FZD5	up_ACOR_EC
GO:0044238	0.0483	0.986	11	3383	primary metabolic process	BP	1	ETFA,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0034138	0.0483	0.993	3	9	toll-like receptor 3 signaling pathway	BP	1	TLR3,F2RL1,PTPN22	up_ACOR_VSMC
GO:0043537	0.0483	0.995	2	15	negative regulation of blood vessel endothelial	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:0003407	0.0483	0.995	2	15	neural retina development	BP	1	IRX5,THRB	up_AFEM_EC
GO:1902369	0.0483	0.995	2	15	negative regulation of RNA catabolic process	BP	1	TENT5C,AXIN2	up_AFEM_EC
GO:0061158	0.0483	0.997	2	4	3'-UTR-mediated mRNA destabilization	BP	1	ZFP36L1,ZFP36L2	up_VSAP_EC
GO:0042391	0.0483	0.995	2	81	regulation of membrane potential	BP	1	NETO1,CAV1	up_VSAP_VSMC
GO:0061333	0.0483	0.999	1	35	renal tubule morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0110110	0.0483	0.999	1	34	positive regulation of animal organ	BP	1	GATA5	up_VCAV_VSMC
GO:0021854	0.0483	0.999	1	6	hypothalamus development	BP	1	SEMA3A	up_VPOR_EC
GO:0048538	0.0483	0.999	1	20	thymus development	BP	1	HOXA3	up_VPOR_VSMC
GO:0042063	0.0484	0.982	7	67	gliogenesis	BP	1	LRP1,NAB2,NDN,AKT2,CSPG4,GLI3,CDH2	down_VCAV_EC
GO:0048514	0.0484	0.991	3	214	blood vessel morphogenesis	BP	1	HOXA3,NTRK2,HOXA1	up_APUL_EC
GO:0030029	0.0484	0.991	3	239	actin filament-based process	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0048713	0.0484	0.996	2	6	regulation of oligodendrocyte	BP	0.874	SLC45A3,CTNNB1	down_VSAP_EC
GO:0031960	0.0484	0.995	2	15	response to corticosteroid	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0051384	0.0484	0.995	2	15	response to glucocorticoid	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0010454	0.0484	1	1	1	negative regulation of cell fate commitment	BP	1	LOXL3	down_VCAV_EC
GO:0018057	0.0484	1	1	1	peptidyl-lysine oxidation	BP	1	LOXL3	down_VCAV_EC
GO:1905590	0.0484	1	1	1	fibronectin fibril organization	BP	1	LOXL3	down_VCAV_EC
GO:2000328	0.0484	1	1	1	regulation of T-helper 17 cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:2000329	0.0484	1	1	1	negative regulation of T-helper 17 cell lineage	BP	1	LOXL3	down_VCAV_EC
GO:1902626	0.0484	1	1	1	assembly of large subunit precursor of preribosome	BP	0.874	RSL24D1	down_VSAP_EC
GO:0007179	0.0484	0.999	1	57	transforming growth factor beta receptor	BP	1	TGFBR1	down_VSAP_VSMC
GO:0030902	0.0484	0.999	1	41	hindbrain development	BP	1	WNT7A	up_AORT_VSMC
GO:0060420	0.0484	0.999	1	18	regulation of heart growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0072283	0.0484	0.999	1	12	metanephric renal vesicle morphogenesis	BP	1	SALL1	up_VSAP_VSMC
GO:0015669	0.048445871	0.9994	1	2	gas transport	BP	1	AQP1	up_ACOR_EC
GO:0015670	0.048445871	0.9994	1	2	carbon dioxide transport	BP	1	AQP1	up_ACOR_EC
GO:0044089	0.0485	0.974	16	170	positive regulation of cellular component biogenesis	BP	0.874	VEGFA,FSCN1,DPYSL3,MSN,DYNLL1,ACTR3,CTNNB1,ANLN,ENSCAFG00000002015,GSK3B,GBP5,SH3GLB1,SDC4,HTT,LRRTM2,NRP1	down_VSAP_EC
GO:0001558	0.0485	0.991	3	101	regulation of cell growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC

GO:0002443	0.0485	0.995	2	71	leukocyte mediated immunity	BP	1	LYN,STX4	down_ACOR_EC
GO:0045597	0.0485	0.995	2	253	positive regulation of cell differentiation	BP	1	LIMK1,GATA5	up_VCAV_VSMC
GO:0001501	0.0485	0.995	2	178	skeletal system development	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0003008	0.0485	1	1	336	system process	BP	1	GATA5	down_AFEM_VSMC
GO:0030809	0.0485	0.999	1	6	negative regulation of nucleotide biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:1900372	0.0485	0.999	1	6	negative regulation of purine nucleotide	BP	1	FBP1	up_VPOR_EC
GO:2001170	0.0485	0.999	1	6	negative regulation of ATP biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0007613	0.0485	0.999	1	20	memory	BP	1	NETO1	up_VFEM_VSMC
GO:0021766	0.0485	0.999	1	20	hippocampus development	BP	1	EMX2	up_VFEM_VSMC
GO:0003148	0.048501708	0.99516	2	13	outflow tract septum morphogenesis	BP	1	SMAD6,NRP1	up_ACOR_EC
GO:0010035	0.0486	0.975	14	107	response to inorganic substance	BP	0.884	TNFAIP3,MEF2C,PPP3CA,TJP1,MAPK13,ITPKB,TIMELESS,GUCY1B1,CREB1,GCH1,BLM,RIPK1,HIF1A,ATRX	up_VCAV_EC
GO:0043902	0.0486	0.984	6	45	positive regulation of multi-organism process	BP	0.874	P4HB,SMARCA4,CNOT7,APOE,RAD23A,INHBA	down_VSAP_EC
GO:0032101	0.0486	0.991	3	173	regulation of response to external stimulus	BP	1	LYN,PDPN,STX4	down_ACOR_EC
GO:0072102	0.0486	0.997	2	4	glomerulus morphogenesis	BP	0.884	MEF2C,MTSS1	up_VCAV_EC
GO:0002009	0.0486	0.995	2	177	morphogenesis of an epithelium	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0051241	0.0486	1	1	336	negative regulation of multicellular organismal	BP	1	GATA5	down_AFEM_VSMC
GO:0048863	0.0486	0.999	1	70	stem cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0070509	0.0486	0.999	1	21	calcium ion import	BP	1	TRPC4	up_VPOR_VSMC
GO:0071407	0.0487	0.974	17	129	cellular response to organic cyclic compound	BP	0.884	PDGFB,TMEM173,PDE4D,MEF2C,TIPARP,RAPGEF1,RALB,TFPI,BMP2,RIOK3,PAK2,SMARCA4,RAPGEF2,CTNNA1,BLM,UFSP2,KDM3A	up_VCAV_EC
GO:0002244	0.0487	0.983	7	35	hematopoietic progenitor cell differentiation	BP	1	BMP4,CITED2,CHD2,PSEN1,JAM3,ENSCAFG00000003530,BVES	up_ACOR_VSMC
GO:0023056	0.0487	0.986	5	462	positive regulation of signaling	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0050868	0.0487	0.988	4	28	negative regulation of T cell activation	BP	1	PRNP,SDC4,GLI3,LOXL3	down_VCAV_EC
GO:0060976	0.0487	0.989	4	22	coronary vasculature development	BP	0.874	PRICKLE1,LTBP1,ADAMTS6,NRP1	down_VSAP_EC
GO:0071260	0.0487	0.989	4	19	cellular response to mechanical stimulus	BP	0.884	TMEM150C,CASP8,TLR3,BCL10	up_VCAV_EC
GO:0051252	0.0487	0.994	3	1051	regulation of RNA metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0043649	0.0487	0.997	2	4	dicarboxylic acid catabolic process	BP	1	GOT1,ADHFE1	up_VSAP_EC
GO:0050820	0.0487	0.999	1	10	positive regulation of coagulation	BP	1	PDPN	down_ACOR_EC
GO:0071333	0.0487	0.999	1	25	cellular response to glucose stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0010835	0.0487	0.999	1	6	regulation of protein ADP-ribosylation	BP	1	PUM3	up_VPOR_EC
GO:0060421	0.0487	0.999	1	14	positive regulation of heart growth	BP	1	TBX5	up_VPUL_EC
GO:0072606	0.0487	0.999	1	12	interleukin-8 secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0098884	0.04875227	0.99939	1	2	postsynaptic neurotransmitter	BP	1	CALY	up_ACOR_EC
GO:0099590	0.04875227	0.99939	1	2	neurotransmitter receptor internalization	BP	1	CALY	up_ACOR_EC
GO:0140239	0.04875227	0.99939	1	2	postsynaptic endocytosis	BP	1	CALY	up_ACOR_EC
GO:0034332	0.048771537	0.99116	3	32	adherens junction organization	BP	1	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0090398	0.0488	0.987	5	24	cellular senescence	BP	0.884	PLK2,ARG2,MAP3K3,SMC5,VASH1	up_VCAV_EC
GO:1901576	0.0488	0.993	4	1877	organic substance biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0071461	0.0488	1	1	1	cellular response to redox state	BP	1	VASN	down_VCAV_EC

GO:0051216	0.0488	0.999	1	70	cartilage development	BP	1	HOXA3	up_APUL_VSMC
GO:0050996	0.0488	0.999	1	6	positive regulation of lipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0060795	0.0488	0.999	1	12	cell fate commitment involved in formation of	BP	1	HOXA11	up_VSAP_VSMC
GO:0034644	0.0489	0.984	6	32	cellular response to UV	BP	1	NEDD4,AURKB,PCNA,NOC2L,POLH,CDC25A	down_ACOR_VSMC
GO:0090342	0.0489	0.989	4	17	regulation of cell aging	BP	0.884	PLK2,ARG2,MAP3K3,VASH1	up_VCAV_EC
GO:0040020	0.0489	0.992	3	10	regulation of meiotic nuclear division	BP	1	FBXO5,CDC20,TTK	down_ACOR_VSMC
GO:0003215	0.0489	0.993	3	9	cardiac right ventricle morphogenesis	BP	0.884	CHD7,GATA3,JAG1	up_VCAV_EC
GO:0050808	0.0489	0.995	2	93	synapse organization	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0048666	0.0489	0.995	2	258	neuron development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0006040	0.0489	0.999	1	12	amino sugar metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:1900180	0.049	0.98	9	50	regulation of protein localization to nucleus	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PARP9,PSEN1,JUP,PARK7	up_ACOR_VSMC
GO:0051046	0.049	0.991	3	174	regulation of secretion	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0001945	0.049	0.993	3	9	lymph vessel development	BP	1	CCBE1,ACVRL1,PPP3CB	up_VSAP_EC
GO:0001946	0.049	0.993	3	9	lymphangiogenesis	BP	1	CCBE1,ACVRL1,PPP3CB	up_VSAP_EC
GO:0036303	0.049	0.993	3	9	lymph vessel morphogenesis	BP	1	CCBE1,ACVRL1,PPP3CB	up_VSAP_EC
GO:0002313	0.049	0.997	2	4	mature B cell differentiation involved in	BP	0.884	MFNG,PLCG2	up_VCAV_EC
GO:0002335	0.049	0.997	2	4	mature B cell differentiation	BP	0.884	MFNG,PLCG2	up_VCAV_EC
GO:0032534	0.049	0.997	2	4	regulation of microvillus assembly	BP	0.884	PODXL,FSCN1	up_VCAV_EC
GO:1900272	0.049	0.997	2	4	negative regulation of long-term synaptic	BP	1	FAM107A,ABL1	up_VSAP_EC
GO:0090596	0.049	0.995	2	84	sensory organ morphogenesis	BP	1	SALL1,IRX5	up_VSAP_VSMC
GO:1902305	0.049	0.999	1	12	regulation of sodium ion transmembrane transport	BP	1	NEDD4	down_ACOR_EC
GO:0018105	0.049	0.999	1	116	peptidyl-serine phosphorylation	BP	1	PLCL1	down_VFEM_EC
GO:0070168	0.049	0.999	1	6	negative regulation of biomineral tissue	BP	1	ASPN	up_VPOR_EC
GO:0001959	0.0491	0.986	5	33	regulation of cytokine-mediated signaling	BP	0.874	NR1H4,PTPN2,ADAM17,CNOT7,CDC37	down_VSAP_EC
GO:0034138	0.0491	0.993	3	9	toll-like receptor 3 signaling pathway	BP	1	F2RL1,UNC93B1,FLOT1	up_VSAP_EC
GO:0061430	0.0491	0.995	2	8	bone trabecula morphogenesis	BP	1	THBS3,GREM1	down_VCAV_EC
GO:0071674	0.0491	0.999	1	23	mononuclear cell migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0046939	0.0491	0.999	1	19	nucleotide phosphorylation	BP	1	FBP1	up_VFEM_VSMC
GO:0051781	0.0492	0.989	4	18	positive regulation of cell division	BP	1	AURKB,CDC6,NUP62,FGF5	down_ACOR_VSMC
GO:0006509	0.0492	0.989	4	15	membrane protein ectodomain proteolysis	BP	1	PTPN3,DAG1,PSEN1,ERAP1	up_ACOR_VSMC
GO:0010648	0.0492	0.988	4	407	negative regulation of cell communication	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0045123	0.0492	0.992	3	11	cellular extravasation	BP	0.884	SELP,SELE,SELL	up_VCAV_EC
GO:0040008	0.0492	0.995	2	179	regulation of growth	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0000165	0.049299175	0.977	11	236	MAPK cascade	BP	1	SOX9,NDRG2,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,MAPK8IP2,SH3RF3,NRP1,PRKCD	up_ACOR_EC
GO:0071363	0.0493	0.974	15	188	cellular response to growth factor stimulus	BP	1	PDGFRB,SMAD9,DCN,NDN,VASN,FBN1,AKT1S1,CHRDL1,NR3C1,ASPN,ZFP36L1,FUT8,SHC1,GREM1,RGMA	down_VCAV_EC
GO:0007405	0.0493	0.989	4	21	neuroblast proliferation	BP	0.874	ARHGEF2,HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0060379	0.0493	0.996	2	6	cardiac muscle cell myoblast differentiation	BP	0.874	PRICKLE1,REST	down_VSAP_EC
GO:0001880	0.0493	1	1	1	Mullerian duct regression	BP	1	BMPR1A	down_VCAV_EC
GO:0048352	0.0493	1	1	1	paraxial mesoderm structural organization	BP	1	BMPR1A	down_VCAV_EC

GO:0060897	0.0493	1	1	1	neural plate regionalization	BP	1	BMPR1A	down_VCAV_EC
GO:1904412	0.0493	1	1	1	regulation of cardiac ventricle development	BP	1	BMPR1A	down_VCAV_EC
GO:1904414	0.0493	1	1	1	positive regulation of cardiac ventricle	BP	1	BMPR1A	down_VCAV_EC
GO:1905285	0.0493	1	1	1	fibrous ring of heart morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0021998	0.0493	1	1	1	neural plate mediolateral regionalization	BP	1	BMPR1A	down_VCAV_EC
GO:0048338	0.0493	1	1	1	mesoderm structural organization	BP	1	BMPR1A	down_VCAV_EC
GO:0060896	0.0493	1	1	1	neural plate pattern specification	BP	1	BMPR1A	down_VCAV_EC
GO:0072676	0.0493	0.999	1	25	lymphocyte migration	BP	1	HSD3B7	down_VPOR_EC
GO:1900078	0.0493	0.999	1	13	positive regulation of cellular response to	BP	1	NR1H4	up_APUL_EC
GO:0033690	0.0494	0.997	2	4	positive regulation of osteoblast proliferation	BP	1	ABL1,HPSE	up_VSAP_EC
GO:0060429	0.0494	1	1	341	epithelium development	BP	1	GATA5	down_AFEM_VSMC
GO:0008626	0.0494	1	1	1	granzyme-mediated apoptotic signaling	BP	0.874	BNIP3	down_VSAP_EC
GO:0050710	0.0494	0.999	1	13	negative regulation of cytokine secretion	BP	1	NR1H4	up_APUL_EC
GO:1901700	0.0495	0.975	14	364	response to oxygen-containing compound	BP	1	LEP,CRY2,CD40,CRYAB,GPAM,FIBIN,CHRM2,AVPR1A,CAMK2A,NR3C1,TBXA2R,ADAM17,KANK1,SOD1	up_AFEM_EC
GO:0046822	0.0495	0.982	7	53	regulation of nucleocytoplasmic	BP	0.874	PTPN14,PTPN11,PPP1R12A,IWS1,ZPR1,GSK3B,CDKN1A	down_VSAP_EC
GO:0002724	0.0495	0.992	3	9	regulation of T cell cytokine production	BP	1	B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051254	0.0495	0.996	2	431	positive regulation of RNA metabolic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0001525	0.0495	0.999	1	173	angiogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0072088	0.0495	0.999	1	36	nephron epithelium morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0001657	0.0495	0.999	1	42	ureteric bud development	BP	1	ARG2	up_AORT_VSMC
GO:0072163	0.0495	0.999	1	42	mesonephric epithelium development	BP	1	ARG2	up_AORT_VSMC
GO:0072164	0.0495	0.999	1	42	mesonephric tubule development	BP	1	ARG2	up_AORT_VSMC
GO:0060795	0.0495	0.999	1	12	cell fate commitment involved in formation of	BP	1	EYA1	up_VFEM_EC
GO:0043500	0.0495	0.999	1	21	muscle adaptation	BP	1	GATM	up_VFEM_VSMC
GO:0022410	0.049585252	0.99937	1	2	circadian sleep/wake cycle process	BP	1	PTGDS	up_ACOR_EC
GO:0042745	0.049585252	0.99937	1	2	circadian sleep/wake cycle	BP	1	PTGDS	up_ACOR_EC
GO:0042749	0.049585252	0.99937	1	2	regulation of circadian sleep/wake cycle	BP	1	PTGDS	up_ACOR_EC
GO:0045187	0.049585252	0.99937	1	2	regulation of circadian sleep/wake cycle, sleep	BP	1	PTGDS	up_ACOR_EC
GO:0050802	0.049585252	0.99937	1	2	circadian sleep/wake cycle, sleep	BP	1	PTGDS	up_ACOR_EC
GO:0009952	0.0496	0.982	7	66	anterior/posterior pattern specification	BP	1	BMPR1A,HOXC4,CLSTN1,SEMA3C,GLI3,PCSK6,ZBTB16	down_VCAV_EC
GO:0061077	0.0496	0.988	4	25	chaperone-mediated protein folding	BP	0.874	ERO1A,FKBP11,PPIB,FKBP10	down_VSAP_EC
GO:0035809	0.0496	0.997	2	4	regulation of urine volume	BP	1	EDN1,INPP5K	up_ACOR_VSMC
GO:0035810	0.0496	0.997	2	4	positive regulation of urine volume	BP	1	EDN1,INPP5K	up_ACOR_VSMC
GO:0060572	0.0496	0.999	1	11	morphogenesis of an epithelial bud	BP	1	SULF1	down_ACOR_EC
GO:0014070	0.0496	0.999	1	172	response to organic cyclic compound	BP	1	JUP	down_VFEM_VSMC
GO:0007219	0.0496	0.999	1	59	Notch signaling pathway	BP	1	GATA5	down_VSAP_VSMC
GO:0031348	0.0496	0.999	1	46	negative regulation of defense response	BP	1	ARG2	up_AORT_VSMC
GO:1901071	0.0496	0.999	1	6	glucosamine-containing compound metabolic	BP	1	OGA	up_VPOR_EC
GO:1903524	0.0496	0.999	1	11	positive regulation of blood circulation	BP	1	AVPR1A	up_VFEM_EC

GO:0045596	0.0497	0.97	25	186	negative regulation of cell differentiation	BP	1	THRB,HOXA7,TWIST2,HOXA9,AXIN2,SLIT2,HDAC7,DLL1,OSR1,ZBTB16,RARG,ZFP36L1,PIK3R1,MYC,IRX3,ZEB1,RTN4RL1,LRP4,ZADH2,FBXO7,LIMD1,FBLN1,ZFP36L2,ACVRL1,LBH	up_VSAP_EC
GO:0048232	0.0497	0.976	13	95	male gamete generation	BP	0.884	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,CDYL,CREM,ARID4B,HIST1H1A,AFF4,KDM3A,ATRX,SPATA6	up_VCAV_EC
GO:0070646	0.0497	0.978	10	63	protein modification by small protein removal	BP	0.884	TNFAIP3,TNIP1,USP33,ENSCAFG00000010893,OTUD4,SENP6,USP28,USP13,USP38,USP37	up_VCAV_EC
GO:2000482	0.0497	0.992	3	9	regulation of interleukin-8 secretion	BP	1	TLR1,F2RL1,PTPN22	up_ACOR_VSMC
GO:0048856	0.0497	1	2	1533	anatomical structure development	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0003149	0.0497	0.997	2	4	membranous septum morphogenesis	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0030098	0.0497	0.995	2	87	lymphocyte differentiation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0002695	0.0497	0.999	1	44	negative regulation of leukocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0050707	0.0497	0.999	1	44	regulation of cytokine secretion	BP	1	ARG2	up_AORT_VSMC
GO:0002761	0.0497	0.999	1	36	regulation of myeloid leukocyte differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0048747	0.0497	0.999	1	20	muscle fiber development	BP	1	SHOX2	up_VFEM_VSMC
GO:0042327	0.0498	0.971	21	289	positive regulation of phosphorylation	BP	1	NOTCH2,PDGFRB,PRNP,GLIPR2,BMPR1A,LMO4,CLIP3,AKT2,CSPG4,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0046661	0.0498	0.995	2	45	male sex differentiation	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0006835	0.0498	0.999	1	13	dicarboxylic acid transport	BP	1	NTRK2	up_APUL_EC
GO:0044381	0.0498	0.999	1	13	glucose import in response to insulin	BP	1	NR1H4	up_APUL_EC
GO:0051099	0.0498	0.999	1	70	positive regulation of binding	BP	1	HOXA3	up_APUL_VSMC
GO:2000027	0.0498	0.999	1	72	regulation of animal organ morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:1990266	0.0498	0.999	1	24	neutrophil migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0002686	0.0498	0.999	1	12	negative regulation of leukocyte migration	BP	1	HOXA7	up_VFEM_EC
GO:0019229	0.0498	0.999	1	12	regulation of vasoconstriction	BP	1	AVPR1A	up_VFEM_EC
GO:1901863	0.0498	0.999	1	25	positive regulation of muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0061036	0.0498	0.999	1	11	positive regulation of cartilage development	BP	1	HOXA11	up_VSAP_VSMC
GO:0050994	0.049811322	0.99491	2	14	regulation of lipid catabolic process	BP	1	RARRES2,PRKCD	up_ACOR_EC
GO:0044281	0.0499	0.966	41	622	small molecule metabolic process	BP	1	GPAM,DCN,ADCY6,VKORC1,AKT2,LCAT,ACAA1,ME3,H6PD,CYB5R3,UROS,NT5C2,EPHX1,ENTPD3,THNSL2,PGLS,POFUT1,ATP5MC1,GFPT2,UQCR10,SUOX,CYP1B1,ADK,AHCYL1,PEX5,B4GALT1,RETSAT,PARK7,AMPD2,ENSCAFG00000002977,HPDL,FUT8,ACSS2,RDH10,CRTAP,LONP2,NAPEPLD,GLS2,SOAT1,BCKDHB,ACAT1	down_VCAV_EC
GO:0048588	0.0499	0.981	8	44	developmental cell growth	BP	1	SLIT2,ABL1,PLXNA4,RARG,DPYSL2,TTL,ULK1,TGFBR2	up_VSAP_EC
GO:0030030	0.0499	0.986	5	377	cell projection organization	BP	1	LYN,SPG11,PDPN,NRP2,NEDD4	down_ACOR_EC
GO:0051702	0.0499	0.988	4	24	interaction with symbiont	BP	0.874	SMARCA4,APOE,REST,CALM1	down_VSAP_EC
GO:0023057	0.0499	0.988	4	409	negative regulation of signaling	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0009790	0.0499	0.991	3	335	embryo development	BP	1	HOXA3,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0034220	0.0499	0.991	3	188	ion transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0034645	0.0499	1	2	1546	cellular macromolecule biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1904683	0.0499	0.997	2	4	regulation of metalloendopeptidase	BP	1	MBP,RECK	up_ACOR_VSMC
GO:0051489	0.049959504	0.99489	2	14	regulation of filopodium assembly	BP	1	NRP1,PRKCD	up_ACOR_EC

GO:1905477	0.049971887	0.99085	3	32	positive regulation of protein localization to	BP	1	KCNB1,PLS1,LRP4	up_ACOR_EC
GO:0001822	0.05	0.975	14	98	kidney development	BP	0.884	HOXB7,PDGFB,PODXL,MEF2C,TIPARP,GPR4,GATA3,MTSS1,ODC1,ARG2,BMP2,PROX1,JAG1,BASP1	up_VCAV_EC
GO:0000082	0.05	0.982	7	57	G1/S transition of mitotic cell cycle	BP	0.874	PLK3,ZPR1,EIF4EBP1,BACH1,RBBP8,INHBA,CDKN1A	down_VSAP_EC
GO:0034440	0.05	0.991	3	35	lipid oxidation	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC
GO:0060429	0.05	0.991	3	341	epithelium development	BP	1	EYA1,SPINK5,HOXA11	up_VFEM_VSMC
GO:0030949	0.05	0.996	2	6	positive regulation of vascular endothelial growth factor receptor	BP	0.874	VEGFA,HIF1A	down_VSAP_EC
GO:0006836	0.05	0.999	1	47	neurotransmitter transport	BP	1	WNT7A	up_AORT_VSMC
GO:0035773	0.05	0.999	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0071359	0.05	0.999	1	11	cellular response to dsRNA	BP	1	CAV1	up_VSAP_VSMC
GO:0030970	0.050079277	0.99487	2	14	retrograde protein transport, ER to cytosol	BP	1	EDEM2,HM13	up_ACOR_EC
GO:1903513	0.050079277	0.99487	2	14	endoplasmic reticulum to cytosol transport	BP	1	EDEM2,HM13	up_ACOR_EC
GO:0051056	0.0501	0.975	13	87	regulation of small GTPase mediated signal transduction	BP	1	CDON,ARHGEF5,ARHGEF6,SLIT2,ABL1,F2RL1,MFN2,TIAM1,DLC1,FGD4,PSD4,ARHGAP12,FLOT1	up_VSAP_EC
GO:0050768	0.0501	0.98	8	66	negative regulation of neurogenesis	BP	0.874	DPYSL3,HOOK3,IFRD1,CTNNB1,APOE,REST,NRP1,YWHAH	down_VSAP_EC
GO:0046907	0.0501	0.984	6	536	intracellular transport	BP	1	LYN,SPG11,IPO7,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0055007	0.0501	0.984	6	31	cardiac muscle cell differentiation	BP	0.884	MEF2C,EDN1,MTOR,BMP2,PROX1,ENSCAFG00000010596	up_VCAV_EC
GO:0060502	0.0501	0.992	3	9	epithelial cell proliferation involved in lung	BP	1	FGF7,NFIB,MAP2K2	up_VSAP_EC
GO:0008610	0.0501	0.995	2	177	lipid biosynthetic process	BP	1	HSD3B7,GBGT1	down_VPOR_EC
GO:0055078	0.0501	0.997	2	4	sodium ion homeostasis	BP	1	EDN1,SLC8A1	up_ACOR_VSMC
GO:0007610	0.0501	0.995	2	146	behavior	BP	1	GATM,NETO1	up_VFEM_VSMC
GO:0048701	0.0501	0.999	1	25	embryonic cranial skeleton morphogenesis	BP	1	TBX15	down_VPOR_EC
GO:0032635	0.0501	0.999	1	37	interleukin-6 production	BP	1	TLR2	up_AFEM_VSMC
GO:0030101	0.0501	0.999	1	12	natural killer cell activation	BP	1	TOX	up_VFEM_EC
GO:0033043	0.050103074	0.97203	18	446	regulation of organelle organization	BP	1	TMOD1,PKIB,ARHGAP6,SYNPO2,DIXDC1,ACTN2,ARHGAP28,PAK3,PTGER4,ARHGDIB,PREB,MAVS,CHMP4B,VPS16,NRP1,PRKCD,PYGO2,TUBB4A	up_ACOR_EC
GO:0022406	0.0502	0.991	3	35	membrane docking	BP	1	CAMK2A,BVES,RAB7A	up_AFEM_EC
GO:0071248	0.0502	0.991	3	35	cellular response to metal ion	BP	1	MT2A,ENSCAFG00000009113,CPNE7	up_AFEM_EC
GO:0007351	0.0502	0.997	2	4	tripartite regional subdivision	BP	1	FRS2,PCSK6	up_ACOR_VSMC
GO:0008595	0.0502	0.997	2	4	anterior/posterior axis specification, embryo	BP	1	FRS2,PCSK6	up_ACOR_VSMC
GO:2000484	0.0502	0.997	2	4	positive regulation of interleukin-8 secretion	BP	1	TLR1,F2RL1	up_ACOR_VSMC
GO:0003149	0.0502	0.997	2	4	membranous septum morphogenesis	BP	1	FZD1,TGFBR2	up_VSAP_EC
GO:0048505	0.0502	0.997	2	4	regulation of timing of cell differentiation	BP	1	DLL1,GDPD5	up_VSAP_EC
GO:0002221	0.0502	0.999	1	46	pattern recognition receptor signaling	BP	1	ESR1	up_AORT_VSMC
GO:0002758	0.0502	0.999	1	46	innate immune response-activating signal	BP	1	ESR1	up_AORT_VSMC
GO:0007416	0.0502	0.999	1	36	synapse assembly	BP	1	SLITRK5	up_VCAV_VSMC
GO:0001960	0.0502	0.999	1	15	negative regulation of cytokine-mediated	BP	1	NR1H4	up_VPUL_EC
GO:0060761	0.0502	0.999	1	15	negative regulation of response to cytokine	BP	1	NR1H4	up_VPUL_EC
GO:0006862	0.050229759	0.99936	1	2	nucleotide transport	BP	1	SLC25A42	up_ACOR_EC
GO:1901679	0.050229759	0.99936	1	2	nucleotide transmembrane transport	BP	1	SLC25A42	up_ACOR_EC

GO:0019355	0.050291033	0.99935	1	2	nicotinamide nucleotide biosynthetic process from aspartate	BP	1	NMNAT2	up_ACOR_EC
GO:0034627	0.050291033	0.99935	1	2	'de novo' NAD biosynthetic process	BP	1	NMNAT2	up_ACOR_EC
GO:0034628	0.050291033	0.99935	1	2	'de novo' NAD biosynthetic process from	BP	1	NMNAT2	up_ACOR_EC
GO:0048731	0.0503	0.962	74	1247	system development	BP	1	ADAMTS2,NOTCH2,HSPB6,PDGFRB,SMAD9,LRP1,DCN,NAB2,NDN,ANGPT1,SDC4,VASN,FBN1,GLIPR2,KANK2,THBS3,BMPR1A,LOX,LMO4,RECK,TRPV2,ANPEP,NUMBL,NAGLU,CHRDL1,TBX15,AKT2,TFE3,ENSCAFG00000018277,HOXC4,CLSTN1,CSPG4,PKD1,SEMA3C,ASPN,THY1,TEAD1,HAPLN3,PEX5,TLX2,VCAN,B4GALT1,GLI3,EEF2,ZFP36L1,MYDGF,SASH1,NCDN,IFT57,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,IRX5,TSC22D3,UST,GLIS2,PRKCSH,DDR2,SHC1,RDH10,OMD,GREM1,CLIC4,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,SEC61A1,BRSK1	down_VCAV_EC
GO:0048869	0.0503	0.985	6	1119	cellular developmental process	BP	1	CHL1,BARX1,NKX2-5,BAMBI,TRPC4,CYP26B1	up_VPOR_VSMC
GO:0051193	0.0503	0.989	4	15	regulation of cofactor metabolic process	BP	1	PDK2,CLYBL,ZNF205,DDIT4	up_VSAP_EC
GO:0003008	0.0503	0.991	3	336	system process	BP	1	HOXC10,GATM,NETO1	up_VFEM_VSMC
GO:0033622	0.0503	0.996	2	6	integrin activation	BP	0.874	FBLIM1,TLN1	down_VSAP_EC
GO:0034135	0.0503	0.997	2	4	regulation of toll-like receptor 2 signaling	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0032801	0.0503	0.999	1	10	receptor catabolic process	BP	1	NEDD4	down_ACOR_EC
GO:0045576	0.0503	0.999	1	12	mast cell activation	BP	1	LYN	down_ACOR_EC
GO:0046040	0.0503	0.999	1	9	IMP metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0000413	0.0503	1	1	1	protein peptidyl-prolyl isomerization	BP	0.874	PPIB	down_VSAP_EC
GO:0030004	0.0503	0.999	1	36	cellular monovalent inorganic cation	BP	1	CA2	up_VCAV_VSMC
GO:0046326	0.0503	0.999	1	15	positive regulation of glucose import	BP	1	NR1H4	up_VPUL_EC
GO:0051270	0.0504	0.966	37	296	regulation of cellular component movement	BP	1	HOXA7,TWIST2,WNT11,FAM107A,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,KCNE3,FUZ,PDGFD,PLXNA4,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,FBLN1,ZNF580,STX4,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0001649	0.0504	0.983	6	54	osteoblast differentiation	BP	1	BMPR1A,CLSTN1,GLI3,TWIST2,DDR2,GREM1	down_VCAV_EC
GO:0035510	0.0504	0.992	3	10	DNA dealkylation	BP	0.884	GATA3,OTUD4,TET2	up_VCAV_EC
GO:1903053	0.0504	0.999	1	10	regulation of extracellular matrix organization	BP	1	PDPN	down_ACOR_EC
GO:0051224	0.0504	0.999	1	47	negative regulation of protein transport	BP	1	ARG2	up_AORT_VSMC
GO:1904950	0.0504	0.999	1	47	negative regulation of establishment of protein localization	BP	1	ARG2	up_AORT_VSMC
GO:1905209	0.0504	0.999	1	13	positive regulation of cardiocyte differentiation	BP	1	TBX5	up_APUL_EC
GO:0035637	0.0504	0.999	1	21	multicellular organismal signaling	BP	1	NKX2-5	up_VPOR_VSMC
GO:0008284	0.0505	0.967	31	238	positive regulation of cell proliferation	BP	1	CDON,C5AR2,OSR2,PTGFR,MAB21L1,IL6R,CRIP2,FGF7,ABL1,EMP2,DLL1,OSR1,PDGFD,HPSE,RARG,STAT5A,DDR2,MFN2,TIAM1,MYC,FBXW4,SHOX2,MYD88,PNP,ZNF580,STX4,ACVRL1,NCK1,HMOX1,TGFBR2,LBH	up_VSAP_EC
GO:0007286	0.0505	0.984	6	34	spermatid development	BP	0.884	KIT,PSME4,NECTIN2,CDYL,AFF4,KDM3A	up_VCAV_EC
GO:0019693	0.0505	0.995	2	172	ribose phosphate metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0006573	0.0505	0.997	2	4	valine metabolic process	BP	1	ALDH6A1,ENSCAFG00000002977	up_VSAP_EC
GO:0000245	0.0505	0.999	1	24	spliceosomal complex assembly	BP	1	SRSF6	down_AFEM_EC
GO:0045843	0.0505	0.999	1	13	negative regulation of striated muscle tissue	BP	1	TBX5	up_APUL_EC

GO:0060602	0.0505	0.999	1	12	branch elongation of an epithelium	BP	1	SIX1	up_VFEM_EC
GO:1904211	0.050524297	0.99935	1	2	membrane protein proteolysis involved in retrograde protein	BP	1	HM13	up_ACOR_EC
GO:0009306	0.05054773	0.98112	7	127	protein secretion	BP	1	NR1H4,KCNB1,FZD5,NOD2,PTGER4,PREB,MAVS	up_ACOR_EC
GO:0046877	0.050599406	0.99935	1	2	regulation of saliva secretion	BP	1	AQP1	up_ACOR_EC
GO:0046632	0.0506	0.984	6	29	alpha-beta T cell differentiation	BP	1	ABL1,ZBTB16,STAT6,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0002573	0.0506	0.995	2	71	myeloid leukocyte differentiation	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0045601	0.0506	0.999	1	10	regulation of endothelial cell differentiation	BP	1	ACVRL1	down_ACOR_EC
GO:0048646	0.0506	1	1	349	anatomical structure formation involved in	BP	1	GATA5	down_AFEM_VSMC
GO:0048871	0.0506	0.999	1	120	multicellular organismal homeostasis	BP	1	PLCL1	down_VFEM_EC
GO:0030878	0.0506	0.999	1	13	thyroid gland development	BP	1	HOXA3	up_APUL_EC
GO:0006355	0.0507	0.98	9	974	regulation of transcription, DNA-	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0030001	0.0507	0.991	3	172	metal ion transport	BP	1	LYN,HOXA3,NEDD4	down_ACOR_EC
GO:0046530	0.0507	0.991	3	17	photoreceptor cell differentiation	BP	1	NAGLU,THY1,THRB	down_VCAV_EC
GO:0001773	0.0507	0.996	2	4	myeloid dendritic cell activation	BP	1	BATF2,TGFBR2	up_VSAP_EC
GO:0043011	0.0507	0.996	2	4	myeloid dendritic cell differentiation	BP	1	BATF2,TGFBR2	up_VSAP_EC
GO:2001046	0.0507	0.996	2	4	positive regulation of integrin-mediated	BP	1	LIMS2,EMP2	up_VSAP_EC
GO:0006816	0.0507	0.994	2	84	calcium ion transport	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0071326	0.0507	0.999	1	26	cellular response to monosaccharide stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0071331	0.0507	0.999	1	26	cellular response to hexose stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0022408	0.0507	0.999	1	44	negative regulation of cell-cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0045926	0.0507	0.999	1	72	negative regulation of growth	BP	1	TBX5	up_APUL_VSMC
GO:1905523	0.0507	0.999	1	6	positive regulation of macrophage migration	BP	1	C3AR1	up_VPOR_EC
GO:0055017	0.0507	0.999	1	19	cardiac muscle tissue growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010464	0.0507	0.999	1	21	regulation of mesenchymal cell	BP	1	SHOX2	up_VFEM_VSMC
GO:0045764	0.050716629	0.99934	1	2	positive regulation of cellular amino acid	BP	1	NR1H4	up_ACOR_EC
GO:0060456	0.050781662	0.99934	1	2	positive regulation of digestive system process	BP	1	AQP1	up_ACOR_EC
GO:0072488	0.050781662	0.99934	1	2	ammonium transmembrane transport	BP	1	AQP1	up_ACOR_EC
GO:0006898	0.0508	0.981	7	57	receptor-mediated endocytosis	BP	0.874	VEGFA,SERPINE1,CANX,TFRC,APOE,GPR107,LRRTM2	down_VSAP_EC
GO:0051924	0.0508	0.983	6	53	regulation of calcium ion transport	BP	1	PRNP,TRPV2,CACNB3,THY1,CYBA,PACSIN3	down_VCAV_EC
GO:0048519	0.0508	1	2	1554	negative regulation of biological process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0009314	0.0508	0.995	2	143	response to radiation	BP	1	EYA1,NETO1	up_VFEM_VSMC
GO:0003433	0.0508	0.996	2	4	chondrocyte development involved in endochondral bone morphogenesis	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:0072567	0.0508	0.996	2	4	chemokine (C-X-C motif) ligand 2 production	BP	1	F2RL1,MYD88	up_VSAP_EC
GO:1904646	0.0508	0.999	1	6	cellular response to amyloid-beta	BP	1	IGF1R	down_ACOR_EC
GO:0060541	0.0508	0.999	1	73	respiratory system development	BP	1	TBX5	up_APUL_VSMC
GO:0030334	0.050877139	0.97527	12	267	regulation of cell migration	BP	1	SOX9,AQP1,SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,FOXC2,LRRC15,TBX5,RARRES2,NRP1	up_ACOR_EC
GO:0045664	0.0509	0.971	20	144	regulation of neuron differentiation	BP	1	THRB,CDON,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,CYB5D2,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC

GO:0009100	0.0509	0.975	12	139	glycoprotein metabolic process	BP	1	DCN,KRTCAP2,DDOST,GFPT2,NECAB3,B4GALT1,PARK7,FUT8,PRKCSH,PCSK6,RPN2,SOAT1	down_VCAV_EC
GO:0045861	0.0509	0.98	8	71	negative regulation of proteolysis	BP	0.874	SERPINE1,PTGS2,UCHL5,CRYAB,PAK2,A2M,SPINK2,USP14	down_VSAP_EC
GO:0034249	0.0509	0.985	5	41	negative regulation of cellular amide metabolic	BP	1	PRNP,SAMD4B,ZFP36L1,ORMDL3,EIF4EBP1	down_VCAV_EC
GO:1902750	0.0509	0.986	5	24	negative regulation of cell cycle G2/M phase	BP	0.884	TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0090317	0.0509	0.989	4	16	negative regulation of intracellular protein	BP	1	FERMT1,OS9,INPP5K,PARK7	up_ACOR_VSMC
GO:0007399	0.0509	0.988	4	564	nervous system development	BP	1	CHL1,HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0006351	0.0509	0.993	3	1069	transcription, DNA-templated	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0060712	0.0509	0.996	2	4	spongiotrophoblast layer development	BP	1	GJB5,ZFP36L1	up_VSAP_EC
GO:0071941	0.0509	0.996	2	4	nitrogen cycle metabolic process	BP	1	SUOX,ASS1	up_VSAP_EC
GO:0050650	0.0509	0.999	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	CSGALNACT1	down_ACOR_EC
GO:0021849	0.0509	1	1	1	neuroblast division in subventricular zone	BP	1	NUMBL	down_VCAV_EC
GO:0042445	0.0509	0.999	1	46	hormone metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0050891	0.0509	0.999	1	12	multicellular organismal water homeostasis	BP	1	CYP26B1	up_VFEM_EC
GO:0051347	0.051	0.97	22	182	positive regulation of transferase activity	BP	0.884	TEK,KIT,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,NEDD9,MAP3K3,BMP2,SLK,PROX1,MADD,HMBOX1,PAK2,SH3GLB1,MMD,RAPGEF2,RIPK1,PDGFD	up_VCAV_EC
GO:0051648	0.051	0.98	8	69	vesicle localization	BP	0.874	MYH9,SHROOM2,MYO1C,KIF5B,CTNNB1,GSK3B,HTT,AP3S1	down_VSAP_EC
GO:0018022	0.051	0.982	7	36	peptidyl-lysine methylation	BP	0.884	IWS1,GATA3,ARID4B,NSD1,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0001823	0.051	0.983	6	45	mesonephros development	BP	0.874	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0002702	0.051	0.984	6	28	positive regulation of production of molecular mediator of immune	BP	1	TP53BP1,F2RL1,PTPN22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0008104	0.051	0.992	3	763	protein localization	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0044089	0.051	0.995	2	170	positive regulation of cellular component	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0009059	0.051	1	2	1563	macromolecule biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0042692	0.051	0.994	2	105	muscle cell differentiation	BP	1	TBX5,MYBPC2	up_VPUL_EC
GO:0030855	0.051	0.995	2	183	epithelial cell differentiation	BP	1	GATA5,HOXB5	up_VPUL_VSMC
GO:0001765	0.051	0.996	2	4	membrane raft assembly	BP	1	EMP2,FLOT1	up_VSAP_EC
GO:0015693	0.051	0.996	2	4	magnesium ion transport	BP	1	NIPAL3,NIPAL1	up_VSAP_EC
GO:0034433	0.051	0.996	2	4	steroid esterification	BP	1	LCAT,SOAT1	up_VSAP_EC
GO:0034434	0.051	0.996	2	4	sterol esterification	BP	1	LCAT,SOAT1	up_VSAP_EC
GO:0034435	0.051	0.996	2	4	cholesterol esterification	BP	1	LCAT,SOAT1	up_VSAP_EC
GO:0002088	0.051	0.999	1	26	lens development in camera-type eye	BP	1	CITED2	down_VPOR_EC
GO:0032677	0.051	0.999	1	22	regulation of interleukin-8 production	BP	1	BPI	up_AORT_EC
GO:0032495	0.051	0.999	1	15	response to muramyl dipeptide	BP	1	ARHGEF2	up_VPUL_EC
GO:2000649	0.051	0.999	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	NETO1	up_VSAP_VSMC
GO:2000275	0.051054914	0.99933	1	2	regulation of oxidative phosphorylation uncoupler activity	BP	1	PM20D1	up_ACOR_EC
GO:0030185	0.051087603	0.99933	1	2	nitric oxide transport	BP	1	AQP1	up_ACOR_EC
GO:0009607	0.0511	0.967	30	232	response to biotic stimulus	BP	1	VEGFD,TLR1,PLCG2,TMEM255A,COCH,MX1,ABCA1,TLR3,ISG15,CD274,PTGIR,SASH1,PLAC8B,ANKRD1,F2RL1,BNIP3,SLC17A5,PTPN22,GPM6A,PRKCE,PARP9,CHD7,CCL5,NOD2,DDIT4,NAALADL2,B2M,SERINC3,TNFRSF11B,WASL	up_ACOR_VSMC

GO:0140058	0.0511	0.996	2	4	neuron projection arborization	BP	1	ZNF365,NRP1	up_ACOR_VSMC
GO:0071294	0.0511	0.996	2	4	cellular response to zinc ion	BP	1	ENSCAFG00000009113,MT2A	up_VSAP_EC
GO:0072028	0.0511	0.999	1	37	nephron morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0050770	0.0511	0.999	1	39	regulation of axonogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0032768	0.0511	0.999	1	12	regulation of monooxygenase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0072014	0.051197048	0.99933	1	2	proximal tubule development	BP	1	AQP1	up_ACOR_EC
GO:0033554	0.0512	0.963	54	708	cellular response to stress	BP	0.874	ARHGEF2,VEGFA,P4HB,ASNS,PLK3,ENSCAFG00000013214,HSPA5,SOCS5,HM13,SGK1,ERO1A,HSP90B1,CBX5,CASP3,ENSCAFG00000003477,HYOU1,PGK1,NUAK1,PTPN11,SESN2,PTGS2,SEL1L,HIF1A,DNAJC10,TNIK,UBA6,PTPN2,DDX39B,PDIA4,DNAJB9,CTNNB1,UBA5,LYN,BNIP3,DDIT3,PDS5B,FAM162A,BACH1,ATF3,GSK3B,CDC37,GTF2H1,RBBP8,MAPK10,EIF2S1,RAD23A,PAK2,CREB3L2,HIF1AN,CDKN1A,TMTC3,SH3RF3,USP14,MID1	down_VSAP_EC
GO:0046903	0.0512	0.968	28	255	secretion	BP	0.884	GBP5,KIT,EXOC3L2,MEF2C,FERMT1,CHD7,TLR4,STC1,GATA3,EDN1,RAB11A,RAB27A,EXOC6,SNCAIP,ARG2,SNAP23,SCAMP1,RSC1A1,ABCA1,EXOC5,CD200,FES,CREB1,STX11,HMGB1,NOS2,MCU,HIF1A	up_VCAV_EC
GO:0018345	0.0512	0.991	3	12	protein palmitoylation	BP	0.884	ZDHHC22,HHAT,ZDHHC6	up_VCAV_EC
GO:0031268	0.0512	0.992	3	9	pseudopodium organization	BP	1	CDC42EP5,CDC42EP2,F2RL1	up_VSAP_EC
GO:0031269	0.0512	0.992	3	9	pseudopodium assembly	BP	1	CDC42EP5,CDC42EP2,F2RL1	up_VSAP_EC
GO:0003211	0.0512	0.996	2	4	cardiac ventricle formation	BP	1	SMARCD3,TBX5	up_ACOR_VSMC
GO:0048568	0.0512	0.995	2	148	embryonic organ development	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:1901652	0.0512	0.994	2	105	response to peptide	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0001502	0.0512	0.999	1	8	cartilage condensation	BP	1	SULF1	down_ACOR_EC
GO:0098743	0.0512	0.999	1	8	cell aggregation	BP	1	SULF1	down_ACOR_EC
GO:0042493	0.0512	0.999	1	178	response to drug	BP	1	JUP	down_VFEM_VSMC
GO:0060759	0.0512	0.999	1	37	regulation of response to cytokine stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0006940	0.0512	0.999	1	14	regulation of smooth muscle contraction	BP	1	NPNT	up_APUL_EC
GO:0055021	0.0512	0.999	1	15	regulation of cardiac muscle tissue growth	BP	1	TBX5	up_VPUL_EC
GO:0050708	0.05121385	0.98256	6	101	regulation of protein secretion	BP	1	NR1H4,KCNB1,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:2001234	0.05122669	0.98468	5	75	negative regulation of apoptotic signaling	BP	1	IFI6,MAPK8IP2,FIGNL1,CLU,NRP1	up_ACOR_EC
GO:0001816	0.0513	0.968	26	194	cytokine production	BP	1	WNT11,CD274,C5AR2,IL6R,ABL1,HDAC7,DLL1,IL17RC,ANXA4,HPSE,CCBE1,F2RL1,PIK3R1,SULF2,MYD88,NLRX1,TKFC,CD83,RNF216,PNP,MAPKBP1,ZNF580,CYBA,PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:1903506	0.0513	0.98	9	977	regulation of nucleic acid-templated transcription	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0040014	0.0513	0.984	6	27	regulation of multicellular organism growth	BP	1	FGFR2,ATRN,PLAC8B,APP,CHD7,STC2	up_ACOR_VSMC
GO:0044260	0.0513	1	3	2593	cellular macromolecule metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0001937	0.0513	0.991	3	15	negative regulation of endothelial cell	BP	0.874	SULF1,SPARC,APOE	down_VSAP_EC
GO:0097659	0.0513	0.993	3	1072	nucleic acid-templated transcription	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0009887	0.0513	0.995	2	314	animal organ morphogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0048705	0.0513	0.994	2	95	skeletal system morphogenesis	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0048872	0.0514	0.985	5	85	homeostasis of number of cells	BP	1	GPAM,NFE2L1,CYLD,NAPEPLD,GCNT4	up_AFEM_EC
GO:0048666	0.0514	0.987	4	258	neuron development	BP	1	LYN,SPG11,NRP2,NEDD4	down_ACOR_EC
GO:0032774	0.0514	0.993	3	1073	RNA biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC

GO:0006163	0.0514	0.995	2	174	purine nucleotide metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0002091	0.0514	0.996	2	4	negative regulation of receptor internalization	BP	1	ATXN2,LRPAP1	up_ACOR_VSMC
GO:0030878	0.0514	0.999	1	13	thyroid gland development	BP	1	HOXA3	down_ACOR_EC
GO:0032024	0.0514	0.999	1	12	positive regulation of insulin secretion	BP	1	STX4	down_ACOR_EC
GO:0090277	0.0514	0.999	1	12	positive regulation of peptide hormone	BP	1	STX4	down_ACOR_EC
GO:0001544	0.0514	1	1	1	initiation of primordial ovarian follicle growth	BP	1	FOXO3	down_VCAV_EC
GO:0007043	0.0514	0.999	1	28	cell-cell junction assembly	BP	1	HDAC7	down_VPOR_EC
GO:0021675	0.0514	0.999	1	29	nerve development	BP	1	CITED2	down_VPOR_EC
GO:0097581	0.0514	0.999	1	26	lamellipodium organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0050794	0.0515	0.977	18	3075	regulation of cellular process	BP	1	EYA1,HOXA9,TOX,MAP2K6,HOXA10,TRIM9,HOXA7,ENSCAFG00000018194,SIX1,YBX3,MAB21L1,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3	up_VFEM_EC
GO:0035239	0.0515	0.975	12	299	tube morphogenesis	BP	1	IRX3,LEP,ANGPT4,HOXA7,DLL1,F3,TMEM100,GREM1,LUZP1,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0040029	0.0515	0.976	11	74	regulation of gene expression, epigenetic	BP	1	ATAD2,SRRT,RAN,EZH2,UHRF1,BRCA1,SUV39H1,RBM14,HAT1,HIST2H2AC,H2AFX	down_ACOR_VSMC
GO:0031330	0.0515	0.985	5	85	negative regulation of cellular catabolic process	BP	1	LEP,TENT5C,CLEC16A,AXIN2,ACACB	up_AFEM_EC
GO:0007219	0.0515	0.987	4	59	Notch signaling pathway	BP	1	ANGPT4,DLL1,TMEM100,POSTN	up_AFEM_EC
GO:0007267	0.0515	0.987	4	332	cell-cell signaling	BP	1	NETO1,SALL1,TLR2,CAV1	up_VSAP_VSMC
GO:0009309	0.0515	0.996	2	4	amine biosynthetic process	BP	1	MOXD1,AZIN2	up_ACOR_VSMC
GO:0042401	0.0515	0.996	2	4	cellular biogenic amine biosynthetic process	BP	1	MOXD1,AZIN2	up_ACOR_VSMC
GO:0006955	0.0515	0.995	2	327	immune response	BP	1	ARG2,ESR1	up_AORT_VSMC
GO:0045602	0.0515	0.996	2	4	negative regulation of endothelial cell	BP	0.884	JAG1,ZEB1	up_VCAV_EC
GO:0000902	0.0515	0.995	2	266	cell morphogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0035295	0.0515	1	1	356	tube development	BP	1	GATA5	down_AFEM_VSMC
GO:0046474	0.0516	0.98	8	44	glycerophospholipid biosynthetic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,PIGN,PIGS,PIGG,CRLS1	up_ACOR_VSMC
GO:0001952	0.0516	0.983	6	34	regulation of cell-matrix adhesion	BP	0.884	TEK,FERMT1,SLK,APOD,JAG1,ENSCAFG00000002015	up_VCAV_EC
GO:0007338	0.0516	0.988	4	16	single fertilization	BP	1	GLRB,DKKL1,SPINK2,WDR48	up_ACOR_VSMC
GO:0060421	0.0516	0.999	1	14	positive regulation of heart growth	BP	1	TBX5	up_APUL_EC
GO:0071398	0.0516	0.999	1	14	cellular response to fatty acid	BP	1	NR1H4	up_APUL_EC
GO:0035567	0.0516	0.999	1	19	non-canonical Wnt signaling pathway	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030961	0.051650571	0.99932	1	2	peptidyl-arginine hydroxylation	BP	1	RIOX2	up_ACOR_EC
GO:0051223	0.051658373	0.97783	9	181	regulation of protein transport	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,MAVS,PRKCD	up_ACOR_EC
GO:0051149	0.0517	0.985	5	25	positive regulation of muscle cell differentiation	BP	0.884	KIT,MEF2C,EDN1,MTOR,PROX1	up_VCAV_EC
GO:0002934	0.0517	0.996	2	4	desmosome organization	BP	1	JUP,PERP	up_ACOR_VSMC
GO:0008283	0.0517	0.996	2	545	cell proliferation	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0060291	0.0517	0.999	1	11	long-term synaptic potentiation	BP	1	STX4	down_ACOR_EC
GO:0030155	0.0517	0.999	1	180	regulation of cell adhesion	BP	1	JUP	down_VFEM_VSMC
GO:0048209	0.051728485	0.99932	1	2	regulation of vesicle targeting, to, from or	BP	1	PREB	up_ACOR_EC
GO:0006972	0.05176157	0.99932	1	2	hyperosmotic response	BP	1	AQP1	up_ACOR_EC
GO:0071474	0.05176157	0.99932	1	2	cellular hyperosmotic response	BP	1	AQP1	up_ACOR_EC
GO:0010760	0.051770463	0.99932	1	2	negative regulation of macrophage chemotaxis	BP	1	MMP28	up_ACOR_EC
GO:1905522	0.051770463	0.99932	1	2	negative regulation of macrophage migration	BP	1	MMP28	up_ACOR_EC

GO:0042045	0.051793512	0.99932	1	2	epithelial fluid transport	BP	1	AQP1	up_ACOR_EC
GO:0001934	0.0518	0.966	35	274	positive regulation of protein phosphorylation	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,F2RL1,FAM129A,NRP1,PTPN22,NPNT,PRKCE,CCNT1,FRS2,PARP9,APP,PSEN1,CCL5,DDR2,DUSP22,EDN1,AKTIP,NOD2,SH3RF3,MAP3K7,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0051129	0.0518	0.968	26	221	negative regulation of cellular component organization	BP	1	HMGB1,ATAD2,ZW10,CAPG,TRIP13,SLC25A5,FBXO5,PRELID1,BIRC5,INSIG1,CAV1,LIMA1,STMN1,NEK2,BRCA1,NOC2L,NDC80,ENSCAFG00000005299,BUB1,RBM14,CORO1A,TTK,ARHGEF2,TINF2,MTBP,GEN1	down_ACOR_VSMC
GO:2001141	0.0518	0.979	9	979	regulation of RNA biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0009058	0.0518	0.993	4	1910	biosynthetic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:1903727	0.0518	0.988	4	16	positive regulation of phospholipid metabolic	BP	0.884	TEK,ADGRF5,PDGFB,SH3GLB1	up_VCAV_EC
GO:0019221	0.0518	0.99	3	102	cytokine-mediated signaling pathway	BP	1	ENSCAFG00000002015,ASPN,ENSCAFG00000032731	up_VPOR_EC
GO:0071621	0.0518	0.999	1	27	granulocyte chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0071383	0.0519	0.977	10	58	cellular response to steroid hormone stimulus	BP	1	LBH,SKP2,BMP4,MED14,AR,CREBRF,NR3C1,FAM107A,DDIT4,PARK7	up_ACOR_VSMC
GO:0007292	0.0519	0.983	6	32	female gamete generation	BP	1	TRIP13,FBXO5,NCAPH,FOSL1,TTK,ASPM	down_ACOR_VSMC
GO:0010556	0.0519	0.985	6	1137	regulation of macromolecule	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0032528	0.0519	0.992	3	9	microvillus organization	BP	0.884	PODXL,RAPGEF2,FSCN1	up_VCAV_EC
GO:0042986	0.0519	1	1	1	positive regulation of amyloid precursor protein biosynthetic process	BP	1	SOAT1	down_VCAV_EC
GO:0043473	0.0519	0.999	1	28	pigmentation	BP	1	RAB11B	down_VPOR_EC
GO:0002065	0.0519	0.999	1	37	columnar/cuboidal epithelial cell	BP	1	GATA5	up_VCAV_VSMC
GO:2001259	0.0519	0.999	1	13	positive regulation of cation channel activity	BP	1	STIM1	up_VSAP_VSMC
GO:0051146	0.051944499	0.9844	5	76	striated muscle cell differentiation	BP	1	MYOZ2,TMOD1,ACTN2,TBX5,RBM38	up_ACOR_EC
GO:1904154	0.051959737	0.99931	1	2	positive regulation of retrograde protein	BP	1	EDEM2	up_ACOR_EC
GO:0033043	0.052	0.963	48	446	regulation of organelle organization	BP	0.884	PLK2,TEK,HCLS1,ARHGEF15,PDGFB,BAIAP2L1,IWS1,MEF2C,GATA3,EDN1,RALB,ARHGAP28,TMOD1,MTOR,CNOT6,NCKAP1,PROX1,UHRF2,IQGAP2,STMN1,HMBOX1,PRKD2,SH3GLB1,SWAP70,NCK1,FES,NSD1,SENP6,PAN3,TAOK1,TBC1D1,PMAIP1,ARPC5L,SMC5,RAD21,ARHGDIB,ZW10,KDM5A,HIF1A,KDM3A,ATRX,DCP2,TMOD3,RABGAP1,ARHGEF2,FSCN1,FBXO5,USP6NL	up_VCAV_EC
GO:0002520	0.052	0.987	4	279	immune system development	BP	1	LYN,HOXA3,PDPN,HOXA7	down_ACOR_EC
GO:0110111	0.052	0.991	3	17	negative regulation of animal organ	BP	1	ASPN,GREM1,THRB	down_VCAV_EC
GO:0006956	0.052	0.995	2	8	complement activation	BP	1	CFD,A2M	down_VCAV_EC
GO:0001944	0.052	0.995	2	263	vasculature development	BP	1	C6,TGFBI	up_VCAV_VSMC
GO:0042128	0.052	1	1	1	nitrate assimilation	BP	1	SUOX	down_VCAV_EC
GO:0050679	0.052	0.999	1	62	positive regulation of epithelial cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0051146	0.052	0.999	1	76	striated muscle cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0072079	0.052	0.999	1	12	nephron tubule formation	BP	1	SIX1	up_VFEM_EC
GO:0046622	0.052	0.999	1	15	positive regulation of organ growth	BP	1	TBX5	up_VPUL_EC
GO:0048675	0.052	0.999	1	26	axon extension	BP	1	SLIT2	up_VPUL_VSMC
GO:0051182	0.052004021	0.99931	1	2	coenzyme transport	BP	1	SLC25A42	up_ACOR_EC
GO:0072009	0.0521	0.98	8	48	nephron epithelium development	BP	0.884	HOXB7,PODXL,MEF2C,GATA3,MTSS1,BMP2,JAG1,BASP1	up_VCAV_EC
GO:0002753	0.0521	0.988	4	17	cytoplasmic pattern recognition receptor	BP	0.884	TNFAIP3,TLR4,RIOK3,LSM14A	up_VCAV_EC

GO:0021515	0.0521	0.992	3	9	cell differentiation in spinal cord	BP	1	LMO4,TBX20,CLN8	up_ACOR_VSMC
GO:0002673	0.0521	0.995	2	6	regulation of acute inflammatory response	BP	0.874	PTGS2,A2M	down_VSAP_EC
GO:0010718	0.0521	0.999	1	21	positive regulation of epithelial to mesenchymal	BP	1	BAMBI	up_VPOR_VSMC
GO:0035115	0.0521	0.999	1	12	embryonic forelimb morphogenesis	BP	1	HOXA9	up_VFEM_EC
GO:0021954	0.0521	0.999	1	26	central nervous system neuron development	BP	1	SLIT2	up_VPUL_VSMC
GO:1902750	0.0522	0.985	5	24	negative regulation of cell cycle G2/M phase	BP	1	CDK1,FANCI,TOPBP1,DTL,CLSPN	down_ACOR_VSMC
GO:0051240	0.0522	0.985	5	489	positive regulation of multicellular organismal	BP	1	TOX,AVPR1A,HOXB7,SIX1,CYP26B1	up_VFEM_EC
GO:0002534	0.0522	0.988	4	18	cytokine production involved in inflammatory	BP	0.884	GBP5,TLR4,APOD,NOS2	up_VCAV_EC
GO:0033631	0.0522	0.996	2	4	cell-cell adhesion mediated by integrin	BP	0.884	PODXL,SWAP70	up_VCAV_EC
GO:0061178	0.0522	0.999	1	12	regulation of insulin secretion involved in cellular response to	BP	1	STX4	down_ACOR_EC
GO:0051223	0.0522	0.999	1	181	regulation of protein transport	BP	1	JUP	down_VFEM_VSMC
GO:0048592	0.052242551	0.98693	4	53	eye morphogenesis	BP	1	SOX9,AQP1,FZD5,EFEMP1	up_ACOR_EC
GO:1902742	0.052270454	0.99451	2	14	apoptotic process involved in development	BP	1	FZD5,FOXC2	up_ACOR_EC
GO:0001817	0.052277134	0.97751	9	182	regulation of cytokine production	BP	1	CDH3,NR1H4,NDRG2,FZD5,NOD2,IL33,PTGER4,MAVS,AGPAT2	up_ACOR_EC
GO:0016567	0.0523	0.966	30	232	protein ubiquitination	BP	1	PCGF5,SKP2,SH3RF2,ISG15,SASH1,KLHL20,MARCH5,PTPN22,OS9,UBE2H,SH3RF1,RNF24,PRKCE,RNF19A,PSEN1,SHPRH,RNF141,NOD2,FAM107A,SH3RF3,DCUN1D4,RNF181,HERPUD1,CNOT4,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,PARK7	up_ACOR_VSMC
GO:0090596	0.0523	0.974	13	84	sensory organ morphogenesis	BP	1	THRB,CDON,OSR2,INSIG2,LRIG3,IRX5,DLL1,OSR1,RARG,MFN2,ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:0001932	0.0523	0.988	4	416	regulation of protein phosphorylation	BP	1	CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0006099	0.0523	0.988	4	15	tricarboxylic acid cycle	BP	1	DLST,IDH1,IDH3A,ENSCAFG00000006639	up_VSAP_EC
GO:0009190	0.0523	0.992	3	8	cyclic nucleotide biosynthetic process	BP	0.884	NPR1,GUCY1A1,GUCY1B1	up_VCAV_EC
GO:0052652	0.0523	0.992	3	8	cyclic purine nucleotide metabolic process	BP	0.884	NPR1,GUCY1A1,GUCY1B1	up_VCAV_EC
GO:0019367	0.0523	0.996	2	5	fatty acid elongation, saturated fatty acid	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0019368	0.0523	0.996	2	5	fatty acid elongation, unsaturated fatty acid	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0034625	0.0523	0.996	2	5	fatty acid elongation, monounsaturated fatty	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0034626	0.0523	0.996	2	5	fatty acid elongation, polyunsaturated fatty acid	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0035338	0.0523	0.996	2	5	long-chain fatty-acyl-CoA biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0030855	0.0523	0.999	1	183	epithelial cell differentiation	BP	1	GATA5	down_VFEM_VSMC
GO:0001823	0.0523	0.999	1	45	mesonephros development	BP	1	ARG2	up_AORT_VSMC
GO:0060231	0.0523	0.999	1	12	mesenchymal to epithelial transition	BP	1	SALL1	up_VSAP_VSMC
GO:1903035	0.052311495	0.99451	2	14	negative regulation of response to wounding	BP	1	RGMA,PRKCD	up_ACOR_EC
GO:0046459	0.052379949	0.9993	1	2	short-chain fatty acid metabolic process	BP	1	THNSL2	up_ACOR_EC
GO:0051790	0.052379949	0.9993	1	2	short-chain fatty acid biosynthetic process	BP	1	THNSL2	up_ACOR_EC
GO:0048856	0.0524	0.984	7	1533	anatomical structure development	BP	1	HOXC10,DKK2,HOXA9,HOXC6,SGCD,TAOK1,DUSP2	up_AORT_EC
GO:0045665	0.0524	0.982	6	55	negative regulation of neuron differentiation	BP	1	THY1,TLX2,GLI3,PRKCSH,THRB,RGMA	down_VCAV_EC
GO:0030168	0.0524	0.988	4	23	platelet activation	BP	0.874	APOE,LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0006139	0.0524	0.993	4	1909	nucleobase-containing compound metabolic	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0032506	0.0524	0.995	2	8	cytokinetic process	BP	1	SNX18,ANXA11	down_VCAV_EC
GO:0048749	0.0524	1	1	1	compound eye development	BP	1	CHRDL1	down_VCAV_EC

GO:0007186	0.0524	0.999	1	124	G protein-coupled receptor signaling	BP	1	PLCL1	down_VFEM_EC
GO:0048247	0.0524	0.999	1	16	lymphocyte chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0060443	0.0524	0.999	1	13	mammary gland morphogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:0006928	0.0525	0.961	66	557	movement of cell or subcellular component	BP	1	TNNT2,FGF13,RHOT1,VEGFD,LGR6,DNAH7,KCNE3,HTR2B,TCAF1,ZRANB1,RECK,FEZ1,FERMT1,BMP4,GJA1,HRH1,SH3RF2,TP53INP1,SASH1,LMO4,TMEM108,FGF18,IFT43,KIF1A,F2RL1,NRP1,PTPN22,GPM6A,UNC5B,EVL,SPINT2,TBX20,TBX5,PRKCE,FZD3,MYO1B,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,DYNC1I2,ARID5B,FAM107A,JAM3,DISC1,KIF9,FEZ2,SUN1,WASL,DOCK5,ENSCAFG00000029553,DYNC1I1,ENSCAFG00000013536,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0001958	0.0525	0.999	1	11	endochondral ossification	BP	1	CSGALNACT1	down_ACOR_EC
GO:0036075	0.0525	0.999	1	11	replacement ossification	BP	1	CSGALNACT1	down_ACOR_EC
GO:0071612	0.0525	1	1	1	IP-10 production	BP	1	MAVS	down_VCAV_EC
GO:0071651	0.0525	1	1	1	positive regulation of chemokine (C-C motif)	BP	1	MAVS	down_VCAV_EC
GO:0071658	0.0525	1	1	1	regulation of IP-10 production	BP	1	MAVS	down_VCAV_EC
GO:0071660	0.0525	1	1	1	positive regulation of IP-10 production	BP	1	MAVS	down_VCAV_EC
GO:0002905	0.0525	1	1	1	regulation of mature B cell apoptotic process	BP	0.884	BCL10	up_VCAV_EC
GO:0002906	0.0525	1	1	1	negative regulation of mature B cell apoptotic	BP	0.884	BCL10	up_VCAV_EC
GO:0045414	0.0525	1	1	1	regulation of interleukin-8 biosynthetic process	BP	0.884	BCL10	up_VCAV_EC
GO:0045416	0.0525	1	1	1	positive regulation of interleukin-8 biosynthetic	BP	0.884	BCL10	up_VCAV_EC
GO:0002901	0.0525	1	1	1	mature B cell apoptotic process	BP	0.884	BCL10	up_VCAV_EC
GO:0048565	0.0525	0.999	1	38	digestive tract development	BP	1	GATA5	up_VCAV_VSMC
GO:0061383	0.0525	0.999	1	20	trabecula morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0034969	0.052551194	0.99929	1	2	histone arginine methylation	BP	1	NR1H4	up_ACOR_EC
GO:0006528	0.052599696	0.99929	1	2	asparagine metabolic process	BP	1	NIT2	up_ACOR_EC
GO:0045785	0.0526	0.972	16	107	positive regulation of cell adhesion	BP	1	LEP,CD83,FERMT1,CITED2,CD274,NRP1,PTPN22,NPNT,PRKCE,ECM2,JUP,NID1,DUSP26,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0060840	0.0526	0.98	8	42	artery development	BP	1	SMAD6,BMP4,SEC24B,CITED2,NRP1,CHD7,HPGD,AP2B1	up_ACOR_VSMC
GO:0006754	0.0526	0.985	5	36	ATP biosynthetic process	BP	0.874	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0044380	0.0526	0.991	3	14	protein localization to cytoskeleton	BP	0.874	HOOK3,GSK3B,MID1	down_VSAP_EC
GO:0045637	0.0526	0.994	2	73	regulation of myeloid cell differentiation	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0021510	0.0526	0.999	1	23	spinal cord development	BP	1	HOXC10	up_AORT_EC
GO:0003209	0.0526	0.999	1	14	cardiac atrium morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0003230	0.0526	0.999	1	14	cardiac atrium development	BP	1	TBX5	up_APUL_EC
GO:0071624	0.0526	0.999	1	6	positive regulation of granulocyte chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0090023	0.0526	0.999	1	6	positive regulation of neutrophil chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0006040	0.0526	0.999	1	12	amino sugar metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0055022	0.052689359	0.99929	1	2	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0060044	0.052689359	0.99929	1	2	negative regulation of cardiac muscle cell	BP	1	TBX5	up_ACOR_EC
GO:0061117	0.052689359	0.99929	1	2	negative regulation of heart growth	BP	1	TBX5	up_ACOR_EC
GO:0022407	0.0527	0.974	13	96	regulation of cell-cell adhesion	BP	0.884	IL7R,PODXL,GATA3,PELI1,ARG2,BMP2,ITPKB,SWAP70,NCK1,JAG1,BCL10,HMGB1,ITGA6	up_VCAV_EC

GO:0051926	0.0527	0.999	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	down_ACOR_EC
GO:0018209	0.0527	0.999	1	125	peptidyl-serine modification	BP	1	PLCL1	down_VFEM_EC
GO:0060612	0.0527	0.999	1	14	adipose tissue development	BP	1	NR1H4	up_APUL_EC
GO:0072077	0.0527	0.999	1	13	renal vesicle morphogenesis	BP	1	SALL1	up_VSAP_VSMC
GO:0072273	0.0527	0.999	1	13	metanephric nephron morphogenesis	BP	1	SALL1	up_VSAP_VSMC
GO:0032757	0.052754214	0.99444	2	14	positive regulation of interleukin-8 production	BP	1	NOD2,MAVS	up_ACOR_EC
GO:0001941	0.052787819	0.99443	2	14	postsynaptic membrane organization	BP	1	LRP4,LRRC4	up_ACOR_EC
GO:0009968	0.0528	0.964	42	392	negative regulation of signal transduction	BP	0.884	CXCL8,TNFAIP3,TNIP1,PDE4D,FERMT1,ATF3,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,APLNR,ARAP3,HOMER3,EGFL7,FIGNL1,CASP8,MTOR,BMP2,HHEX,PREX2,GDPD5,RIOK3,STMN1,MCC,SMARCA4,APOD,NCK1,OTUD4,PTGS2,CTDSPL2,CTNNA1,CNOT7,RIPK1,ITGA6,RGS2,SKIL,HIF1A,TNFAIP1,IVNS1ABP,ARHGEF2,PEAR1	up_VCAV_EC
GO:2000179	0.0528	0.988	4	14	positive regulation of neural precursor cell	BP	0.884	DLL4,PROX1,HIF1A,CDON	up_VCAV_EC
GO:0086004	0.0528	0.991	3	10	regulation of cardiac muscle cell contraction	BP	1	FGF13,KCNE3,JUP	up_ACOR_VSMC
GO:0060592	0.0528	0.996	2	4	mammary gland formation	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0006549	0.0528	1	1	1	isoleucine metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0006550	0.0528	1	1	1	isoleucine catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0016480	0.0528	1	1	1	negative regulation of transcription by RNA polymerase III	BP	1	NAB2	down_VCAV_EC
GO:0046952	0.0528	1	1	1	ketone body catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:1901373	0.0528	1	1	1	lipid hydroperoxide transport	BP	1	SCP2	down_VCAV_EC
GO:1902858	0.0528	1	1	1	propionyl-CoA metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:1902860	0.0528	1	1	1	propionyl-CoA biosynthetic process	BP	1	ACAT1	down_VCAV_EC
GO:0006957	0.0528	1	1	1	complement activation, alternative pathway	BP	1	CFD	down_VCAV_EC
GO:0097194	0.0528	0.999	1	23	execution phase of apoptosis	BP	1	TAOK1	up_AORT_EC
GO:0043433	0.0528	0.999	1	49	negative regulation of DNA-binding transcription factor activity	BP	1	ESR1	up_AORT_VSMC
GO:0001947	0.0528	0.999	1	21	heart looping	BP	1	NKX2-5	up_VPOR_VSMC
GO:0061371	0.0528	0.999	1	21	determination of heart left/right asymmetry	BP	1	NKX2-5	up_VPOR_VSMC
GO:0061043	0.052877902	0.99929	1	2	regulation of vascular wound healing	BP	1	FOXC2	up_ACOR_EC
GO:0080134	0.052893481	0.97134	16	386	regulation of response to stress	BP	1	NR1H4,FNDC4,EDEM2,FZD5,NOD2,IL33,RGMA,TNFRSF19,PTGER4,MAPK8IP2,MAVS,FOXC2,FIGNL1,SH3RF3,CLU,PRKCD	up_ACOR_EC
GO:0001701	0.0529	0.971	17	134	in utero embryonic development	BP	0.884	PCDH12,TIE1,AMOT,PDGFB,CHD7,GATA3,EDN1,SOX18,BMP2,HHEX,MDFI,SKIL,CUL4A,HIF1A,RBBP6,VASH1,GINS4	up_VCAV_EC
GO:0071478	0.0529	0.978	9	58	cellular response to radiation	BP	1	NEDD4,INTS7,RAD51,AURKB,MAP3K20,PCNA,NOC2L,POLH,CDC25A	down_ACOR_VSMC
GO:0031345	0.0529	0.994	2	46	negative regulation of cell projection organization	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0060425	0.0529	0.999	1	25	lung morphogenesis	BP	1	SRSF6	down_AFEM_EC
GO:0005988	0.0529	1	1	1	lactose metabolic process	BP	1	B4GALT1	down_VCAV_EC
GO:0005989	0.0529	1	1	1	lactose biosynthetic process	BP	1	B4GALT1	down_VCAV_EC
GO:0060057	0.0529	1	1	1	apoptotic process involved in mammary	BP	1	B4GALT1	down_VCAV_EC
GO:0060058	0.0529	1	1	1	positive regulation of apoptotic process involved in mammary	BP	1	B4GALT1	down_VCAV_EC
GO:1903519	0.0529	1	1	1	regulation of mammary gland involution	BP	1	B4GALT1	down_VCAV_EC

GO:1903521	0.0529	1	1	1	positive regulation of mammary gland	BP	1	B4GALT1	down_VCAV_EC
GO:0007619	0.0529	1	1	1	courtship behavior	BP	1	THRB	down_VCAV_EC
GO:0007621	0.0529	1	1	1	negative regulation of female receptivity	BP	1	THRB	down_VCAV_EC
GO:0008050	0.0529	1	1	1	female courtship behavior	BP	1	THRB	down_VCAV_EC
GO:0042480	0.0529	1	1	1	negative regulation of eye photoreceptor cell	BP	1	THRB	down_VCAV_EC
GO:0045924	0.0529	1	1	1	regulation of female receptivity	BP	1	THRB	down_VCAV_EC
GO:0060180	0.0529	1	1	1	female mating behavior	BP	1	THRB	down_VCAV_EC
GO:0097474	0.0529	1	1	1	retinal cone cell apoptotic process	BP	1	THRB	down_VCAV_EC
GO:0050770	0.0529	0.999	1	39	regulation of axonogenesis	BP	1	LIMK1	up_VCAV_VSMC
GO:0008306	0.0529	0.999	1	21	associative learning	BP	1	NETO1	up_VFEM_VSMC
GO:0060548	0.053	0.967	25	294	negative regulation of cell death	BP	0.874	ARHGEF2,VEGFA,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,HYOU1,AARS,FHL2,PTGS2,HIF1A,ZPR1,MTDH,CTNNB1,CRYAB,APOE,BNIP3,GSK3B,HTT,GLO1,PAK2,SIX4,NRP1,ARF4	down_VSAP_EC
GO:0070085	0.053	0.973	14	95	glycosylation	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,B3GNT7,CCDC126,MAGT1,STT3B,FUT11,FUT8,POMK,PSEN1,EOGT,LMF1	up_ACOR_VSMC
GO:0022612	0.053	0.979	8	44	gland morphogenesis	BP	1	LIMS2,FGF7,RARG,STAT6,SULF2,NTN4,NFIB,TGFBR2	up_VSAP_EC
GO:0030004	0.053	0.99	3	36	cellular monovalent inorganic cation	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0043691	0.053	0.996	2	4	reverse cholesterol transport	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0048532	0.053	0.999	1	9	anatomical structure arrangement	BP	1	NRP2	down_ACOR_EC
GO:0030644	0.053	1	1	1	cellular chloride ion homeostasis	BP	1	ENSCAFG00000018277	down_VCAV_EC
GO:0055064	0.053	1	1	1	chloride ion homeostasis	BP	1	ENSCAFG00000018277	down_VCAV_EC
GO:0060040	0.053	1	1	1	retinal bipolar neuron differentiation	BP	1	IRX5	down_VCAV_EC
GO:0001824	0.053	0.999	1	27	blastocyst development	BP	1	CITED2	down_VPOR_EC
GO:0008584	0.053	0.999	1	39	male gonad development	BP	1	HOXA9	up_AFEM_VSMC
GO:0046546	0.053	0.999	1	39	development of primary male sexual	BP	1	HOXA9	up_AFEM_VSMC
GO:0032944	0.053	0.999	1	48	regulation of mononuclear cell	BP	1	ARG2	up_AORT_VSMC
GO:0050670	0.053	0.999	1	48	regulation of lymphocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0001934	0.0531	0.969	20	274	positive regulation of protein phosphorylation	BP	1	NOTCH2,PDGFRB,PRNP,GLIPR2,BMPR1A,CLIP3,AKT2,CSPG4,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0098660	0.0531	0.974	12	141	inorganic ion transmembrane transport	BP	1	PRNP,FXYD1,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SCARA5,CYBA,ARHGAP1,CLIC4	down_VCAV_EC
GO:0010975	0.0531	0.975	11	103	regulation of neuron projection development	BP	0.874	SIPA1L1,DPYSL3,IFRD1,TNIK,UST,APOE,LYN,VLDLR,DISC1,NRP1,YWHAH	down_VSAP_EC
GO:0030336	0.0531	0.984	5	86	negative regulation of cell migration	BP	1	ANGPT4,HOXA7,RECK,TBXA2R,KANK1	up_AFEM_EC
GO:0044728	0.0531	0.988	4	17	DNA methylation or demethylation	BP	0.884	GATA3,OTUD4,MTA2,TET2	up_VCAV_EC
GO:0071495	0.0531	1	1	365	cellular response to endogenous stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0016056	0.0531	1	1	1	rhodopsin mediated signaling pathway	BP	0.874	RDH11	down_VSAP_EC
GO:0036367	0.0531	1	1	1	light adaption	BP	0.874	RDH11	down_VSAP_EC
GO:0016062	0.0531	1	1	1	adaptation of rhodopsin mediated signaling	BP	0.874	RDH11	down_VSAP_EC
GO:0022612	0.0531	0.999	1	44	gland morphogenesis	BP	1	ESR1	up_AORT_VSMC
GO:0060026	0.0531	0.999	1	7	convergent extension	BP	1	PTK7	up_VPOR_EC
GO:1990868	0.0531	0.999	1	16	response to chemokine	BP	1	CCL24	up_VPUL_EC
GO:1990869	0.0531	0.999	1	16	cellular response to chemokine	BP	1	CCL24	up_VPUL_EC

GO:1903524	0.0531	0.999	1	11	positive regulation of blood circulation	BP	1	CAV1	up_VSAP_VSMC
GO:0048681	0.053126613	0.99928	1	2	negative regulation of axon regeneration	BP	1	RGMA	up_ACOR_EC
GO:0090154	0.053127462	0.99928	1	2	positive regulation of sphingolipid biosynthetic	BP	1	PRKCD	up_ACOR_EC
GO:2000304	0.053127462	0.99928	1	2	positive regulation of ceramide biosynthetic	BP	1	PRKCD	up_ACOR_EC
GO:2000145	0.0532	0.965	35	279	regulation of cell motility	BP	1	HOXA7,TWIST2,WNT11,FAM107A,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,FUZ,PDGFD,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,FBLN1,ZNF580,STX4,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0042254	0.0532	0.971	16	128	ribosome biogenesis	BP	1	NOP56,RAN,FBL,DIS3,NOC4L,NOC2L,DDX28,RSL1D1,RRP1,ENSCAFG00000019620,NOP14,NOP58,ENSCAFG00000015189,EMG1,EXOSC5,NOB1	down_ACOR_VSMC
GO:0035107	0.0532	0.987	4	60	appendage morphogenesis	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0035108	0.0532	0.987	4	60	limb morphogenesis	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0042304	0.0532	0.991	3	15	regulation of fatty acid biosynthetic process	BP	0.874	TRIB3,PTGS2,SLC45A3	down_VSAP_EC
GO:0060462	0.0532	0.996	2	4	lung lobe development	BP	1	FGFR2,SEC24B	up_ACOR_VSMC
GO:0060463	0.0532	0.996	2	4	lung lobe morphogenesis	BP	1	FGFR2,SEC24B	up_ACOR_VSMC
GO:1905063	0.0532	0.996	2	5	regulation of vascular smooth muscle cell	BP	0.884	KIT,PDGFB	up_VCAV_EC
GO:0035313	0.0532	0.999	1	7	wound healing, spreading of epidermal cells	BP	1	ACVRL1	down_ACOR_EC
GO:1901379	0.0532	0.999	1	12	regulation of potassium ion transmembrane	BP	1	NEDD4	down_ACOR_EC
GO:0006169	0.0532	1	1	1	adenosine salvage	BP	1	ADK	down_VCAV_EC
GO:0006175	0.0532	1	1	1	dATP biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0009153	0.0532	1	1	1	purine deoxyribonucleotide	BP	1	ADK	down_VCAV_EC
GO:0009202	0.0532	1	1	1	deoxyribonucleoside triphosphate biosynthetic	BP	1	ADK	down_VCAV_EC
GO:0018400	0.0532	1	1	1	peptidyl-proline hydroxylation to 3-	BP	1	CRTAP	down_VCAV_EC
GO:0046086	0.0532	1	1	1	adenosine biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0009216	0.0532	1	1	1	purine deoxyribonucleoside	BP	1	ADK	down_VCAV_EC
GO:0070170	0.0532	1	1	1	regulation of tooth mineralization	BP	1	ASPN	down_VCAV_EC
GO:0070171	0.0532	1	1	1	negative regulation of tooth mineralization	BP	1	ASPN	down_VCAV_EC
GO:0090107	0.0532	1	1	1	regulation of high-density lipoprotein particle	BP	1	LCAT	down_VCAV_EC
GO:0014031	0.0532	0.999	1	27	mesenchymal cell development	BP	1	CITED2	down_VPOR_EC
GO:0014032	0.0532	0.999	1	27	neural crest cell development	BP	1	CITED2	down_VPOR_EC
GO:0006707	0.0532	1	1	1	cholesterol catabolic process	BP	0.874	APOE	down_VSAP_EC
GO:0010873	0.0532	1	1	1	positive regulation of cholesterol esterification	BP	0.874	APOE	down_VSAP_EC
GO:0010877	0.0532	1	1	1	lipid transport involved in lipid storage	BP	0.874	APOE	down_VSAP_EC
GO:0032802	0.0532	1	1	1	low-density lipoprotein particle receptor catabolic	BP	0.874	APOE	down_VSAP_EC
GO:0032803	0.0532	1	1	1	regulation of low-density lipoprotein particle receptor catabolic process	BP	0.874	APOE	down_VSAP_EC
GO:0032805	0.0532	1	1	1	positive regulation of low-density lipoprotein particle receptor catabolic	BP	0.874	APOE	down_VSAP_EC
GO:0090731	0.0532	1	1	1	cellular response to very-low-density lipoprotein particle stimulus	BP	0.874	APOE	down_VSAP_EC
GO:0097113	0.0532	1	1	1	AMPA glutamate receptor clustering	BP	0.874	APOE	down_VSAP_EC
GO:0097688	0.0532	1	1	1	glutamate receptor clustering	BP	0.874	APOE	down_VSAP_EC

GO:1901630	0.0532	1	1	1	negative regulation of presynaptic membrane	BP	0.874	APOE	down_VSAP_EC
GO:1902952	0.0532	1	1	1	positive regulation of dendritic spine	BP	0.874	APOE	down_VSAP_EC
GO:1902994	0.0532	1	1	1	regulation of phospholipid efflux	BP	0.874	APOE	down_VSAP_EC
GO:1902995	0.0532	1	1	1	positive regulation of phospholipid efflux	BP	0.874	APOE	down_VSAP_EC
GO:1903000	0.0532	1	1	1	regulation of lipid transport across blood	BP	0.874	APOE	down_VSAP_EC
GO:1903002	0.0532	1	1	1	positive regulation of lipid transport across blood brain barrier	BP	0.874	APOE	down_VSAP_EC
GO:1905853	0.0532	1	1	1	regulation of heparan sulfate binding	BP	0.874	APOE	down_VSAP_EC
GO:1905855	0.0532	1	1	1	positive regulation of heparan sulfate binding	BP	0.874	APOE	down_VSAP_EC
GO:1905858	0.0532	1	1	1	regulation of heparan sulfate proteoglycan	BP	0.874	APOE	down_VSAP_EC
GO:1905860	0.0532	1	1	1	positive regulation of heparan sulfate	BP	0.874	APOE	down_VSAP_EC
GO:1905890	0.0532	1	1	1	regulation of cellular response to very-low-density lipoprotein	BP	0.874	APOE	down_VSAP_EC
GO:1990379	0.0532	1	1	1	lipid transport across blood brain barrier	BP	0.874	APOE	down_VSAP_EC
GO:0016127	0.0532	1	1	1	sterol catabolic process	BP	0.874	APOE	down_VSAP_EC
GO:0008038	0.0532	0.999	1	7	neuron recognition	BP	1	SEMA3A	up_VPOR_EC
GO:0072615	0.053219172	0.99928	1	2	interleukin-17 secretion	BP	1	NR1H4	up_ACOR_EC
GO:0072173	0.053299059	0.99927	1	2	metanephric tubule morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0072174	0.053299059	0.99927	1	2	metanephric tubule formation	BP	1	SOX9	up_ACOR_EC
GO:0072282	0.053299059	0.99927	1	2	metanephric nephron tubule morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0072289	0.053299059	0.99927	1	2	metanephric nephron tubule formation	BP	1	SOX9	up_ACOR_EC
GO:0030833	0.0533	0.978	9	59	regulation of actin filament polymerization	BP	0.884	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0048731	0.0533	0.981	8	1247	system development	BP	1	TBX5,HOXA3,NR1H4,EVI2B,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0072172	0.0533	0.995	2	7	mesonephric tubule formation	BP	0.874	ENSCAFG00000032470,SIX4	down_VSAP_EC
GO:0072359	0.0533	1	1	368	circulatory system development	BP	1	GATA5	down_AFEM_VSMC
GO:0060979	0.0533	1	1	1	vasculogenesis involved in coronary vascular	BP	1	SPRED1	down_VCAV_EC
GO:0071484	0.0533	1	1	1	cellular response to light intensity	BP	1	AKT2	down_VCAV_EC
GO:0071486	0.0533	1	1	1	cellular response to high light intensity	BP	1	AKT2	down_VCAV_EC
GO:0097473	0.0533	1	1	1	retinal rod cell apoptotic process	BP	1	AKT2	down_VCAV_EC
GO:2001136	0.0533	1	1	1	negative regulation of endocytic recycling	BP	1	ARHGAP1	down_VCAV_EC
GO:0010918	0.0533	1	1	1	positive regulation of mitochondrial membrane potential	BP	1	AKT2	down_VCAV_EC
GO:0021527	0.0533	1	1	1	spinal cord association neuron differentiation	BP	1	LMO4	down_VCAV_EC
GO:0042078	0.0533	1	1	1	germ-line stem cell division	BP	1	ZBTB16	down_VCAV_EC
GO:0048133	0.0533	1	1	1	male germ-line stem cell asymmetric division	BP	1	ZBTB16	down_VCAV_EC
GO:0098728	0.0533	1	1	1	germline stem cell asymmetric division	BP	1	ZBTB16	down_VCAV_EC
GO:0090087	0.0533	0.999	1	185	regulation of peptide transport	BP	1	JUP	down_VFEM_VSMC
GO:0030239	0.0533	0.999	1	21	myofibril assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007215	0.0533	0.999	1	13	glutamate receptor signaling pathway	BP	1	NETO1	up_VSAP_VSMC
GO:0042398	0.0533	0.999	1	12	cellular modified amino acid biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0007352	0.053328539	0.99927	1	2	zygotic specification of dorsal/ventral axis	BP	1	SMAD6	up_ACOR_EC

GO:0010988	0.053391673	0.99927	1	2	regulation of low-density lipoprotein particle	BP	1	NR1H4	up_ACOR_EC
GO:0009888	0.0534	0.985	5	545	tissue development	BP	1	NR1H4,TBX5,HOXA3,ARHGEF26,NPNT	up_APUL_EC
GO:0035150	0.0534	0.99	3	36	regulation of tube size	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0050880	0.0534	0.99	3	36	regulation of blood vessel size	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0019953	0.0534	0.994	2	152	sexual reproduction	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0097193	0.0534	0.994	2	109	intrinsic apoptotic signaling pathway	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0002438	0.0534	1	1	1	acute inflammatory response to antigenic	BP	1	PARK7	down_VCAV_EC
GO:0002866	0.0534	1	1	1	positive regulation of acute inflammatory response to antigenic	BP	1	PARK7	down_VCAV_EC
GO:0006030	0.0534	1	1	1	chitin metabolic process	BP	1	CHID1	down_VCAV_EC
GO:0006032	0.0534	1	1	1	chitin catabolic process	BP	1	CHID1	down_VCAV_EC
GO:0006780	0.0534	1	1	1	uroporphyrinogen III biosynthetic process	BP	1	UROS	down_VCAV_EC
GO:0010273	0.0534	1	1	1	detoxification of copper ion	BP	1	PARK7	down_VCAV_EC
GO:0015680	0.0534	1	1	1	protein maturation by copper ion transfer	BP	1	ATOX1	down_VCAV_EC
GO:0017187	0.0534	1	1	1	peptidyl-glutamic acid carboxylation	BP	1	VKORC1	down_VCAV_EC
GO:0018323	0.0534	1	1	1	enzyme active site formation via L-cysteine	BP	1	PARK7	down_VCAV_EC
GO:0032905	0.0534	1	1	1	transforming growth factor beta1 production	BP	1	LUM	down_VCAV_EC
GO:0032908	0.0534	1	1	1	regulation of transforming growth factor beta1	BP	1	LUM	down_VCAV_EC
GO:0032914	0.0534	1	1	1	positive regulation of transforming growth factor beta1 production	BP	1	LUM	down_VCAV_EC
GO:0033860	0.0534	1	1	1	regulation of NAD(P)H oxidase activity	BP	1	PARK7	down_VCAV_EC
GO:0033864	0.0534	1	1	1	positive regulation of NAD(P)H oxidase activity	BP	1	PARK7	down_VCAV_EC
GO:0002158	0.0534	1	1	1	osteoclast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0034164	0.0534	1	1	1	negative regulation of toll-like receptor 9 signaling	BP	1	RAB7B	down_VCAV_EC
GO:0036525	0.0534	1	1	1	protein deglycation	BP	1	PARK7	down_VCAV_EC
GO:0036526	0.0534	1	1	1	peptidyl-cysteine deglycation	BP	1	PARK7	down_VCAV_EC
GO:0036527	0.0534	1	1	1	peptidyl-arginine deglycation	BP	1	PARK7	down_VCAV_EC
GO:0036528	0.0534	1	1	1	peptidyl-lysine deglycation	BP	1	PARK7	down_VCAV_EC
GO:0036529	0.0534	1	1	1	protein deglycation, glyoxal removal	BP	1	PARK7	down_VCAV_EC
GO:0036530	0.0534	1	1	1	protein deglycation, methylglyoxal removal	BP	1	PARK7	down_VCAV_EC
GO:0036531	0.0534	1	1	1	glutathione deglycation	BP	1	PARK7	down_VCAV_EC
GO:0042373	0.0534	1	1	1	vitamin K metabolic process	BP	1	VKORC1	down_VCAV_EC
GO:0046826	0.0534	1	1	1	negative regulation of protein export from	BP	1	PARK7	down_VCAV_EC
GO:0046851	0.0534	1	1	1	negative regulation of bone remodeling	BP	1	GREM1	down_VCAV_EC
GO:0002863	0.0534	1	1	1	positive regulation of inflammatory response to antigenic stimulus	BP	1	PARK7	down_VCAV_EC
GO:0002864	0.0534	1	1	1	regulation of acute inflammatory response to	BP	1	PARK7	down_VCAV_EC
GO:0050787	0.0534	1	1	1	detoxification of mercury ion	BP	1	PARK7	down_VCAV_EC
GO:0060081	0.0534	1	1	1	membrane hyperpolarization	BP	1	PARK7	down_VCAV_EC
GO:0061687	0.0534	1	1	1	detoxification of inorganic compound	BP	1	PARK7	down_VCAV_EC
GO:0090086	0.0534	1	1	1	negative regulation of protein deubiquitination	BP	1	PARK7	down_VCAV_EC

GO:0090289	0.0534	1	1	1	regulation of osteoclast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0090291	0.0534	1	1	1	negative regulation of osteoclast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0097238	0.0534	1	1	1	cellular response to methylglyoxal	BP	1	PARK7	down_VCAV_EC
GO:0097501	0.0534	1	1	1	stress response to metal ion	BP	1	PARK7	down_VCAV_EC
GO:0106044	0.0534	1	1	1	guanine deglycation	BP	1	PARK7	down_VCAV_EC
GO:0106045	0.0534	1	1	1	guanine deglycation, methylglyoxal removal	BP	1	PARK7	down_VCAV_EC
GO:0106046	0.0534	1	1	1	guanine deglycation, glyoxal removal	BP	1	PARK7	down_VCAV_EC
GO:0140041	0.0534	1	1	1	cellular detoxification of methylglyoxal	BP	1	PARK7	down_VCAV_EC
GO:1901671	0.0534	1	1	1	positive regulation of superoxide dismutase	BP	1	PARK7	down_VCAV_EC
GO:1902938	0.0534	1	1	1	regulation of intracellular calcium activated chloride	BP	1	PRNP	down_VCAV_EC
GO:1902958	0.0534	1	1	1	positive regulation of mitochondrial electron transport, NADH to	BP	1	PARK7	down_VCAV_EC
GO:1903031	0.0534	1	1	1	regulation of microtubule plus-end binding	BP	1	MAPRE3	down_VCAV_EC
GO:1903033	0.0534	1	1	1	positive regulation of microtubule plus-end	BP	1	MAPRE3	down_VCAV_EC
GO:1903094	0.0534	1	1	1	negative regulation of protein K48-linked	BP	1	PARK7	down_VCAV_EC
GO:1903122	0.0534	1	1	1	negative regulation of TRAIL-activated apoptotic signaling pathway	BP	1	PARK7	down_VCAV_EC
GO:1903167	0.0534	1	1	1	regulation of pyrroline-5-carboxylate reductase	BP	1	PARK7	down_VCAV_EC
GO:1903168	0.0534	1	1	1	positive regulation of pyrroline-5-carboxylate	BP	1	PARK7	down_VCAV_EC
GO:1903184	0.0534	1	1	1	L-dopa metabolic process	BP	1	PARK7	down_VCAV_EC
GO:1903185	0.0534	1	1	1	L-dopa biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:1903189	0.0534	1	1	1	glyoxal metabolic process	BP	1	PARK7	down_VCAV_EC
GO:1903195	0.0534	1	1	1	regulation of L-dopa biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:1903197	0.0534	1	1	1	positive regulation of L-dopa biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:1903383	0.0534	1	1	1	regulation of hydrogen peroxide-induced neuron intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:1903384	0.0534	1	1	1	negative regulation of hydrogen peroxide-induced neuron intrinsic	BP	1	PARK7	down_VCAV_EC
GO:1903750	0.0534	1	1	1	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	PARK7	down_VCAV_EC
GO:1903751	0.0534	1	1	1	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	PARK7	down_VCAV_EC
GO:1903795	0.0534	1	1	1	regulation of inorganic anion transmembrane	BP	1	PRNP	down_VCAV_EC
GO:1904833	0.0534	1	1	1	positive regulation of removal of superoxide	BP	1	PARK7	down_VCAV_EC
GO:1905258	0.0534	1	1	1	regulation of nitrosative stress-induced intrinsic apoptotic signaling	BP	1	PARK7	down_VCAV_EC
GO:1905259	0.0534	1	1	1	negative regulation of nitrosative stress-induced intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:2000284	0.0534	1	1	1	positive regulation of cellular amino acid	BP	1	PARK7	down_VCAV_EC
GO:0009441	0.0534	1	1	1	glycolate metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0018214	0.0534	1	1	1	protein carboxylation	BP	1	VKORC1	down_VCAV_EC
GO:0031204	0.0534	1	1	1	posttranslational protein targeting to membrane, translocation	BP	1	SEC61B	down_VCAV_EC
GO:0036376	0.0534	1	1	1	sodium ion export across plasma membrane	BP	1	FXYD1	down_VCAV_EC

GO:0036471	0.0534	1	1	1	cellular response to glyoxal	BP	1	PARK7	down_VCAV_EC
GO:0036482	0.0534	1	1	1	neuron intrinsic apoptotic signaling pathway in response to hydrogen	BP	1	PARK7	down_VCAV_EC
GO:0046295	0.0534	1	1	1	glycolate biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0046360	0.0534	1	1	1	2-oxobutyrate biosynthetic process	BP	1	THNSL2	down_VCAV_EC
GO:0046361	0.0534	1	1	1	2-oxobutyrate metabolic process	BP	1	THNSL2	down_VCAV_EC
GO:0046502	0.0534	1	1	1	uroporphyrinogen III metabolic process	BP	1	UROS	down_VCAV_EC
GO:0048874	0.0534	1	1	1	host-mediated regulation of intestinal microbiota	BP	1	NAPEPLD	down_VCAV_EC
GO:0070291	0.0534	1	1	1	N-acylethanolamine metabolic process	BP	1	NAPEPLD	down_VCAV_EC
GO:0070292	0.0534	1	1	1	N-acylphosphatidylethanola	BP	1	NAPEPLD	down_VCAV_EC
GO:0097403	0.0534	1	1	1	cellular response to raffinose	BP	1	ZFP36L1	down_VCAV_EC
GO:1901545	0.0534	1	1	1	response to raffinose	BP	1	ZFP36L1	down_VCAV_EC
GO:1903259	0.0534	1	1	1	exon-exon junction complex disassembly	BP	1	PYM1	down_VCAV_EC
GO:1903276	0.0534	1	1	1	regulation of sodium ion export across plasma	BP	1	FXYD1	down_VCAV_EC
GO:1903278	0.0534	1	1	1	positive regulation of sodium ion export across	BP	1	FXYD1	down_VCAV_EC
GO:1904580	0.0534	1	1	1	regulation of intracellular mRNA localization	BP	1	ZFP36L1	down_VCAV_EC
GO:1904582	0.0534	1	1	1	positive regulation of intracellular mRNA	BP	1	ZFP36L1	down_VCAV_EC
GO:1990169	0.0534	1	1	1	stress response to copper ion	BP	1	PARK7	down_VCAV_EC
GO:2000152	0.0534	1	1	1	regulation of ubiquitin-specific protease activity	BP	1	PARK7	down_VCAV_EC
GO:2000157	0.0534	1	1	1	negative regulation of ubiquitin-specific	BP	1	PARK7	down_VCAV_EC
GO:2000277	0.0534	1	1	1	positive regulation of oxidative phosphorylation uncoupler activity	BP	1	PARK7	down_VCAV_EC
GO:0007498	0.0534	0.999	1	38	mesoderm development	BP	1	EYA1	up_AFEM_VSMC
GO:0048639	0.0534	0.999	1	39	positive regulation of developmental growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0003197	0.0534	0.999	1	16	endocardial cushion development	BP	1	TBX5	up_VPUL_EC
GO:0060079	0.0534	0.999	1	15	excitatory postsynaptic potential	BP	1	NETO1	up_VSAP_VSMC
GO:0003285	0.053406829	0.99927	1	2	septum secundum development	BP	1	GATA4	up_ACOR_EC
GO:0032502	0.053417361	0.96248	54	1661	developmental process	BP	1	SH3TC2,MYOZ2,CPAMD8,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TRPS1,TBX18,SOX9,RHOU,PTH1R,NDRG2,AQP1,ENSCAFG00000004331,FZD5,CCDC3,SEMA6D,DIXDC1,PDLIM3,RGMA,LHX9,SMAD6,PLS1,ACTN2,ESM1,PAK3,IL11RA,DLX3,TRIM8,TNFRSF19,PTGER4,ARHGDIB,PIAS1,DCLK2,ADAMTSL2,MAPK8IP2,FOXC2,FIGNL1,TBX5,LRP4,CLSTN1,PRELP,RBM38,C23H3orf58,TP53INP2,RARRES2,NRP1,ARHGEF26,PRKCD,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:0003209	0.053420275	0.99433	2	14	cardiac atrium morphogenesis	BP	1	GATA4,TBX5	up_ACOR_EC
GO:0003230	0.053420275	0.99433	2	14	cardiac atrium development	BP	1	GATA4,TBX5	up_ACOR_EC
GO:0048865	0.053435013	0.99927	1	2	stem cell fate commitment	BP	1	SOX9	up_ACOR_EC
GO:0048866	0.053435013	0.99927	1	2	stem cell fate specification	BP	1	SOX9	up_ACOR_EC
GO:0046813	0.053449184	0.99927	1	2	receptor-mediated virion attachment to host cell	BP	1	LRRC15	up_ACOR_EC
GO:0048870	0.053450813	0.96992	18	451	cell motility	BP	1	SOX9,AQP1,ENSCAFG00000004331,SEMA6D,DIXDC1,ZMYND8,PAK3,MMP28,PTGER4,ARHGDIB,ELMO2,FOXC2,LRRC15,TBX5,RARRES2,NRP1,PRKCD,CCNYL1	up_ACOR_EC

GO:0051674	0.053450813	0.96992	18	451	localization of cell	BP	1	SOX9,AQP1,ENSCAFG00000004331,SEMA6D,DIXDC1,ZMYND8,PAK3,MMP28,PTGER4,ARHGDIB,ELMO2,FOXC2,LRRC15,TBX5,RARRES2,NRP1,PRKCD,CCNYL1	up_ACOR_EC
GO:0003164	0.053475349	0.99927	1	2	His-Purkinje system development	BP	1	TBX5	up_ACOR_EC
GO:0003166	0.053475349	0.99927	1	2	bundle of His development	BP	1	TBX5	up_ACOR_EC
GO:0040008	0.0535	0.967	24	179	regulation of growth	BP	1	ENSCAFG00000009113,WNT11,HNF4A,FAM107A,ACACB,SLIT2,SLC6A4,ABL1,DLL1,SAV1,PLXNA4,MT2A,FXN,MYD88,DPYSL2,WISP2,KDM2B,IGFBP6,TTL,SMARCA2,ACVRL1,HTRA2,TGFBR2,LATS2	up_VSAP_EC
GO:0022603	0.0535	0.974	12	301	regulation of anatomical structure morphogenesis	BP	1	LEP,ANGPT4,DLL1,F3,PLXNA4,THRB,TMEM100,GREM1,TBXA2R,BVES,CDC42EP5,KANK1	up_AFEM_EC
GO:0043542	0.0535	0.984	5	86	endothelial cell migration	BP	1	ANGPT4,GREM1,TBXA2R,FAP,ADAM17	up_AFEM_EC
GO:1990001	0.0535	0.996	2	5	inhibition of cysteine-type endopeptidase activity involved in apoptotic	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0071363	0.0535	0.994	2	188	cellular response to growth factor stimulus	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0044706	0.0535	0.999	1	27	multi-multicellular organism process	BP	1	CITED2	down_VPOR_EC
GO:2000117	0.0535	0.999	1	27	negative regulation of cysteine-type	BP	1	CST3	down_VPOR_EC
GO:0030010	0.0535	0.999	1	41	establishment of cell polarity	BP	1	WNT7A	up_AORT_VSMC
GO:0010922	0.0535	0.999	1	14	positive regulation of phosphatase activity	BP	1	NPNT	up_APUL_EC
GO:0060330	0.0536	0.995	2	6	regulation of response to interferon-gamma	BP	0.874	PTPN2,CDC37	down_VSAP_EC
GO:0060334	0.0536	0.995	2	6	regulation of interferon-gamma-mediated	BP	0.874	PTPN2,CDC37	down_VSAP_EC
GO:0089718	0.0536	0.996	2	4	amino acid import across plasma membrane	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:1902475	0.0536	0.996	2	4	L-alpha-amino acid transmembrane transport	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0043090	0.0536	0.996	2	4	amino acid import	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0050866	0.0536	0.999	1	48	negative regulation of cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0060043	0.0536	0.999	1	14	regulation of cardiac muscle cell proliferation	BP	1	TBX5	up_APUL_EC
GO:0038034	0.0536	0.999	1	21	signal transduction in absence of ligand	BP	1	EYA1	up_VFEM_VSMC
GO:0097192	0.0536	0.999	1	21	extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_VFEM_VSMC
GO:0010828	0.0536	0.999	1	16	positive regulation of glucose transmembrane	BP	1	NR1H4	up_VPUL_EC
GO:1902714	0.053630067	0.99927	1	2	negative regulation of interferon-gamma	BP	1	NR1H4	up_ACOR_EC
GO:1904425	0.053652523	0.99926	1	2	negative regulation of GTP binding	BP	1	ARHGAP28	up_ACOR_EC
GO:0055021	0.0537	0.988	4	15	regulation of cardiac muscle tissue growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0045600	0.0537	0.987	4	21	positive regulation of fat cell differentiation	BP	0.884	PPARG,BMP2,PTGS2,CREB1	up_VCAV_EC
GO:0071363	0.0537	0.999	1	188	cellular response to growth factor stimulus	BP	1	GATA5	down_VFEM_VSMC
GO:0045055	0.0537	0.999	1	52	regulated exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0097178	0.0537	0.999	1	14	ruffle assembly	BP	1	ARHGEF26	up_APUL_EC
GO:0048813	0.0537	0.999	1	39	dendrite morphogenesis	BP	1	SLITRK5	up_VCAV_VSMC
GO:0007350	0.0537	0.999	1	7	blastoderm segmentation	BP	1	SEMA3A	up_VPOR_EC
GO:0001569	0.053700717	0.99428	2	14	branching involved in blood vessel	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:1902308	0.053725797	0.99926	1	2	regulation of peptidyl-serine dephosphorylation	BP	1	DUSP26	up_ACOR_EC
GO:0071398	0.053783166	0.99427	2	14	cellular response to fatty acid	BP	1	NR1H4,PTGER4	up_ACOR_EC
GO:0051648	0.0538	0.994	2	69	vesicle localization	BP	1	SPG11,STX4	down_ACOR_EC
GO:0038083	0.0538	0.994	2	16	peptidyl-tyrosine autophosphorylation	BP	1	HCK,GREM1	up_AFEM_EC

GO:0002704	0.0538	0.996	2	5	negative regulation of leukocyte mediated	BP	0.884	IL7R,THOC1	up_VCAV_EC
GO:0006635	0.0538	0.999	1	25	fatty acid beta-oxidation	BP	1	ETFA	down_AFEM_EC
GO:0097581	0.0538	0.999	1	26	lamellipodium organization	BP	1	FSCN1	down_AFEM_EC
GO:0070201	0.0538	0.999	1	187	regulation of establishment of protein	BP	1	JUP	down_VFEM_VSMC
GO:0014916	0.0538	1	1	1	regulation of lung blood pressure	BP	0.884	GCH1	up_VCAV_EC
GO:0046654	0.0538	1	1	1	tetrahydrofolate biosynthetic process	BP	0.884	GCH1	up_VCAV_EC
GO:0006720	0.0538	0.999	1	25	isoprenoid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:2000736	0.0538	0.999	1	21	regulation of stem cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0001523	0.0538	0.999	1	12	retinoid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0035136	0.0538	0.999	1	16	forelimb morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0014904	0.0538	0.999	1	12	myotube cell development	BP	1	SHOX2	up_VSAP_VSMC
GO:0048741	0.0538	0.999	1	12	skeletal muscle fiber development	BP	1	SHOX2	up_VSAP_VSMC
GO:1901628	0.053805325	0.99926	1	2	positive regulation of postsynaptic membrane organization	BP	1	LRP4	up_ACOR_EC
GO:1901629	0.053805325	0.99926	1	2	regulation of presynaptic membrane organization	BP	1	LRP4	up_ACOR_EC
GO:0030837	0.053863716	0.99425	2	14	negative regulation of actin filament	BP	1	TMOD1,PRKCD	up_ACOR_EC
GO:0045666	0.0539	0.978	8	68	positive regulation of neuron differentiation	BP	0.874	ARHGEF2,DPYSL3,APOE,LYN,MMD,VLDLR,REST,NRP1	down_VSAP_EC
GO:0002687	0.0539	0.99	3	36	positive regulation of leukocyte migration	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:0032682	0.0539	0.995	2	7	negative regulation of chemokine production	BP	0.874	NR1H4,SOCS5	down_VSAP_EC
GO:0106049	0.0539	0.996	2	4	regulation of cellular response to osmotic	BP	0.884	PTGS2,ARHGEF2	up_VCAV_EC
GO:1902218	0.0539	0.996	2	4	regulation of intrinsic apoptotic signaling pathway in response to	BP	0.884	PTGS2,ARHGEF2	up_VCAV_EC
GO:1902219	0.0539	0.996	2	4	negative regulation of intrinsic apoptotic signaling pathway in	BP	0.884	PTGS2,ARHGEF2	up_VCAV_EC
GO:0034439	0.0539	1	1	1	lipoprotein lipid oxidation	BP	0.884	APOD	up_VCAV_EC
GO:0034442	0.0539	1	1	1	regulation of lipoprotein oxidation	BP	0.884	APOD	up_VCAV_EC
GO:0034443	0.0539	1	1	1	negative regulation of lipoprotein oxidation	BP	0.884	APOD	up_VCAV_EC
GO:0042160	0.0539	1	1	1	lipoprotein modification	BP	0.884	APOD	up_VCAV_EC
GO:0042161	0.0539	1	1	1	lipoprotein oxidation	BP	0.884	APOD	up_VCAV_EC
GO:0050748	0.0539	1	1	1	negative regulation of lipoprotein metabolic	BP	0.884	APOD	up_VCAV_EC
GO:0060587	0.0539	1	1	1	regulation of lipoprotein lipid oxidation	BP	0.884	APOD	up_VCAV_EC
GO:0060588	0.0539	1	1	1	negative regulation of lipoprotein lipid oxidation	BP	0.884	APOD	up_VCAV_EC
GO:2000405	0.0539	1	1	1	negative regulation of T cell migration	BP	0.884	APOD	up_VCAV_EC
GO:2001258	0.0539	0.999	1	11	negative regulation of cation channel activity	BP	1	CAV1	up_VSAP_VSMC
GO:0070858	0.053948127	0.99926	1	2	negative regulation of bile acid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:1904252	0.053948127	0.99926	1	2	negative regulation of bile acid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:2000145	0.054	0.967	24	279	regulation of cell motility	BP	0.874	ARHGEF2,VEGFA,SULF1,HSPA5,SERPINE1,SPARC,JCAD,DPYSL3,PRCP,MYO1C,PIK3C2A,MSN,HIF1A,ADAM17,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,NEXN,SDC4,ZMYND8,NRP1	down_VSAP_EC
GO:0050849	0.054	0.99	3	15	negative regulation of calcium-mediated	BP	0.874	FHL2,GSK3B,CALM1	down_VSAP_EC
GO:0014823	0.054	0.996	2	5	response to activity	BP	0.884	SLC25A25,HIF1A	up_VCAV_EC
GO:0032504	0.054	0.994	2	152	multicellular organism reproduction	BP	1	HOXA9,HOXA11	up_VFEM_VSMC

GO:0048609	0.054	0.994	2	152	multicellular organismal reproductive process	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0035493	0.054	0.999	1	11	SNARE complex assembly	BP	1	STX4	down_ACOR_EC
GO:0060041	0.054	0.999	1	41	retina development in camera-type eye	BP	1	IRX5	up_AFEM_VSMC
GO:0043393	0.054	0.999	1	77	regulation of protein binding	BP	1	HOXA3	up_APUL_VSMC
GO:0016998	0.054	1	1	1	cell wall macromolecule catabolic process	BP	0.884	LYZ	up_VCAV_EC
GO:0044036	0.054	1	1	1	cell wall macromolecule metabolic process	BP	0.884	LYZ	up_VCAV_EC
GO:0071554	0.054	1	1	1	cell wall organization or biogenesis	BP	0.884	LYZ	up_VCAV_EC
GO:0006680	0.054090452	0.99925	1	2	glucosylceramide catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0031324	0.0541	0.961	55	735	negative regulation of cellular metabolic process	BP	0.874	PRICKLE1,NR1H4,PLK3,SERPINE1,SOCS5,ETV6,ENPP1,ERRFI1,SNX25,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,PEG3,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,APOE,WWC3,KLF5,LYN,BNIP3,STRAP,DDIT3,CBLC,ATF3,VLDLR,REST,ZMYND8,EIF2S1,ARFGEF3,CDYL,PAK2,LRRTM2,A2M,HIF1AN,SIX4,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:0007167	0.0541	0.968	20	274	enzyme linked receptor protein signaling pathway	BP	1	PDGFRB,SMAD9,DCN,NDN,ANGPT1,VASN,FBN1,BMPR1A,IGFBP6,ENSCAFG00000014978,AKT1S1,CHRDL1,AKT2,CSPG4,ASPN,FUT8,ENSCAFG00000017708,SHC1,GREM1,RGMA	down_VCAV_EC
GO:0034641	0.0541	0.987	6	2171	cellular nitrogen compound metabolic	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:1903959	0.0541	0.995	2	8	regulation of anion transmembrane transport	BP	1	PRNP,AKT2	down_VCAV_EC
GO:0043586	0.0541	0.995	2	6	tongue development	BP	0.874	CTNNB1,SIX4	down_VSAP_EC
GO:0007632	0.0541	0.999	1	14	visual behavior	BP	1	HOXA1	up_APUL_EC
GO:0048635	0.0541	0.999	1	14	negative regulation of muscle organ	BP	1	TBX5	up_APUL_EC
GO:2000826	0.0541	0.999	1	14	regulation of heart morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0010524	0.0541	0.999	1	12	positive regulation of calcium ion transport into	BP	1	CAV1	up_VSAP_VSMC
GO:1901021	0.0541	0.999	1	13	positive regulation of calcium ion transmembrane	BP	1	STIM1	up_VSAP_VSMC
GO:0035356	0.054176071	0.99925	1	2	cellular triglyceride homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:1904177	0.054176071	0.99925	1	2	regulation of adipose tissue development	BP	1	NR1H4	up_ACOR_EC
GO:1904179	0.054176071	0.99925	1	2	positive regulation of adipose tissue	BP	1	NR1H4	up_ACOR_EC
GO:0019222	0.0542	0.976	13	1934	regulation of metabolic process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,HOXC10,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0048008	0.0542	0.985	5	24	platelet-derived growth factor receptor signaling	BP	0.884	PDGFB,TIPARP,RAPGEF1,APOD,PDGFD	up_VCAV_EC
GO:0042987	0.0542	0.991	3	10	amyloid precursor protein catabolic process	BP	1	PSEN2,APP,PSEN1	up_ACOR_VSMC
GO:0031579	0.0542	0.995	2	6	membrane raft organization	BP	1	CAV1,EMP2	down_ACOR_VSMC
GO:0032490	0.0542	0.996	2	4	detection of molecule of bacterial origin	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0035136	0.0542	0.994	2	16	forelimb morphogenesis	BP	1	HOXA9,RECK	up_AFEM_EC
GO:0034142	0.0542	0.999	1	14	toll-like receptor 4 signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:1901862	0.0542	0.999	1	14	negative regulation of muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0090331	0.054214401	0.99925	1	2	negative regulation of platelet aggregation	BP	1	PRKCD	up_ACOR_EC
GO:1903532	0.05421703	0.98351	5	78	positive regulation of secretion by cell	BP	1	NR1H4,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0001951	0.054225243	0.99925	1	2	intestinal D-glucose absorption	BP	1	PLS1	up_ACOR_EC
GO:0032532	0.054225243	0.99925	1	2	regulation of microvillus length	BP	1	PLS1	up_ACOR_EC

GO:0106001	0.054225243	0.99925	1	2	intestinal hexose absorption	BP	1	PLS1	up_ACOR_EC
GO:1902896	0.054225243	0.99925	1	2	terminal web assembly	BP	1	PLS1	up_ACOR_EC
GO:2000826	0.054269018	0.99419	2	14	regulation of heart morphogenesis	BP	1	FOXC2,TBX5	up_ACOR_EC
GO:0008219	0.0543	0.962	46	611	cell death	BP	0.874	ARHGEF2,VEGFA,P4HB,ASNS,NR1H4,PLK3,HSPA5,SERPINE1,ETV6,ERO1A,CASP3,HYOU1,EXOC5,AARS,FHL2,PTGS2,UACA,HIF1A,DNAJC10,TNIK,ZPR1,PTPN2,MTDH,MAGED1,CTNNB1,CRYAB,APOE,LYN,BNIP3,DDIT3,FAM162A,ATF3,GSK3B,SH3GLB1,HTT,REST,EIF2S1,GLO1,PAK2,INHBA,SIX4,CDKN1A,NRP1,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0006873	0.0543	0.968	22	160	cellular ion homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,DMXL1,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0051341	0.0543	0.985	5	22	regulation of oxidoreductase activity	BP	1	LEP,HTR2B,ATP7A,EDN1,PARK7	up_ACOR_VSMC
GO:0032653	0.0543	0.991	3	11	regulation of interleukin-10 production	BP	0.884	CD34,TLR4,HMGB1	up_VCAV_EC
GO:0023052	0.0543	1	2	1602	signaling	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0030900	0.0543	0.994	2	101	forebrain development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0043277	0.0543	0.999	1	9	apoptotic cell clearance	BP	1	SPG11	down_ACOR_EC
GO:1903707	0.0543	0.999	1	48	negative regulation of hemopoiesis	BP	1	HOXA9	up_AORT_VSMC
GO:0019229	0.0543	0.999	1	12	regulation of vasoconstriction	BP	1	CAV1	up_VSAP_VSMC
GO:0060717	0.054366379	0.99924	1	2	chorion development	BP	1	FZD5	up_ACOR_EC
GO:0060718	0.054366379	0.99924	1	2	chorionic trophoblast cell differentiation	BP	1	FZD5	up_ACOR_EC
GO:0008360	0.0544	0.982	6	46	regulation of cell shape	BP	0.874	VEGFA,MYH9,FMNL3,AKAP2,WDR1,MSN	down_VSAP_EC
GO:0046888	0.0544	0.99	3	14	negative regulation of hormone secretion	BP	0.874	PTPN11,REST,RAB11FIP1	down_VSAP_EC
GO:0060339	0.0544	0.995	2	5	negative regulation of type I interferon-mediated signaling	BP	0.884	NLRC5,CNOT7	up_VCAV_EC
GO:1903312	0.0544	0.999	1	25	negative regulation of mRNA metabolic process	BP	1	SRSF6	down_AFEM_EC
GO:0051098	0.0544	0.999	1	129	regulation of binding	BP	1	PLCL1	down_VFEM_EC
GO:0006749	0.0544	0.999	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	up_APUL_EC
GO:0051926	0.0544	0.999	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_APUL_EC
GO:0048638	0.0544	0.999	1	82	regulation of developmental growth	BP	1	TBX5	up_APUL_VSMC
GO:0003104	0.0544	1	1	1	positive regulation of glomerular filtration	BP	0.884	PDGFB	up_VCAV_EC
GO:0010046	0.0544	1	1	1	response to mycotoxin	BP	0.884	PDGFB	up_VCAV_EC
GO:0035655	0.0544	1	1	1	interleukin-18-mediated signaling pathway	BP	0.884	PDGFB	up_VCAV_EC
GO:0035787	0.0544	1	1	1	cell migration involved in kidney development	BP	0.884	PDGFB	up_VCAV_EC
GO:0035789	0.0544	1	1	1	metanephric mesenchymal cell	BP	0.884	PDGFB	up_VCAV_EC
GO:0035793	0.0544	1	1	1	positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor	BP	0.884	PDGFB	up_VCAV_EC
GO:0036146	0.0544	1	1	1	cellular response to mycotoxin	BP	0.884	PDGFB	up_VCAV_EC
GO:0038001	0.0544	1	1	1	paracrine signaling	BP	0.884	PDGFB	up_VCAV_EC
GO:0043696	0.0544	1	1	1	dedifferentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:0043697	0.0544	1	1	1	cell dedifferentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:0071351	0.0544	1	1	1	cellular response to interleukin-18	BP	0.884	PDGFB	up_VCAV_EC
GO:0071505	0.0544	1	1	1	response to mycophenolic acid	BP	0.884	PDGFB	up_VCAV_EC

GO:0071506	0.0544	1	1	1	cellular response to mycophenolic acid	BP	0.884	PDGFB	up_VCAV_EC
GO:0072126	0.0544	1	1	1	positive regulation of glomerular mesangial cell	BP	0.884	PDGFB	up_VCAV_EC
GO:0072209	0.0544	1	1	1	metanephric mesangial cell differentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:0072223	0.0544	1	1	1	metanephric glomerular mesangium development	BP	0.884	PDGFB	up_VCAV_EC
GO:0072254	0.0544	1	1	1	metanephric glomerular mesangial cell	BP	0.884	PDGFB	up_VCAV_EC
GO:0072255	0.0544	1	1	1	metanephric glomerular mesangial cell	BP	0.884	PDGFB	up_VCAV_EC
GO:0090193	0.0544	1	1	1	positive regulation of glomerulus development	BP	0.884	PDGFB	up_VCAV_EC
GO:0090677	0.0544	1	1	1	reversible differentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:0090678	0.0544	1	1	1	cell dedifferentiation involved in phenotypic	BP	0.884	PDGFB	up_VCAV_EC
GO:1900127	0.0544	1	1	1	positive regulation of hyaluronan biosynthetic	BP	0.884	PDGFB	up_VCAV_EC
GO:1900238	0.0544	1	1	1	regulation of metanephric mesenchymal cell migration by platelet-derived growth factor	BP	0.884	PDGFB	up_VCAV_EC
GO:1900241	0.0544	1	1	1	positive regulation of phenotypic switching	BP	0.884	PDGFB	up_VCAV_EC
GO:1901724	0.0544	1	1	1	positive regulation of cell proliferation involved in kidney development	BP	0.884	PDGFB	up_VCAV_EC
GO:1905174	0.0544	1	1	1	regulation of vascular smooth muscle cell	BP	0.884	PDGFB	up_VCAV_EC
GO:1905176	0.0544	1	1	1	positive regulation of vascular smooth muscle cell dedifferentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:1990936	0.0544	1	1	1	vascular smooth muscle cell dedifferentiation	BP	0.884	PDGFB	up_VCAV_EC
GO:2000589	0.0544	1	1	1	regulation of metanephric mesenchymal cell	BP	0.884	PDGFB	up_VCAV_EC
GO:2000591	0.0544	1	1	1	positive regulation of metanephric mesenchymal cell	BP	0.884	PDGFB	up_VCAV_EC
GO:0010512	0.0544	1	1	1	negative regulation of phosphatidylinositol biosynthetic process	BP	0.884	PDGFB	up_VCAV_EC
GO:0035788	0.0544	1	1	1	cell migration involved in metanephros	BP	0.884	PDGFB	up_VCAV_EC
GO:0043271	0.0544	0.999	1	28	negative regulation of ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0002692	0.054417727	0.99924	1	2	negative regulation of cellular extravasation	BP	1	PTGER4	up_ACOR_EC
GO:1900063	0.054464932	0.99924	1	2	regulation of peroxisome organization	BP	1	MAVS	up_ACOR_EC
GO:0015846	0.054491371	0.99924	1	2	polyamine transport	BP	1	AZIN2	up_ACOR_EC
GO:1902047	0.054491371	0.99924	1	2	polyamine transmembrane transport	BP	1	AZIN2	up_ACOR_EC
GO:1902267	0.054491371	0.99924	1	2	regulation of polyamine transmembrane transport	BP	1	AZIN2	up_ACOR_EC
GO:1902269	0.054491371	0.99924	1	2	positive regulation of polyamine	BP	1	AZIN2	up_ACOR_EC
GO:0071732	0.054494275	0.99924	1	2	cellular response to nitric oxide	BP	1	GUCY1B1	up_ACOR_EC
GO:0051338	0.0545	0.986	4	288	regulation of transferase activity	BP	1	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0048589	0.0545	0.994	2	188	developmental growth	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0006885	0.0545	0.999	1	39	regulation of pH	BP	1	CA2	up_VCAV_VSMC
GO:0043408	0.054518488	0.97518	10	211	regulation of MAPK cascade	BP	1	NDRG2,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,MAPK8IP2,SH3RF3,NRP1,PRKCD	up_ACOR_EC
GO:0019953	0.0546	0.969	19	152	sexual reproduction	BP	1	NDC1,TRIP13,CTDNEP1,FBXO5,AAAS,NCAPH,POC1A,B4GALT1,HIST1H1A,FOSL1,HMGB2,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,CCT4,TTLL1	down_ACOR_VSMC
GO:0007166	0.0546	0.98	7	686	cell surface receptor signaling pathway	BP	1	ACVRL1,LYN,NRP2,SULF1,WDR12,STX4,ASPN	down_ACOR_EC
GO:0002088	0.0546	0.984	5	26	lens development in camera-type eye	BP	0.884	GATA3,TMOD1,PROX1,SKIL,CDON	up_VCAV_EC
GO:0014904	0.0546	0.991	3	12	myotube cell development	BP	0.884	PPP3CA,CAV2,P2RX2	up_VCAV_EC

GO:0048741	0.0546	0.991	3	12	skeletal muscle fiber development	BP	0.884	PPP3CA,CAV2,P2RX2	up_VCAV_EC
GO:0032530	0.0546	0.995	2	6	regulation of microvillus organization	BP	0.874	FSCN1,KLF5	down_VSAP_EC
GO:0042775	0.0546	0.999	1	28	mitochondrial ATP synthesis coupled	BP	1	NDUFA10	down_AFEM_EC
GO:1902750	0.0546	0.999	1	24	negative regulation of cell cycle G2/M phase	BP	1	TAOK1	up_AORT_EC
GO:2000378	0.0546	0.999	1	12	negative regulation of reactive oxygen species	BP	1	CAV1	up_VSAP_VSMC
GO:2000739	0.05460252	0.99924	1	2	regulation of mesenchymal stem cell	BP	1	SOX9	up_ACOR_EC
GO:0090176	0.054609228	0.99924	1	2	microtubule cytoskeleton organization involved in establishment of planar	BP	1	BRSK1	up_ACOR_EC
GO:0050680	0.0547	0.98	7	44	negative regulation of epithelial cell proliferation	BP	0.884	MEF2C,DLL4,GATA3,MTSS1,CAV2,MCC,VASH1	up_VCAV_EC
GO:0001932	0.0547	0.984	5	416	regulation of protein phosphorylation	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0043933	0.0547	0.988	4	698	protein-containing complex subunit	BP	1	EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:0035050	0.0547	0.999	1	28	embryonic heart tube development	BP	1	CITED2	down_VPOR_EC
GO:0006551	0.0547	1	1	1	leucine metabolic process	BP	0.874	BCAT1	down_VSAP_EC
GO:0009098	0.0547	1	1	1	leucine biosynthetic process	BP	0.874	BCAT1	down_VSAP_EC
GO:0009099	0.0547	1	1	1	valine biosynthetic process	BP	0.874	BCAT1	down_VSAP_EC
GO:0009082	0.0547	1	1	1	branched-chain amino acid biosynthetic process	BP	0.874	BCAT1	down_VSAP_EC
GO:0070663	0.0547	0.999	1	50	regulation of leukocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0021602	0.0547	0.999	1	16	cranial nerve morphogenesis	BP	1	HOXA3	up_VPUL_EC
GO:0061476	0.054762266	0.99923	1	2	response to anticoagulant	BP	1	SOX9	up_ACOR_EC
GO:0071503	0.054762266	0.99923	1	2	response to heparin	BP	1	SOX9	up_ACOR_EC
GO:0071504	0.054762266	0.99923	1	2	cellular response to heparin	BP	1	SOX9	up_ACOR_EC
GO:0030595	0.0548	0.978	8	57	leukocyte chemotaxis	BP	0.884	EDNRB,KIT,CXCL8,PDGFB,PDE4D,MMP28,SWAP70,HMGB1	up_VCAV_EC
GO:0035023	0.0548	0.978	8	46	regulation of Rho protein signal transduction	BP	1	ARHGEF5,ARHGEF6,ABL1,F2RL1,TIAM1,DLC1,FGD4,FLOT1	up_VSAP_EC
GO:0051239	0.0548	0.985	5	859	regulation of multicellular organismal process	BP	1	NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0060113	0.0548	0.99	3	18	inner ear receptor cell differentiation	BP	1	SDC4,NAGLU,GSDME	down_VCAV_EC
GO:0071310	0.0548	0.991	3	634	cellular response to organic substance	BP	1	CYP1A1,GATA5,CA2	up_VCAV_VSMC
GO:2000479	0.0548	0.999	1	8	regulation of cAMP-dependent protein kinase	BP	1	PRKAR2A	down_ACOR_EC
GO:0048817	0.054816115	0.99923	1	2	negative regulation of hair follicle maturation	BP	1	CDH3	up_ACOR_EC
GO:0035977	0.054880787	0.99923	1	2	protein deglycosylation involved in glycoprotein	BP	1	EDEM2	up_ACOR_EC
GO:0036507	0.054880787	0.99923	1	2	protein demannosylation	BP	1	EDEM2	up_ACOR_EC
GO:0036508	0.054880787	0.99923	1	2	protein alpha-1,2-demannosylation	BP	1	EDEM2	up_ACOR_EC
GO:0097466	0.054880787	0.99923	1	2	ubiquitin-dependent glycoprotein ERAD	BP	1	EDEM2	up_ACOR_EC
GO:1904382	0.054880787	0.99923	1	2	mannose trimming involved in glycoprotein	BP	1	EDEM2	up_ACOR_EC
GO:1904587	0.054880787	0.99923	1	2	response to glycoprotein	BP	1	EDEM2	up_ACOR_EC
GO:0071635	0.054881257	0.99923	1	2	negative regulation of transforming growth factor beta production	BP	1	CDH3	up_ACOR_EC
GO:0042221	0.054892142	0.96379	35	1012	response to chemical	BP	1	NR1H4,GATA4,SOX9,FNDC4,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,CCDC3,AGRN,PTGIR,NOD2,RGMA,PDE4A,SMAD6,ACTN2,PAK3,MMP28,GUCY1B1,PTGER4,ELMO2,ADAMTSL2,MAVS,FOXC2,LRRC15,IFIT2,LRP4,LRRC4,CLU,RARRES2,PRKACA,NRP1,HM13,PRKCD	up_ACOR_EC

GO:0042325	0.0549	0.964	31	463	regulation of phosphorylation	BP	1	NOTCH2,PDGFRB,KIRREL1,DCN,PRNP,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,ASPN,THY1,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,SPRED1,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0002526	0.0549	0.987	4	17	acute inflammatory response	BP	0.884	PRCP,F8,IL6,PTGS2	up_VCAV_EC
GO:0043066	0.0549	0.99	3	253	negative regulation of apoptotic process	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0071803	0.0549	0.995	2	6	positive regulation of podosome assembly	BP	0.874	FSCN1,MSN	down_VSAP_EC
GO:1904645	0.0549	0.999	1	7	response to amyloid-beta	BP	1	IGF1R	down_ACOR_EC
GO:0007268	0.0549	0.999	1	130	chemical synaptic transmission	BP	1	PLCL1	down_VFEM_EC
GO:0098916	0.0549	0.999	1	130	anterograde trans-synaptic signaling	BP	1	PLCL1	down_VFEM_EC
GO:0038110	0.0549	1	1	1	interleukin-2-mediated signaling pathway	BP	0.874	PTPN2	down_VSAP_EC
GO:0060331	0.0549	1	1	1	negative regulation of response to interferon-	BP	0.874	PTPN2	down_VSAP_EC
GO:0060336	0.0549	1	1	1	negative regulation of interferon-gamma-mediated signaling	BP	0.874	PTPN2	down_VSAP_EC
GO:0070103	0.0549	1	1	1	regulation of interleukin-6-mediated signaling	BP	0.874	PTPN2	down_VSAP_EC
GO:0070104	0.0549	1	1	1	negative regulation of interleukin-6-mediated	BP	0.874	PTPN2	down_VSAP_EC
GO:0070669	0.0549	1	1	1	response to interleukin-2	BP	0.874	PTPN2	down_VSAP_EC
GO:0071352	0.0549	1	1	1	cellular response to interleukin-2	BP	0.874	PTPN2	down_VSAP_EC
GO:1902205	0.0549	1	1	1	regulation of interleukin-2-mediated signaling	BP	0.874	PTPN2	down_VSAP_EC
GO:1902206	0.0549	1	1	1	negative regulation of interleukin-2-mediated	BP	0.874	PTPN2	down_VSAP_EC
GO:1902214	0.0549	1	1	1	regulation of interleukin-4-mediated signaling	BP	0.874	PTPN2	down_VSAP_EC
GO:1902215	0.0549	1	1	1	negative regulation of interleukin-4-mediated	BP	0.874	PTPN2	down_VSAP_EC
GO:1902232	0.0549	1	1	1	regulation of positive thymic T cell selection	BP	0.874	PTPN2	down_VSAP_EC
GO:1902233	0.0549	1	1	1	negative regulation of positive thymic T cell	BP	0.874	PTPN2	down_VSAP_EC
GO:0010633	0.0549	0.999	1	28	negative regulation of epithelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0060669	0.0549	0.999	1	12	embryonic placenta morphogenesis	BP	1	GJB5	up_VSAP_VSMC
GO:0031348	0.055	0.981	6	46	negative regulation of defense response	BP	0.874	NR1H4,SOCS5,PTPN2,CNOT7,APOE,A2M	down_VSAP_EC
GO:0090175	0.055	0.987	4	15	regulation of establishment of planar	BP	1	MLLT3,SEC24B,ZNRF3,FZD3	up_ACOR_VSMC
GO:0051457	0.055	0.995	2	8	maintenance of protein location in nucleus	BP	1	PARK7,ARL2BP	down_VCAV_EC
GO:0042219	0.055	0.996	2	4	cellular modified amino acid catabolic process	BP	1	SARDH,PCYOX1	up_ACOR_VSMC
GO:0015991	0.055	0.994	2	16	ATP hydrolysis coupled proton transport	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0090662	0.055	0.994	2	16	ATP hydrolysis coupled transmembrane transport	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0099131	0.055	0.994	2	16	ATP hydrolysis coupled ion transmembrane	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0060546	0.055	0.999	1	7	negative regulation of necroptotic process	BP	1	ARHGEF2	up_VPOR_EC
GO:0060547	0.055	0.999	1	7	negative regulation of necrotic cell death	BP	1	ARHGEF2	up_VPOR_EC
GO:1903727	0.055	0.999	1	16	positive regulation of phospholipid metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0060481	0.055005143	0.99923	1	2	lobar bronchus epithelium development	BP	1	ADAMTSL2	up_ACOR_EC
GO:0060482	0.055005143	0.99923	1	2	lobar bronchus development	BP	1	ADAMTSL2	up_ACOR_EC
GO:0045333	0.0551	0.974	12	74	cellular respiration	BP	1	DLST,COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,FXN,NDUFS2,MTFR1L,IDH1,IDH3A,ENSCAFG00000006639,NDUFV1	up_VSAP_EC
GO:0010557	0.0551	0.984	5	492	positive regulation of macromolecule biosynthetic process	BP	1	HOXA11,HOXA9,SALL1,PRR16,SHOX2	up_VSAP_VSMC

GO:0070848	0.0551	0.999	1	193	response to growth factor	BP	1	GATA5	down_VFEM_VSMC
GO:0006517	0.0551	0.999	1	7	protein deglycosylation	BP	1	OGA	up_VPOR_EC
GO:0003143	0.0551	0.999	1	22	embryonic heart tube morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071621	0.0551	0.999	1	27	granulocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0030104	0.0551	0.999	1	13	water homeostasis	BP	1	CYP26B1	up_VFEM_EC
GO:0070266	0.0551	0.999	1	14	necroptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:1901890	0.0551	0.999	1	13	positive regulation of cell junction assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0009117	0.0552	0.966	24	208	nucleotide metabolic process	BP	1	PRPSAP1,ACLY,HMGCR,NNT,RRM1,RAN,CDK1,PFAS,RNASEH2B,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,DCK,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,PGD,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0071219	0.0552	0.978	8	50	cellular response to molecule of bacterial	BP	0.884	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,TLR4,IRF8,ABCA1	up_VCAV_EC
GO:0050793	0.0552	0.982	6	731	regulation of developmental process	BP	1	NR1H4,TBX5,SLITRK5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0002709	0.0552	0.987	4	19	regulation of T cell mediated immunity	BP	0.884	IL7R,GATA3,NECTIN2,HMGB1	up_VCAV_EC
GO:0034109	0.0552	0.99	3	14	homotypic cell-cell adhesion	BP	0.874	LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0003094	0.0552	0.999	1	11	glomerular filtration	BP	1	SULF1	down_ACOR_EC
GO:0002042	0.0552	0.999	1	29	cell migration involved in sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0002062	0.0552	0.999	1	48	chondrocyte differentiation	BP	1	WNT7A	up_AORT_VSMC
GO:0070542	0.0552	0.999	1	15	response to fatty acid	BP	1	NR1H4	up_APUL_EC
GO:1900120	0.0552	0.999	1	7	regulation of receptor binding	BP	1	HOXA3	up_VPOR_EC
GO:0046660	0.0552	0.999	1	28	female sex differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:1900452	0.055222993	0.99922	1	2	regulation of long-term synaptic depression	BP	1	KCNB1	up_ACOR_EC
GO:0007166	0.0553	0.967	23	686	cell surface receptor signaling pathway	BP	1	LEP,GAS1,ANGPT4,DLL1,F3,PLXNA4,MLLT11,HCK,TMEM100,GREM1,FAM53B,GREM2,CYLD,POSTN,LRRC15,RECK,LGR6,RAB7A,AXIN2,CCL5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:1901699	0.0553	0.967	21	164	cellular response to nitrogen compound	BP	0.884	PPARG,BAIAP2L1,TMEM173,PDE4D,MEF2C,RAPGEF1,RALB,MTOR,MAPK13,RIOK3,NCK1,TIMELESS,GUCY1B1,RAPGEF2,CTNNA1,BLM,PDGFD,ATRX,NR4A1,ZEB1,ARHGEF2	up_VCAV_EC
GO:0045216	0.0553	0.981	6	44	cell-cell junction organization	BP	0.874	NR1H4,FSCN1,WDR1,MYO1C,CTNNB1,ENSCAFG00000002015	down_VSAP_EC
GO:0098773	0.0553	0.982	6	29	skin epidermis development	BP	1	FGF7,DLL1,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0046889	0.0553	0.987	4	24	positive regulation of lipid biosynthetic process	BP	0.874	NR1H4,PTGS2,SLC45A3,APOE	down_VSAP_EC
GO:0070542	0.0553	0.987	4	15	response to fatty acid	BP	1	PRKAA2,ADCY6,PTGDR,PRKCE	up_ACOR_VSMC
GO:0010720	0.0553	0.989	3	110	positive regulation of cell development	BP	1	ARHGEF2,ENSCAFG00000002015,SEMA3A	up_VPOR_EC
GO:0002347	0.0553	0.995	2	6	response to tumor cell	BP	0.884	NECTIN2,HMGB1	up_VCAV_EC
GO:0099537	0.0553	0.999	1	131	trans-synaptic signaling	BP	1	PLCL1	down_VFEM_EC
GO:0042742	0.0553	0.999	1	39	defense response to bacterium	BP	1	TLR2	up_AFEM_VSMC
GO:0055123	0.0553	0.999	1	40	digestive system development	BP	1	GATA5	up_VCAV_VSMC
GO:0045880	0.0553	0.999	1	14	positive regulation of smoothened signaling	BP	1	SHOX2	up_VSAP_VSMC
GO:1902305	0.0553	0.999	1	12	regulation of sodium ion transmembrane transport	BP	1	NETO1	up_VSAP_VSMC
GO:0150018	0.055377795	0.99922	1	2	basal dendrite development	BP	1	NRP1	up_ACOR_EC
GO:0150019	0.055377795	0.99922	1	2	basal dendrite morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0150020	0.055377795	0.99922	1	2	basal dendrite arborization	BP	1	NRP1	up_ACOR_EC
GO:1901606	0.0554	0.984	5	22	alpha-amino acid catabolic process	BP	1	GOT1,ADHFE1,ALDH6A1,ENSCAFG00000002977,IDO2	up_VSAP_EC

GO:0001709	0.0554	0.991	3	11	cell fate determination	BP	0.884	MEF2C,GATA3,PROX1	up_VCAV_EC
GO:1904666	0.0554	0.995	2	5	regulation of ubiquitin protein ligase activity	BP	1	UBE2S,CDC20	down_ACOR_VSMC
GO:0048247	0.0554	0.994	2	16	lymphocyte chemotaxis	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0051051	0.0554	0.994	2	112	negative regulation of transport	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:0048485	0.0554	0.999	1	9	sympathetic nervous system development	BP	1	NRP2	down_ACOR_EC
GO:1901983	0.0554	0.999	1	24	regulation of protein acetylation	BP	1	TAOK1	up_AORT_EC
GO:0046622	0.0554	0.999	1	15	positive regulation of organ growth	BP	1	TBX5	up_APUL_EC
GO:0061010	0.0554	1	1	1	gall bladder development	BP	0.884	HHEX	up_VCAV_EC
GO:0061011	0.0554	1	1	1	hepatic duct development	BP	0.884	HHEX	up_VCAV_EC
GO:0061017	0.0554	1	1	1	hepatoblast differentiation	BP	0.884	HHEX	up_VCAV_EC
GO:0021545	0.0554	0.999	1	21	cranial nerve development	BP	1	HOXA3	up_VPOR_VSMC
GO:0021510	0.0554	0.999	1	23	spinal cord development	BP	1	HOXC10	up_VFEM_VSMC
GO:0045834	0.0555	0.98	7	41	positive regulation of lipid metabolic process	BP	0.884	TEK,ADGRF5,PDGFB,MTOR,SH3GLB1,PTGS2,CREB1	up_VCAV_EC
GO:0050804	0.0555	0.983	5	87	modulation of chemical synaptic transmission	BP	1	KCNC4,CHRM2,SLC6A6,CAMK2A,DMPK	up_AFEM_EC
GO:0099177	0.0555	0.983	5	87	regulation of trans-synaptic signaling	BP	1	KCNC4,CHRM2,SLC6A6,CAMK2A,DMPK	up_AFEM_EC
GO:0070613	0.0555	0.986	4	25	regulation of protein processing	BP	0.874	MYH9,SERPINE1,PRKACB,A2M	down_VSAP_EC
GO:1903317	0.0555	0.986	4	25	regulation of protein maturation	BP	0.874	MYH9,SERPINE1,PRKACB,A2M	down_VSAP_EC
GO:0050767	0.0555	0.986	4	184	regulation of neurogenesis	BP	1	HOOK3,ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0061213	0.0555	0.991	3	11	positive regulation of mesonephros	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0032507	0.0555	0.99	3	18	maintenance of protein location in cell	BP	1	TLN2,PARK7,ARL2BP	down_VCAV_EC
GO:0018196	0.0555	0.99	3	15	peptidyl-asparagine modification	BP	0.874	STT3A,HIF1AN,RPN1	down_VSAP_EC
GO:0016048	0.0555	0.995	2	5	detection of temperature stimulus	BP	0.884	EPHB1,MMP24	up_VCAV_EC
GO:0050951	0.0555	0.995	2	5	sensory perception of temperature stimulus	BP	0.884	EPHB1,MMP24	up_VCAV_EC
GO:0050961	0.0555	0.995	2	5	detection of temperature stimulus involved in sensory perception	BP	0.884	EPHB1,MMP24	up_VCAV_EC
GO:0050965	0.0555	0.995	2	5	detection of temperature stimulus involved in sensory perception of	BP	0.884	EPHB1,MMP24	up_VCAV_EC
GO:0060840	0.0555	0.999	1	42	artery development	BP	1	EYA1	up_AFEM_VSMC
GO:1901164	0.0555	1	1	1	negative regulation of trophoblast cell migration	BP	0.884	ARHGDIB	up_VCAV_EC
GO:0032535	0.055515491	0.97882	7	128	regulation of cellular component size	BP	1	TMOD1,AQP1,PLS1,ACTN2,PAK3,NRP1,PRKCD	up_ACOR_EC
GO:1903909	0.05559869	0.99921	1	2	regulation of receptor clustering	BP	1	LRP4	up_ACOR_EC
GO:1904393	0.05559869	0.99921	1	2	regulation of skeletal muscle acetylcholine-gated channel clustering	BP	1	LRP4	up_ACOR_EC
GO:0048545	0.0556	0.974	11	68	response to steroid hormone	BP	1	FAM107A,PPARGC1B,SLIT2,GOT1,ZFP36L1,CREBRF,PRMT2,ZFP36L2,NCOA2,LBH,DDIT4	up_VSAP_EC
GO:0051046	0.0556	0.977	8	174	regulation of secretion	BP	1	LEP,KCNC4,CRY2,GPAM,CHRM2,CAMK2A,RAB7A,CCL5	up_AFEM_EC
GO:0034622	0.0556	0.99	3	421	cellular protein-containing complex assembly	BP	1	EIF3M,SRSF6,NDUFA10	down_AFEM_EC
GO:0007154	0.0556	1	2	1622	cell communication	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0001759	0.0556	0.999	1	13	organ induction	BP	1	SIX1	up_VFEM_EC
GO:0050830	0.0556	0.999	1	12	defense response to Gram-positive bacterium	BP	1	TLR2	up_VSAP_VSMC
GO:0072202	0.0556	0.999	1	13	cell differentiation involved in metanephros	BP	1	SALL1	up_VSAP_VSMC
GO:0021649	0.05561755	0.99921	1	2	vestibulocochlear nerve structural organization	BP	1	NRP1	up_ACOR_EC

GO:0061552	0.05561755	0.99921	1	2	ganglion morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0097374	0.05561755	0.99921	1	2	sensory neuron axon guidance	BP	1	NRP1	up_ACOR_EC
GO:1904835	0.05561755	0.99921	1	2	dorsal root ganglion morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0042144	0.055624625	0.99921	1	2	vacuole fusion, non-autophagic	BP	1	VPS16	up_ACOR_EC
GO:0097576	0.055624625	0.99921	1	2	vacuole fusion	BP	1	VPS16	up_ACOR_EC
GO:0007409	0.0557	0.994	2	109	axonogenesis	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0006929	0.0557	0.999	1	10	substrate-dependent cell migration	BP	1	NRP2	down_ACOR_EC
GO:0055011	0.0557	1	1	1	atrial cardiac muscle cell differentiation	BP	0.874	FHL2	down_VSAP_EC
GO:0055014	0.0557	1	1	1	atrial cardiac muscle cell development	BP	0.874	FHL2	down_VSAP_EC
GO:0010959	0.0557	0.999	1	79	regulation of metal ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0002548	0.0557	0.999	1	17	monocyte chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0050772	0.0557	0.999	1	13	positive regulation of axonogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:1901018	0.055713201	0.99921	1	2	positive regulation of potassium ion transmembrane	BP	1	ACTN2	up_ACOR_EC
GO:0060978	0.055728307	0.99921	1	2	angiogenesis involved in coronary vascular	BP	1	NRP1	up_ACOR_EC
GO:0048699	0.0558	0.971	14	371	generation of neurons	BP	1	IRX3,IRX5,HOXC10,LEP,DLL1,VXN,PLXNA4,NEFH,THRB,LGI4,CAMK2A,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0051017	0.0558	0.978	8	49	actin filament bundle assembly	BP	0.886	ARHGEF15,BAIAP2L1,ARHGAP28,MTOR,STMN1,SWAP70,TNFAIP1,FSCN1	up_VCAV_EC
GO:0006811	0.0558	0.986	4	330	ion transport	BP	1	NETO1,SLC16A12,STIM1,CAV1	up_VSAP_VSMC
GO:0035295	0.0558	0.99	3	356	tube development	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0003157	0.0558	0.995	2	5	endocardium development	BP	0.886	SOX18,PROX1	up_VCAV_EC
GO:0030003	0.0558	0.994	2	157	cellular cation homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0001678	0.0558	0.999	1	29	cellular glucose homeostasis	BP	1	RAB11B	down_VPOR_EC
GO:0006879	0.0558	0.999	1	23	cellular iron ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0007097	0.0558	0.999	1	7	nuclear migration	BP	1	HOOK3	up_VPOR_EC
GO:0051647	0.0558	0.999	1	7	nucleus localization	BP	1	HOOK3	up_VPOR_EC
GO:0090259	0.055848505	0.9992	1	2	regulation of retinal ganglion cell axon	BP	1	NRP1	up_ACOR_EC
GO:0009653	0.0559	0.96	48	773	anatomical structure morphogenesis	BP	1	NOTCH2,HSPB6,PDGFRB,DCN,NAB2,NDN,ANGPT1,SDC4,FBN1,THBS3,BMPR1A,LOX,LMO4,RECK,TRPV2,ANPEP,COL6A1,NUMBL,NAGLU,TBX15,HOXC4,LAMA3,CLSTN1,SEMA3C,ASPN,POLDIP2,CRISPLD2,THY1,TLX2,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,IFT57,CDH2,ENSCAFG00000017708,SPRED1,IRX5,UST,SHC1,RDH10,GREM1,CLIC4,FOXO3,THRB,ZBTB16,BRSK1	down_VCAV_EC
GO:2000113	0.0559	0.961	42	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,EIF4A3,SREBF2,SMC1A,NEDD4,MTDH,NAB2,BIRC5,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,NCL,SUV39H1,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:0090257	0.0559	0.978	8	52	regulation of muscle system process	BP	0.886	DOCK4,PDE4D,STC1,EDN1,PPP3CA,GUCY1A1,KCNJ2,ATP2A1	up_VCAV_EC
GO:0060048	0.0559	0.982	6	30	cardiac muscle contraction	BP	1	TNNT2,ADRA1B,KCNE3,PDE5A,JUP,GAA	up_ACOR_VSMC
GO:0060402	0.0559	0.983	5	35	calcium ion transport into cytosol	BP	0.874	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0003171	0.0559	0.991	3	10	atrioventricular valve development	BP	1	SMAD6,TBX20,TBX5	up_ACOR_VSMC
GO:0071559	0.0559	0.994	2	75	response to transforming growth factor beta	BP	1	ACVRL1,ASPN	down_ACOR_EC

GO:0042531	0.0559	0.999	1	13	positive regulation of tyrosine phosphorylation	BP	1	LYN	down_ACOR_EC
GO:0007507	0.0559	0.999	1	194	heart development	BP	1	GATA5	down_VFEM_VSMC
GO:0043985	0.0559	1	1	1	histone H4-R3 methylation	BP	0.874	PRMT1	down_VSAP_EC
GO:0048593	0.0559	0.999	1	41	camera-type eye morphogenesis	BP	1	IRX5	up_AFEM_VSMC
GO:0031110	0.0559	0.999	1	24	regulation of microtubule polymerization or depolymerization	BP	1	TAOK1	up_AORT_EC
GO:0050795	0.0559	0.999	1	15	regulation of behavior	BP	1	HOXA1	up_APUL_EC
GO:0010977	0.055942237	0.98927	3	33	negative regulation of neuron projection	BP	1	RGMA,LRP4,NRP1	up_ACOR_EC
GO:0040017	0.056	0.986	4	180	positive regulation of locomotion	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0060713	0.056	0.991	3	10	labyrinthine layer morphogenesis	BP	1	FGFR2,SPINT1,SPINT2	up_ACOR_VSMC
GO:0048646	0.056	0.99	3	349	anatomical structure formation involved in	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0051094	0.056	1	1	388	positive regulation of developmental process	BP	1	GATA5	down_AFEM_VSMC
GO:0010896	0.056	1	1	1	regulation of triglyceride catabolic process	BP	0.874	ABHD5	down_VSAP_EC
GO:0010898	0.056	1	1	1	positive regulation of triglyceride catabolic	BP	0.874	ABHD5	down_VSAP_EC
GO:0001704	0.056	0.999	1	43	formation of primary germ layer	BP	1	EYA1	up_AFEM_VSMC
GO:0061326	0.056	0.999	1	41	renal tubule development	BP	1	EYA1	up_AFEM_VSMC
GO:0072080	0.056	0.999	1	41	nephron tubule development	BP	1	EYA1	up_AFEM_VSMC
GO:0007196	0.056	1	1	1	adenylate cyclase-inhibiting G protein-coupled glutamate	BP	0.886	GRM8	up_VCAV_EC
GO:0007216	0.056	1	1	1	G protein-coupled glutamate receptor	BP	0.886	GRM8	up_VCAV_EC
GO:0048731	0.0561	0.955	137	1247	system development	BP	1	EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,LBH,GATA5,GATA4,CD83,ANGPT1,EPYC,HTR2B,RASSF2,MBP,PRDX4,RECK,SHROOM3,FEZ1,MLLT3,ITM2C,FERMT1,BMP4,LNPK,TBX18,FGFR2,TP53BP1,GJA1,ATRX,TLR3,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,CITED2,SPINT1,GLRB,ISG15,ACSL6,ZNRF3,CD274,ZNF365,SASH1,LMO4,TMEM108,FGF18,FAM210B,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,LIMS2,ANKRD1,F2RL1,CAMK2D,CTSB,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,GPM6A,CHD2,ULK2,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,TBX20,BBX,TBX5,FZD3,FRS2,CPAMD8,RND1,DAG1,POMK,APP,PSEN1,SEMA6D,TGFBR1,SYNJ2BP,CHD7,JUP,SPINK2,SIPA1L1,DDR2,CLN8,FOSL2,PERP,PSKH1,RTKN2,SSH3,EDN1,NID1,HPGD,ARID5B,ASAP1,DMC1,SERPINB5,JAM3,B2M,DISC1,AP2B1,TNFRSF11B,TACC1,GAA,ATXN10,FEZ2,SUN1,CNOT4,LHX9,WFS1,WDR48,WASL,ACP2,ERAP1,ID3,SLC8A1,TEAD1,ENSCAFG00000003530,IL18R1,BVES,RREB1,ZDHHC21,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0042221	0.0561	0.977	9	1012	response to chemical	BP	1	ACVRL1,LYN,IGF1R,PDPN,NRP2,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0046483	0.0561	0.992	4	1948	heterocycle metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0001960	0.0561	0.99	3	15	negative regulation of cytokine-mediated	BP	0.874	NR1H4,PTPN2,CNOT7	down_VSAP_EC
GO:0060761	0.0561	0.99	3	15	negative regulation of response to cytokine	BP	0.874	NR1H4,PTPN2,CNOT7	down_VSAP_EC
GO:0050919	0.0561	0.991	3	10	negative chemotaxis	BP	1	SLIT2,PLXNA4,SEMA5A	up_VSAP_EC
GO:0070848	0.0561	0.994	2	193	response to growth factor	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0099536	0.0561	0.999	1	133	synaptic signaling	BP	1	PLCL1	down_VFEM_EC
GO:0050902	0.0561	1	1	1	leukocyte adhesive activation	BP	0.874	CX3CL1	down_VSAP_EC
GO:0002690	0.0561	0.999	1	26	positive regulation of leukocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC

GO:0002520	0.0562	0.965	24	279	immune system development	BP	0.874	VEGFA,MYH9,ACTN1,SOCS5,ETV6,CASP3,PTPN11,WDR1,HOXB7,HIF1A,PTPN2,EVI2B,CTNNB1,ANLN,TFRC,LYN,MYO1E,REST,PRMT1,SH2B3,GLO1,INHBA,BTK,SIX4	down_VSAP_EC
GO:0032269	0.0562	0.986	4	306	negative regulation of cellular protein metabolic	BP	1	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0002682	0.0562	0.986	4	343	regulation of immune system process	BP	1	HOXA9,TOX,HOXA7,CYP26B1	up_VFEM_EC
GO:0030225	0.0562	0.99	3	12	macrophage differentiation	BP	0.889	HCLS1,CASP8,RIPK1	up_VCAV_EC
GO:0031641	0.0562	0.995	2	6	regulation of myelination	BP	0.874	ZPR1,CTNNB1	down_VSAP_EC
GO:2000008	0.0562	0.999	1	12	regulation of protein localization to cell surface	BP	1	STX4	down_ACOR_EC
GO:0048844	0.0562	0.999	1	30	artery morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0032722	0.0562	0.999	1	14	positive regulation of chemokine production	BP	1	TLR2	up_VSAP_VSMC
GO:0050794	0.0563	0.954	202	3075	regulation of cellular process	BP	0.874	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,ASNS,MYH9,NR1H4,FMNL3,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,MEIS2,SGK1,ERO1A,PRKACB,PTPN14,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CBX5,CASP3,FAM49B,ENSCAFG00000003477,HYOU1,AKAP2,WSB1,BCAR3,NUAK1,PTPN11,FSCN1,AARS,DPYSL3,LRRC8A,HOOK3,TRIB3,PGAM1,IFRD1,FARP1,PUM3,PM20D2,FBLIM1,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,REM1,WDR1,MYO1C,PIK3C2A,CHSY1,MSN,UACA,KIF5B,LMAN1,HIF1A,CX3CL1,ENSCAFG00000000562,DYNLL1,SLC45A3,TUBB,IWS1,DNAJC10,YIPF5,TNIK,NAA10,NXN,RGS2,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,EIF2B1,EVI2B,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,ESM1,DDX39B,ADAM17,AGRN,BRD2,EIF4EBP1,SKAP2,UST,PDIA4,CNOT7,CDH11,ACTR3,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,ANLN,CRYAB,STARD13,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,PTP4A1,WWC3,PDE1A,ZC3H15,IGFBP7,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,FAM162A,BACH1,CCNYL1,PLEKHG2,TLN1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,NEXN,CDC37,GTF2H1,ARMCX3,IT	down_VSAP_EC
GO:0040017	0.0563	0.966	24	180	positive regulation of locomotion	BP	1	TWIST2,WNT11,FAM107A,ENPP2,SLIT2,FGF7,ABL1,HDAC7,PDGFD,CCBE1,STAT5A,F2RL1,DDR2,PIK3R1,TIAM1,CFAP69,SASH1,PC,ZNF580,STX4,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0001655	0.0563	0.98	6	116	urogenital system development	BP	1	IRX3,DLL1,GREM1,OVOL1,GCNT4,TNC	up_AFEM_EC
GO:0042092	0.0563	0.99	3	11	type 2 immune response	BP	0.889	BCL6B,GATA3,ARG2	up_VCAV_EC
GO:0051092	0.0563	0.993	2	47	positive regulation of NF-kappaB transcription	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0007568	0.0563	0.999	1	50	aging	BP	1	ARG2	up_AORT_VSMC
GO:0010646	0.0564	0.964	30	945	regulation of cell communication	BP	1	CMKLR1,LEP,KCNC4,LBH,CRY2,GAS1,DLL1,F3,MLLT11,LMCD1,CHRM2,TMEM100,SLC6A6,PLAGL2,GREM1,FAM53B,CAMK2A,GREM2,CLEC16A,CYLD,POSTN,LRRC15,RECK,LGR6,RAB7A,AXIN2,CCL5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0042493	0.0564	0.966	24	178	response to drug	BP	1	GATA4,HTR2B,PRKAA2,ATRX,CASTOR1,TP53INP1,ADCY6,ANKRD1,EGLN1,P2RX7,PTPN22,TCN2,PRKCE,AGRN,PSEN1,JUP,CLN8,NR3C1,EDN1,NOD2,DDIT4,GNAQ,CAT,PARK7	up_ACOR_VSMC
GO:0098542	0.0564	0.97	15	100	defense response to other organism	BP	1	MAP3K14,IL17RC,F2RL1,BATF2,PLA2G6,MYD88,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,PQBP1,MAVS,JCHAIN,DDIT4	up_VSAP_EC
GO:0031589	0.0564	0.972	13	93	cell-substrate adhesion	BP	0.889	EPHB1,TEK,ADAMTS9,VWF,CD34,FERMT1,NEDD9,SLK,ANGPT2,APOD,JAG1,ITGA6,ENSCAFG00000002015	up_VCAV_EC
GO:0050663	0.0564	0.976	9	52	cytokine secretion	BP	1	CD274,C5AR2,ABL1,IL17RC,ANXA4,F2RL1,PNP,MAPKBP1,MAVS	up_VSAP_EC
GO:0050707	0.0564	0.978	8	44	regulation of cytokine secretion	BP	1	CD274,C5AR2,ABL1,IL17RC,ANXA4,F2RL1,MAPKBP1,MAVS	up_VSAP_EC
GO:0007530	0.0564	0.995	2	5	sex determination	BP	1	SF1,SIX4	down_ACOR_VSMC

GO:0033578	0.0564	0.996	2	4	protein glycosylation in Golgi	BP	1	FUT8,LMF1	up_ACOR_VSMC
GO:0048864	0.0564	0.999	1	29	stem cell development	BP	1	CITED2	down_VPOR_EC
GO:0021885	0.0564	0.999	1	24	forebrain cell migration	BP	1	EMX2	up_VFEM_VSMC
GO:0045844	0.0564	0.999	1	24	positive regulation of striated muscle tissue	BP	1	SHOX2	up_VFEM_VSMC
GO:0048636	0.0564	0.999	1	24	positive regulation of muscle organ	BP	1	SHOX2	up_VFEM_VSMC
GO:0044057	0.0565	0.971	14	110	regulation of system process	BP	0.889	DOCK4,PDGFB,RELN,PDE4D,STC1,EDN1,HOMER3,PPP3CA,GUCY1A1,ACPP,KCNJ2,GCH1,SPTBN4,ATP2A1	up_VCAV_EC
GO:0045944	0.0565	0.994	2	287	positive regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0072109	0.0565	0.995	2	6	glomerular mesangium development	BP	0.889	PDGFB,GPR4	up_VCAV_EC
GO:0035914	0.0565	0.999	1	22	skeletal muscle cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0035904	0.0565	0.999	1	25	aorta development	BP	1	EYA1	up_VFEM_VSMC
GO:0009142	0.0566	0.993	2	46	nucleoside triphosphate biosynthetic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0071346	0.0566	0.999	1	41	cellular response to interferon-gamma	BP	1	TLR2	up_AFEM_VSMC
GO:0044106	0.0566	0.999	1	17	cellular amine metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0002763	0.0566	0.999	1	17	positive regulation of myeloid leukocyte	BP	1	EVI2B	up_VPUL_EC
GO:0009893	0.0567	0.978	8	995	positive regulation of metabolic process	BP	1	HOXA11,HOXA9,GATM,SALL1,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0030835	0.0567	0.99	3	11	negative regulation of actin filament	BP	0.891	TMOD1,SWAP70,TMOD3	up_VCAV_EC
GO:0010603	0.0567	0.996	2	4	regulation of cytoplasmic mRNA processing body	BP	0.891	CNOT6,PAN3	up_VCAV_EC
GO:0007283	0.0567	0.993	2	91	spermatogenesis	BP	1	HOXA9,CYP26B1	up_VFEM_EC
GO:0006679	0.0567	1	1	1	glucosylceramide biosynthetic process	BP	0.874	UGCG	down_VSAP_EC
GO:0099003	0.0567	0.999	1	50	vesicle-mediated transport in synapse	BP	1	WNT7A	up_AORT_VSMC
GO:0001759	0.0567	0.999	1	13	organ induction	BP	1	HOXA11	up_VSAP_VSMC
GO:0070371	0.0568	0.972	12	91	ERK1 and ERK2 cascade	BP	0.891	EPHB1,TEK,TNIP1,PDGFB,ATF3,RAPGEF1,TLR4,BMP2,PRKD2,RAPGEF2,HMGB1,PDGFD	up_VCAV_EC
GO:0048522	0.0568	0.982	7	1484	positive regulation of cellular process	BP	1	FGF5,HOXA3,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0043244	0.0568	0.983	5	34	regulation of protein complex disassembly	BP	0.874	ARHGEF2,WDR1,BNIP3,CAPG,MID1	down_VSAP_EC
GO:0016477	0.0568	0.986	4	426	cell migration	BP	1	TBX5,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0046637	0.0568	0.99	3	18	regulation of alpha-beta T cell differentiation	BP	1	GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0071322	0.0568	0.999	1	29	cellular response to carbohydrate stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0032057	0.0568	1	1	1	negative regulation of translational initiation in response to stress	BP	0.874	EIF2S1	down_VSAP_EC
GO:0010243	0.056898105	0.97282	11	238	response to organonitrogen compound	BP	1	NR1H4,SOX9,AQP1,ENSCAFG00000004331,EDEM2,NOD2,ACTN2,FOXC2,RARRES2,HM13,PRKCD	up_ACOR_EC
GO:0071900	0.0569	0.971	13	131	regulation of protein serine/threonine kinase activity	BP	0.874	VEGFA,PTPN11,TRIB3,SESN2,TNIK,MAGED1,APOE,LYN,CCNYL1,CBLC,HTT,CDKN1A,MADD	down_VSAP_EC
GO:0002040	0.0569	0.981	6	46	sprouting angiogenesis	BP	0.874	VEGFA,JCAD,PIK3C2A,ESM1,STARD13,NRP1	down_VSAP_EC
GO:0032481	0.0569	0.984	5	24	positive regulation of type I interferon production	BP	0.892	TMEM173,TLR4,RIOK3,TLR3,PLCG2	up_VCAV_EC
GO:0006725	0.0569	0.992	4	1956	cellular aromatic compound metabolic	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0047496	0.0569	0.99	3	15	vesicle transport along microtubule	BP	0.874	KIF5B,HTT,AP3S1	down_VSAP_EC
GO:0007507	0.0569	0.994	2	194	heart development	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0001960	0.0569	0.999	1	15	negative regulation of cytokine-mediated	BP	1	NR1H4	up_APUL_EC
GO:0060761	0.0569	0.999	1	15	negative regulation of response to cytokine	BP	1	NR1H4	up_APUL_EC

GO:0030878	0.0569	0.999	1	13	thyroid gland development	BP	1	SIX1	up_VFEM_EC
GO:1903578	0.0569	0.999	1	22	regulation of ATP metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0010225	0.057	0.995	2	5	response to UV-C	BP	1	POLH,HMGN1	down_ACOR_VSMC
GO:0050877	0.057	0.994	2	164	nervous system process	BP	1	HOXC10,GPR155	up_AORT_EC
GO:0022617	0.057	0.999	1	11	extracellular matrix disassembly	BP	1	PDPN	down_ACOR_EC
GO:0021884	0.057	0.999	1	10	forebrain neuron development	BP	1	NRP2	down_ACOR_EC
GO:0060384	0.057	0.999	1	9	innervation	BP	1	SULF1	down_ACOR_EC
GO:0120034	0.057	0.999	1	28	positive regulation of plasma membrane bounded cell projection	BP	1	FSCN1	down_AFEM_EC
GO:0001300	0.057	1	1	1	chronological cell aging	BP	0.874	SERPINE1	down_VSAP_EC
GO:0002538	0.057	1	1	1	arachidonic acid metabolite production involved in inflammatory	BP	0.874	SERPINE1	down_VSAP_EC
GO:0002540	0.057	1	1	1	leukotriene production involved in inflammatory	BP	0.874	SERPINE1	down_VSAP_EC
GO:0035490	0.057	1	1	1	regulation of leukotriene production involved in inflammatory response	BP	0.874	SERPINE1	down_VSAP_EC
GO:0035491	0.057	1	1	1	positive regulation of leukotriene production involved in inflammatory	BP	0.874	SERPINE1	down_VSAP_EC
GO:0061044	0.057	1	1	1	negative regulation of vascular wound healing	BP	0.874	SERPINE1	down_VSAP_EC
GO:0097187	0.057	1	1	1	dentinogenesis	BP	0.874	SERPINE1	down_VSAP_EC
GO:1901329	0.057	1	1	1	regulation of odontoblast differentiation	BP	0.874	SERPINE1	down_VSAP_EC
GO:1901331	0.057	1	1	1	positive regulation of odontoblast	BP	0.874	SERPINE1	down_VSAP_EC
GO:1902913	0.057	1	1	1	positive regulation of neuroepithelial cell differentiation	BP	0.874	SERPINE1	down_VSAP_EC
GO:0007492	0.057	0.998	1	27	endoderm development	BP	1	DUSP2	up_AORT_EC
GO:0055024	0.057	0.999	1	22	regulation of cardiac muscle tissue	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002683	0.0571	0.968	18	126	negative regulation of immune system process	BP	1	HOXA7,HOXA9,CD274,C5AR2,TBC1D10C,SLIT2,DLL1,TRAFD1,ZBTB16,STAT6,F2RL1,ZFP36L1,PIK3R1,MYC,FBXO7,NLRX1,TKFC,PPP3CB	up_VSAP_EC
GO:0019221	0.0571	0.971	13	102	cytokine-mediated signaling pathway	BP	0.893	ACKR1,KIT,CXCL8,CXCR4,PDGFB,NLRC5,IFNGR1,OTUD4,CNOT7,ADIPOR2,LSM14A,ENSCAFG00000002015,TJP2	up_VCAV_EC
GO:0099601	0.0571	0.99	3	10	regulation of neurotransmitter	BP	0.893	RELN,MEF2C,HOMER3	up_VCAV_EC
GO:0048729	0.0571	0.989	3	209	tissue morphogenesis	BP	1	HOXA11,SALL1,SHOX2	up_VSAP_VSMC
GO:0045595	0.0571	0.995	2	469	regulation of cell differentiation	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0030162	0.0571	0.999	1	202	regulation of proteolysis	BP	1	CST3	down_AORT_EC
GO:0002042	0.0571	0.999	1	29	cell migration involved in sprouting angiogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0008542	0.0571	0.999	1	13	visual learning	BP	1	NETO1	up_VSAP_VSMC
GO:0010459	0.057113736	0.99916	1	2	negative regulation of heart rate	BP	1	RNLS	up_ACOR_EC
GO:0044332	0.057121713	0.99916	1	2	Wnt signaling pathway involved in dorsal/ventral	BP	1	LRP4	up_ACOR_EC
GO:0009966	0.0572	0.984	5	868	regulation of signal transduction	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0072521	0.0572	0.994	2	185	purine-containing compound metabolic	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0098876	0.0572	0.999	1	29	vesicle-mediated transport to the plasma	BP	1	RAB11B	down_VPOR_EC
GO:0019563	0.0572	1	1	1	glycerol catabolic process	BP	0.874	TPI1	down_VSAP_EC
GO:1905207	0.0572	0.998	1	17	regulation of cardiocyte differentiation	BP	1	TBX5	up_VPUL_EC
GO:0048663	0.0572	0.999	1	13	neuron fate commitment	BP	1	HOXC10	up_VSAP_VSMC

GO:0032872	0.057265821	0.98232	5	77	regulation of stress-activated MAPK cascade	BP	1	FZD5,NOD2,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC
GO:0002262	0.0573	0.977	8	54	myeloid cell homeostasis	BP	0.895	HCLS1,ADGRF5,KIT,GATA3,ITPKB,HMGB1,HIF1A,TMOD3	up_VCAV_EC
GO:0065009	0.0573	0.981	6	735	regulation of molecular function	BP	1	NR1H4,HOXA3,PLCL1,PCSK1N,NPNT,NTRK2	up_APUL_EC
GO:0051155	0.0573	0.986	4	18	positive regulation of striated muscle cell	BP	0.895	MEF2C,EDN1,MTOR,PROX1	up_VCAV_EC
GO:0048762	0.0573	0.993	2	77	mesenchymal cell differentiation	BP	1	PDPN,NRP2	down_ACOR_EC
GO:0043268	0.0573	0.996	2	4	positive regulation of potassium ion transport	BP	1	ACTN2,AKAP6	up_ACOR_VSMC
GO:0003007	0.0573	0.993	2	94	heart morphogenesis	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0021783	0.0573	0.999	1	9	preganglionic parasympathetic fiber	BP	1	NRP2	down_ACOR_EC
GO:0071675	0.0573	0.998	1	13	regulation of mononuclear cell	BP	1	LYN	down_ACOR_EC
GO:0055021	0.0573	0.998	1	15	regulation of cardiac muscle tissue growth	BP	1	TBX5	up_APUL_EC
GO:0050810	0.0573	0.998	1	17	regulation of steroid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0051965	0.0573	0.998	1	17	positive regulation of synapse assembly	BP	1	FLRT3	up_VPUL_EC
GO:0060042	0.0573	0.998	1	14	retina morphogenesis in camera-type eye	BP	1	IRX5	up_VSAP_VSMC
GO:0044267	0.057302888	0.95982	51	1583	cellular protein metabolic process	BP	1	NR1H4,BRSK1,PLCL1,PKIB,SOX9,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,IFI6,DUSP26,NOD2,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,CLU,CHMP4B,TP53INP2,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,HM13,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0009790	0.0574	0.961	37	335	embryo development	BP	1	ACSL4,EIF4A3,HINFP,HOXA3,GINS4,INSIG1,PRMT1,XYLT1,NF2,MMP14,SLC30A1,GREM1,MAP3K20,NEK2,RNASEH2B,HOXA7,HOXC10,HOXB7,BRCA1,E2F8,UGDH,FOSL1,PLK4,HOXC6,SMARCB1,HOXB5,RBBP8,HOXC4,NOLC1,PHACTR4,TBX15,ITGA2,HOXA9,GLI1,EMG1,RTCB,SIX4	down_ACOR_VSMC
GO:0001654	0.0574	0.969	16	110	eye development	BP	1	THRB,CDON,OSR2,MAB21L1,IRX5,DLL1,RARG,MFN2,ZEB1,CTNS,CLCN2,SMG9,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0048880	0.0574	0.969	16	110	sensory system development	BP	1	THRB,CDON,OSR2,MAB21L1,IRX5,DLL1,RARG,MFN2,ZEB1,CTNS,CLCN2,SMG9,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0150063	0.0574	0.969	16	110	visual system development	BP	1	THRB,CDON,OSR2,MAB21L1,IRX5,DLL1,RARG,MFN2,ZEB1,CTNS,CLCN2,SMG9,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0030282	0.0574	0.989	3	37	bone mineralization	BP	1	GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:1904706	0.0574	0.994	2	7	negative regulation of vascular smooth muscle	BP	0.874	ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:0031349	0.0574	0.993	2	90	positive regulation of defense response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0045682	0.0574	0.998	1	27	regulation of epidermis development	BP	1	SRSF6	down_AFEM_EC
GO:0009719	0.0574	1	1	395	response to endogenous stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0009566	0.0574	0.998	1	24	fertilization	BP	1	HOXA9	up_AORT_EC
GO:0046326	0.0574	0.998	1	15	positive regulation of glucose import	BP	1	NR1H4	up_APUL_EC
GO:0006940	0.0574	0.998	1	14	regulation of smooth muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0043009	0.0575	0.964	26	227	chordate embryonic development	BP	0.896	HOXB7,PCDH12,ADGRF5,TIE1,AMOT,PDGFB,MEF2C,CHD7,GATA3,EDN1,HOXB8,SOX18,BMP2,HHEX,MDFI,HOXB5,BCL10,NUP133,SKIL,CUL4A,HIF1A,LUZP1,RBBP6,VASH1,ZEB1,GINS4	up_VCAV_EC
GO:0051270	0.0575	0.964	25	296	regulation of cellular component movement	BP	0.874	ARHGEF2,VEGFA,SULF1,HSPA5,SERPINE1,ACTN1,SPARC,JCAD,DPYSL3,PRCP,MYO1C,PIK3C2A,MSN,HIF1A,ADAM17,STARD13,APOE,PTP4A1,MMP28,LYN,STRAP,NEXN,SDC4,ZMYND8,NRP1	down_VSAP_EC
GO:0008284	0.0575	0.974	10	238	positive regulation of cell proliferation	BP	1	LEP,LBH,DLL1,F3,GPAM,MAB21L1,GREM1,ADAM17,FOSL2,TNC	up_AFEM_EC

GO:2000112	0.0575	0.992	3	1119	regulation of cellular macromolecule biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0001503	0.0575	0.989	3	109	ossification	BP	1	HOXA3,ASPN,ACVR2A	up_VPOR_EC
GO:0051962	0.0575	0.993	2	112	positive regulation of nervous system	BP	1	FLRT3,ARHGEF2	up_VPUL_EC
GO:0044346	0.0575	0.999	1	7	fibroblast apoptotic process	BP	1	STK17B	up_VPOR_EC
GO:2000269	0.0575	0.999	1	7	regulation of fibroblast apoptotic process	BP	1	STK17B	up_VPOR_EC
GO:0005976	0.0576	0.983	5	34	polysaccharide metabolic process	BP	0.874	ENPP1,ENSCAFG00000032470,PPP1R3C,GSK3B,EXT1	down_VSAP_EC
GO:0035295	0.0576	0.989	3	356	tube development	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0021522	0.0576	0.994	2	8	spinal cord motor neuron differentiation	BP	1	LMO4,GLI3	down_VCAV_EC
GO:0055025	0.0576	0.998	1	17	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0019076	0.057664246	0.99356	2	15	viral release from host cell	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0035890	0.057664246	0.99356	2	15	exit from host	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0035891	0.057664246	0.99356	2	15	exit from host cell	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0052126	0.057664246	0.99356	2	15	movement in host environment	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0052192	0.057664246	0.99356	2	15	movement in environment of other organism involved in	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0001763	0.057671931	0.98215	5	78	morphogenesis of a branching structure	BP	1	SOX9,FZD5,FOXC2,CLSTN1,NRP1	up_ACOR_EC
GO:0006941	0.0577	0.981	6	36	striated muscle contraction	BP	0.896	PDE4D,STC1,ARG2,MTOR,KCNJ2,ATP2A1	up_VCAV_EC
GO:0016045	0.0577	0.996	2	4	detection of bacterium	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0098543	0.0577	0.996	2	4	detection of other organism	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0021773	0.0577	1	1	1	striatal medium spiny neuron differentiation	BP	0.874	INHBA	down_VSAP_EC
GO:0032276	0.0577	1	1	1	regulation of gonadotropin secretion	BP	0.874	INHBA	down_VSAP_EC
GO:0046884	0.0577	1	1	1	follicle-stimulating hormone secretion	BP	0.874	INHBA	down_VSAP_EC
GO:0060278	0.0577	1	1	1	regulation of ovulation	BP	0.874	INHBA	down_VSAP_EC
GO:0060279	0.0577	1	1	1	positive regulation of ovulation	BP	0.874	INHBA	down_VSAP_EC
GO:0046880	0.0577	1	1	1	regulation of follicle-stimulating hormone	BP	0.874	INHBA	down_VSAP_EC
GO:0060993	0.0577	0.999	1	42	kidney morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0035773	0.0577	0.998	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	NR1H4	up_APUL_EC
GO:0046718	0.0577	0.998	1	13	viral entry into host cell	BP	1	CAV1	up_VSAP_VSMC
GO:0030154	0.0578	0.98	7	1040	cell differentiation	BP	1	TBX5,EVI2B,MYBPC2,WIF1,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0030512	0.0578	0.986	4	24	negative regulation of transforming growth factor beta receptor	BP	0.874	HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:1903845	0.0578	0.986	4	24	negative regulation of cellular response to transforming growth	BP	0.874	HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:0006509	0.0578	0.99	3	15	membrane protein ectodomain proteolysis	BP	0.874	MYH9,ADAM17,APOE	down_VSAP_EC
GO:0002263	0.0578	0.993	2	68	cell activation involved in immune response	BP	1	LYN,STX4	down_ACOR_EC
GO:0050878	0.0578	0.993	2	75	regulation of body fluid levels	BP	1	LYN,PDPN	down_ACOR_EC
GO:0098542	0.0578	0.993	2	100	defense response to other organism	BP	1	NR1H4,BPI	up_APUL_EC
GO:0046470	0.0578	0.998	1	13	phosphatidylcholine metabolic process	BP	1	ACSL3	down_ACOR_EC
GO:0002218	0.0578	0.999	1	53	activation of innate immune response	BP	1	ESR1	up_AORT_VSMC
GO:0090050	0.057804376	0.99354	2	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	FOXC2,NRP1	up_ACOR_EC

GO:0001959	0.05782273	0.98876	3	33	regulation of cytokine-mediated signaling	BP	1	NR1H4,CCDC3,MAVS	up_ACOR_EC
GO:0002682	0.0579	0.96	42	343	regulation of immune system process	BP	1	HOXA7,HOXA9,CD274,C5AR2,SLC8B1,PPARGC1B,TBC1D10C,SLIT2,ABL1,DLL1,TRAFD1,ANKRD54,ZBTB16,TOX,RARG,STAT6,F2RL1,ZFP36L1,PIK3R1,RBCK1,MYC,ZEB1,MYD88,TFE3,CFD,FBXO7,NLRX1,TKFC,CD83,RNF216,ZFP36L2,PNP,ZNF580,CYBA,STX4,PQBP1,UNC93B1,FLOT1,PPP3CB,NCK1,MAVS,TGFBR2	up_VSAP_EC
GO:0060341	0.0579	0.965	22	255	regulation of cellular localization	BP	0.874	NR1H4,PLK3,PTPN14,PTPN11,PPP1R12A,SESN2,MYO1C,MSN,KIF5B,HIF1A,IWS1,YIPF5,ZPR1,CTNNB1,CRYAB,LYN,GSK3B,SH3GLB1,TAX1BP3,HTT,CALM1,CDKN1A	down_VSAP_EC
GO:0061515	0.0579	0.983	5	24	myeloid cell development	BP	0.896	ADGRF5,KIT,FLI1,TMOD3,TJP2	up_VCAV_EC
GO:0002287	0.0579	0.986	4	17	alpha-beta T cell activation involved in	BP	0.896	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0002292	0.0579	0.986	4	17	T cell differentiation involved in immune	BP	0.896	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0002293	0.0579	0.986	4	17	alpha-beta T cell differentiation involved in	BP	0.896	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0002294	0.0579	0.986	4	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	0.896	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0042093	0.0579	0.986	4	17	T-helper cell differentiation	BP	0.896	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0061351	0.0579	0.993	2	50	neural precursor cell proliferation	BP	1	HOOK3,ARHGEF2	up_VPOR_EC
GO:0097242	0.0579	0.999	1	7	amyloid-beta clearance	BP	1	IGF1R	down_ACOR_EC
GO:0120093	0.0579	1	1	1	regulation of peptidyl-lysine crotonylation	BP	0.874	CDYL	down_VSAP_EC
GO:0120094	0.0579	1	1	1	negative regulation of peptidyl-lysine	BP	0.874	CDYL	down_VSAP_EC
GO:0140066	0.0579	1	1	1	peptidyl-lysine crotonylation	BP	0.874	CDYL	down_VSAP_EC
GO:0106106	0.0579	0.999	1	48	cold-induced thermogenesis	BP	1	HOXC10	up_AORT_VSMC
GO:0120161	0.0579	0.999	1	48	regulation of cold-induced thermogenesis	BP	1	HOXC10	up_AORT_VSMC
GO:0043124	0.0579	0.998	1	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	up_VPUL_EC
GO:0021675	0.0579	0.998	1	29	nerve development	BP	1	HOXA3	up_VPUL_VSMC
GO:0032613	0.0579	0.998	1	14	interleukin-10 production	BP	1	TLR2	up_VSAP_VSMC
GO:0032757	0.0579	0.998	1	14	positive regulation of interleukin-8 production	BP	1	TLR2	up_VSAP_VSMC
GO:0072087	0.0579	0.998	1	14	renal vesicle development	BP	1	SALL1	up_VSAP_VSMC
GO:1903115	0.0579	0.998	1	12	regulation of actin filament-based movement	BP	1	CAV1	up_VSAP_VSMC
GO:0098815	0.058	0.991	3	9	modulation of excitatory postsynaptic potential	BP	1	TMEM108,DMPK,APP	up_ACOR_VSMC
GO:0032075	0.058	0.995	2	5	positive regulation of nuclease activity	BP	1	PCNA,HMGB2	down_ACOR_VSMC
GO:0006873	0.058	0.993	2	160	cellular ion homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0014033	0.058	0.998	1	30	neural crest cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:1903670	0.058	0.998	1	30	regulation of sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0010595	0.058	0.999	1	52	positive regulation of endothelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0006816	0.058	0.999	1	84	calcium ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0034754	0.058	0.998	1	24	cellular hormone metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0002791	0.058037524	0.97961	6	104	regulation of peptide secretion	BP	1	NR1H4,KCNB1,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0090087	0.058056955	0.97452	9	185	regulation of peptide transport	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,MAVS,PRKCD	up_ACOR_EC
GO:0045605	0.0581	0.995	2	5	negative regulation of epidermal cell	BP	1	EZH2,HOXA7	down_ACOR_VSMC
GO:0042982	0.0581	0.998	1	15	amyloid precursor protein metabolic process	BP	1	LYN	down_ACOR_EC
GO:0016101	0.0581	0.998	1	13	diterpenoid metabolic process	BP	1	CYP26B1	up_VFEM_EC

GO:0097300	0.0581	0.998	1	17	programmed necrotic cell death	BP	1	ARHGEF2	up_VPUL_EC
GO:0006950	0.0582	0.954	107	1102	response to stress	BP	1	ELK3,HMGB1,SREBF1,FLNB,USP1,IRAK1,MCM7,RPA1,DDX39A,CBX5,HMGA1,TFPI,SREBF2,SMC1A,TFPI2,HINFP,NEDD4,WDR76,INTS7,MNDA,POLA1,SLC29A1,TRIP13,PPP1R15B,PARPBP,GINS4,SDC1,RAD54L,POLE,HM13,UBE2T,RFC2,INSIG1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,FANCD2,TIMELESS,TOPBP1,EZH2,MAP3K20,RFC4,ADIPOR2,FEN1,TRIM35,MND1,RNASEH2B,PLK3,PCNA,TONSL,ARG2,MCM10,RNF152,DHCR24,BRCA1,B4GALT1,PRCP,PPARD,POLH,ITGB3,NEIL3,UBE2J2,AHSA1,DTL,SUV39H1,RSL1D1,CACTIN,HMGB2,DMAP1,CDC42EP4,SMARCB1,DDX39B,ENSCAFG00000030087,RBBP8,EZR,CLSPN,SMC6,RBM14,MIOS,RBM17,RAD23A,CORO1A,POLR3F,SIGMAR1,BAP1,MELK,SMARCAL1,ELF4,TXNDC12,PSMC1,AIFM1,ARHGEF2,GLI1,H2AFX,CDC5L,ATRIP,NUDT1,EXOSC5,HMGN1,APEX1,GEN1,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0009888	0.0582	0.957	63	545	tissue development	BP	1	HOXA11,FZD1,THRB,HOXA7,CDON,WNT11,HNF4A,AXIN2,OSR2,GJB5,SLIT2,HOXD3,FGF7,ABL1,EBF2,BTG1,DLL1,OSR1,FUZ,ADAMTSL4,SAV1,KLF15,ANXA4,HPSE,RILPL2,ZBTB16,TOX,RARG,STAT6,HOXC4,GTF3C5,AMBRA1,F2RL1,DLX3,DDR2,ZFP36L1,TIAM1,OMD,IRX3,ZEB1,FBXW4,SULF2,SHOX2,MYD88,LRP4,FRMD6,E2F4,NTN4,KDM2B,NFIB,ZFAND5,ARHGAP12,ACVRL1,FLOT1,BGLAP,MAP2K2,TGFBR2,NPRL3,CITED2,TRADD,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0002682	0.0582	0.964	24	343	regulation of immune system process	BP	1	GPAM,NOTCH2,CFD,PRNP,SDC4,FBN1,TFE3,CLSTN1,THY1,RNF216,GLI3,PARK7,ZFP36L1,BPI,CYBA,MAVS,LOXL3,RAB7B,A2M,TSC22D3,RAC2,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0008361	0.0582	0.993	2	50	regulation of cell size	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0009719	0.0582	1	1	395	response to endogenous stimulus	BP	1	MXRA5	down_AORT_VSMC
GO:0097699	0.0582	1	1	1	vascular endothelial cell response to fluid shear	BP	0.874	SOCS5	down_VSAP_EC
GO:0001657	0.0582	0.998	1	42	ureteric bud development	BP	1	EYA1	up_AFEM_VSMC
GO:0072163	0.0582	0.998	1	42	mesonephric epithelium development	BP	1	EYA1	up_AFEM_VSMC
GO:0072164	0.0582	0.998	1	42	mesonephric tubule development	BP	1	EYA1	up_AFEM_VSMC
GO:0007268	0.058230247	0.97754	7	130	chemical synaptic transmission	BP	1	CNTNAP4,BRSK1,PLCL1,KCNB1,INSYN1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0098916	0.058230247	0.97754	7	130	anterograde trans-synaptic signaling	BP	1	CNTNAP4,BRSK1,PLCL1,KCNB1,INSYN1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0001960	0.058265545	0.99345	2	15	negative regulation of cytokine-mediated	BP	1	NR1H4,CCDC3	up_ACOR_EC
GO:0060761	0.058265545	0.99345	2	15	negative regulation of response to cytokine	BP	1	NR1H4,CCDC3	up_ACOR_EC

GO:0051716	0.0583	0.951	212	2001	cellular response to stimulus	BP	1	SH3TC2,FGF13,RHOT1,ADRA1B,VEGFD,TLR1,SMAD6,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,IFNGR1,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,ENSCAFG00000016285,HTR2B,RASSF2,MBP,ZRANB1,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,TM7SF3,FGFR2,TP53BP1,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,RERG,GLRB,ARHGAP29,ZBTB40,ZNRF3,CD274,ZNF365,PLPP2,AR,PTGIR,SASH1,SLC2A5,GPR155,TMEM108,FGF18,FAM210B,ARHGEF26,NDRG2,TMX3,CHN2,CDKN2B,ADCY6,ZBTB4,POLK,ITPR1,GRK7,LIMS2,BLNK,ANKRD1,F2RL1,ADGRL1,FAM129A,CAMK2D,PSEN2,PPP2R5E,GABARAPL1,DAPK1,CTSB,ARHGAP5,BNIP3,NCEH1,AKAP6,CDKN1A,JMY,GNA14,CRLF3,CLSTN1,LRRC8C,CREBRF,NRP1,UBR1,PDE1A,PTPN22,CHD2,DMPK,NPNT,OS9,UNC5B,STT3B,EVL,SMPD1,RCAN2,APLP1,PTGDR,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,MARF1,FZD3,FRS2,AGRN,RND1,SCG5,RGS2,DAG1,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,TESK2,SHPRH,PIK3C3,LAMP2,JUP,SIPA1L1,SENP7,CCL5,NR3C1,WWC2,PERP,PSKH1,RTKN2,D	up_ACOR_VSMC
GO:0051172	0.0583	0.958	50	663	negative regulation of nitrogen compound metabolic process	BP	0.874	PRICKLE1,NR1H4,PLK3,SERPINE1,SOCS5,ETV6,ENPP1,ERRFI1,SNX25,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTGS2,DNAJC10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,PEG3,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,APOE,WWC3,KLF5,LYN,STRAP,DDIT3,CBLC,ATF3,VLDLR,REST,ZMYND8,EIF2S1,CDYL,PAK2,A2M,HIF1AN,SIX4,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:0033157	0.0583	0.971	13	82	regulation of intracellular protein transport	BP	1	SH3TC2,LEP,TCAF1,FERMT1,BMP4,CDKN1A,PTPN22,OS9,PSEN1,JUP,INPP5K,PARK7,PTPN14	up_ACOR_VSMC
GO:0051654	0.0583	0.995	2	6	establishment of mitochondrion	BP	0.874	HIF1A,TRAK1	down_VSAP_EC
GO:0044087	0.0583	0.994	2	339	regulation of cellular component biogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0036138	0.0583	1	1	1	peptidyl-histidine hydroxylation	BP	0.874	HIF1AN	down_VSAP_EC
GO:0042265	0.0583	1	1	1	peptidyl-asparagine hydroxylation	BP	0.874	HIF1AN	down_VSAP_EC
GO:0061428	0.0583	1	1	1	negative regulation of transcription from RNA polymerase II promoter in response to hypoxia	BP	0.874	HIF1AN	down_VSAP_EC
GO:1903727	0.0583	0.998	1	16	positive regulation of phospholipid metabolic	BP	1	NR1H4	up_APUL_EC
GO:0014855	0.0583	0.998	1	22	striated muscle cell proliferation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0030204	0.0583	0.998	1	14	chondroitin sulfate metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0009135	0.0583	0.998	1	22	purine nucleoside diphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0009179	0.0583	0.998	1	22	purine ribonucleoside diphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0046031	0.0583	0.998	1	22	ADP metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0006809	0.0583	0.998	1	14	nitric oxide biosynthetic process	BP	1	CAV1	up_VSAP_VSMC
GO:0046209	0.0583	0.998	1	14	nitric oxide metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0001570	0.0584	0.979	7	37	vasculogenesis	BP	1	ACKR3,HDAC7,EMP2,WARS2,ZFP36L1,TGFBR2,CITED2	up_VSAP_EC
GO:0032502	0.0584	1	2	1661	developmental process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0030182	0.0584	0.994	2	327	neuron differentiation	BP	1	HOXC10,WNT7A	up_AORT_VSMC
GO:0021554	0.0584	0.996	2	4	optic nerve development	BP	0.899	EPHB1,NAV2	up_VCAV_EC
GO:0006865	0.0584	0.998	1	23	amino acid transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0060419	0.0584	0.998	1	22	heart growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003229	0.0584	0.998	1	17	ventricular cardiac muscle tissue development	BP	1	TBX5	up_VPUL_EC

GO:0007015	0.0585	0.967	18	144	actin filament organization	BP	0.899	HCLS1,ARHGEF15,BAIAP2L1,ARHGAP28,TMOD1,MTOR,NCKAP1,PROX1,IQGAP2,STMN1,SWAP70,NCK1,CTNNA1,ARPC5L,TNFAIP1,TMOD3,ARHGEF2,FSCN1	up_VCAV_EC
GO:0031638	0.0585	0.989	3	15	zymogen activation	BP	0.874	SERPINE1,ENSCAFG00000005575,PGK1	down_VSAP_EC
GO:0048562	0.0585	0.993	2	102	embryonic organ morphogenesis	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0035709	0.0585	1	1	1	memory T cell activation	BP	0.874	FAM49B	down_VSAP_EC
GO:2000567	0.0585	1	1	1	regulation of memory T cell activation	BP	0.874	FAM49B	down_VSAP_EC
GO:2000568	0.0585	1	1	1	positive regulation of memory T cell activation	BP	0.874	FAM49B	down_VSAP_EC
GO:1901863	0.0585	0.998	1	25	positive regulation of muscle tissue	BP	1	SHOX2	up_VFEM_VSMC
GO:0016070	0.0586	0.981	7	1479	RNA metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0032781	0.0586	0.99	3	10	positive regulation of ATPase activity	BP	1	TNNT2,DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:0044764	0.0586	0.99	3	11	multi-organism cellular process	BP	0.899	NECTIN2,RIOK3,LSM14A	up_VCAV_EC
GO:0051047	0.0586	0.993	2	84	positive regulation of secretion	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0050798	0.0586	0.994	2	8	activated T cell proliferation	BP	1	GPAM,PRNP	down_VCAV_EC
GO:0032964	0.0586	0.994	2	7	collagen biosynthetic process	BP	0.874	SERPINH1,P3H4	down_VSAP_EC
GO:0003012	0.0586	0.993	2	90	muscle system process	BP	1	GATM,CAV1	up_VSAP_VSMC
GO:0002765	0.0586	1	1	1	immune response-inhibiting signal	BP	0.874	LYN	down_VSAP_EC
GO:0002767	0.0586	1	1	1	immune response-inhibiting cell surface receptor signaling	BP	0.874	LYN	down_VSAP_EC
GO:0002774	0.0586	1	1	1	Fc receptor mediated inhibitory signaling	BP	0.874	LYN	down_VSAP_EC
GO:0034136	0.0586	1	1	1	negative regulation of toll-like receptor 2 signaling	BP	0.874	LYN	down_VSAP_EC
GO:0070667	0.0586	1	1	1	negative regulation of mast cell proliferation	BP	0.874	LYN	down_VSAP_EC
GO:2001022	0.0586	0.998	1	42	positive regulation of response to DNA damage	BP	1	EYA1	up_AFEM_VSMC
GO:0030336	0.0586	0.999	1	86	negative regulation of cell migration	BP	1	TBX5	up_APUL_VSMC
GO:0055067	0.0586	0.998	1	42	monovalent inorganic cation homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0055008	0.0586	0.998	1	24	cardiac muscle tissue morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048660	0.0587	0.98	6	35	regulation of smooth muscle cell proliferation	BP	0.899	CALCRL,TNFAIP3,PDGFB,MEF2C,EDN1,APOD	up_VCAV_EC
GO:0051261	0.0587	0.98	6	33	protein depolymerization	BP	0.899	TMOD1,STMN1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0003215	0.0587	0.99	3	9	cardiac right ventricle morphogenesis	BP	1	SMARCD3,TBX20,CHD7	up_ACOR_VSMC
GO:0015711	0.0587	0.993	2	81	organic anion transport	BP	1	PDPN,ACSL3	down_ACOR_EC
GO:0050926	0.0587	0.994	2	6	regulation of positive chemotaxis	BP	0.899	CXCL8,ANGPT2	up_VCAV_EC
GO:0003281	0.0587	0.998	1	30	ventricular septum development	BP	1	TBX5	up_VPUL_VSMC
GO:0044087	0.0588	0.962	28	339	regulation of cellular component biogenesis	BP	0.874	VEGFA,PTPN11,FSCN1,DPYSL3,FBLIM1,ANKRA2,MYO1C,MSN,DYNLL1,ACTR3,CTNNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,KLF5,TWF1,PLEKHG2,GSK3B,GBP5,SH3GLB1,SDC4,HTT,REST,LRRTM2,CAPG,SIX4,NRP1	down_VSAP_EC
GO:0048016	0.0588	0.986	4	19	inositol phosphate-mediated signaling	BP	0.899	EDN1,HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0070664	0.0588	0.989	3	18	negative regulation of leukocyte proliferation	BP	1	PRNP,SDC4,GREM1	down_VCAV_EC
GO:0048518	0.0588	1	2	1676	positive regulation of biological process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0002686	0.0588	0.998	1	12	negative regulation of leukocyte migration	BP	1	HOXA7	down_ACOR_EC
GO:0061099	0.0588	0.998	1	13	negative regulation of protein tyrosine kinase	BP	1	CAV1	up_VSAP_VSMC
GO:0009880	0.0589	0.983	5	22	embryonic pattern specification	BP	1	SMAD6,FGFR2,NRP1,FRS2,PCSK6	up_ACOR_VSMC
GO:0050856	0.0589	0.99	3	12	regulation of T cell receptor signaling	BP	0.899	NECTIN2,PRKD2,BCL10	up_VCAV_EC

GO:0003094	0.0589	0.99	3	11	glomerular filtration	BP	0.899	ADGRF5,PDGFB,CD34	up_VCAV_EC
GO:0051130	0.0589	0.994	2	342	positive regulation of cellular component	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0070163	0.0589	1	1	1	regulation of adiponectin secretion	BP	0.874	RAB11FIP1	down_VSAP_EC
GO:0070164	0.0589	1	1	1	negative regulation of adiponectin secretion	BP	0.874	RAB11FIP1	down_VSAP_EC
GO:0070162	0.0589	1	1	1	adiponectin secretion	BP	0.874	RAB11FIP1	down_VSAP_EC
GO:0032637	0.0589	0.998	1	26	interleukin-8 production	BP	1	BPI	up_AORT_EC
GO:2001239	0.0589	0.998	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	EYA1	up_VFEM_EC
GO:0051640	0.059	0.988	3	174	organelle localization	BP	1	LYN,SPG11,STX4	down_ACOR_EC
GO:0046599	0.059	0.99	3	11	regulation of centriole replication	BP	1	NUP62,PLK4,RBM14	down_ACOR_VSMC
GO:0090279	0.059	0.994	2	8	regulation of calcium ion import	BP	1	PRNP,TRPV2	down_VCAV_EC
GO:0003421	0.059	1	1	1	growth plate cartilage axis specification	BP	0.899	STC1	up_VCAV_EC
GO:0003422	0.059	1	1	1	growth plate cartilage morphogenesis	BP	0.899	STC1	up_VCAV_EC
GO:0044722	0.059	1	1	1	renal phosphate excretion	BP	0.899	STC1	up_VCAV_EC
GO:1903402	0.059	1	1	1	regulation of renal phosphate excretion	BP	0.899	STC1	up_VCAV_EC
GO:1903403	0.059	1	1	1	negative regulation of renal phosphate excretion	BP	0.899	STC1	up_VCAV_EC
GO:0098742	0.059	0.998	1	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5	up_VCAV_VSMC
GO:0042493	0.0591	0.965	21	178	response to drug	BP	0.899	TNFAIP3,PDGFB,P2RX7,SELL,MEF2C,EDN1,PPP3CA,RALBP1,MAPK13,APOD,TIMELESS,JAG1,GUCY1B1,TOP1,CREB1,CTNNA1,BLM,RIPK1,ATRX,P2RX2,ARHGEF2	up_VCAV_EC
GO:0006875	0.0591	0.968	16	129	cellular metal ion homeostasis	BP	0.899	CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0070848	0.0591	0.968	15	193	response to growth factor	BP	1	PDGFRB,SMAD9,DCN,NDN,VASN,FBN1,AKT1S1,CHRDL1,NR3C1,ASPN,ZFP36L1,FUT8,SHC1,GREM1,RGMA	down_VCAV_EC
GO:0048639	0.0591	0.978	7	39	positive regulation of developmental growth	BP	0.899	MEF2C,CHD7,EDN1,RAB11A,PROX1,CREB1,SPTBN4	up_VCAV_EC
GO:0090090	0.0591	0.982	5	44	negative regulation of canonical Wnt signaling	BP	1	GLI3,CDH2,GREM1,NPHP4,FOXO3	down_VCAV_EC
GO:0043628	0.0591	0.986	4	19	ncRNA 3'-end processing	BP	1	INTS7,FBL,ENSCAFG00000019620,EXOSC5	down_ACOR_VSMC
GO:0003281	0.0591	0.998	1	30	ventricular septum development	BP	1	CITED2	down_VPOR_EC
GO:2000042	0.0591	0.998	1	8	negative regulation of double-strand break repair via homologous	BP	1	CXHXorf57	up_VPOR_EC
GO:0055085	0.0592	0.96	35	284	transmembrane transport	BP	1	ACTN2,PLCG2,LEP,SLC26A7,KCNE3,HTR2B,TCAF1,GJA1,SLC2A5,GPR155,PTPN3,CLCN3,MICU2,ITPR1,DAPK1,CACNB3,AKAP6,LRRC8C,KCNJ4,PRKCE,PSEN1,CHD7,MFSD9,CLN8,ATP6V0E1,EDN1,KCNC4,FXYD1,INPP5K,AZIN2,SLC25A12,NDUFA4L2,PARK7,SLC8A1,SLC2A12	up_ACOR_VSMC
GO:0032273	0.0592	0.978	7	44	positive regulation of protein polymerization	BP	0.899	BAIAP2L1,MTOR,NCKAP1,IQGAP2,NCK1,FES,ARPC5L	up_VCAV_EC
GO:0060485	0.0592	0.993	2	93	mesenchyme development	BP	1	SIX1,TIAM1	up_VFEM_EC
GO:0099156	0.0592	1	1	1	cell-cell signaling via exosome	BP	0.874	KLF5	down_VSAP_EC
GO:0007399	0.0593	0.982	5	564	nervous system development	BP	1	MAPK10,HOXA3,SLITRK5,NTRK2,HOXA1	up_APUL_EC
GO:0031111	0.0593	0.99	3	11	negative regulation of microtubule polymerization or	BP	0.9	STMN1,TAOK1,ARHGEF2	up_VCAV_EC
GO:0051238	0.0593	0.998	1	7	sequestering of metal ion	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0001953	0.0593	0.998	1	14	negative regulation of cell-matrix adhesion	BP	1	HOXA7	up_VFEM_EC
GO:0022408	0.0594	0.976	8	44	negative regulation of cell-cell adhesion	BP	1	MBP,BMP4,PDE5A,CD274,PTPN22,SPINT2,DUSP22,PAG1	up_ACOR_VSMC
GO:0097300	0.0594	0.986	4	17	programmed necrotic cell death	BP	0.9	PELI1,TLR3,RIPK1,ARHGEF2	up_VCAV_EC

GO:1904355	0.0594	0.99	3	11	positive regulation of telomere capping	BP	1	HNRNPD,AURKB,NEK2	down_ACOR_VSMC
GO:0006085	0.0594	0.994	2	8	acetyl-CoA biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0002253	0.0594	0.993	2	92	activation of immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0007632	0.0594	0.998	1	14	visual behavior	BP	1	HOXA1	down_ACOR_EC
GO:0021879	0.059472616	0.99324	2	15	forebrain neuron differentiation	BP	1	DCLK2,NRP1	up_ACOR_EC
GO:0048514	0.0595	0.965	19	214	blood vessel morphogenesis	BP	0.874	VEGFA,SULF1,MYH9,SERPINE1,SPARC,JCAD,PGK1,PRCP,PIK3C2A,HIF1A,THBS2,MTDH,ESM1,CTNNB1,STARD13,APOE,KLF5,MYO1E,NRP1	down_VSAP_EC
GO:0021561	0.0595	0.998	1	8	facial nerve development	BP	1	SEMA3A	up_VPOR_EC
GO:0021610	0.0595	0.998	1	8	facial nerve morphogenesis	BP	1	SEMA3A	up_VPOR_EC
GO:0006942	0.0595	0.998	1	26	regulation of striated muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0046887	0.0595	0.998	1	18	positive regulation of hormone secretion	BP	1	NR1H4	up_VPUL_EC
GO:0003338	0.0595	0.998	1	15	metanephros morphogenesis	BP	1	SALL1	up_VSAP_VSMC
GO:0061572	0.0596	0.976	8	50	actin filament bundle organization	BP	0.902	ARHGEF15,BAIAP2L1,ARHGAP28,MTOR,STMN1,SWAP70,TNFAIP1,FSCN1	up_VCAV_EC
GO:0032675	0.0596	0.98	6	34	regulation of interleukin-6 production	BP	0.902	TNFAIP3,TLR4,MAPK13,TLR3,HMGB1,ARHGEF2	up_VCAV_EC
GO:1903313	0.0596	0.986	4	16	positive regulation of mRNA metabolic process	BP	1	ZFP36L1,NUP98,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0009798	0.0596	0.998	1	31	axis specification	BP	1	CITED2	down_VPOR_EC
GO:1902010	0.0596	1	1	1	negative regulation of translation in response to endoplasmic reticulum	BP	0.874	SESN2	down_VSAP_EC
GO:0034341	0.0596	0.998	1	43	response to interferon-gamma	BP	1	TLR2	up_AFEM_VSMC
GO:0035136	0.0597	0.986	4	16	forelimb morphogenesis	BP	1	RECK,LNPK,ATRX,TBX5	up_ACOR_VSMC
GO:0070231	0.0597	0.989	3	18	T cell apoptotic process	BP	1	GPAM,GLI3,TSC22D3	down_VCAV_EC
GO:0006290	0.0597	0.995	2	5	pyrimidine dimer repair	BP	1	POLH,HMGN1	down_ACOR_VSMC
GO:0043029	0.0597	0.994	2	8	T cell homeostasis	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0010817	0.0597	0.993	2	102	regulation of hormone levels	BP	1	NR1H4,PCSK1N	up_APUL_EC
GO:0098876	0.0597	0.998	1	29	vesicle-mediated transport to the plasma	BP	1	ANKRD50	down_AFEM_EC
GO:0006808	0.0597	1	1	1	regulation of nitrogen utilization	BP	0.874	NR1H4	down_VSAP_EC
GO:0019676	0.0597	1	1	1	ammonia assimilation cycle	BP	0.874	NR1H4	down_VSAP_EC
GO:0019740	0.0597	1	1	1	nitrogen utilization	BP	0.874	NR1H4	down_VSAP_EC
GO:0034255	0.0597	1	1	1	regulation of urea metabolic process	BP	0.874	NR1H4	down_VSAP_EC
GO:0034971	0.0597	1	1	1	histone H3-R17 methylation	BP	0.874	NR1H4	down_VSAP_EC
GO:0038183	0.0597	1	1	1	bile acid signaling pathway	BP	0.874	NR1H4	down_VSAP_EC
GO:0038185	0.0597	1	1	1	intracellular bile acid receptor signaling	BP	0.874	NR1H4	down_VSAP_EC
GO:0045848	0.0597	1	1	1	positive regulation of nitrogen utilization	BP	0.874	NR1H4	down_VSAP_EC
GO:1903314	0.0597	1	1	1	regulation of nitrogen cycle metabolic process	BP	0.874	NR1H4	down_VSAP_EC
GO:1905693	0.0597	1	1	1	regulation of phosphatidic acid biosynthetic process	BP	0.874	NR1H4	down_VSAP_EC
GO:1905695	0.0597	1	1	1	positive regulation of phosphatidic acid biosynthetic process	BP	0.874	NR1H4	down_VSAP_EC
GO:2000211	0.0597	1	1	1	regulation of glutamate metabolic process	BP	0.874	NR1H4	down_VSAP_EC
GO:2000213	0.0597	1	1	1	positive regulation of glutamate metabolic	BP	0.874	NR1H4	down_VSAP_EC
GO:2001248	0.0597	1	1	1	regulation of ammonia assimilation cycle	BP	0.874	NR1H4	down_VSAP_EC
GO:2001250	0.0597	1	1	1	positive regulation of ammonia assimilation	BP	0.874	NR1H4	down_VSAP_EC

GO:0071695	0.0597	0.998	1	45	anatomical structure maturation	BP	1	IRX5	up_AFEM_VSMC
GO:0046620	0.0597	0.998	1	30	regulation of organ growth	BP	1	TBX5	up_VPUL_VSMC
GO:0001934	0.059741546	0.97021	12	274	positive regulation of protein phosphorylation	BP	1	SOX9,ENSCAFG00000004331,FZD5,NOD2,PAK3,TNFRSF19,MAVS,LRP4,SH3RF3,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0008610	0.0598	0.964	21	177	lipid biosynthetic process	BP	1	SCD,ACSL3,SQLE,LSS,SREBF1,HMGCR,SF1,CTDNEP1,INSIG1,ENSCAFG00000018572,CDK4,DHCR24,BRCA1,MVD,ELOVL1,VAC14,ELOVL6,FDFT1,LIPC,NUS1,PDSS1	down_ACOR_VSMC
GO:0034762	0.0598	0.97	12	122	regulation of transmembrane transport	BP	0.874	NR1H4,ENPP1,PTPN11,TRIB3,REM1,WDR1,YES1,LYN,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0051216	0.0598	0.977	7	70	cartilage development	BP	1	SMAD9,THBS3,BMPR1A,HOXC4,GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:1903038	0.0598	0.985	4	30	negative regulation of leukocyte cell-cell	BP	1	PRNP,SDC4,GLI3,LOXL3	down_VCAV_EC
GO:0010556	0.0598	0.992	3	1137	regulation of macromolecule	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0006012	0.0598	0.994	2	6	galactose metabolic process	BP	0.902	GALE,CHST1	up_VCAV_EC
GO:0006874	0.0598	0.993	2	91	cellular calcium ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0001834	0.0598	1	1	1	trophectodermal cell proliferation	BP	0.874	ZPR1	down_VSAP_EC
GO:0006713	0.0598	1	1	1	glucocorticoid catabolic process	BP	0.874	YWHAH	down_VSAP_EC
GO:0033566	0.0598	1	1	1	gamma-tubulin complex localization	BP	0.874	MZT1	down_VSAP_EC
GO:0042447	0.0598	1	1	1	hormone catabolic process	BP	0.874	YWHAH	down_VSAP_EC
GO:0044324	0.0598	1	1	1	regulation of transcription involved in anterior/posterior axis	BP	0.874	DDIT3	down_VSAP_EC
GO:0071931	0.0598	1	1	1	positive regulation of transcription involved in G1/S transition of mitotic	BP	0.874	ZPR1	down_VSAP_EC
GO:1903026	0.0598	1	1	1	negative regulation of RNA polymerase II regulatory region	BP	0.874	DDIT3	down_VSAP_EC
GO:1990261	0.0598	1	1	1	pre-mRNA catabolic process	BP	0.874	ZPR1	down_VSAP_EC
GO:2000016	0.0598	1	1	1	negative regulation of determination of dorsal	BP	0.874	DDIT3	down_VSAP_EC
GO:0009311	0.0598	0.998	1	21	oligosaccharide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0070302	0.05988216	0.98127	5	78	regulation of stress-activated protein kinase	BP	1	FZD5,NOD2,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC
GO:0035265	0.05988877	0.98432	4	54	organ growth	BP	1	SOX9,FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0048699	0.0599	0.958	41	371	generation of neurons	BP	0.902	EPHB1,EDNRB,PRKCH,IFRD1,RELN,MEF2C,CHD7,DLL4,RAPGEF1,GATA3,RAB11A,TCF4,NTN4,PPP3CA,MTOR,HOOK3,BMP2,HMG20A,PREX2,GDPD5,PROX1,ENSCAFG00000010224,STMN1,PAK2,APOD,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,ZC4H2,CTNNA1,SPTBN4,SKIL,HIF1A,ALS2,ZEB1,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:2000145	0.0599	0.965	20	279	regulation of cell motility	BP	1	PDGFRB,DCN,SDC4,GLIPR2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,LAMA3,SEMA3C,THY1,SASH1,SPRED1,TWIST2,DDR2,RAC2,FOXO3	down_VCAV_EC
GO:0045664	0.0599	0.969	14	144	regulation of neuron differentiation	BP	0.874	ARHGEF2,SIPA1L1,DPYSL3,IFRD1,TNIK,UST,APOE,LYN,MMD,VLDLR,REST,DISC1,NRP1,YWHAH	down_VSAP_EC
GO:0048592	0.0599	0.974	9	53	eye morphogenesis	BP	1	THRB,CDON,IRX5,DLL1,RARG,MFN2,ZEB1,KDM2B,CITED2	up_VSAP_EC
GO:0006997	0.0599	0.978	7	42	nucleus organization	BP	1	NDC1,SF1,CTDNEP1,REEP4,HMGB2,NOLC1,EMG1	down_ACOR_VSMC
GO:0051261	0.0599	0.98	6	33	protein depolymerization	BP	1	CAPG,LIMA1,STMN1,PDXP,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0051028	0.0599	0.98	6	33	mRNA transport	BP	0.902	IWS1,QKI,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0043069	0.0599	0.988	3	262	negative regulation of programmed cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0045596	0.0599	0.993	2	186	negative regulation of cell differentiation	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:1901879	0.0599	0.998	1	26	regulation of protein depolymerization	BP	1	TAOK1	up_AORT_EC

GO:0035136	0.0599	0.998	1	16	forelimb morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0006054	0.0599	1	1	1	N-acetylneuraminate metabolic process	BP	0.902	ST6GAL1	up_VCAV_EC
GO:0046622	0.06	0.986	4	15	positive regulation of organ growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0046602	0.06	0.995	2	5	regulation of mitotic centrosome separation	BP	1	NEK2,KIF11	down_ACOR_VSMC
GO:0045992	0.06	0.998	1	12	negative regulation of embryonic development	BP	1	SULF1	down_ACOR_EC
GO:0033628	0.06	0.998	1	14	regulation of cell adhesion mediated by integrin	BP	1	LYN	down_ACOR_EC
GO:0050707	0.06	0.998	1	44	regulation of cytokine secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0050663	0.06	0.998	1	52	cytokine secretion	BP	1	ARG2	up_AORT_VSMC
GO:0048588	0.06	0.998	1	44	developmental cell growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0032652	0.06	0.998	1	18	regulation of interleukin-1 production	BP	1	NR1H4	up_VPUL_EC
GO:0098771	0.0601	0.963	24	180	inorganic ion homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,CNNM2,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,PRKCE,APP,PSEN1,CHD7,DMXL1,EDN1,B2M,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC
GO:0072089	0.0601	0.976	8	43	stem cell proliferation	BP	1	FERMT1,FGFR2,ACSL6,ZNRF3,SMARCD3,FZD3,FRS2,DISC1	up_ACOR_VSMC
GO:0061448	0.0601	0.981	5	89	connective tissue development	BP	1	LEP,GREM1,PTHLH,AXIN2,PPARGC1A	up_AFEM_EC
GO:1900024	0.0601	0.986	4	16	regulation of substrate adhesion-dependent cell	BP	1	NRP1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:1902895	0.0601	0.989	3	15	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	0.874	SMARCA4,HIF1A,KLF5	down_VSAP_EC
GO:0046461	0.0601	0.995	2	5	neutral lipid catabolic process	BP	1	ABHD5,LIPC	down_ACOR_VSMC
GO:0046464	0.0601	0.995	2	5	acylglycerol catabolic process	BP	1	ABHD5,LIPC	down_ACOR_VSMC
GO:0050806	0.0601	0.998	1	25	positive regulation of synaptic transmission	BP	1	NETO1	up_VFEM_VSMC
GO:1900182	0.060109853	0.98813	3	33	positive regulation of protein localization to	BP	1	TRIM8,MAVS,PRKCD	up_ACOR_EC
GO:0048870	0.0602	0.961	30	451	cell motility	BP	1	PDGFRB,DCN,NDN,SDC4,GLIPR2,KANK2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,HSD3B7,LAMA3,CSPG4,SEMA3C,THY1,PEX5,B4GALT1,GLI3,SASH1,CDH2,FUT8,SPRED1,TWIST2,DDR2,GREM1,RAC2,FOXO3	down_VCAV_EC
GO:0051674	0.0602	0.961	30	451	localization of cell	BP	1	PDGFRB,DCN,NDN,SDC4,GLIPR2,KANK2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,HSD3B7,LAMA3,CSPG4,SEMA3C,THY1,PEX5,B4GALT1,GLI3,SASH1,CDH2,FUT8,SPRED1,TWIST2,DDR2,GREM1,RAC2,FOXO3	down_VCAV_EC
GO:0006357	0.0602	0.98	6	547	regulation of transcription by RNA polymerase II	BP	1	ACVRL1,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0032615	0.0602	0.985	4	18	interleukin-12 production	BP	0.904	TLR4,IRF8,TLR3,HMGB1	up_VCAV_EC
GO:0048869	0.0602	0.987	4	1119	cellular developmental process	BP	1	SLITRK5,LIMK1,GATA5,LRRC17	up_VCAV_VSMC
GO:0002762	0.0602	0.989	3	15	negative regulation of myeloid leukocyte	BP	0.874	PTPN2,CTNNB1,LYN	down_VSAP_EC
GO:0014015	0.0602	0.99	3	11	positive regulation of gliogenesis	BP	0.904	PRKCH,MTOR,BMP2	up_VCAV_EC
GO:0045893	0.0602	1	1	413	positive regulation of transcription, DNA-	BP	1	GATA5	down_AFEM_VSMC
GO:1901222	0.0602	0.998	1	32	regulation of NIK/NF-kappaB signaling	BP	1	HDAC7	down_VPOR_EC
GO:0016477	0.060211142	0.96617	17	426	cell migration	BP	1	SOX9,AQP1,ENSCAFG00000004331,SEMA6D,DIXDC1,ZMYND8,PAK3,MMP28,PTGER4,ARHGDIB,ELMO2,FOXC2,LRRC15,TBX5,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0002065	0.0603	0.978	7	37	columnar/cuboidal epithelial cell	BP	1	WNT11,HNF4A,ABL1,DLL1,SAV1,RARG,DLX3	up_VSAP_EC
GO:0048771	0.0603	0.981	5	43	tissue remodeling	BP	1	NOTCH2,SEMA3C,B4GALT1,NCDN,GREM1	down_VCAV_EC
GO:0048523	0.0603	0.989	4	1399	negative regulation of cellular process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0034340	0.0603	0.989	3	15	response to type I interferon	BP	0.874	PTPN2,CNOT7,CDC37	down_VSAP_EC
GO:0048232	0.0603	0.993	2	95	male gamete generation	BP	1	HOXA9,CYP26B1	up_VFEM_EC

GO:0007283	0.0603	0.993	2	91	spermatogenesis	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0032413	0.0603	0.998	1	15	negative regulation of ion transmembrane transporter activity	BP	1	NEDD4	down_ACOR_EC
GO:0007043	0.0603	0.998	1	28	cell-cell junction assembly	BP	1	FSCN1	down_AFEM_EC
GO:0061548	0.0603	0.998	1	8	ganglion development	BP	1	SEMA3A	up_VPOR_EC
GO:0009749	0.06034159	0.98804	3	34	response to glucose	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0099537	0.060347598	0.97654	7	131	trans-synaptic signaling	BP	1	CNTNAP4,BRSK1,PLCL1,KCNB1,INSYN1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0031128	0.060363937	0.99308	2	15	developmental induction	BP	1	SOX9,FZD5	up_ACOR_EC
GO:2001235	0.0604	0.974	9	69	positive regulation of apoptotic signaling	BP	0.904	ATF3,PAK2,SH3GLB1,NCK1,BCL10,CTNNA1,PMAIP1,RIPK1,SKIL	up_VCAV_EC
GO:0045667	0.0604	0.988	3	38	regulation of osteoblast differentiation	BP	1	TWIST2,GREM1,AXIN2	up_AFEM_EC
GO:0007608	0.0604	0.995	2	5	sensory perception of smell	BP	1	B3GNT2,NAV2	down_ACOR_VSMC
GO:0045898	0.0604	0.995	2	5	regulation of RNA polymerase II transcriptional	BP	1	HMGB1,PSMC1	down_ACOR_VSMC
GO:0050905	0.0604	0.998	1	26	neuromuscular process	BP	1	HOXC10	up_AORT_EC
GO:0002030	0.0604	1	1	1	inhibitory G protein-coupled receptor	BP	0.904	APLNR	up_VCAV_EC
GO:1904323	0.0604	1	1	1	regulation of inhibitory G protein-coupled receptor	BP	0.904	APLNR	up_VCAV_EC
GO:1904325	0.0604	1	1	1	positive regulation of inhibitory G protein-coupled receptor	BP	0.904	APLNR	up_VCAV_EC
GO:0030857	0.0604	0.998	1	15	negative regulation of epithelial cell	BP	1	CAV1	up_VSAP_VSMC
GO:0051270	0.0605	0.964	21	296	regulation of cellular component movement	BP	1	PDGFRB,DCN,SDC4,GLIPR2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,LAMA3,SEMA3C,THY1,B4GALT1,SASH1,SPRED1,TWIST2,DDR2,RAC2,FOXO3	down_VCAV_EC
GO:0034220	0.0605	0.988	3	188	ion transmembrane transport	BP	1	LYN,PDPN,NEDD4	down_ACOR_EC
GO:0051171	0.0605	1	2	1697	regulation of nitrogen compound metabolic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0001756	0.0605	0.993	2	17	somitogenesis	BP	1	DLL1,AXIN2	up_AFEM_EC
GO:0042058	0.0605	0.993	2	17	regulation of epidermal growth factor receptor	BP	1	RAB7A,ADAM17	up_AFEM_EC
GO:0002158	0.0605	1	1	1	osteoclast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:0046851	0.0605	1	1	1	negative regulation of bone remodeling	BP	1	GREM1	down_ACOR_VSMC
GO:0090289	0.0605	1	1	1	regulation of osteoclast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:0090291	0.0605	1	1	1	negative regulation of osteoclast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:1902680	0.0605	1	1	415	positive regulation of RNA biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:1903508	0.0605	1	1	415	positive regulation of nucleic acid-templated	BP	1	GATA5	down_AFEM_VSMC
GO:0048729	0.0605	0.999	1	209	tissue morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:1902624	0.0605	0.998	1	7	positive regulation of neutrophil migration	BP	1	C3AR1	up_VPOR_EC
GO:0019359	0.0605	0.998	1	23	nicotinamide nucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0019363	0.0605	0.998	1	23	pyridine nucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0003209	0.0605	0.998	1	14	cardiac atrium morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0003230	0.0605	0.998	1	14	cardiac atrium development	BP	1	SHOX2	up_VSAP_VSMC
GO:0050795	0.060583875	0.99304	2	15	regulation of behavior	BP	1	CNTNAP4,PTGDS	up_ACOR_EC
GO:0032874	0.0606	0.974	9	57	positive regulation of stress-activated MAPK	BP	0.905	MAP3K11,TLR4,EDN1,MAP3K3,BMP2,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0046320	0.0606	0.99	3	10	regulation of fatty acid oxidation	BP	1	ACACB,C1QTNF2,LONP2	up_VSAP_EC
GO:0098927	0.0606	0.993	2	17	vesicle-mediated transport between endosomal compartments	BP	1	MYO1D,RAB7A	up_AFEM_EC

GO:1905207	0.0606	0.993	2	17	regulation of cardiocyte differentiation	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0071560	0.0606	0.998	1	72	cellular response to transforming growth	BP	1	TGFBR1	down_VSAP_VSMC
GO:0030512	0.0606	0.998	1	24	negative regulation of transforming growth factor beta receptor	BP	1	BAMBI	up_VPOR_VSMC
GO:1903845	0.0606	0.998	1	24	negative regulation of cellular response to transforming growth	BP	1	BAMBI	up_VPOR_VSMC
GO:0006094	0.0606	0.998	1	24	gluconeogenesis	BP	1	FBP1	up_VFEM_VSMC
GO:0009185	0.0606	0.998	1	23	ribonucleoside diphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:1902903	0.0607	0.966	18	125	regulation of supramolecular fiber organization	BP	1	SYNPO2L,FGF13,ARHGAP28,ACTN2,MID1,SYNPO2,TUBB4A,F2RL1,JMY,NRP1,EVL,PRKCE,APP,PSEN1,SSH3,EDN1,INPP5K,WASL	up_ACOR_VSMC
GO:0072395	0.0607	0.989	3	11	signal transduction involved in cell cycle	BP	1	CASP2,DTL,CDC5L	down_ACOR_VSMC
GO:0072401	0.0607	0.989	3	11	signal transduction involved in DNA integrity	BP	1	CASP2,DTL,CDC5L	down_ACOR_VSMC
GO:0072422	0.0607	0.989	3	11	signal transduction involved in DNA damage	BP	1	CASP2,DTL,CDC5L	down_ACOR_VSMC
GO:0008217	0.0607	0.988	3	38	regulation of blood pressure	BP	1	DLL1,AVPR1A,TBXA2R	up_AFEM_EC
GO:0044091	0.0607	0.99	3	10	membrane biogenesis	BP	1	EMP2,LRP4,FLOT1	up_VSAP_EC
GO:0042692	0.0607	0.993	2	105	muscle cell differentiation	BP	1	TBX5,NPNT	up_APUL_EC
GO:0006482	0.0607	0.995	2	5	protein demethylation	BP	1	KDM2B,KDM3B	up_VSAP_EC
GO:0008214	0.0607	0.995	2	5	protein dealkylation	BP	1	KDM2B,KDM3B	up_VSAP_EC
GO:0016577	0.0607	0.995	2	5	histone demethylation	BP	1	KDM2B,KDM3B	up_VSAP_EC
GO:0070076	0.0607	0.995	2	5	histone lysine demethylation	BP	1	KDM2B,KDM3B	up_VSAP_EC
GO:0006835	0.0607	0.998	1	13	dicarboxylic acid transport	BP	1	PDPN	down_ACOR_EC
GO:2001271	0.0607	1	1	1	negative regulation of cysteine-type endopeptidase activity involved in execution	BP	0.874	PAK2	down_VSAP_EC
GO:2000027	0.0607	0.998	1	72	regulation of animal organ morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0070570	0.0608	0.994	2	8	regulation of neuron projection regeneration	BP	1	THY1,RGMA	down_VCAV_EC
GO:0050886	0.0608	0.993	2	17	endocrine process	BP	1	CRY2,AVPR1A	up_AFEM_EC
GO:0110111	0.0608	0.993	2	17	negative regulation of animal organ	BP	1	THRB,GREM1	up_AFEM_EC
GO:2000108	0.0608	0.998	1	12	positive regulation of leukocyte apoptotic	BP	1	LYN	down_ACOR_EC
GO:0007528	0.0608	0.998	1	17	neuromuscular junction development	BP	1	NTRK2	up_APUL_EC
GO:0046626	0.0608	0.998	1	18	regulation of insulin receptor signaling	BP	1	NR1H4	up_VPUL_EC
GO:0051253	0.0609	0.958	39	359	negative regulation of RNA metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,SREBF2,NEDD4,U2AF2,MTDH,NAB2,BIRC5,CAV1,TIMELESS,THRAP3,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,SUV39H1,HMGB2,DMAP1,CDK2,ENSCAFG00000005299,EZR,ERF,TCERG1,HAT1,HIST2H2AC,H2AFX,SIX4	down_ACOR_VSMC
GO:0048641	0.0609	0.986	4	16	regulation of skeletal muscle tissue	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0090304	0.0609	1	2	1694	nucleic acid metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0045604	0.0609	0.993	2	17	regulation of epidermal cell differentiation	BP	1	HOXA7,DLL1	up_AFEM_EC
GO:1901654	0.0609	0.998	1	31	response to ketone	BP	1	SLIT2	up_VPUL_VSMC
GO:0070201	0.060904286	0.97302	9	187	regulation of establishment of protein	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,MAVS,PRKCD	up_ACOR_EC
GO:0055082	0.061	0.962	25	189	cellular chemical homeostasis	BP	1	ADRA1B,PLCG2,SLC26A7,HTR2B,PRKAA2,MICU2,ITPR1,F2RL1,EGLN1,DMPK,ATP7A,ORMDL3,PRKCE,APP,PSEN1,CHD7,DMXL1,RAB11B,EDN1,DISC1,HERPUD1,WFS1,ATP2C1,SLC8A1,STC2	up_ACOR_VSMC

GO:0044106	0.061	0.993	2	17	cellular amine metabolic process	BP	1	MOXD1,NAPEPLD	up_AFEM_EC
GO:0090100	0.061	0.998	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:1904888	0.061	0.998	1	31	cranial skeletal system development	BP	1	TBX15	down_VPOR_EC
GO:0006352	0.061	0.998	1	56	DNA-templated transcription, initiation	BP	1	ESR1	up_AORT_VSMC
GO:0060078	0.061	0.998	1	17	regulation of postsynaptic membrane potential	BP	1	NETO1	up_VSAP_VSMC
GO:0099565	0.061	0.998	1	17	chemical synaptic transmission, postsynaptic	BP	1	NETO1	up_VSAP_VSMC
GO:1904029	0.0611	0.982	5	28	regulation of cyclin-dependent protein kinase	BP	0.905	TNFAIP3,PDGFB,HHEX,PROX1,BLM	up_VCAV_EC
GO:0120039	0.0611	0.988	3	158	plasma membrane bounded cell projection	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0051149	0.0611	0.998	1	25	positive regulation of muscle cell differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0044093	0.0612	0.956	52	437	positive regulation of molecular function	BP	1	TNNT2,ACTN2,PLCG2,LEP,PLCL1,MAP3K8,HTR2B,RASSF2,TCAF1,USP6NL,MBP,BMP4,EVI5L,FGFR2,TLR3,PPARGC1A,PDE5A,PKP4,AR,SASH1,LMO4,FGF18,F2RL1,DAPK1,AKAP6,JMY,NPNT,ATP7A,CCNT1,FRS2,PARP9,APP,PSEN1,SGSM2,JUP,CCL5,DDR2,PERP,EDN1,DYNC1I2,AKTIP,NOD2,ARID5B,B2M,DCUN1D4,HERPUD1,MAP3K7,DYNC1I1,PARK7,IL18R1,HMBOX1,LMF1	up_ACOR_VSMC
GO:0034655	0.0612	0.966	17	135	nucleobase-containing compound catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,AIFM1,ENSCAFG00000015189,RNASEH2C,NUDT1,EXOSC5,NUDT3	down_ACOR_VSMC
GO:0044237	0.0612	0.982	11	3491	cellular metabolic process	BP	1	ETFA,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0033135	0.0612	0.977	7	40	regulation of peptidyl-serine phosphorylation	BP	0.905	HCLS1,PDE4D,PRKD2,NCK1,NSD1,PTGS2,SPTBN4	up_VCAV_EC
GO:0072359	0.0612	0.988	3	368	circulatory system development	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0006098	0.0612	0.994	2	8	pentose-phosphate shunt	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0051156	0.0612	0.994	2	8	glucose 6-phosphate metabolic process	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0048598	0.0612	0.993	2	207	embryonic morphogenesis	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0090200	0.0612	0.993	2	10	positive regulation of release of cytochrome c	BP	0.874	BNIP3,FAM162A	down_VSAP_EC
GO:0032989	0.0612	0.993	2	292	cellular component morphogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0018105	0.0612	0.993	2	116	peptidyl-serine phosphorylation	BP	1	STK32B,PTGER2	up_VPUL_EC
GO:0048486	0.0612	0.998	1	10	parasympathetic nervous system development	BP	1	NRP2	down_ACOR_EC
GO:0000041	0.0612	0.998	1	31	transition metal ion transport	BP	1	RAB11B	down_VPOR_EC
GO:0048514	0.0612	0.999	1	214	blood vessel morphogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0010828	0.0612	0.998	1	16	positive regulation of glucose transmembrane	BP	1	NR1H4	up_APUL_EC
GO:0060038	0.0612	0.998	1	18	cardiac muscle cell proliferation	BP	1	TBX5	up_VPUL_EC
GO:0055007	0.0612	0.998	1	31	cardiac muscle cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0070542	0.061240418	0.99293	2	15	response to fatty acid	BP	1	NR1H4,PTGER4	up_ACOR_EC
GO:0032675	0.061281293	0.98778	3	34	regulation of interleukin-6 production	BP	1	NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0043604	0.0613	0.963	21	288	amide biosynthetic process	BP	1	UBA52,LARP6,COA1,SAMD4B,RPL23,RPL13,EIF3K,MRPL37,RPL27A,EEF2,ZFP36L1,RPL27,MRPS11,ORMDL3,RPS27,ACSS2,ENSCAFG00000015122,PYM1,FOXO3,EIF4EBP1,ACAT1	down_VCAV_EC
GO:0034113	0.0613	0.989	3	10	heterotypic cell-cell adhesion	BP	1	MBP,JUP,PERP	up_ACOR_VSMC
GO:0006692	0.0613	0.989	3	11	prostanoid metabolic process	BP	0.905	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:0006693	0.0613	0.989	3	11	prostaglandin metabolic process	BP	0.905	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:1903428	0.0613	0.994	2	8	positive regulation of reactive oxygen species biosynthetic process	BP	1	PARK7,CYBA	down_VCAV_EC

GO:0015988	0.0613	0.993	2	17	energy coupled proton transmembrane transport, against	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0046661	0.0613	0.998	1	45	male sex differentiation	BP	1	HOXA9	up_AFEM_VSMC
GO:0030857	0.0613	0.998	1	15	negative regulation of epithelial cell	BP	1	HOXA7	up_VFEM_EC
GO:0002762	0.0613	0.998	1	15	negative regulation of myeloid leukocyte	BP	1	HOXA7	up_VFEM_EC
GO:0008652	0.0613	0.998	1	24	cellular amino acid biosynthetic process	BP	1	GATM	up_VFEM_VSMC
GO:1901607	0.0613	0.998	1	24	alpha-amino acid biosynthetic process	BP	1	GATM	up_VFEM_VSMC
GO:0007165	0.0614	0.98	7	1496	signal transduction	BP	1	FGF5,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0015672	0.0614	0.981	5	89	monovalent inorganic cation transport	BP	1	KCNC4,ATP6V1B2,FXYD1,ATP6V0B,DMPK	up_AFEM_EC
GO:0006336	0.0614	0.989	3	11	DNA replication-independent nucleosome	BP	0.905	NASP,ASF1A,ATRX	up_VCAV_EC
GO:0048514	0.0614	0.988	3	214	blood vessel morphogenesis	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0099132	0.0614	0.993	2	17	ATP hydrolysis coupled cation transmembrane	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0003197	0.0614	0.998	1	16	endocardial cushion development	BP	1	TBX5	up_APUL_EC
GO:0051049	0.0615	0.958	37	479	regulation of transport	BP	0.874	VEGFA,NR1H4,PLK3,SERPINE1,PTPN14,ENPP1,PTPN11,TRIB3,PPP1R12A,REM1,WDR1,MYO1C,MSN,KIF5B,HIF1A,IWS1,YIPF5,ZPR1,YES1,CTNNB1,CRYAB,APOE,LYN,GSK3B,NKAIN1,SH3GLB1,SDC4,HTT,REST,CALM1,RAB11FIP1,LRRTM2,INHBA,CDKN1A,RHBDF2,YWHAH,HOMER1	down_VSAP_EC
GO:0045892	0.0615	0.958	36	328	negative regulation of transcription, DNA-templated	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,SREBF2,NEDD4,MTDH,NAB2,BIRC5,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,SUV39H1,HMGB2,DMAP1,CDK2,ENSCAFG00000005299,EZR,ERF,TCERG1,HAT1,HIST2H2AC,H2AFX,SIX4	down_ACOR_VSMC
GO:0060326	0.0615	0.971	11	84	cell chemotaxis	BP	0.905	EPHB1,EDNRB,KIT,CXCL8,DOCK4,PDGFB,PDE4D,MMP28,PRKD2,SWAP70,HMGB1	up_VCAV_EC
GO:0043536	0.0615	0.998	1	32	positive regulation of blood vessel endothelial	BP	1	HDAC7	down_VPOR_EC
GO:0043316	0.0615	1	1	1	cytotoxic T cell degranulation	BP	0.905	RAB27A	up_VCAV_EC
GO:1903433	0.0615	1	1	1	regulation of constitutive secretory pathway	BP	0.905	RAB27A	up_VCAV_EC
GO:0097278	0.0615	1	1	1	complement-dependent cytotoxicity	BP	0.905	RAB27A	up_VCAV_EC
GO:1903435	0.0615	1	1	1	positive regulation of constitutive secretory	BP	0.905	RAB27A	up_VCAV_EC
GO:0060420	0.0615	0.998	1	18	regulation of heart growth	BP	1	TBX5	up_VPUL_EC
GO:0006605	0.0616	0.973	9	99	protein targeting	BP	1	PRNP,RHOD,AKT2,SSR2,SSR3,PEX5,SEC61B,LONP2,SEC61A1	down_VCAV_EC
GO:0071705	0.0616	0.979	6	582	nitrogen compound transport	BP	1	LYN,PDPN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0051493	0.0616	0.993	2	188	regulation of cytoskeleton organization	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0022414	0.0616	0.993	2	294	reproductive process	BP	1	HOXA9,IRX5	up_AFEM_VSMC
GO:0042773	0.0616	0.998	1	32	ATP synthesis coupled electron transport	BP	1	NDUFA10	down_AFEM_EC
GO:0017157	0.0616	0.998	1	58	regulation of exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0061448	0.0616	0.998	1	89	connective tissue development	BP	1	HOXA3	up_APUL_VSMC
GO:0030593	0.0616	0.998	1	19	neutrophil chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0097305	0.0616	0.998	1	31	response to alcohol	BP	1	SLIT2	up_VPUL_VSMC
GO:0098662	0.0617	0.965	18	131	inorganic cation transmembrane transport	BP	1	ACTN2,PLCG2,KCNE3,HTR2B,PTPN3,MICU2,ITPR1,CACNB3,AKAP6,KCNJ4,PRKCE,CHD7,ATP6V0E1,KCNC4,FXYD1,NDUFA4L2,PARK7,SLC8A1	up_ACOR_VSMC
GO:0048858	0.0617	0.988	3	159	cell projection morphogenesis	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0071825	0.0617	0.998	1	12	protein-lipid complex subunit organization	BP	1	ACSL3	down_ACOR_EC

GO:0071827	0.0617	0.998	1	12	plasma lipoprotein particle organization	BP	1	ACSL3	down_ACOR_EC
GO:0006434	0.0617	1	1	1	seryl-tRNA aminoacylation	BP	0.874	SARS	down_VSAP_EC
GO:0061351	0.0617	0.998	1	50	neural precursor cell proliferation	BP	1	WNT7A	up_AORT_VSMC
GO:0007026	0.0617	0.998	1	8	negative regulation of microtubule	BP	1	ARHGEF2	up_VPOR_EC
GO:0031326	0.0618	0.974	10	1176	regulation of cellular biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,ACSL3,NEDD4	down_ACOR_EC
GO:0051248	0.0618	0.984	4	316	negative regulation of protein metabolic process	BP	1	LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0000132	0.0618	0.989	3	11	establishment of mitotic spindle orientation	BP	1	ZW10,CENPA,NDC80	down_ACOR_VSMC
GO:0051294	0.0618	0.989	3	11	establishment of spindle orientation	BP	1	ZW10,CENPA,NDC80	down_ACOR_VSMC
GO:0019219	0.0618	0.991	3	1151	regulation of nucleobase-containing compound metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0055002	0.0618	0.998	1	45	striated muscle cell development	BP	1	BEND2	up_AFEM_VSMC
GO:0048522	0.0619	0.95	140	1484	positive regulation of cellular process	BP	1	ACSL3,FSCN1,HMGB1,RNPS1,SREBF1,IRAK1,ANLN,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,NEDD4,U2AF2,MNDA,SLC29A1,MTDH,HOXA3,COLGALT1,SLC25A5,SRRT,SDC1,CTDNEP1,FBXO5,SLC35C2,PRELID1,CDCA7L,RFC2,BIRC5,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,CASP2,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,NF2,AURKB,MMP14,ABHD5,EZH2,STMN1,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FEN1,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,PCNA,DHX33,BID,ARG2,SF3B4,CKS2,PDCD2,RNF152,POC1A,BRCA1,MVD,FASTKD3,EIF5A,E2F8,B4GALT1,TFRC,NRAS,PPARD,CDC6,NDC80,RAP2C,HIST1H1A,CYCS,FAM49B,NCL,RAC1,NUP62,EMP2,DTL,PDXP,FOSL1,PLK4,IQGAP2,HMGB2,GSTO1,CDC42EP4,CDK2,FGF5,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,SMC6,TOX,RBM14,MIOS,RAD23A,CORO1A,BEND6,CDC20,ASPM,MELK,ARPC1B,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,CDC25A,SUPT16H,TWIST2,TADA2A,HOXA9,GLI1,JMJD6,UBE2C,NUS1,CCT4,AMOTL1,MTBP,DEPDC1B,TPBG,ENSCAFG00000017103,GEN1,AMER1,DCUN1D5,PIK3CD	down_ACOR_VSMC
GO:0006641	0.0619	0.984	4	25	triglyceride metabolic process	BP	0.874	PTPN11,SEL1L,APOE,ABHD5	down_VSAP_EC
GO:0050900	0.0619	0.992	2	89	leukocyte migration	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0001822	0.0619	0.992	2	98	kidney development	BP	1	HOXA11,SALL1	up_VSAP_VSMC
GO:0003229	0.0619	0.998	1	17	ventricular cardiac muscle tissue development	BP	1	TBX5	up_APUL_EC
GO:0071225	0.0619	0.998	1	8	cellular response to muramyl dipeptide	BP	1	ARHGEF2	up_VPOR_EC
GO:0003170	0.0619	0.998	1	25	heart valve development	BP	1	SHOX2	up_VFEM_VSMC
GO:0048660	0.061949341	0.98757	3	35	regulation of smooth muscle cell proliferation	BP	1	NDRG2,PTGIR,CLSTN1	up_ACOR_EC
GO:0031327	0.062	0.956	44	412	negative regulation of cellular biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,EIF4A3,SREBF2,SMC1A,NEDD4,MTDH,NAB2,BIRC5,INSIG1,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,BRCA1,NOC2L,PPARD,NCL,SUV39H1,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:0032147	0.062	0.971	11	77	activation of protein kinase activity	BP	0.905	KIT,MAP3K11,PDGFB,STK10,TLR4,MAP3K3,BMP2,SLK,MADD,PAK2,RIPK1	up_VCAV_EC
GO:0000003	0.062	0.993	2	295	reproduction	BP	1	HOXA9,IRX5	up_AFEM_VSMC
GO:0010575	0.062	0.998	1	8	positive regulation of vascular endothelial growth factor production	BP	1	C3AR1	up_VPOR_EC
GO:0034637	0.062	0.998	1	25	cellular carbohydrate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0002053	0.062	0.998	1	15	positive regulation of mesenchymal cell	BP	1	SHOX2	up_VSAP_VSMC

GO:0050879	0.0621	0.985	4	16	multicellular organismal movement	BP	1	ITPR1,DMPK,CLN8,GAA	up_ACOR_VSMC
GO:0050881	0.0621	0.985	4	16	musculoskeletal movement	BP	1	ITPR1,DMPK,CLN8,GAA	up_ACOR_VSMC
GO:0042737	0.0621	0.988	3	18	drug catabolic process	BP	1	MAOA,CHID1,ACAT1	down_VCAV_EC
GO:0010571	0.0621	0.995	2	4	positive regulation of nuclear cell cycle DNA	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0048709	0.0621	0.998	1	17	oligodendrocyte differentiation	BP	1	NTRK2	up_APUL_EC
GO:0007632	0.0621	0.998	1	14	visual behavior	BP	1	NETO1	up_VSAP_VSMC
GO:0035116	0.0621	0.998	1	15	embryonic hindlimb morphogenesis	BP	1	PITX1	up_VSAP_VSMC
GO:0048646	0.0622	0.961	24	349	anatomical structure formation involved in morphogenesis	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,SDC4,THBS3,BMPR1A,LMO4,ANPEP,COL6A1,LAMA3,SEMA3C,THY1,TLX2,B4GALT1,GLI3,MYDGF,SASH1,IFT57,SPRED1,SHC1,RDH10,GREM1,CLIC4	down_VCAV_EC
GO:0043410	0.0622	0.964	18	144	positive regulation of MAPK cascade	BP	0.905	TEK,KIT,MAP3K11,PDGFB,TLR4,EDN1,MAP3K3,BMP2,MADD,PRKD2,TLR3,RAPGEF2,TAOK1,HMGB1,RIPK1,PDGFD,JCAD,CDON	up_VCAV_EC
GO:0043931	0.0622	0.993	2	9	ossification involved in bone maturation	BP	1	THBS3,GREM1	down_VCAV_EC
GO:0070977	0.0622	0.993	2	9	bone maturation	BP	1	THBS3,GREM1	down_VCAV_EC
GO:0050862	0.0622	0.994	2	5	positive regulation of T cell receptor signaling	BP	0.905	NECTIN2,PRKD2	up_VCAV_EC
GO:0006721	0.0622	0.998	1	14	terpenoid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0003401	0.0622	0.998	1	15	axis elongation	BP	1	SIX1	up_VFEM_EC
GO:0060996	0.0623	0.981	5	26	dendritic spine development	BP	0.905	EPHB1,RELN,MEF2C,ENSCAFG00000010224,PAK2	up_VCAV_EC
GO:0045601	0.0623	0.989	3	10	regulation of endothelial cell differentiation	BP	1	BTG1,ZEB1,ACVRL1	up_VSAP_EC
GO:0045844	0.0623	0.998	1	24	positive regulation of striated muscle tissue	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048636	0.0623	0.998	1	24	positive regulation of muscle organ	BP	1	CYP26B1	up_VPOR_VSMC
GO:0071396	0.0624	0.964	19	134	cellular response to lipid	BP	1	LBH,SKP2,PRKAA2,BMP4,ABCA1,MED14,AR,SASH1,FAM210B,ADCY6,ANKRD1,CREBRF,PTGDR,PRKCE,NR3C1,NOD2,FAM107A,DDIT4,PARK7	up_ACOR_VSMC
GO:0030282	0.0624	0.977	7	37	bone mineralization	BP	1	WNT11,AXIN2,OSR2,OSR1,DDR2,OMD,BGLAP	up_VSAP_EC
GO:2000648	0.0624	0.988	3	14	positive regulation of stem cell proliferation	BP	0.874	HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0034142	0.0624	0.998	1	14	toll-like receptor 4 signaling pathway	BP	1	LYN	down_ACOR_EC
GO:0030216	0.0624	0.998	1	29	keratinocyte differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0031397	0.0624	0.998	1	30	negative regulation of protein ubiquitination	BP	1	IVNS1ABP	down_AFEM_EC
GO:1990845	0.0624	0.998	1	51	adaptive thermogenesis	BP	1	HOXC10	up_AORT_VSMC
GO:0060544	0.0624	0.998	1	8	regulation of necroptotic process	BP	1	ARHGEF2	up_VPOR_EC
GO:0040007	0.0625	0.97	11	276	growth	BP	1	MT2A,LEP,ENSCAFG00000009113,GAS1,DLL1,PLXNA4,GPAM,DCUN1D3,LGR6,ACACB,ADAM17	up_AFEM_EC
GO:1903670	0.0625	0.979	6	30	regulation of sprouting angiogenesis	BP	1	ABL1,HDAC7,DLL1,EPN2,TBXA2R,HMOX1	up_VSAP_EC
GO:0030855	0.0625	0.987	3	183	epithelial cell differentiation	BP	1	ACVRL1,PDPN,HOXA7	down_ACOR_EC
GO:0015672	0.0625	0.992	2	89	monovalent inorganic cation transport	BP	1	NETO1,CAV1	up_VSAP_VSMC
GO:0097205	0.0625	0.998	1	12	renal filtration	BP	1	SULF1	down_ACOR_EC
GO:1904464	0.0625	1	1	1	regulation of matrix metallopeptidase	BP	0.905	CD200	up_VCAV_EC
GO:1904465	0.0625	1	1	1	negative regulation of matrix metallopeptidase	BP	0.905	CD200	up_VCAV_EC
GO:1990773	0.0625	1	1	1	matrix metallopeptidase secretion	BP	0.905	CD200	up_VCAV_EC
GO:0008045	0.0625	0.998	1	9	motor neuron axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0050654	0.0625	0.998	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	CHST7	up_VFEM_EC

GO:0034330	0.062578839	0.98017	5	80	cell junction organization	BP	1	NR1H4,ARHGAP6,FZD5,ACTN2,NRP1	up_ACOR_EC
GO:0035966	0.0626	0.975	8	47	response to topologically incorrect protein	BP	1	TM7SF3,CREBRF,STT3B,JKAMP,HERPUD1,WFS1,DZIP3,STC2	up_ACOR_VSMC
GO:0003012	0.0626	0.98	5	90	muscle system process	BP	1	LMCD1,CHRM2,HTR1D,TBXA2R,DMPK	up_AFEM_EC
GO:0007229	0.0626	0.984	4	32	integrin-mediated signaling pathway	BP	1	ITGB5,THY1,LOXL3,FUT8	down_VCAV_EC
GO:0045766	0.0626	0.983	4	63	positive regulation of angiogenesis	BP	1	ANGPT4,DLL1,F3,GREM1	up_AFEM_EC
GO:0006312	0.0626	0.989	3	11	mitotic recombination	BP	1	RAD51,SMC6,GEN1	down_ACOR_VSMC
GO:0001775	0.0626	0.987	3	219	cell activation	BP	1	HOXA9,TOX,CYP26B1	up_VFEM_EC
GO:0090232	0.0626	0.994	2	5	positive regulation of spindle checkpoint	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:0090267	0.0626	0.994	2	5	positive regulation of mitotic cell cycle spindle	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:0045935	0.0626	0.994	2	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0009967	0.0626	1	1	435	positive regulation of signal transduction	BP	1	GATA5	down_AFEM_VSMC
GO:0060411	0.0626	0.998	1	33	cardiac septum morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:2000146	0.0626	0.998	1	92	negative regulation of cell motility	BP	1	TBX5	up_APUL_VSMC
GO:0010469	0.0626	0.998	1	26	regulation of signaling receptor activity	BP	1	NETO1	up_VFEM_VSMC
GO:0045446	0.0626	0.998	1	32	endothelial cell differentiation	BP	1	HOXB5	up_VPUL_VSMC
GO:0006753	0.0627	0.961	24	211	nucleoside phosphate metabolic process	BP	1	PRPSAP1,ACLY,HMGCR,NNT,RRM1,RAN,CDK1,PFAS,RNASEH2B,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,DCK,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,PGD,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0002822	0.0627	0.976	7	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	0.905	IL7R,TNFAIP3,MEF2C,GATA3,NECTIN2,THOC1,HMGB1	up_VCAV_EC
GO:0071482	0.0627	0.979	6	34	cellular response to light stimulus	BP	1	NEDD4,AURKB,PCNA,NOC2L,POLH,CDC25A	down_ACOR_VSMC
GO:1901879	0.0627	0.981	5	26	regulation of protein depolymerization	BP	0.905	TMOD1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0015698	0.0627	0.984	4	24	inorganic anion transport	BP	0.874	ENPP1,SLC20A1,CLCN3,SLC20A2	down_VSAP_EC
GO:0050918	0.0627	0.989	3	10	positive chemotaxis	BP	1	VEGFD,F2RL1,NRP1	up_ACOR_VSMC
GO:0045824	0.0627	0.989	3	11	negative regulation of innate immune response	BP	0.905	TNFAIP3,NLRC5,CNOT7	up_VCAV_EC
GO:0010557	0.0627	0.994	2	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:1904754	0.0627	0.995	2	4	positive regulation of vascular associated smooth muscle cell	BP	0.905	DOCK4,PDGFB	up_VCAV_EC
GO:0046061	0.0627	1	1	1	dATP catabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0001823	0.0627	0.998	1	45	mesonephros development	BP	1	EYA1	up_AFEM_VSMC
GO:0007164	0.0627	0.998	1	23	establishment of tissue polarity	BP	1	ANKRD6	up_VPOR_VSMC
GO:0001736	0.0627	0.998	1	23	establishment of planar polarity	BP	1	ANKRD6	up_VPOR_VSMC
GO:0002053	0.0627	0.998	1	15	positive regulation of mesenchymal cell	BP	1	SIX1	up_VFEM_EC
GO:0042472	0.0627	0.998	1	27	inner ear morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0050905	0.0627	0.998	1	26	neuromuscular process	BP	1	HOXC10	up_VFEM_VSMC
GO:0032635	0.0628	0.977	7	37	interleukin-6 production	BP	1	TLR1,LEP,MBP,TLR3,F2RL1,PTPN22,NOD2	up_ACOR_VSMC
GO:0060438	0.0628	0.989	3	10	trachea development	BP	1	RARG,MAP2K2,TGFBR2	up_VSAP_EC
GO:0060571	0.0628	0.998	1	13	morphogenesis of an epithelial fold	BP	1	SULF1	down_ACOR_EC
GO:0051254	0.0628	1	1	431	positive regulation of RNA metabolic process	BP	1	GATA5	down_AFEM_VSMC

GO:0032621	0.0628	1	1	1	interleukin-18 production	BP	0.874	GBP5	down_VSAP_EC
GO:0072616	0.0628	1	1	1	interleukin-18 secretion	BP	0.874	GBP5	down_VSAP_EC
GO:0018108	0.0629	0.992	2	79	peptidyl-tyrosine phosphorylation	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0008203	0.063	0.976	7	37	cholesterol metabolic process	BP	1	LEP,LCAT,ABCA1,LIPE,APP,CLN8,LMF1	up_ACOR_VSMC
GO:0009064	0.063	0.981	5	23	glutamine family amino acid metabolic process	BP	1	GOT1,GLUL,ADHFE1,ENSCAFG00000016140,ASS1	up_VSAP_EC
GO:0034637	0.063	0.984	4	25	cellular carbohydrate biosynthetic process	BP	0.874	ENPP1,ENSCAFG00000032470,PPP1R3C,EXT1	down_VSAP_EC
GO:1901360	0.063	0.991	4	2016	organic cyclic compound metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0006101	0.063	0.985	4	16	citrate metabolic process	BP	1	DLST,IDH1,IDH3A,ENSCAFG00000006639	up_VSAP_EC
GO:0002369	0.063	0.989	3	10	T cell cytokine production	BP	1	B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0040036	0.063	0.998	1	11	regulation of fibroblast growth factor receptor	BP	1	SULF1	down_ACOR_EC
GO:0060539	0.063	1	1	1	diaphragm development	BP	1	MSC	down_ACOR_VSMC
GO:0033277	0.063	1	1	1	abortive mitotic cell cycle	BP	0.874	PTPN11	down_VSAP_EC
GO:0043400	0.063	1	1	1	cortisol secretion	BP	0.874	PTPN11	down_VSAP_EC
GO:0051462	0.063	1	1	1	regulation of cortisol secretion	BP	0.874	PTPN11	down_VSAP_EC
GO:0051463	0.063	1	1	1	negative regulation of cortisol secretion	BP	0.874	PTPN11	down_VSAP_EC
GO:0060125	0.063	1	1	1	negative regulation of growth hormone	BP	0.874	PTPN11	down_VSAP_EC
GO:0009653	0.0631	0.951	88	773	anatomical structure morphogenesis	BP	1	TNNT2,VEGFD,SMAD6,ACTN2,LEP,AFF3,GATA5,GATA4,CDC7,ANGPT1,EPYC,HTR2B,MBP,ZRANB1,RECK,SHROOM3,FEZ1,MLLT3,BMP4,LNPK,FGFR2,GJA1,ATRX,TLR3,SEC24B,WASF3,LATS2,CITED2,SPINT1,ZNRF3,ZNF365,SASH1,LMO4,TMEM108,FGF18,ARHGEF26,NEBL,ZMYM2,LIMS2,ANKRD1,MARCH5,BNIP3,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,GPM6A,ULK2,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,TBX20,TBX5,FZD3,FRS2,DAG1,APP,LAMA3,PSEN1,TGFBR1,SYNJ2BP,CHD7,JUP,SIPA1L1,PERP,SSH3,C10H2orf49,EDN1,HPGD,ARID5B,SERPINB5,JAM3,TNFRSF11B,GAA,FEZ2,LHX9,WDR48,WASL,DOCK5,ERAP1,BVES,RREB1,CRKL,MYOZ2,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0097435	0.0631	0.959	30	230	supramolecular fiber organization	BP	1	SYNPO2L,PDLIM3,FGF13,FMOD,ARHGAP28,ACTN2,MID1,SYNPO2,TUBB4A,MFAP4,NEBL,F2RL1,JMY,NRP1,EVL,P4HA1,DES,PRKCE,MYO1B,TTC17,RND1,APP,PSEN1,DDR2,SSH3,EDN1,FAM107A,INPP5K,WASL,MYOZ2	up_ACOR_VSMC
GO:0045859	0.0631	0.96	25	219	regulation of protein kinase activity	BP	0.905	KIT,TNFAIP3,MAP3K11,PDGFB,STK10,RELN,TLR4,EDN1,RALB,NEDD9,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,PROX1,MADD,PAK2,MMD,RAPGEF2,BLM,RIPK1,PDGFD	up_VCAV_EC
GO:0036503	0.0631	0.978	6	47	ERAD pathway	BP	0.874	HM13,HSP90B1,SEL1L,DNAJC10,DNAJB9,USP14	down_VSAP_EC
GO:0080090	0.0631	1	2	1734	regulation of primary metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0009060	0.0631	0.998	1	31	aerobic respiration	BP	1	SUCLG2	down_AFEM_EC
GO:0006551	0.0631	1	1	1	leucine metabolic process	BP	0.905	BCAT1	up_VCAV_EC
GO:0009082	0.0631	1	1	1	branched-chain amino acid biosynthetic process	BP	0.905	BCAT1	up_VCAV_EC
GO:0009098	0.0631	1	1	1	leucine biosynthetic process	BP	0.905	BCAT1	up_VCAV_EC
GO:0009099	0.0631	1	1	1	valine biosynthetic process	BP	0.905	BCAT1	up_VCAV_EC
GO:0045739	0.0631	0.998	1	26	positive regulation of DNA repair	BP	1	EYA1	up_VFEM_VSMC
GO:0070670	0.0632	0.989	3	11	response to interleukin-4	BP	1	SLC29A1,CDK4,CORO1A	down_ACOR_VSMC
GO:0071353	0.0632	0.989	3	11	cellular response to interleukin-4	BP	1	SLC29A1,CDK4,CORO1A	down_ACOR_VSMC
GO:0045835	0.0632	0.994	2	5	negative regulation of meiotic nuclear division	BP	1	FBXO5,TTK	down_ACOR_VSMC

GO:0071559	0.0632	0.998	1	75	response to transforming growth factor beta	BP	1	TGFBR1	down_VSAP_VSMC
GO:0048706	0.0632	0.998	1	59	embryonic skeletal system development	BP	1	HOXA9	up_AORT_VSMC
GO:0051149	0.0632	0.998	1	25	positive regulation of muscle cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0021761	0.0632	0.998	1	27	limbic system development	BP	1	EMX2	up_VFEM_VSMC
GO:0003151	0.063262581	0.98722	3	34	outflow tract morphogenesis	BP	1	SMAD6,FOXC2,NRP1	up_ACOR_EC
GO:0009719	0.063291092	0.96486	16	395	response to endogenous stimulus	BP	1	NR1H4,SOX9,FNDC4,AQP1,ENSCAFG00000004331,AGRN,NOD2,RGMA,SMAD6,ACTN2,PTGER4,ADAMTSL2,FOXC2,LRP4,RARRES2,PRKCD	up_ACOR_EC
GO:1902531	0.0633	0.953	63	536	regulation of intracellular signal transduction	BP	1	ADRA1B,LEP,MID1,HTR2B,RASSF2,C28H10orf71,NACC2,PRKAA2,BMP4,FGFR2,ABCA1,CASTOR1,TLR3,SH3RF2,PDE5A,SASH1,FGF18,ARHGEF26,NDRG2,CHN2,ITPR1,ANKRD1,F2RL1,CRLF3,NRP1,UBR1,PTPN22,NPNT,UNC5B,SMPD1,APLP1,SESN3,SH3RF1,PRKCE,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,SIPA1L1,CCL5,WWC2,DUSP22,SIAH1,EDN1,SESN1,DUSP26,NOD2,LRRC4,DDIT4,SH3RF3,SERINC3,HERPUD1,MAP3K7,INPP5K,BMT2,WFS1,SH3BP4,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0051249	0.0633	0.967	14	107	regulation of lymphocyte activation	BP	0.905	IL7R,TNFAIP3,MEF2C,TLR4,GATA3,PELI1,ARG2,ITPKB,THOC1,NCK1,BCL10,HMGB1,ATP11C,ZEB1	up_VCAV_EC
GO:0031328	0.0633	0.981	5	512	positive regulation of cellular biosynthetic	BP	1	HOXA11,HOXA9,SALL1,PRR16,SHOX2	up_VSAP_VSMC
GO:0003229	0.0633	0.985	4	17	ventricular cardiac muscle tissue development	BP	0.905	ADAMTS9,CHD7,DLL4,PROX1	up_VCAV_EC
GO:0090207	0.0633	0.989	3	11	regulation of triglyceride metabolic process	BP	1	SREBF1,CTDNEP1,ABHD5	down_ACOR_VSMC
GO:0006654	0.0633	0.993	2	7	phosphatidic acid biosynthetic process	BP	0.874	NR1H4,SH3GLB1	down_VSAP_EC
GO:0046473	0.0633	0.993	2	7	phosphatidic acid metabolic process	BP	0.874	NR1H4,SH3GLB1	down_VSAP_EC
GO:0038061	0.0633	0.998	1	34	NIK/NF-kappaB signaling	BP	1	HDAC7	down_VPOR_EC
GO:0006529	0.0633	1	1	1	asparagine biosynthetic process	BP	0.874	ASNS	down_VSAP_EC
GO:0032944	0.0634	0.978	6	48	regulation of mononuclear cell	BP	0.874	CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0050670	0.0634	0.978	6	48	regulation of lymphocyte proliferation	BP	0.874	CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0035282	0.0634	0.979	6	30	segmentation	BP	1	MLLT3,BMP4,NRP1,FRS2,PSEN1,PCSK6	up_ACOR_VSMC
GO:0036294	0.0634	0.978	6	37	cellular response to decreased oxygen levels	BP	0.905	CD34,MTOR,PTGS2,PMAIP1,HIF1A,HP1BP3	up_VCAV_EC
GO:0071456	0.0634	0.978	6	37	cellular response to hypoxia	BP	0.905	CD34,MTOR,PTGS2,PMAIP1,HIF1A,HP1BP3	up_VCAV_EC
GO:0016999	0.0634	0.979	6	30	antibiotic metabolic process	BP	1	DLST,ACSS2,ZNF205,IDH1,IDH3A,ENSCAFG00000006639	up_VSAP_EC
GO:0030334	0.0634	0.987	3	267	regulation of cell migration	BP	1	TBX5,CCL24,ARHGEF2	up_VPUL_EC
GO:0072659	0.0634	0.992	2	82	protein localization to plasma membrane	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0032957	0.0634	0.994	2	5	inositol trisphosphate metabolic process	BP	0.905	ITPKB,PLCG2	up_VCAV_EC
GO:0003333	0.0634	0.998	1	12	amino acid transmembrane transport	BP	1	PDPN	down_ACOR_EC
GO:0006622	0.0634	0.998	1	11	protein targeting to lysosome	BP	1	NEDD4	down_ACOR_EC
GO:0010644	0.0634	1	1	1	cell communication by electrical coupling	BP	1	CAV1	down_ACOR_VSMC
GO:0048550	0.0634	1	1	1	negative regulation of pinocytosis	BP	1	CAV1	down_ACOR_VSMC
GO:0072584	0.0634	1	1	1	caveolin-mediated endocytosis	BP	1	CAV1	down_ACOR_VSMC
GO:0075509	0.0634	1	1	1	endocytosis involved in viral entry into host cell	BP	1	CAV1	down_ACOR_VSMC
GO:0086064	0.0634	1	1	1	cell communication by electrical coupling involved in cardiac	BP	1	CAV1	down_ACOR_VSMC
GO:0086098	0.0634	1	1	1	angiotensin-activated signaling pathway	BP	1	CAV1	down_ACOR_VSMC

GO:1901844	0.0634	1	1	1	regulation of cell communication by electrical coupling	BP	1	CAV1	down_ACOR_VSMC
GO:1901979	0.0634	1	1	1	regulation of inward rectifier potassium	BP	1	CAV1	down_ACOR_VSMC
GO:1903596	0.0634	1	1	1	regulation of gap junction assembly	BP	1	CAV1	down_ACOR_VSMC
GO:1903598	0.0634	1	1	1	positive regulation of gap junction assembly	BP	1	CAV1	down_ACOR_VSMC
GO:1903609	0.0634	1	1	1	negative regulation of inward rectifier potassium channel activity	BP	1	CAV1	down_ACOR_VSMC
GO:0010649	0.0634	1	1	1	regulation of cell communication by	BP	1	CAV1	down_ACOR_VSMC
GO:0019065	0.0634	1	1	1	receptor-mediated endocytosis of virus by	BP	1	CAV1	down_ACOR_VSMC
GO:0033484	0.0634	1	1	1	nitric oxide homeostasis	BP	1	CAV1	down_ACOR_VSMC
GO:0044860	0.0634	1	1	1	protein localization to plasma membrane raft	BP	1	CAV1	down_ACOR_VSMC
GO:1900085	0.0634	1	1	1	negative regulation of peptidyl-tyrosine	BP	1	CAV1	down_ACOR_VSMC
GO:0097530	0.0634	0.998	1	33	granulocyte migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0007033	0.063494456	0.97978	5	82	vacuole organization	BP	1	ATG16L2,CHMP4B,TP53INP2,VPS16,ENSCAFG00000010493	up_ACOR_EC
GO:0042490	0.0635	0.988	3	19	mechanoreceptor differentiation	BP	1	SDC4,NAGLU,GSDME	down_VCAV_EC
GO:1900746	0.0635	0.993	2	7	regulation of vascular endothelial growth factor	BP	0.874	JCAD,MYO1C	down_VSAP_EC
GO:1902547	0.0635	0.993	2	7	regulation of cellular response to vascular endothelial growth factor	BP	0.874	JCAD,MYO1C	down_VSAP_EC
GO:0000460	0.0635	0.998	1	15	maturation of 5.8S rRNA	BP	1	WDR12	down_ACOR_EC
GO:0061951	0.0635	0.998	1	16	establishment of protein localization to plasma	BP	1	ACSL3	down_ACOR_EC
GO:0010466	0.0635	0.998	1	32	negative regulation of peptidase activity	BP	1	CST3	down_VPOR_EC
GO:0010951	0.0635	0.998	1	32	negative regulation of endopeptidase activity	BP	1	CST3	down_VPOR_EC
GO:0072525	0.0635	0.998	1	24	pyridine-containing compound biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0045595	0.0636	0.958	31	469	regulation of cell differentiation	BP	1	NOTCH2,VASN,FBN1,GLIPR2,BMPR1A,LMO4,TRPV2,NUMBL,TFE3,CLSTN1,SEMA3C,THY1,TLX2,GLI3,ZFP36L1,RBM38,CDH2,LOXL3,RAB7B,UST,TWIST2,PRKCSH,DDR2,GREM1,NAPEPLD,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC
GO:0060976	0.0636	0.981	5	22	coronary vasculature development	BP	1	SMAD6,BMP4,SEC24B,NRP1,AP2B1	up_ACOR_VSMC
GO:0031086	0.0636	0.994	2	5	nuclear-transcribed mRNA catabolic process, deadenylation-	BP	1	EDC3,EDC4	down_ACOR_VSMC
GO:0031087	0.0636	0.994	2	5	deadenylation-independent decapping of nuclear-transcribed mRNA	BP	1	EDC3,EDC4	down_ACOR_VSMC
GO:0090025	0.0636	0.993	2	7	regulation of monocyte chemotaxis	BP	0.874	SERPINE1,LYN	down_VSAP_EC
GO:0006244	0.0636	1	1	1	pyrimidine nucleotide catabolic process	BP	0.874	ENTPD4	down_VSAP_EC
GO:0006256	0.0636	1	1	1	UDP catabolic process	BP	0.874	ENTPD4	down_VSAP_EC
GO:0009138	0.0636	1	1	1	pyrimidine nucleoside diphosphate metabolic	BP	0.874	ENTPD4	down_VSAP_EC
GO:0009140	0.0636	1	1	1	pyrimidine nucleoside diphosphate catabolic	BP	0.874	ENTPD4	down_VSAP_EC
GO:0009193	0.0636	1	1	1	pyrimidine ribonucleoside diphosphate metabolic	BP	0.874	ENTPD4	down_VSAP_EC
GO:0009195	0.0636	1	1	1	pyrimidine ribonucleoside diphosphate catabolic	BP	0.874	ENTPD4	down_VSAP_EC
GO:0009222	0.0636	1	1	1	pyrimidine ribonucleotide catabolic process	BP	0.874	ENTPD4	down_VSAP_EC
GO:0046048	0.0636	1	1	1	UDP metabolic process	BP	0.874	ENTPD4	down_VSAP_EC
GO:0010944	0.0636	1	1	1	negative regulation of transcription by competitive promoter	BP	0.905	CREB1	up_VCAV_EC
GO:0051289	0.0636	0.998	1	25	protein homotetramerization	BP	1	FBP1	up_VFEM_VSMC

GO:0016042	0.063680064	0.97972	5	80	lipid catabolic process	BP	1	PLCL1,PLCE1,CFI,RARRES2,PRKCD	up_ACOR_EC
GO:0007166	0.0637	0.955	43	686	cell surface receptor signaling pathway	BP	1	NOTCH2,PDGFRB,SMAD9,ITGB5,DCN,NDN,ANGPT1,PRNP,VASN,FBN1,BGN,BMPR1A,EVC,RECK,IGFBP6,NUMBL,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,AKT2,CLSTN1,CSPG4,SEMA3C,ASPN,THY1,ATP6V0C,GLI3,PARK7,SASH1,IFT57,MAVS,CDH2,LOXL3,FUT8,ENSCAFG00000017708,GLIS2,SHC1,GREM1,NPHP4,FOXO3,RGMA,CDK14	down_VCAV_EC
GO:0035264	0.0637	0.972	9	56	multicellular organism growth	BP	0.905	PDE4D,CHD7,MTOR,HHEX,SLC25A25,CREB1,SPTBN4,ATRX,RBBP6	up_VCAV_EC
GO:0003334	0.0637	0.995	2	4	keratinocyte development	BP	1	EXPH5,FOSL2	up_ACOR_VSMC
GO:0002155	0.0637	1	1	1	regulation of thyroid hormone mediated	BP	0.874	PRCP	down_VSAP_EC
GO:0002353	0.0637	1	1	1	plasma kallikrein-kinin cascade	BP	0.874	PRCP	down_VSAP_EC
GO:0002254	0.0637	1	1	1	kinin cascade	BP	0.874	PRCP	down_VSAP_EC
GO:0021953	0.0637	0.998	1	49	central nervous system neuron differentiation	BP	1	HOXC10	up_AFEM_VSMC
GO:0003007	0.0637	0.998	1	94	heart morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0021602	0.0637	0.998	1	16	cranial nerve morphogenesis	BP	1	SIX1	up_VFEM_EC
GO:0032663	0.0637	0.998	1	19	regulation of interleukin-2 production	BP	1	NR1H4	up_VPUL_EC
GO:1902679	0.0638	0.957	36	329	negative regulation of RNA biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,SREBF2,NEDD4,MTDH,NAB2,BIRC5,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,SUV39H1,HMGB2,DMAP1,CDK2,ENSCAFG00000005299,EZR,ERF,TCERG1,HAT1,HIST2H2AC,H2AFX,SIX4	down_ACOR_VSMC
GO:1903507	0.0638	0.957	36	329	negative regulation of nucleic acid-templated transcription	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,SREBF2,NEDD4,MTDH,NAB2,BIRC5,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,SUV39H1,HMGB2,DMAP1,CDK2,ENSCAFG00000005299,EZR,ERF,TCERG1,HAT1,HIST2H2AC,H2AFX,SIX4	down_ACOR_VSMC
GO:0001819	0.0638	0.964	17	120	positive regulation of cytokine production	BP	1	TLR1,PLCG2,LEP,CD83,HTR2B,MBP,FERMT1,TLR3,CD274,F2RL1,PTPN22,NOD2,B2M,SCAMP5,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0051251	0.0638	0.971	10	69	positive regulation of lymphocyte activation	BP	0.905	IL7R,MEF2C,TLR4,GATA3,PELI1,ITPKB,NCK1,BCL10,HMGB1,ATP11C	up_VCAV_EC
GO:1903038	0.0638	0.978	6	30	negative regulation of leukocyte cell-cell	BP	1	BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0042035	0.0638	0.984	4	20	regulation of cytokine biosynthetic process	BP	0.905	TLR4,GATA3,TLR3,BCL10	up_VCAV_EC
GO:0044092	0.0638	0.987	3	270	negative regulation of molecular function	BP	1	NR1H4,PTGER2,FLRT3	up_VPUL_EC
GO:0046503	0.0638	0.989	3	10	glycerolipid catabolic process	BP	1	LIPC,ENPP2,ABHD16A	up_VSAP_EC
GO:0006282	0.0638	0.998	1	48	regulation of DNA repair	BP	1	EYA1	up_AFEM_VSMC
GO:1901491	0.0638	1	1	1	negative regulation of lymphangiogenesis	BP	0.905	VASH1	up_VCAV_EC
GO:0008344	0.0638	0.998	1	25	adult locomotory behavior	BP	1	CHL1	up_VPOR_VSMC
GO:0003208	0.0638	0.998	1	24	cardiac ventricle morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:2000026	0.0639	0.978	6	560	regulation of multicellular organismal development	BP	1	ACVRL1,LYN,PDPN,HOXA7,SULF1,ASPN	down_ACOR_EC
GO:0043010	0.0639	0.992	2	96	camera-type eye development	BP	1	IRX5,MAB21L1	up_VSAP_VSMC
GO:0048232	0.0639	0.992	2	95	male gamete generation	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0046530	0.0639	0.998	1	17	photoreceptor cell differentiation	BP	1	NTRK2	up_APUL_EC
GO:0031128	0.0639	0.998	1	15	developmental induction	BP	1	SIX1	up_VFEM_EC
GO:0038083	0.0639	0.998	1	16	peptidyl-tyrosine autophosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0051100	0.064	0.972	9	53	negative regulation of binding	BP	1	ARHGAP28,XIRP1,CLSTN1,LRPAP1,PSEN1,MITD1,B2M,DISC1,PARK7	up_ACOR_VSMC
GO:0035556	0.064	0.979	6	845	intracellular signal transduction	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC

GO:2000311	0.064	0.995	2	4	regulation of AMPA receptor activity	BP	0.905	RELN,MEF2C	up_VCAV_EC
GO:0046717	0.064	0.998	1	17	acid secretion	BP	1	NTRK2	up_APUL_EC
GO:0002699	0.064	0.998	1	46	positive regulation of immune effector process	BP	1	C6	up_VCAV_VSMC
GO:0097006	0.064	0.998	1	19	regulation of plasma lipoprotein particle levels	BP	1	NR1H4	up_VPUL_EC
GO:0009991	0.0641	0.965	16	110	response to extracellular stimulus	BP	1	LEP,PRKAA2,CASTOR1,PPARGC1A,CDKN2B,GABARAPL1,CDKN1A,P2RX7,ULK2,SESN3,PIK3C3,LAMP2,SESN1,FAM107A,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0040017	0.0641	0.973	8	180	positive regulation of locomotion	BP	1	CMKLR1,ANGPT4,TWIST2,LRRC15,BVES,LGR6,CCL5,ADAM17	up_AFEM_EC
GO:0003281	0.0641	0.978	6	30	ventricular septum development	BP	1	FZD1,WNT11,SAV1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0045730	0.0641	0.993	2	8	respiratory burst	BP	1	CYBA,RAC2	down_VCAV_EC
GO:0051651	0.0641	0.998	1	31	maintenance of location in cell	BP	1	GPSM2	down_AFEM_EC
GO:0000103	0.0641	1	1	1	sulfate assimilation	BP	0.874	PAPSS1	down_VSAP_EC
GO:0034036	0.0641	1	1	1	purine ribonucleoside bisphosphate biosynthetic process	BP	0.874	PAPSS1	down_VSAP_EC
GO:0035508	0.0641	1	1	1	positive regulation of myosin-light-chain-	BP	0.874	PPP1R12A	down_VSAP_EC
GO:0050428	0.0641	1	1	1	3'-phosphoadenosine 5'-phosphosulfate biosynthetic process	BP	0.874	PAPSS1	down_VSAP_EC
GO:0002221	0.0641	0.998	1	46	pattern recognition receptor signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0002758	0.0641	0.998	1	46	innate immune response-activating signal	BP	1	TLR2	up_AFEM_VSMC
GO:0044773	0.0641	0.998	1	28	mitotic DNA damage checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0055001	0.0642	0.998	1	47	muscle cell development	BP	1	BEND2	up_AFEM_VSMC
GO:0038159	0.0642	1	1	1	C-X-C chemokine receptor CXCR4 signaling pathway	BP	0.905	CXCR4	up_VCAV_EC
GO:0038160	0.0642	1	1	1	CXCL12-activated CXCR4 signaling pathway	BP	0.905	CXCR4	up_VCAV_EC
GO:0043271	0.0642	0.998	1	28	negative regulation of ion transport	BP	1	HOXA3	up_VPOR_VSMC
GO:1901880	0.0642	0.998	1	19	negative regulation of protein depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0008593	0.0642	0.998	1	33	regulation of Notch signaling pathway	BP	1	GATA5	up_VPUL_VSMC
GO:0009725	0.064234236	0.97125	9	188	response to hormone	BP	1	NR1H4,AQP1,ENSCAFG00000004331,AGRN,ACTN2,PTGER4,FOXC2,RARRES2,PRKCD	up_ACOR_EC
GO:0021915	0.0643	0.977	6	58	neural tube development	BP	1	SDC4,LMO4,SEMA3C,GLI3,ZFP36L1,IFT57	down_VCAV_EC
GO:0016999	0.0643	0.998	1	30	antibiotic metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0021783	0.0643	0.998	1	9	preganglionic parasympathetic fiber	BP	1	SEMA3A	up_VPOR_EC
GO:0070265	0.0643	0.998	1	19	necrotic cell death	BP	1	ARHGEF2	up_VPUL_EC
GO:0048641	0.0643	0.998	1	16	regulation of skeletal muscle tissue	BP	1	SHOX2	up_VSAP_VSMC
GO:0045785	0.0644	0.966	14	107	positive regulation of cell adhesion	BP	0.905	TEK,IL7R,PODXL,FERMT1,GATA3,NEDD9,PPP3CA,ITPKB,PRKD2,NCK1,BCL10,HMGB1,ITGA6,ENSCAFG00000002015	up_VCAV_EC
GO:0055074	0.0644	0.992	2	95	calcium ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0048024	0.0644	0.998	1	30	regulation of mRNA splicing, via spliceosome	BP	1	SRSF6	down_AFEM_EC
GO:0072009	0.0644	0.998	1	48	nephron epithelium development	BP	1	EYA1	up_AFEM_VSMC
GO:0043124	0.0644	0.998	1	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	up_APUL_EC
GO:0071539	0.0644	0.998	1	8	protein localization to centrosome	BP	1	HOOK3	up_VPOR_EC
GO:1905508	0.0644	0.998	1	8	protein localization to microtubule organizing	BP	1	HOOK3	up_VPOR_EC
GO:0003179	0.0644	0.998	1	19	heart valve morphogenesis	BP	1	TBX5	up_VPUL_EC

GO:0009967	0.0645	0.956	34	435	positive regulation of signal transduction	BP	0.874	VEGFA,SULF1,NR1H4,JCAD,PTPN11,ILK,SMARCA4,MYO1C,CHSY1,HIF1A,TNIK,PTPN2,NEO1,MTDH,ESM1,ADAM17,MAGED1,CTNNB1,ENSCAFG00000002015,LYN,BNIP3,FAM162A,ATF3,SH3GLB1,HTT,CALM1,DISC1,PAK2,INHBA,NRP1,SH3RF3,MADD,SEC13,MID1	down_VSAP_EC
GO:0051223	0.0645	0.987	3	181	regulation of protein transport	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0003151	0.0645	0.998	1	34	outflow tract morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0048701	0.0645	0.998	1	25	embryonic cranial skeleton morphogenesis	BP	1	TBX15	up_VFEM_VSMC
GO:0055017	0.0645	0.998	1	19	cardiac muscle tissue growth	BP	1	TBX5	up_VPUL_EC
GO:2001293	0.0645	1	1	1	malonyl-CoA metabolic process	BP	1	ACACB	up_VSAP_EC
GO:2001295	0.0645	1	1	1	malonyl-CoA biosynthetic process	BP	1	ACACB	up_VSAP_EC
GO:0099536	0.064513878	0.97453	7	133	synaptic signaling	BP	1	CNTNAP4,BRSK1,PLCL1,KCNB1,INSYN1,MAPK8IP2,LRRC4	up_ACOR_EC
GO:0015748	0.06458545	0.99226	2	16	organophosphate ester transport	BP	1	SLC25A42,PRKCD	up_ACOR_EC
GO:0070555	0.0646	0.98	5	29	response to interleukin-1	BP	0.905	SELE,CXCL8,MAPK13,OTUD4,HIF1A	up_VCAV_EC
GO:0016310	0.0646	0.981	5	641	phosphorylation	BP	1	STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0030048	0.0646	0.981	5	23	actin filament-based movement	BP	1	EMP2,KCNE3,FRMD6,WIPF1,MYO1B	up_VSAP_EC
GO:0035295	0.0646	0.983	4	356	tube development	BP	1	HOXA11,SALL1,CAV1,SHOX2	up_VSAP_VSMC
GO:0006885	0.0646	0.987	3	39	regulation of pH	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0070302	0.0646	0.992	2	78	regulation of stress-activated protein kinase	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0071300	0.0646	0.998	1	12	cellular response to retinoic acid	BP	1	LYN	down_ACOR_EC
GO:0051092	0.0646	0.998	1	47	positive regulation of NF-kappaB transcription	BP	1	TLR2	up_AFEM_VSMC
GO:0050810	0.0646	0.998	1	17	regulation of steroid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0060485	0.0646	0.998	1	93	mesenchyme development	BP	1	TBX5	up_APUL_VSMC
GO:0007528	0.0646	0.998	1	17	neuromuscular junction development	BP	1	SIX1	up_VFEM_EC
GO:0001959	0.0646	0.998	1	33	regulation of cytokine-mediated signaling	BP	1	SLIT2	up_VPUL_VSMC
GO:0007612	0.0646	0.998	1	33	learning	BP	1	LRRN4	up_VPUL_VSMC
GO:0070838	0.0647	0.97	10	96	divalent metal ion transport	BP	0.874	SLC39A7,ERO1A,ATP2B1,REM1,CTNNB1,LYN,DDIT3,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0001919	0.0647	0.994	2	5	regulation of receptor recycling	BP	1	PSEN1,BVES	up_ACOR_VSMC
GO:0007631	0.0647	0.998	1	17	feeding behavior	BP	1	NTRK2	up_APUL_EC
GO:0010976	0.0647	0.998	1	47	positive regulation of neuron projection	BP	1	LIMK1	up_VCAV_VSMC
GO:0009410	0.0647	0.998	1	27	response to xenobiotic stimulus	BP	1	CYP26B1	up_VPOR_VSMC
GO:0010977	0.0647	0.998	1	33	negative regulation of neuron projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0008654	0.064782766	0.98255	4	58	phospholipid biosynthetic process	BP	1	NR1H4,CHPT1,PIGS,AGPAT2	up_ACOR_EC
GO:0048259	0.0648	0.981	5	24	regulation of receptor-mediated endocytosis	BP	1	DNAJC6,PLCG2,ATXN2,LRPAP1,B2M	up_ACOR_VSMC
GO:0003014	0.0648	0.98	5	27	renal system process	BP	0.905	ADGRF5,PDGFB,CD34,STC1,EDN1	up_VCAV_EC
GO:0048026	0.0648	0.994	2	5	positive regulation of mRNA splicing, via	BP	1	THRAP3,SF3B4	down_ACOR_VSMC
GO:0042311	0.0648	0.993	2	7	vasodilation	BP	0.874	APOE,PLOD3	down_VSAP_EC
GO:0055025	0.0648	0.998	1	17	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0031128	0.0648	0.998	1	15	developmental induction	BP	1	HOXA11	up_VSAP_VSMC
GO:0048754	0.064817253	0.98255	4	57	branching morphogenesis of an epithelial tube	BP	1	SOX9,FOXC2,CLSTN1,NRP1	up_ACOR_EC
GO:0009746	0.064850636	0.98675	3	35	response to hexose	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC

GO:0034284	0.064850636	0.98675	3	35	response to monosaccharide	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0015672	0.0649	0.967	13	89	monovalent inorganic cation transport	BP	1	FGF13,ACTN2,KCNE3,PTPN3,AKAP6,DMPK,KCNJ4,ATP6V0E1,KCNC4,FXYD1,NDUFA4L2,PARK7,SLC8A1	up_ACOR_VSMC
GO:0009889	0.0649	0.972	10	1190	regulation of biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,ACSL3,NEDD4	down_ACOR_EC
GO:0002573	0.0649	0.973	8	71	myeloid leukocyte differentiation	BP	0.874	VEGFA,MYH9,PTPN2,EVI2B,CTNNB1,TFRC,LYN,GLO1	down_VSAP_EC
GO:0044242	0.0649	0.977	6	57	cellular lipid catabolic process	BP	1	AKT2,ACAA1,PEX5,ENSCAFG00000017708,LONP2,ACAT1	down_VCAV_EC
GO:0071363	0.0649	0.987	3	188	cellular response to growth factor stimulus	BP	1	ACVRL1,SULF1,ASPN	down_ACOR_EC
GO:2000725	0.0649	0.989	3	10	regulation of cardiac muscle cell differentiation	BP	1	BMP4,FRS2,EDN1	up_ACOR_VSMC
GO:0071495	0.0649	0.987	3	365	cellular response to endogenous stimulus	BP	1	FGF5,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0061564	0.0649	0.992	2	119	axon development	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0048645	0.0649	0.998	1	33	animal organ formation	BP	1	CITED2	down_VPOR_EC
GO:1904716	0.0649	1	1	1	positive regulation of chaperone-mediated	BP	0.874	PLK3	down_VSAP_EC
GO:2000777	0.0649	1	1	1	positive regulation of proteasomal ubiquitin-dependent protein catabolic process involved	BP	0.874	PLK3	down_VSAP_EC
GO:0001659	0.0649	0.998	1	54	temperature homeostasis	BP	1	HOXC10	up_AORT_VSMC
GO:0044106	0.0649	0.998	1	17	cellular amine metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0120163	0.0649	0.998	1	17	negative regulation of cold-induced	BP	1	PLCL1	up_APUL_EC
GO:0014861	0.0649	1	1	1	regulation of skeletal muscle contraction via regulation of action	BP	0.905	KCNJ2	up_VCAV_EC
GO:0100001	0.0649	1	1	1	regulation of skeletal muscle contraction by	BP	0.905	KCNJ2	up_VCAV_EC
GO:0060411	0.0649	0.998	1	33	cardiac septum morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0001937	0.0649	0.998	1	15	negative regulation of endothelial cell	BP	1	CAV1	up_VSAP_VSMC
GO:0071495	0.064959492	0.96453	15	365	cellular response to endogenous stimulus	BP	1	NR1H4,SOX9,AQP1,ENSCAFG00000004331,AGRN,NOD2,RGMA,SMAD6,ACTN2,PTGER4,ADAMTSL2,FOXC2,LRP4,RARRES2,PRKCD	up_ACOR_EC
GO:0031348	0.065	0.975	7	46	negative regulation of defense response	BP	0.905	TNFAIP3,NLRC5,GATA3,ARG2,RIOK3,APOD,CNOT7	up_VCAV_EC
GO:0048515	0.065	0.977	6	36	spermatid differentiation	BP	0.905	KIT,PSME4,NECTIN2,CDYL,AFF4,KDM3A	up_VCAV_EC
GO:0035239	0.065	0.993	2	299	tube morphogenesis	BP	1	C6,TGFBI	up_VCAV_VSMC
GO:0071345	0.065	0.992	2	210	cellular response to cytokine stimulus	BP	1	IL22RA1,SLIT2	up_VPUL_VSMC
GO:0032418	0.065	0.998	1	17	lysosome localization	BP	1	LYN	down_ACOR_EC
GO:0035773	0.065	0.998	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	STX4	down_ACOR_EC
GO:0009749	0.065	0.998	1	34	response to glucose	BP	1	RAB11B	down_VPOR_EC
GO:0035265	0.065	0.998	1	54	organ growth	BP	1	ESR1	up_AORT_VSMC
GO:0050803	0.065	0.998	1	55	regulation of synapse structure or activity	BP	1	WNT7A	up_AORT_VSMC
GO:0050807	0.065	0.998	1	55	regulation of synapse organization	BP	1	WNT7A	up_AORT_VSMC
GO:0060384	0.065	0.998	1	9	innervation	BP	1	SEMA3A	up_VPOR_EC
GO:0003407	0.065	0.998	1	15	neural retina development	BP	1	IRX5	up_VSAP_VSMC
GO:0018212	0.0651	0.992	2	81	peptidyl-tyrosine modification	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0048514	0.0651	0.992	2	214	blood vessel morphogenesis	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0010563	0.0652	0.959	26	203	negative regulation of phosphorus metabolic process	BP	1	SMAD6,RASSF2,BMP4,SH3RF2,LATS2,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,PTPN22,SMPD1,MARF1,DAG1,PPP1R26,PSEN1,SYNJ2BP,DUSP22,DUSP26,LRRC4,DDIT4,INPP5K,PARK7,GPATCH2,ZFYVE1,CRKL	up_ACOR_VSMC

GO:0045936	0.0652	0.959	26	203	negative regulation of phosphate metabolic process	BP	1	SMAD6,RASSF2,BMP4,SH3RF2,LATS2,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,PTPN22,SMPD1,MARF1,DAG1,PPP1R26,PSEN1,SYNJ2BP,DUSP22,DUSP26,LRRC4,DDIT4,INPP5K,PARK7,GPATCH2,ZFYVE1,CRKL	up_ACOR_VSMC
GO:1903530	0.0652	0.96	22	165	regulation of secretion by cell	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FBXL20,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,SCG5,CHD7,CCL5,EDN1,KCNC4,NOD2,SCAMP5,PREPL,PFKL	up_ACOR_VSMC
GO:0007265	0.0652	0.967	12	121	Ras protein signal transduction	BP	0.874	ARHGEF2,FARP1,KPNB1,APOE,PLEKHG2,TAX1BP3,ARFGEF3,PAK2,CDKN1A,NRP1,TNFAIP1,MADD	down_VSAP_EC
GO:0070304	0.0652	0.972	9	58	positive regulation of stress-activated protein kinase signaling cascade	BP	0.905	MAP3K11,TLR4,EDN1,MAP3K3,BMP2,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0008344	0.0652	0.98	5	25	adult locomotory behavior	BP	0.905	CHD7,HOXB8,TMOD1,PREX2,SPTBN4	up_VCAV_EC
GO:0048144	0.0652	0.981	5	23	fibroblast proliferation	BP	1	PEX2,MORC3,DDR2,MYC,FBXO4	up_VSAP_EC
GO:0048145	0.0652	0.981	5	23	regulation of fibroblast proliferation	BP	1	PEX2,MORC3,DDR2,MYC,FBXO4	up_VSAP_EC
GO:0031326	0.0652	0.991	3	1176	regulation of cellular biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0034123	0.0652	0.989	3	10	positive regulation of toll-like receptor signaling	BP	1	F2RL1,CYBA,FLOT1	up_VSAP_EC
GO:0010867	0.0652	0.994	2	5	positive regulation of triglyceride biosynthetic	BP	1	SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0043552	0.0652	0.998	1	11	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	LYN	down_ACOR_EC
GO:0090218	0.0652	0.998	1	11	positive regulation of lipid kinase activity	BP	1	LYN	down_ACOR_EC
GO:1901863	0.0652	0.998	1	25	positive regulation of muscle tissue	BP	1	CYP26B1	up_VPOR_VSMC
GO:0097178	0.0652	0.998	1	14	ruffle assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0035107	0.0653	0.97	10	60	appendage morphogenesis	BP	1	AFF3,RECK,BMP4,LNPK,FGFR2,GJA1,ATRX,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0035108	0.0653	0.97	10	60	limb morphogenesis	BP	1	AFF3,RECK,BMP4,LNPK,FGFR2,GJA1,ATRX,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0046883	0.0653	0.977	6	49	regulation of hormone secretion	BP	0.874	NR1H4,PTPN11,HIF1A,REST,RAB11FIP1,INHBA	down_VSAP_EC
GO:0048659	0.0653	0.977	6	36	smooth muscle cell proliferation	BP	0.905	CALCRL,TNFAIP3,PDGFB,MEF2C,EDN1,APOD	up_VCAV_EC
GO:0070167	0.0653	0.98	5	29	regulation of biomineral tissue development	BP	0.905	MEF2C,BMP2,BMP2K,HIF1A,FBXO5	up_VCAV_EC
GO:0050867	0.0653	0.992	2	83	positive regulation of cell activation	BP	1	PDPN,STX4	down_ACOR_EC
GO:0070838	0.0653	0.992	2	96	divalent metal ion transport	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0070489	0.0653	1	1	1	T cell aggregation	BP	0.874	MSN	down_VSAP_EC
GO:0106106	0.0653	0.998	1	48	cold-induced thermogenesis	BP	1	HOXC10	up_AFEM_VSMC
GO:0120161	0.0653	0.998	1	48	regulation of cold-induced thermogenesis	BP	1	HOXC10	up_AFEM_VSMC
GO:1905207	0.0653	0.998	1	17	regulation of cardiocyte differentiation	BP	1	TBX5	up_APUL_EC
GO:0009066	0.065354241	0.99212	2	16	aspartate family amino acid metabolic process	BP	1	NMNAT2,NIT2	up_ACOR_EC
GO:0050921	0.0654	0.987	3	39	positive regulation of chemotaxis	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:1902105	0.0654	0.992	2	80	regulation of leukocyte differentiation	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0017144	0.0654	0.992	2	199	drug metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0048485	0.0654	0.998	1	9	sympathetic nervous system development	BP	1	SEMA3A	up_VPOR_EC
GO:0042326	0.06549206	0.97217	8	163	negative regulation of phosphorylation	BP	1	PKIB,NDRG2,DUSP26,SMAD6,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0010558	0.0655	0.954	42	392	negative regulation of macromolecule biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,EIF4A3,SREBF2,SMC1A,NEDD4,MTDH,NAB2,BIRC5,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,NCL,SUV39H1,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC

GO:0031098	0.0655	0.964	16	109	stress-activated protein kinase signaling cascade	BP	1	LEP,MAP3K8,MID1,RASSF2,TLR3,SH3RF2,SASH1,F2RL1,PTPN22,SH3RF1,APP,DUSP22,EDN1,NOD2,SH3RF3,MAP3K7	up_ACOR_VSMC
GO:0062013	0.0655	0.983	4	27	positive regulation of small molecule metabolic	BP	0.874	NR1H4,PTGS2,SLC45A3,PTPN2	down_VSAP_EC
GO:0001775	0.0655	0.987	3	219	cell activation	BP	1	HOXA9,TLR2,CAV1	up_VSAP_VSMC
GO:0007000	0.0655	0.994	2	5	nucleolus organization	BP	1	NOLC1,EMG1	down_ACOR_VSMC
GO:0002688	0.0655	0.998	1	34	regulation of leukocyte chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0048771	0.0656	0.975	7	43	tissue remodeling	BP	0.905	MEF2C,CHD7,DLL4,PPP3CA,JAG1,HMGB1,HIF1A	up_VCAV_EC
GO:2000104	0.0656	0.988	3	11	negative regulation of DNA-dependent DNA	BP	1	SMC1A,GMNN,SMC3	down_ACOR_VSMC
GO:0001893	0.0656	0.993	2	8	maternal placenta development	BP	0.874	TMED2,PTGS2	down_VSAP_EC
GO:0086005	0.0656	0.994	2	5	ventricular cardiac muscle cell action potential	BP	1	KCNE3,JUP	up_ACOR_VSMC
GO:0035759	0.0656	1	1	1	mesangial cell-matrix adhesion	BP	0.905	CD34	up_VCAV_EC
GO:1900035	0.0656	1	1	1	negative regulation of cellular response to heat	BP	0.905	CD34	up_VCAV_EC
GO:0030260	0.0656	0.998	1	15	entry into host cell	BP	1	CAV1	up_VSAP_VSMC
GO:0044409	0.0656	0.998	1	15	entry into host	BP	1	CAV1	up_VSAP_VSMC
GO:0051806	0.0656	0.998	1	15	entry into cell of other organism involved in	BP	1	CAV1	up_VSAP_VSMC
GO:0051828	0.0656	0.998	1	15	entry into other organism involved in symbiotic	BP	1	CAV1	up_VSAP_VSMC
GO:0018193	0.0657	0.954	39	368	peptidyl-amino acid modification	BP	0.905	PLK2,HCLS1,KIT,PRKCH,PDGFB,RELN,ST6GAL1,PDE4D,IWS1,GATA3,NEDD9,YES1,MTOR,HMG20A,SH3BP5,ST3GAL6,MAPK13,ARID4B,PAK2,PRKD2,NCK1,ESCO1,DPH5,FES,NSD1,PTGS2,TOP1,SENP6,CNOT7,NOS2,SPTBN4,RIPK1,PDGFD,BMX,KDM3A,LMTK2,ATRX,TET2,ARHGEF2	up_VCAV_EC
GO:0043409	0.0657	0.971	9	54	negative regulation of MAPK cascade	BP	1	BMP4,NDRG2,F2RL1,PTPN22,SMPD1,DAG1,SYNJ2BP,DUSP26,INPP5K	up_ACOR_VSMC
GO:0006633	0.0657	0.975	7	38	fatty acid biosynthetic process	BP	1	ACSM3,LIPC,INSIG2,ACACB,HSD17B8,PTGES,HACD4	up_VSAP_EC
GO:0034446	0.0657	0.98	5	23	substrate adhesion-dependent cell spreading	BP	1	NRP1,DOCK5,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0090114	0.0657	0.987	3	15	COPII-coated vesicle budding	BP	0.874	SEC24D,SEC23A,SEC13	down_VSAP_EC
GO:1902175	0.0657	0.993	2	7	regulation of oxidative stress-induced intrinsic apoptotic signaling	BP	0.874	P4HB,HIF1A	down_VSAP_EC
GO:1902667	0.0657	0.994	2	5	regulation of axon guidance	BP	1	SLIT2,PLXNA4	up_VSAP_EC
GO:0055074	0.0657	0.998	1	95	calcium ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0010830	0.0657	0.998	1	16	regulation of myotube differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0001960	0.0657	0.998	1	15	negative regulation of cytokine-mediated	BP	1	CAV1	up_VSAP_VSMC
GO:0060761	0.0657	0.998	1	15	negative regulation of response to cytokine	BP	1	CAV1	up_VSAP_VSMC
GO:0060326	0.065773283	0.97883	5	84	cell chemotaxis	BP	1	MMP28,ELMO2,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0001841	0.0658	0.973	8	44	neural tube formation	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0010972	0.0658	0.984	4	18	negative regulation of G2/M transition of mitotic	BP	1	CDK1,FANCI,TOPBP1,CLSPN	down_ACOR_VSMC
GO:0070228	0.0658	0.983	4	20	regulation of lymphocyte apoptotic process	BP	0.905	IL7R,ARG2,BCL10,HIF1A	up_VCAV_EC
GO:0050927	0.0658	0.994	2	5	positive regulation of positive chemotaxis	BP	1	VEGFD,F2RL1	up_ACOR_VSMC
GO:0001503	0.0658	0.992	2	109	ossification	BP	1	HOXA3,NPNT	up_APUL_EC
GO:0030204	0.0658	0.998	1	14	chondroitin sulfate metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0071109	0.0658	1	1	1	superior temporal gyrus development	BP	0.874	GSK3B	down_VSAP_EC
GO:1905319	0.0658	1	1	1	mesenchymal stem cell migration	BP	0.905	FBXO5	up_VCAV_EC
GO:1905320	0.0658	1	1	1	regulation of mesenchymal stem cell	BP	0.905	FBXO5	up_VCAV_EC

GO:1905322	0.0658	1	1	1	positive regulation of mesenchymal stem cell	BP	0.905	FBXO5	up_VCAV_EC
GO:0007056	0.0658	1	1	1	spindle assembly involved in female meiosis	BP	0.905	FBXO5	up_VCAV_EC
GO:0007057	0.0658	1	1	1	spindle assembly involved in female meiosis I	BP	0.905	FBXO5	up_VCAV_EC
GO:0007399	0.0659	0.955	36	564	nervous system development	BP	1	SMAD9,LRP1,NAB2,NDN,SDC4,BMPR1A,LMO4,TRPV2,NUMBL,NAGLU,AKT2,ENSCAFG00000018277,CSPG4,SEMA3C,THY1,HAPLN3,PEX5,TLX2,VCAN,GLI3,ZFP36L1,NCDN,IFT57,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,IRX5,UST,PRKCSH,FOXO3,THRB,ZBTB16,RGMA,BRSK1	down_VCAV_EC
GO:0006607	0.0659	0.994	2	5	NLS-bearing protein import into nucleus	BP	1	ENSCAFG00000011598,IPO4	down_ACOR_VSMC
GO:0060740	0.0659	0.998	1	13	prostate gland epithelium morphogenesis	BP	1	SULF1	down_ACOR_EC
GO:1903674	0.0659	1	1	1	regulation of cap-dependent translational	BP	0.905	NCK1	up_VCAV_EC
GO:1903676	0.0659	1	1	1	positive regulation of cap-dependent translational	BP	0.905	NCK1	up_VCAV_EC
GO:0019319	0.0659	0.998	1	26	hexose biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0048546	0.0659	0.998	1	16	digestive tract morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0098900	0.0659	0.998	1	15	regulation of action potential	BP	1	CAV1	up_VSAP_VSMC
GO:0003215	0.066	0.993	2	9	cardiac right ventricle morphogenesis	BP	1	BMPR1A,SEMA3C	down_VCAV_EC
GO:0061912	0.066	0.992	2	18	selective autophagy	BP	1	CLEC16A,RAB7A	up_AFEM_EC
GO:0019369	0.066	0.994	2	5	arachidonic acid metabolic process	BP	0.905	PTGS1,PTGS2	up_VCAV_EC
GO:0070252	0.066	0.998	1	17	actin-mediated cell contraction	BP	1	PDPN	down_ACOR_EC
GO:2000242	0.066	0.998	1	15	negative regulation of reproductive process	BP	1	SULF1	down_ACOR_EC
GO:1903707	0.066	0.998	1	48	negative regulation of hemopoiesis	BP	1	HOXA9	up_AFEM_VSMC
GO:0060395	0.066	0.998	1	27	SMAD protein signal transduction	BP	1	LNPEP	up_AORT_EC
GO:0048754	0.066	0.998	1	57	branching morphogenesis of an epithelial tube	BP	1	ESR1	up_AORT_VSMC
GO:0007422	0.066	0.998	1	18	peripheral nervous system development	BP	1	NTRK2	up_APUL_EC
GO:0060415	0.066	0.998	1	27	muscle tissue morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0023014	0.066031952	0.96763	11	248	signal transduction by protein phosphorylation	BP	1	SOX9,NDRG2,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,MAPK8IP2,SH3RF3,NRP1,PRKCD	up_ACOR_EC
GO:0140056	0.0661	0.98	5	28	organelle localization by membrane tethering	BP	0.905	EXOC6,CAV2,PDZD8,EXOC5,STX11	up_VCAV_EC
GO:0065002	0.0661	0.983	4	30	intracellular protein transmembrane transport	BP	1	AKT2,PEX5,SEC61B,LONP2	down_VCAV_EC
GO:0071806	0.0661	0.983	4	30	protein transmembrane transport	BP	1	AKT2,PEX5,SEC61B,LONP2	down_VCAV_EC
GO:0010647	0.0661	1	1	460	positive regulation of cell communication	BP	1	GATA5	down_AFEM_VSMC
GO:0032272	0.0661	0.998	1	18	negative regulation of protein polymerization	BP	1	TUBB4A	up_APUL_EC
GO:0010758	0.0661	0.998	1	8	regulation of macrophage chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0060415	0.0661	0.998	1	27	muscle tissue morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0046426	0.0661	0.998	1	20	negative regulation of JAK-STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:1904893	0.0661	0.998	1	20	negative regulation of STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:0032270	0.0662	0.954	37	479	positive regulation of cellular protein metabolic process	BP	0.874	ARHGEF2,PRICKLE1,VEGFA,MYH9,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,ILK,PPP1R12A,PTGS2,MSN,TNIK,YES1,ADAM17,MAGED1,CTNNB1,APOE,LYN,FAM162A,MMD,GSK3B,VLDLR,REST,CALM1,DISC1,RAD23A,PAK2,INHBA,TMTC3,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0007283	0.0662	0.967	12	91	spermatogenesis	BP	0.905	KIT,TSPAN8,PSME4,NECTIN2,CDYL,CREM,ARID4B,HIST1H1A,AFF4,KDM3A,ATRX,SPATA6	up_VCAV_EC
GO:0002695	0.0662	0.979	5	44	negative regulation of leukocyte activation	BP	1	PRNP,SDC4,GLI3,BPI,LOXL3	down_VCAV_EC

GO:0009132	0.0662	0.998	1	25	nucleoside diphosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0110110	0.0662	0.998	1	34	positive regulation of animal organ	BP	1	GATA5	up_VPUL_VSMC
GO:0031401	0.0663	0.954	38	358	positive regulation of protein modification process	BP	0.905	TEK,HCLS1,KIT,PPP2R5A,MAP3K11,TNIP1,PDGFB,STK10,RELN,TLR4,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,TLR3,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,HMGB1,RIPK1,PDGFD,UBE2D1,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0060337	0.0663	0.988	3	12	type I interferon signaling pathway	BP	0.905	NLRC5,CNOT7,LSM14A	up_VCAV_EC
GO:0071357	0.0663	0.988	3	12	cellular response to type I interferon	BP	0.905	NLRC5,CNOT7,LSM14A	up_VCAV_EC
GO:0002697	0.0663	0.992	2	85	regulation of immune effector process	BP	1	LYN,STX4	down_ACOR_EC
GO:0001654	0.0663	0.992	2	110	eye development	BP	1	ZDHHC16,NTRK2	up_APUL_EC
GO:0048880	0.0663	0.992	2	110	sensory system development	BP	1	ZDHHC16,NTRK2	up_APUL_EC
GO:0150063	0.0663	0.992	2	110	visual system development	BP	1	ZDHHC16,NTRK2	up_APUL_EC
GO:0090085	0.0663	0.994	2	5	regulation of protein deubiquitination	BP	0.905	TNIP1,OTUD4	up_VCAV_EC
GO:0072511	0.0663	0.992	2	97	divalent inorganic cation transport	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0035136	0.0663	0.998	1	16	forelimb morphogenesis	BP	1	HOXA9	up_VFEM_EC
GO:0048538	0.0663	0.998	1	20	thymus development	BP	1	HOXA3	up_VPUL_EC
GO:0048518	0.0664	0.984	5	1676	positive regulation of biological process	BP	1	SLITRK5,LIMK1,GATA5,CA2,C6	up_VCAV_VSMC
GO:0006576	0.0664	0.988	3	10	cellular biogenic amine metabolic process	BP	1	NAPEPLD,AZIN2,IDO2	up_VSAP_EC
GO:0001914	0.0664	0.993	2	8	regulation of T cell mediated cytotoxicity	BP	0.874	FAM49B,PVR	down_VSAP_EC
GO:0023056	0.0664	1	1	462	positive regulation of signaling	BP	1	GATA5	down_AFEM_VSMC
GO:0050679	0.0664	0.998	1	62	positive regulation of epithelial cell proliferation	BP	1	WNT7A	up_AORT_VSMC
GO:0051271	0.0664	0.998	1	98	negative regulation of cellular component	BP	1	TBX5	up_APUL_VSMC
GO:0009308	0.0664	0.998	1	20	amine metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0003156	0.0664	0.998	1	20	regulation of animal organ formation	BP	1	TBX5	up_VPUL_EC
GO:0060760	0.0664	0.998	1	17	positive regulation of response to cytokine	BP	1	TLR2	up_VSAP_VSMC
GO:1901020	0.0665	0.993	2	8	negative regulation of calcium ion transmembrane	BP	0.874	REM1,CALM1	down_VSAP_EC
GO:1903170	0.0665	0.993	2	8	negative regulation of calcium ion	BP	0.874	REM1,CALM1	down_VSAP_EC
GO:0007422	0.0665	0.992	2	18	peripheral nervous system development	BP	1	PLXNA4,LGI4	up_AFEM_EC
GO:0009062	0.0665	0.998	1	31	fatty acid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0048532	0.0665	0.998	1	9	anatomical structure arrangement	BP	1	SEMA3A	up_VPOR_EC
GO:0006090	0.0665	0.998	1	26	pyruvate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0048659	0.066506337	0.98625	3	36	smooth muscle cell proliferation	BP	1	NDRG2,PTGIR,CLSTN1	up_ACOR_EC
GO:0009792	0.0666	0.958	26	231	embryo development ending in birth or egg hatching	BP	0.905	HOXB7,PCDH12,ADGRF5,TIE1,AMOT,PDGFB,MEF2C,CHD7,GATA3,EDN1,HOXB8,SOX18,BMP2,HHEX,MDFI,HOXB5,BCL10,NUP133,SKIL,CUL4A,HIF1A,LUZP1,RBBP6,VASH1,ZEB1,GINS4	up_VCAV_EC
GO:0006066	0.0666	0.967	12	89	alcohol metabolic process	BP	1	SQLE,LSS,SREBF1,HMGCR,INSIG1,DHCR24,MVD,FDFT1,LIPC,NUS1,GK5,NUDT3	down_ACOR_VSMC
GO:0045861	0.0666	0.974	7	71	negative regulation of proteolysis	BP	1	CST3,RECK,TIMP2,PSMF1,PARK7,CLEC16A,A2M	down_VCAV_EC
GO:0010467	0.0666	1	2	1787	gene expression	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0050854	0.0666	0.998	1	16	regulation of antigen receptor-mediated	BP	1	LYN	down_ACOR_EC
GO:1903707	0.0666	0.998	1	48	negative regulation of hemopoiesis	BP	1	LRRC17	up_VCAV_VSMC

GO:0042733	0.0666	0.998	1	27	embryonic digit morphogenesis	BP	1	HOXA11	up_VFEM_VSMC
GO:1900542	0.0666	0.998	1	26	regulation of purine nucleotide metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0018209	0.0667	0.963	16	125	peptidyl-serine modification	BP	0.905	PLK2,HCLS1,PRKCH,PDGFB,PDE4D,MTOR,MAPK13,PAK2,PRKD2,NCK1,NSD1,PTGS2,TOP1,SPTBN4,RIPK1,LMTK2	up_VCAV_EC
GO:0006006	0.0667	0.974	7	61	glucose metabolic process	BP	0.874	ENPP1,TPI1,PGAM1,SESN2,SLC45A3,PTPN2,ATF3	down_VSAP_EC
GO:0034763	0.0667	0.98	5	27	negative regulation of transmembrane transport	BP	1	NEDD4,CAV1,SLC30A1,GSTO1,REM1	down_ACOR_VSMC
GO:0033619	0.0667	0.987	3	19	membrane protein proteolysis	BP	1	TIMP2,HM13,PACSIN3	down_VCAV_EC
GO:0032615	0.0667	0.992	2	18	interleukin-12 production	BP	1	CMKLR1,LEP	up_AFEM_EC
GO:0072503	0.0667	0.992	2	97	cellular divalent inorganic cation homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0071544	0.0667	1	1	1	diphosphoinositol polyphosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0051050	0.0667	0.999	1	235	positive regulation of transport	BP	1	JUP	down_VFEM_VSMC
GO:0002339	0.0667	1	1	1	B cell selection	BP	0.874	BTK	down_VSAP_EC
GO:0002343	0.0667	1	1	1	peripheral B cell selection	BP	0.874	BTK	down_VSAP_EC
GO:0002344	0.0667	1	1	1	B cell affinity maturation	BP	0.874	BTK	down_VSAP_EC
GO:0098760	0.0667	1	1	1	response to interleukin-7	BP	0.874	BTK	down_VSAP_EC
GO:0098761	0.0667	1	1	1	cellular response to interleukin-7	BP	0.874	BTK	down_VSAP_EC
GO:0060420	0.0667	0.998	1	18	regulation of heart growth	BP	1	TBX5	up_APUL_EC
GO:0070838	0.0667	0.998	1	96	divalent metal ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:2000145	0.066785918	0.96609	12	279	regulation of cell motility	BP	1	SOX9,AQP1,SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,FOXC2,LRRC15,TBX5,RARRES2,NRP1	up_ACOR_EC
GO:0032943	0.0668	0.974	7	60	mononuclear cell proliferation	BP	0.874	MSN,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0046651	0.0668	0.974	7	60	lymphocyte proliferation	BP	0.874	MSN,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0032990	0.0668	0.986	3	167	cell part morphogenesis	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0061383	0.0668	0.987	3	20	trabecula morphogenesis	BP	1	THBS3,BMPR1A,GREM1	down_VCAV_EC
GO:0016601	0.0668	0.988	3	11	Rac protein signal transduction	BP	0.905	ARAP3,NCKAP1,ELMO1	up_VCAV_EC
GO:0002009	0.0668	0.992	2	177	morphogenesis of an epithelium	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0007186	0.0668	0.992	2	124	G protein-coupled receptor signaling	BP	1	RGS1,CCL24	up_VPUL_EC
GO:0006637	0.0668	0.998	1	32	acyl-CoA metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0035383	0.0668	0.998	1	32	thioester metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0008589	0.0668	0.998	1	28	regulation of smoothened signaling pathway	BP	1	SHOX2	up_VFEM_VSMC
GO:0050701	0.066823181	0.99184	2	16	interleukin-1 secretion	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0060255	0.0669	1	2	1782	regulation of macromolecule metabolic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0043266	0.0669	0.998	1	14	regulation of potassium ion transport	BP	1	NEDD4	down_ACOR_EC
GO:0002244	0.0669	0.998	1	35	hematopoietic progenitor cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:0009746	0.0669	0.998	1	35	response to hexose	BP	1	RAB11B	down_VPOR_EC
GO:0034284	0.0669	0.998	1	35	response to monosaccharide	BP	1	RAB11B	down_VPOR_EC
GO:0016333	0.0669	1	1	1	morphogenesis of follicular epithelium	BP	0.874	WDR1	down_VSAP_EC
GO:0016334	0.0669	1	1	1	establishment or maintenance of polarity	BP	0.874	WDR1	down_VSAP_EC
GO:0042247	0.0669	1	1	1	establishment of planar polarity of follicular	BP	0.874	WDR1	down_VSAP_EC
GO:0048839	0.0669	0.998	1	50	inner ear development	BP	1	EYA1	up_AFEM_VSMC
GO:0032943	0.0669	0.998	1	60	mononuclear cell proliferation	BP	1	ARG2	up_AORT_VSMC

GO:0046651	0.0669	0.998	1	60	lymphocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0002218	0.067	0.971	9	53	activation of innate immune response	BP	1	F2RL1,MYD88,NLRX1,TKFC,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0051961	0.067	0.974	7	73	negative regulation of nervous system	BP	1	BMPR1A,THY1,TLX2,GLI3,PRKCSH,THRB,RGMA	down_VCAV_EC
GO:0051785	0.067	0.987	3	14	positive regulation of nuclear division	BP	0.905	PDGFB,EDN1,SMC5	up_VCAV_EC
GO:0051482	0.067	0.994	2	5	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-	BP	1	F2RL1,EDN1	up_ACOR_VSMC
GO:0002548	0.067	0.998	1	17	monocyte chemotaxis	BP	1	LYN	down_ACOR_EC
GO:0048597	0.067	1	1	1	post-embryonic camera-type eye morphogenesis	BP	1	HMGN1	down_ACOR_VSMC
GO:0030041	0.0671	0.97	9	62	actin filament polymerization	BP	0.905	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0046661	0.0671	0.972	8	45	male sex differentiation	BP	1	GATA4,PRDX4,ATRX,CITED2,SPINK2,ARID5B,LHX9,WDR48	up_ACOR_VSMC
GO:0048870	0.0671	0.983	4	451	cell motility	BP	1	TBX5,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0051674	0.0671	0.983	4	451	localization of cell	BP	1	TBX5,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0007167	0.0671	0.986	3	274	enzyme linked receptor protein signaling pathway	BP	1	NR1H4,FLRT3,NEO1	up_VPUL_EC
GO:0031323	0.0671	1	2	1788	regulation of cellular metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0001525	0.0671	0.992	2	173	angiogenesis	BP	1	HOXA3,C3AR1	up_VPOR_VSMC
GO:0021577	0.0671	1	1	1	hindbrain structural organization	BP	0.874	HSPA5	down_VSAP_EC
GO:0021589	0.0671	1	1	1	cerebellum structural organization	BP	0.874	HSPA5	down_VSAP_EC
GO:0006814	0.0671	0.998	1	28	sodium ion transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:0046324	0.0671	0.998	1	20	regulation of glucose import	BP	1	NR1H4	up_VPUL_EC
GO:0001656	0.067115262	0.98609	3	35	metanephros development	BP	1	SOX9,AQP1,FOXC2	up_ACOR_EC
GO:0071229	0.0672	0.971	9	51	cellular response to acid chemical	BP	1	PRKAA2,ABCA1,CASTOR1,ADCY6,UBR1,PTGDR,SESN3,PRKCE,SH3BP4	up_ACOR_VSMC
GO:2000146	0.0672	0.978	5	92	negative regulation of cell motility	BP	1	ANGPT4,HOXA7,RECK,TBXA2R,KANK1	up_AFEM_EC
GO:0045596	0.0672	0.986	3	186	negative regulation of cell differentiation	BP	1	ACVRL1,LYN,HOXA7	down_ACOR_EC
GO:0009889	0.0672	0.99	3	1190	regulation of biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0001934	0.0672	0.986	3	274	positive regulation of protein phosphorylation	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0032501	0.0672	1	2	1782	multicellular organismal process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0008016	0.0672	0.998	1	48	regulation of heart contraction	BP	1	IRX5	up_AFEM_VSMC
GO:0042339	0.0672	1	1	1	keratan sulfate metabolic process	BP	0.905	CHST1	up_VCAV_EC
GO:0072709	0.0672	1	1	1	cellular response to sorbitol	BP	0.905	MAPK13	up_VCAV_EC
GO:0072740	0.0672	1	1	1	cellular response to anisomycin	BP	0.905	MAPK13	up_VCAV_EC
GO:0010632	0.0673	0.964	14	95	regulation of epithelial cell migration	BP	1	ENPP2,SLIT2,FGF7,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:2001257	0.0673	0.977	6	30	regulation of cation channel activity	BP	1	ACTN2,PLCG2,KCNE3,DAPK1,CACNB3,AKAP6	up_ACOR_VSMC
GO:0032963	0.0673	0.992	2	18	collagen metabolic process	BP	1	MFAP4,FAP	up_AFEM_EC
GO:0044703	0.0673	0.992	2	172	multi-organism reproductive process	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0042908	0.0673	0.998	1	3	xenobiotic transport	BP	1	SLC6A6	up_AFEM_EC
GO:0060038	0.0673	0.998	1	18	cardiac muscle cell proliferation	BP	1	TBX5	up_APUL_EC
GO:0002424	0.0673	1	1	1	T cell mediated immune response to tumor cell	BP	0.905	HMGB1	up_VCAV_EC
GO:0002840	0.0673	1	1	1	regulation of T cell mediated immune	BP	0.905	HMGB1	up_VCAV_EC

GO:0017055	0.0673	1	1	1	negative regulation of RNA polymerase II transcriptional	BP	0.905	HMGB1	up_VCAV_EC
GO:0032072	0.0673	1	1	1	regulation of restriction endodeoxyribonuclease	BP	0.905	HMGB1	up_VCAV_EC
GO:0032425	0.0673	1	1	1	positive regulation of mismatch repair	BP	0.905	HMGB1	up_VCAV_EC
GO:2000425	0.0673	1	1	1	regulation of apoptotic cell clearance	BP	0.905	HMGB1	up_VCAV_EC
GO:2000426	0.0673	1	1	1	negative regulation of apoptotic cell clearance	BP	0.905	HMGB1	up_VCAV_EC
GO:0002009	0.0674	0.958	24	177	morphogenesis of an epithelium	BP	1	SHROOM3,MLLT3,BMP4,FGFR2,GJA1,SEC24B ,CITED2,SPINT1,ZNRF3,LMO4,ENSCAFG0000 0006238,CLSTN1,NRP1,NPNT,SPINT2,TBX20, TBX5,FZD3,FRS2,DAG1,PSEN1,EDN1,SERPINB 5,RREB1	up_ACOR_VSMC
GO:0022008	0.0674	0.979	5	406	neurogenesis	BP	1	LYN,ACSL4,SPG11,NRP2,NEDD4	down_ACOR_EC
GO:0031328	0.0674	0.993	2	512	positive regulation of cellular biosynthetic	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:1901017	0.0674	0.994	2	5	negative regulation of potassium ion transmembrane	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:1901380	0.0674	0.994	2	5	negative regulation of potassium ion	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:0050919	0.0674	0.998	1	10	negative chemotaxis	BP	1	NRP2	down_ACOR_EC
GO:0072511	0.0674	0.998	1	97	divalent inorganic cation transport	BP	1	HOXA3	up_APUL_VSMC
GO:0090066	0.067473032	0.97116	8	162	regulation of anatomical structure size	BP	1	TMOD1,AQP1,PLS1,ACTN2,PAK3,FOXC2,NRP 1,PRKCD	up_ACOR_EC
GO:0071560	0.0675	0.973	7	72	cellular response to transforming growth	BP	1	SMAD9,VASN,FBN1,NR3C1,ASPN,ZFP36L1,FU T8	down_VCAV_EC
GO:0008217	0.0675	0.974	7	38	regulation of blood pressure	BP	1	ADRA1B,SLC2A5,F2RL1,RNLS,EDN1,NCALD,E RAP1	up_ACOR_VSMC
GO:0030838	0.0675	0.976	6	37	positive regulation of actin filament	BP	0.905	BAIAP2L1,MTOR,NCKAP1,IQGAP2,NCK1,ARP C5L	up_VCAV_EC
GO:0043367	0.0675	0.983	4	18	CD4-positive, alpha-beta T cell differentiation	BP	0.905	IL6,GATA3,MTOR,HMGB1	up_VCAV_EC
GO:0051496	0.0675	0.983	4	17	positive regulation of stress fiber assembly	BP	1	WNT11,ARHGEF5,ABL1,BAG4	up_VSAP_EC
GO:0048514	0.0675	0.992	2	214	blood vessel morphogenesis	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:0006418	0.0675	0.998	1	31	tRNA aminoacylation for protein translation	BP	1	DARS	down_AFEM_EC
GO:0021559	0.0675	0.998	1	3	trigeminal nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0021636	0.0675	0.998	1	3	trigeminal nerve morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0021637	0.0675	0.998	1	3	trigeminal nerve structural organization	BP	1	PLXNA4	up_AFEM_EC
GO:0021785	0.0675	0.998	1	3	branchiomotor neuron axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:1902287	0.0675	0.998	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:0051017	0.0675	0.998	1	49	actin filament bundle assembly	BP	1	LIMK1	up_VCAV_VSMC
GO:0008543	0.0675	0.998	1	27	fibroblast growth factor receptor signaling	BP	1	FGF5	up_VPOR_VSMC

GO:0009987	0.067547022	0.95262	143	5086	cellular process	BP	1	CNTNAP4,SH3TC2,MYOZ2,FMOD,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TRPS1,KCTD12,TBX18,PLCL1,PKIB,CALY,THNSL2,SOX9,NMNAT2,RHOU,PKNOX2,ARHGAP6,PTH1R,GALNT5,RGS1,PCSK1N,PHF20,ATG16L2,NDRG2,AQP1,PORCN,ENSCAFG00000004331,SYNPO2,KCNB1,ADAMTS13,SARDH,EDEM2,PI3,FZD5,CCDC3,AGRN,PDE1A,IFI6,SEMA6D,GNAO1,HSF4,DUSP26,DIXDC1,RASL11A,PTGIR,PDLIM3,NOD2,IL33,RGMA,CASP10,LHX9,ENSCAFG00000028814,PDE4A,INSYN1,SMAD6,B3GNT7,DYNC1I1,KLHL25,PLCE1,PLS1,ACTN2,ZMYND8,ARHGAP28,ESM1,NIT2,PTGDS,PAK3,CFI,MMP28,DLX3,GUCY1B1,GRK7,BCL2,TNFRSF19,PTGER4,ARHGDIB,ELMO2,PREB,CST3,PIAS1,DCLK2,ADAMTSL2,USP53,CHPT1,MAPK8IP2,PDRG1,RAPGEF4,MAVS,FOXC2,FIGNL1,LRRC15,IFIT2,KLHDC8B,TBX5,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,PRELP,RBM38,CLU,SLC9A9,SFMBT2,ALDOC,C23H3orf58,ZNF229,CHMP4B,TP53INP2,RARRES2,VPS16,GMEB2,AGBL5,RIOX2,PRKACA,RNF114,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,FKBP11,ARHGEF26,PRKCD,GNAZ,RIN2,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,ENSCAFG00000010493,CCNYL1,MFAP4,ADGRL1,TUBB4A,TLE2	up_ACOR_EC
GO:0048584	0.0676	0.976	6	592	positive regulation of response to stimulus	BP	1	ACVRL1,LYN,PDPN,SULF1,STX4,NEDD4	down_ACOR_EC
GO:0071695	0.0676	0.978	5	45	anatomical structure maturation	BP	1	THBS3,RECK,IRX5,GREM1,FOXO3	down_VCAV_EC
GO:0031060	0.0676	0.98	5	23	regulation of histone methylation	BP	0.905	IWS1,GATA3,NSD1,KDM3A,ATRX	up_VCAV_EC
GO:0002052	0.0676	0.988	3	9	positive regulation of neuroblast proliferation	BP	1	SMARCD3,FZD3,DISC1	up_ACOR_VSMC
GO:0070262	0.0676	0.993	2	6	peptidyl-serine dephosphorylation	BP	0.905	SWAP70,NCK1	up_VCAV_EC
GO:0030201	0.0676	0.998	1	12	heparan sulfate proteoglycan metabolic	BP	1	SULF1	down_ACOR_EC
GO:0002440	0.0676	0.998	1	51	production of molecular mediator of immune	BP	1	TLR2	up_AFEM_VSMC
GO:0006024	0.0676	0.998	1	16	glycosaminoglycan biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:1901655	0.0676	0.998	1	20	cellular response to ketone	BP	1	PTGER2	up_VPUL_EC
GO:2001057	0.0676	0.998	1	16	reactive nitrogen species metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0055085	0.067602285	0.9656	12	284	transmembrane transport	BP	1	NR1H4,CLIC3,AQP1,ENSCAFG00000004331,KCNB1,ACTN2,SLC25A42,MAPK8IP2,SLC9A9,RARRES2,AZIN2,PM20D1	up_ACOR_EC
GO:0060284	0.0677	0.96	19	212	regulation of cell development	BP	0.874	ARHGEF2,SIPA1L1,DPYSL3,HOOK3,IFRD1,HIF1A,SLC45A3,TNIK,UST,CTNNB1,ENSCAFG00000002015,APOE,LYN,MMD,VLDLR,REST,DISC1,NRP1,YWHAH	down_VSAP_EC
GO:0043297	0.0677	0.983	4	17	apical junction assembly	BP	0.905	PRKCH,OCLN,TJP1,CTNNA1	up_VCAV_EC
GO:0006265	0.0677	0.994	2	5	DNA topological change	BP	1	TOP3A,HMGB2	down_ACOR_VSMC
GO:0048730	0.0677	0.993	2	7	epidermis morphogenesis	BP	0.874	CTNNB1,PLOD3	down_VSAP_EC
GO:0051962	0.0677	0.991	2	112	positive regulation of nervous system	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0007517	0.0677	0.991	2	100	muscle organ development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0031998	0.0677	0.994	2	5	regulation of fatty acid beta-oxidation	BP	1	ACACB,LONP2	up_VSAP_EC
GO:0045595	0.0677	1	1	469	regulation of cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0010830	0.0677	0.998	1	16	regulation of myotube differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0097300	0.0677	0.998	1	17	programmed necrotic cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0032874	0.067784641	0.98148	4	57	positive regulation of stress-activated MAPK	BP	1	FZD5,NOD2,TNFRSF19,SH3RF3	up_ACOR_EC
GO:0031503	0.0678	0.967	11	79	protein-containing complex localization	BP	1	DDX39A,STXBP6,NDC1,RAN,BIRC5,NUP62,HASPIN,DDX39B,ENSCAFG00000005299,EZR,MIOS	down_ACOR_VSMC
GO:0065009	0.0678	0.974	7	735	regulation of molecular function	BP	1	LYN,HOXA3,IGF1R,PRKAR2A,MYO1D,ASPN,NEDD4	down_ACOR_EC
GO:0000226	0.0678	0.981	4	197	microtubule cytoskeleton organization	BP	1	MZT1,HOOK3,ARHGEF2,GCC2	up_VPOR_EC

GO:0033036	0.0678	0.989	3	852	macromolecule localization	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0043405	0.0678	0.991	2	85	regulation of MAP kinase activity	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0042116	0.0678	0.998	1	18	macrophage activation	BP	1	BPI	up_APUL_EC
GO:0006554	0.0678	1	1	1	lysine catabolic process	BP	0.905	PIPOX	up_VCAV_EC
GO:0019474	0.0678	1	1	1	L-lysine catabolic process to acetyl-CoA	BP	0.905	PIPOX	up_VCAV_EC
GO:0019477	0.0678	1	1	1	L-lysine catabolic process	BP	0.905	PIPOX	up_VCAV_EC
GO:0033514	0.0678	1	1	1	L-lysine catabolic process to acetyl-CoA via L-	BP	0.905	PIPOX	up_VCAV_EC
GO:0046440	0.0678	1	1	1	L-lysine metabolic process	BP	0.905	PIPOX	up_VCAV_EC
GO:0007389	0.067889239	0.97287	7	137	pattern specification process	BP	1	FZD5,SMAD6,FOXC2,TBX5,LRP4,CLSTN1,NRP1	up_ACOR_EC
GO:0051239	0.0679	0.977	6	859	regulation of multicellular organismal process	BP	1	TBX5,NR1H4,EVI2B,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0009891	0.0679	0.979	5	521	positive regulation of biosynthetic process	BP	1	HOXA11,HOXA9,SALL1,PRR16,SHOX2	up_VSAP_VSMC
GO:0045165	0.0679	0.981	4	65	cell fate commitment	BP	1	HOXC10,GAS1,DLL1,CYLD	up_AFEM_EC
GO:0000272	0.0679	0.994	2	4	polysaccharide catabolic process	BP	1	PYGM,GAA	up_ACOR_VSMC
GO:0009251	0.0679	0.994	2	4	glucan catabolic process	BP	1	PYGM,GAA	up_ACOR_VSMC
GO:0005980	0.0679	0.994	2	4	glycogen catabolic process	BP	1	PYGM,GAA	up_ACOR_VSMC
GO:0044247	0.0679	0.994	2	4	cellular polysaccharide catabolic process	BP	1	PYGM,GAA	up_ACOR_VSMC
GO:0071704	0.068	0.979	11	3535	organic substance metabolic process	BP	1	ETFA,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0044085	0.068	0.981	5	1076	cellular component biogenesis	BP	1	GPSM2,EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:0048227	0.068	0.994	2	5	plasma membrane to endosome transport	BP	1	USP6NL,RAB5C	up_ACOR_VSMC
GO:1904063	0.068	0.998	1	17	negative regulation of cation transmembrane	BP	1	NEDD4	down_ACOR_EC
GO:0060167	0.068	1	1	1	regulation of adenosine receptor signaling	BP	0.905	ACPP	up_VCAV_EC
GO:0060168	0.068	1	1	1	positive regulation of adenosine receptor	BP	0.905	ACPP	up_VCAV_EC
GO:0060048	0.068	0.998	1	30	cardiac muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035270	0.068	0.998	1	35	endocrine system development	BP	1	HOXA3	up_VPUL_VSMC
GO:0046879	0.0681	0.969	10	63	hormone secretion	BP	1	LEP,TM7SF3,PRKCE,SCG5,CHD7,CCL5,RAB11B,EDN1,PFKL,PARK7	up_ACOR_VSMC
GO:0070482	0.0681	0.968	10	75	response to oxygen levels	BP	0.905	CXCR4,CD34,EDN1,MTOR,BMP2,PTGS2,PMAIP1,HIF1A,HP1BP3,P2RX2	up_VCAV_EC
GO:0051171	0.0681	0.984	5	1697	regulation of nitrogen compound metabolic	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0051893	0.0681	0.983	4	20	regulation of focal adhesion assembly	BP	0.905	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0090109	0.0681	0.983	4	20	regulation of cell-substrate junction	BP	0.905	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0007519	0.0681	0.998	1	49	skeletal muscle tissue development	BP	1	BEND2	up_AFEM_VSMC
GO:1903727	0.06816801	0.99158	2	16	positive regulation of phospholipid metabolic	BP	1	NR1H4,PRKCD	up_ACOR_EC
GO:0023052	0.0682	0.971	10	1602	signaling	BP	1	NR1H4,TBX5,MAPK10,HTR7,PLCL1,ARHGEF26,SLITRK5,NPNT,NTRK2,PDE1A	up_APUL_EC
GO:0030198	0.0682	0.97	9	81	extracellular matrix organization	BP	0.874	SULF1,SERPINH1,ERO1A,P4HA1,FSCN1,PLOD3,MYO1E,P3H4,COL12A1	down_VSAP_EC
GO:0090092	0.0682	0.971	8	72	regulation of transmembrane receptor protein serine/threonine	BP	0.874	SULF1,HSPA5,SNX25,ILK,NEO1,ADAM17,STRAP,INHBA	down_VSAP_EC
GO:0006816	0.0682	0.991	2	84	calcium ion transport	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0046040	0.0682	0.992	2	9	IMP metabolic process	BP	1	NT5C2,AMPD2	down_VCAV_EC
GO:0019511	0.0682	0.994	2	5	peptidyl-proline hydroxylation	BP	1	EGLN1,P4HA1	up_ACOR_VSMC
GO:0030888	0.0682	0.998	1	13	regulation of B cell proliferation	BP	1	LYN	down_ACOR_EC
GO:0003197	0.0682	0.998	1	16	endocardial cushion development	BP	1	ACVRL1	down_ACOR_EC

GO:0021960	0.0682	0.998	1	3	anterior commissure morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0071295	0.0682	0.998	1	3	cellular response to vitamin	BP	1	POSTN	up_AFEM_EC
GO:0071219	0.0682	0.998	1	50	cellular response to molecule of bacterial	BP	1	TLR2	up_AFEM_VSMC
GO:0040013	0.0682	0.998	1	100	negative regulation of locomotion	BP	1	TBX5	up_APUL_VSMC
GO:0048870	0.0683	0.962	16	451	cell motility	BP	1	CMKLR1,ANGPT4,HOXA7,TWIST2,HCK,GREM1,CAMK2A,LRRC15,RECK,TBXA2R,BVES,LGR6,CCL5,FAP,ADAM17,KANK1	up_AFEM_EC
GO:0051674	0.0683	0.962	16	451	localization of cell	BP	1	CMKLR1,ANGPT4,HOXA7,TWIST2,HCK,GREM1,CAMK2A,LRRC15,RECK,TBXA2R,BVES,LGR6,CCL5,FAP,ADAM17,KANK1	up_AFEM_EC
GO:0022603	0.0683	0.982	4	301	regulation of anatomical structure morphogenesis	BP	1	ACVRL1,PDPN,SULF1,ASPN	down_ACOR_EC
GO:0097006	0.0683	0.986	3	19	regulation of plasma lipoprotein particle levels	BP	1	LCAT,LRPAP1,SOAT1	down_VCAV_EC
GO:0035725	0.0683	0.998	1	16	sodium ion transmembrane transport	BP	1	NEDD4	down_ACOR_EC
GO:0000117	0.0683	1	1	1	regulation of transcription involved in G2/M transition of mitotic cell	BP	0.874	BACH1	down_VSAP_EC
GO:0010172	0.0683	0.998	1	3	embryonic body morphogenesis	BP	1	GREM2	up_AFEM_EC
GO:0032310	0.0683	0.998	1	3	prostaglandin secretion	BP	1	LEP	up_AFEM_EC
GO:0061502	0.0683	0.998	1	3	early endosome to recycling endosome	BP	1	MYO1D	up_AFEM_EC
GO:0010389	0.0683	0.998	1	30	regulation of G2/M transition of mitotic cell	BP	1	TAOK1	up_AORT_EC
GO:0046626	0.0683	0.998	1	18	regulation of insulin receptor signaling	BP	1	NR1H4	up_APUL_EC
GO:0016925	0.0683	0.998	1	16	protein sumoylation	BP	1	EYA1	up_VFEM_EC
GO:0090066	0.0684	0.958	22	162	regulation of anatomical structure size	BP	1	ADRA1B,ACTN2,HTR2B,NPPB,HRH1,CLCN3,ADCY6,F2RL1,HRH2,SLC12A7,JMY,LRRC8C,NRP1,ULK2,EVL,PTGDR,PRKCE,CLN8,SSH3,EDN1,WASL,DOCK5	up_ACOR_VSMC
GO:0046085	0.0684	0.994	2	5	adenosine metabolic process	BP	1	PTGDR,NT5C2	up_ACOR_VSMC
GO:0032410	0.0684	0.998	1	17	negative regulation of transporter activity	BP	1	NEDD4	down_ACOR_EC
GO:0002181	0.0684	0.998	1	35	cytoplasmic translation	BP	1	EIF3M	down_AFEM_EC
GO:0098856	0.0684	0.998	1	3	intestinal lipid absorption	BP	1	LEP	up_AFEM_EC
GO:0030299	0.0684	0.998	1	3	intestinal cholesterol absorption	BP	1	LEP	up_AFEM_EC
GO:0048251	0.0684	0.998	1	3	elastic fiber assembly	BP	1	MFAP4	up_AFEM_EC
GO:0030177	0.0684	0.998	1	51	positive regulation of Wnt signaling pathway	BP	1	TLR2	up_AFEM_VSMC
GO:0043122	0.0684	0.998	1	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	ESR1	up_AORT_VSMC
GO:0008361	0.0684	0.998	1	50	regulation of cell size	BP	1	LIMK1	up_VCAV_VSMC
GO:0046364	0.0684	0.998	1	27	monosaccharide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0045600	0.0684	0.998	1	21	positive regulation of fat cell differentiation	BP	1	WIF1	up_VPUL_EC
GO:0031952	0.0684	0.998	1	15	regulation of protein autophosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0044270	0.0685	0.96	18	147	cellular nitrogen compound catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,PDXP,AIFM1,ENSCAFG00000015189,RNASEH2C,NUDT1,EXOSC5,NUDT3	down_ACOR_VSMC
GO:0006836	0.0685	0.972	8	47	neurotransmitter transport	BP	1	FBXL20,STX11,PSEN1,CLN8,EDN1,KCNC4,PREPL,PARK7	up_ACOR_VSMC
GO:2000179	0.0685	0.987	3	14	positive regulation of neural precursor cell	BP	0.874	HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0003148	0.0685	0.998	1	13	outflow tract septum morphogenesis	BP	1	NRP2	down_ACOR_EC
GO:0030029	0.0685	0.999	1	239	actin filament-based process	BP	1	JUP	down_VFEM_VSMC
GO:0044774	0.0685	0.998	1	30	mitotic DNA integrity checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0001818	0.0685	0.998	1	65	negative regulation of cytokine production	BP	1	ARG2	up_AORT_VSMC

GO:1990784	0.0685	1	1	1	response to dsDNA	BP	0.905	RIOK3	up_VCAV_EC
GO:1990786	0.0685	1	1	1	cellular response to dsDNA	BP	0.905	RIOK3	up_VCAV_EC
GO:0051153	0.0685	0.998	1	28	regulation of striated muscle cell differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0060491	0.0686	0.973	7	62	regulation of cell projection assembly	BP	0.874	FSCN1,DPYSL3,DYNLL1,ANLN,KLF5,HTT,NRP1	down_VSAP_EC
GO:0120032	0.0686	0.973	7	62	regulation of plasma membrane bounded cell	BP	0.874	FSCN1,DPYSL3,DYNLL1,ANLN,KLF5,HTT,NRP1	down_VSAP_EC
GO:0002088	0.0686	0.982	4	26	lens development in camera-type eye	BP	0.874	BCAR3,CTNNB1,CRYAB,PDS5B	down_VSAP_EC
GO:0015800	0.0686	0.988	3	10	acidic amino acid transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:0071495	0.0686	0.992	2	365	cellular response to endogenous stimulus	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0021615	0.0686	0.998	1	3	glossopharyngeal nerve morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:1901096	0.0686	0.998	1	3	regulation of autophagosome	BP	1	CLEC16A	up_AFEM_EC
GO:0072677	0.068655123	0.99839	1	3	eosinophil migration	BP	1	PTGER4	up_ACOR_EC
GO:0033157	0.068664659	0.97765	5	82	regulation of intracellular protein transport	BP	1	SH3TC2,KCNB1,EDEM2,MAVS,PRKCD	up_ACOR_EC
GO:0071310	0.0687	0.983	4	634	cellular response to organic substance	BP	1	FGF5,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0090189	0.0687	0.987	3	12	regulation of branching involved in ureteric bud	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0045646	0.0687	0.986	3	19	regulation of erythrocyte differentiation	BP	1	ZFP36L1,FOXO3,ANKRD54	down_VCAV_EC
GO:0046885	0.0687	0.993	2	7	regulation of hormone biosynthetic process	BP	0.874	HIF1A,REST	down_VSAP_EC
GO:1903321	0.0687	0.998	1	33	negative regulation of protein modification by small protein conjugation	BP	1	IVNS1ABP	down_AFEM_EC
GO:2000322	0.0687	0.998	1	3	regulation of glucocorticoid receptor	BP	1	CRY2	up_AFEM_EC
GO:2000323	0.0687	0.998	1	3	negative regulation of glucocorticoid receptor signaling pathway	BP	1	CRY2	up_AFEM_EC
GO:0032105	0.0687	0.998	1	3	negative regulation of response to extracellular	BP	1	LEP	up_AFEM_EC
GO:0032108	0.0687	0.998	1	3	negative regulation of response to nutrient	BP	1	LEP	up_AFEM_EC
GO:0046322	0.0687	0.998	1	3	negative regulation of fatty acid oxidation	BP	1	ACACB	up_AFEM_EC
GO:0097343	0.0687	0.998	1	3	ripoptosome assembly	BP	1	CYLD	up_AFEM_EC
GO:1901026	0.0687	0.998	1	3	ripoptosome assembly involved in necroptotic	BP	1	CYLD	up_AFEM_EC
GO:1990845	0.0687	0.998	1	51	adaptive thermogenesis	BP	1	HOXC10	up_AFEM_VSMC
GO:0003179	0.0687	0.998	1	19	heart valve morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0046700	0.0688	0.96	18	147	heterocycle catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,PDXP,AIFM1,ENSCAFG00000015189,RNASEH2C,NUDT1,EXOSC5,NUDT3	down_ACOR_VSMC
GO:0010467	0.0688	0.969	12	1787	gene expression	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0072511	0.0688	0.968	10	97	divalent inorganic cation transport	BP	0.874	SLC39A7,ERO1A,ATP2B1,REM1,CTNNB1,LYN,DDIT3,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0006491	0.0688	0.992	2	9	N-glycan processing	BP	1	FUT8,PRKCSH	down_VCAV_EC
GO:0055089	0.0688	0.993	2	7	fatty acid homeostasis	BP	0.874	NR1H4,APOE	down_VSAP_EC
GO:0030198	0.0688	0.998	1	81	extracellular matrix organization	BP	1	TGFBI	down_VSAP_VSMC
GO:0016358	0.0688	0.998	1	58	dendrite development	BP	1	WNT7A	up_AORT_VSMC
GO:0120093	0.0688	1	1	1	regulation of peptidyl-lysine crotonylation	BP	0.905	CDYL	up_VCAV_EC
GO:0120094	0.0688	1	1	1	negative regulation of peptidyl-lysine	BP	0.905	CDYL	up_VCAV_EC
GO:0140066	0.0688	1	1	1	peptidyl-lysine crotonylation	BP	0.905	CDYL	up_VCAV_EC
GO:0019233	0.0688	0.998	1	16	sensory perception of pain	BP	1	MME	up_VFEM_EC
GO:0010463	0.0688	0.998	1	28	mesenchymal cell proliferation	BP	1	SHOX2	up_VFEM_VSMC

GO:0006816	0.0689	0.969	9	84	calcium ion transport	BP	0.874	ERO1A,ATP2B1,REM1,CTNNB1,LYN,DDIT3,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0002695	0.0689	0.973	7	44	negative regulation of leukocyte activation	BP	0.905	ADGRF5,TNFAIP3,PELI1,ARG2,THOC1,CD200,HMGB1	up_VCAV_EC
GO:0048699	0.0689	0.982	4	371	generation of neurons	BP	1	EMX2,HOXC10,IRX5,SHOX2	up_VSAP_VSMC
GO:0070201	0.0689	0.986	3	187	regulation of establishment of protein	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0060348	0.0689	0.991	2	78	bone development	BP	1	SULF1,CSGALNACT1	down_ACOR_EC
GO:0001842	0.0689	0.998	1	3	neural fold formation	BP	1	LUZP1	up_AFEM_EC
GO:0001955	0.0689	0.998	1	3	blood vessel maturation	BP	1	RECK	up_AFEM_EC
GO:0042490	0.0689	0.998	1	19	mechanoreceptor differentiation	BP	1	NTRK2	up_APUL_EC
GO:0061572	0.0689	0.998	1	50	actin filament bundle organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0032413	0.0689	0.998	1	15	negative regulation of ion transmembrane transporter activity	BP	1	CAV1	up_VSAP_VSMC
GO:0098662	0.069	0.966	11	131	inorganic cation transmembrane transport	BP	1	PRNP,FXYD1,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SCARA5,CYBA,ARHGAP1	down_VCAV_EC
GO:0006937	0.069	0.985	3	40	regulation of muscle contraction	BP	1	CHRM2,TBXA2R,DMPK	up_AFEM_EC
GO:0030810	0.069	0.998	1	3	positive regulation of nucleotide biosynthetic	BP	1	PPARGC1A	up_AFEM_EC
GO:0050995	0.069	0.998	1	3	negative regulation of lipid catabolic process	BP	1	ACACB	up_AFEM_EC
GO:1900373	0.069	0.998	1	3	positive regulation of purine nucleotide	BP	1	PPARGC1A	up_AFEM_EC
GO:0034764	0.069	0.998	1	50	positive regulation of transmembrane transport	BP	1	CA2	up_VCAV_VSMC
GO:0006814	0.069	0.998	1	28	sodium ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0010770	0.069	0.998	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0006464	0.0691	0.945	108	1162	cellular protein modification process	BP	0.905	EPHB1,PLK2,TEK,HCLS1,ST8SIA6,KIT,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,PDE4D,IWS1,MEF2C,ATF3,TIPARP,RAPGEF1,TLR4,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,ZDHHC22,NEDD9,PELI1,YES1,ENSCAFG00000010893,EPHB4,B3GNT5,MTOR,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,ENSCAFG0000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,TLR3,MFNG,NCK1,ESCO1,DPH5,VHL,OTUD4,WSB1,PARP4,FES,NSD1,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,HMGB1,NOS2,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,KDM3A,LMTK2,ATRX,ZDHHC6,IVNS1ABP,JCAD,TET2,ARHGEF2,CDON	up_VCAV_EC
GO:0036211	0.0691	0.945	108	1162	protein modification process	BP	0.905	EPHB1,PLK2,TEK,HCLS1,ST8SIA6,KIT,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,PDE4D,IWS1,MEF2C,ATF3,TIPARP,RAPGEF1,TLR4,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,ZDHHC22,NEDD9,PELI1,YES1,ENSCAFG00000010893,EPHB4,B3GNT5,MTOR,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,ENSCAFG0000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,TLR3,MFNG,NCK1,ESCO1,DPH5,VHL,OTUD4,WSB1,PARP4,FES,NSD1,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,HMGB1,NOS2,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,KDM3A,LMTK2,ATRX,ZDHHC6,IVNS1ABP,JCAD,TET2,ARHGEF2,CDON	up_VCAV_EC
GO:0043648	0.0691	0.982	4	26	dicarboxylic acid metabolic process	BP	0.874	NR1H4,ALDH1L2,NMNAT2,ALDH18A1	down_VSAP_EC

GO:0045665	0.0691	0.991	2	55	negative regulation of neuron differentiation	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0046887	0.0691	0.998	1	18	positive regulation of hormone secretion	BP	1	NR1H4	up_APUL_EC
GO:0035050	0.0691	0.998	1	28	embryonic heart tube development	BP	1	NKX2-5	up_VPOR_VSMC
GO:1902202	0.069183983	0.99836	1	3	regulation of hepatocyte growth factor receptor	BP	1	ESM1	up_ACOR_EC
GO:0007204	0.0692	0.971	8	46	positive regulation of cytosolic calcium ion	BP	1	ADRA1B,PLCG2,HTR2B,ITPR1,F2RL1,PRKCE,CHD7,EDN1	up_ACOR_VSMC
GO:0042552	0.0692	0.976	6	30	myelination	BP	1	SH3TC2,MBP,WASF3,ATRN,DAG1,JAM3	up_ACOR_VSMC
GO:1903580	0.0692	0.993	2	5	positive regulation of ATP metabolic process	BP	1	PPARGC1A,PARK7	up_ACOR_VSMC
GO:0006452	0.0692	1	1	1	translational frameshifting	BP	1	EIF5A	down_ACOR_VSMC
GO:0045905	0.0692	1	1	1	positive regulation of translational termination	BP	1	EIF5A	down_ACOR_VSMC
GO:0001892	0.0692	0.998	1	35	embryonic placenta development	BP	1	CITED2	down_VPOR_EC
GO:0010243	0.0692	0.999	1	238	response to organonitrogen	BP	1	JUP	down_VFEM_VSMC
GO:0034350	0.0692	0.998	1	3	regulation of glial cell apoptotic process	BP	1	DLL1	up_AFEM_EC
GO:0034351	0.0692	0.998	1	3	negative regulation of glial cell apoptotic process	BP	1	DLL1	up_AFEM_EC
GO:0032652	0.0692	0.998	1	18	regulation of interleukin-1 production	BP	1	NR1H4	up_APUL_EC
GO:0031114	0.0692	0.998	1	9	regulation of microtubule depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0061337	0.0692	0.998	1	16	cardiac conduction	BP	1	CAV1	up_VSAP_VSMC
GO:0042592	0.0693	0.96	18	522	homeostatic process	BP	1	CMKLR1,HOXC10,LEP,CRY2,RAB20,DLL1,GPAM,MLLT11,NFE2L1,CYLD,CNNM4,RAB7A,ATP6V0B,ACACB,NAPEPLD,PPARGC1A,DMPK,GCNT4	up_AFEM_EC
GO:0055006	0.0693	0.982	4	18	cardiac cell development	BP	0.905	EDN1,MTOR,PROX1,JAG1	up_VCAV_EC
GO:0035270	0.0693	0.998	1	35	endocrine system development	BP	1	CITED2	down_VPOR_EC
GO:0086013	0.0693	1	1	1	membrane repolarization during cardiac muscle cell action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:0098915	0.0693	1	1	1	membrane repolarization during ventricular cardiac muscle cell action	BP	1	KCNE3	up_ACOR_VSMC
GO:0106135	0.0693	1	1	1	negative regulation of cardiac muscle cell	BP	1	KCNE3	up_ACOR_VSMC
GO:1902302	0.0693	1	1	1	regulation of potassium ion export	BP	1	KCNE3	up_ACOR_VSMC
GO:1902303	0.0693	1	1	1	negative regulation of potassium ion export	BP	1	KCNE3	up_ACOR_VSMC
GO:1903764	0.0693	1	1	1	regulation of potassium ion export across plasma	BP	1	KCNE3	up_ACOR_VSMC
GO:1903765	0.0693	1	1	1	negative regulation of potassium ion export across plasma membrane	BP	1	KCNE3	up_ACOR_VSMC
GO:1903946	0.0693	1	1	1	negative regulation of ventricular cardiac muscle cell action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:1905024	0.0693	1	1	1	regulation of membrane repolarization during ventricular cardiac muscle cell action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:1905025	0.0693	1	1	1	negative regulation of membrane repolarization during ventricular cardiac muscle cell action	BP	1	KCNE3	up_ACOR_VSMC
GO:1905031	0.0693	1	1	1	regulation of membrane repolarization during cardiac muscle cell action	BP	1	KCNE3	up_ACOR_VSMC
GO:1905032	0.0693	1	1	1	negative regulation of membrane repolarization during cardiac muscle cell	BP	1	KCNE3	up_ACOR_VSMC
GO:0002315	0.0693	0.998	1	3	marginal zone B cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:1990523	0.0693	0.998	1	3	bone regeneration	BP	1	LGR6	up_AFEM_EC
GO:0021520	0.0693	0.998	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	up_AFEM_EC

GO:0070602	0.0693	0.998	1	3	regulation of centromeric sister chromatid cohesion	BP	1	AXIN2	up_AFEM_EC
GO:0033030	0.0693	1	1	1	negative regulation of neutrophil apoptotic	BP	0.905	ITPKB	up_VCAV_EC
GO:0045806	0.0693	0.998	1	15	negative regulation of endocytosis	BP	1	CAV1	up_VSAP_VSMC
GO:0051603	0.0694	0.956	25	305	proteolysis involved in cellular protein catabolic process	BP	0.874	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,TRIB3,SEL1L,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,USP48,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0007166	0.0694	0.976	6	686	cell surface receptor signaling pathway	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0070098	0.0694	0.987	3	14	chemokine-mediated signaling pathway	BP	0.905	ACKR1,CXCL8,CXCR4	up_VCAV_EC
GO:0072711	0.0694	0.993	2	5	cellular response to hydroxyurea	BP	1	RAD51,TIMELESS	down_ACOR_VSMC
GO:0009891	0.0694	0.993	2	521	positive regulation of biosynthetic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0033145	0.0694	0.993	2	5	positive regulation of intracellular steroid hormone receptor	BP	1	SKP2,PARK7	up_ACOR_VSMC
GO:0042481	0.0694	0.993	2	5	regulation of odontogenesis	BP	1	BMP4,TNFRSF11B	up_ACOR_VSMC
GO:0036316	0.0694	1	1	1	SREBP-SCAP complex retention in endoplasmic	BP	1	INSIG1	down_ACOR_VSMC
GO:1901303	0.0694	1	1	1	negative regulation of cargo loading into COPII-	BP	1	INSIG1	down_ACOR_VSMC
GO:2000638	0.0694	1	1	1	regulation of SREBP signaling pathway	BP	1	INSIG1	down_ACOR_VSMC
GO:2000639	0.0694	1	1	1	negative regulation of SREBP signaling pathway	BP	1	INSIG1	down_ACOR_VSMC
GO:0070166	0.0694	0.998	1	3	enamel mineralization	BP	1	CNNM4	up_AFEM_EC
GO:0070661	0.0694	0.998	1	63	leukocyte proliferation	BP	1	ARG2	up_AORT_VSMC
GO:1990138	0.0694	0.998	1	35	neuron projection extension	BP	1	SLIT2	up_VPUL_VSMC
GO:0007589	0.0694	0.998	1	16	body fluid secretion	BP	1	CAV1	up_VSAP_VSMC
GO:0090087	0.0695	0.985	3	185	regulation of peptide transport	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0006767	0.0695	0.987	3	12	water-soluble vitamin metabolic process	BP	1	PDXP,GSTO1,ENSCAFG00000005637	down_ACOR_VSMC
GO:0051336	0.0695	0.986	3	251	regulation of hydrolase activity	BP	1	PCSK1N,NPNT,NTRK2	up_APUL_EC
GO:1902903	0.0695	0.991	2	125	regulation of supramolecular fiber	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0043537	0.0695	0.998	1	15	negative regulation of blood vessel endothelial	BP	1	ACVRL1	down_ACOR_EC
GO:0045638	0.0695	0.998	1	33	negative regulation of myeloid cell	BP	1	GABPA	down_AFEM_EC
GO:0007517	0.0695	0.998	1	100	muscle organ development	BP	1	TBX5	up_APUL_VSMC
GO:1904888	0.0696	0.981	4	31	cranial skeletal system development	BP	1	TBX15,GLI3,IRX5,RDH10	down_VCAV_EC
GO:0042509	0.0696	0.986	3	17	regulation of tyrosine phosphorylation of STAT	BP	0.874	PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0032876	0.0696	0.993	2	5	negative regulation of DNA endoreduplication	BP	1	SMC1A,SMC3	down_ACOR_VSMC
GO:0018209	0.0696	0.991	2	125	peptidyl-serine modification	BP	1	STK32B,PTGER2	up_VPUL_EC
GO:0050654	0.0696	0.998	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	CSGALNACT1	down_ACOR_EC
GO:0009650	0.0696	0.998	1	3	UV protection	BP	1	MFAP4	up_AFEM_EC
GO:0035930	0.0696	0.998	1	3	corticosteroid hormone secretion	BP	1	CRY2	up_AFEM_EC
GO:0035933	0.0696	0.998	1	3	glucocorticoid secretion	BP	1	CRY2	up_AFEM_EC
GO:1901525	0.0696	0.998	1	3	negative regulation of mitophagy	BP	1	CLEC16A	up_AFEM_EC
GO:1902459	0.0696	0.998	1	3	positive regulation of stem cell population	BP	1	LBH	up_AFEM_EC
GO:2000832	0.0696	0.998	1	3	negative regulation of steroid hormone	BP	1	CRY2	up_AFEM_EC
GO:2000846	0.0696	0.998	1	3	regulation of corticosteroid hormone	BP	1	CRY2	up_AFEM_EC
GO:2000847	0.0696	0.998	1	3	negative regulation of corticosteroid hormone	BP	1	CRY2	up_AFEM_EC

GO:2000849	0.0696	0.998	1	3	regulation of glucocorticoid secretion	BP	1	CRY2	up_AFEM_EC
GO:2000850	0.0696	0.998	1	3	negative regulation of glucocorticoid secretion	BP	1	CRY2	up_AFEM_EC
GO:0051055	0.0696	0.998	1	21	negative regulation of lipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0044088	0.069664821	0.99124	2	17	regulation of vacuole organization	BP	1	CHMP4B,VPS16	up_ACOR_EC
GO:0033365	0.0697	0.957	23	276	protein localization to organelle	BP	0.874	PRICKLE1,HSPA5,TRAM1,HOOK3,SESN2,SRP54,MSN,ZPR1,SRPRA,KPNB1,SRP72,KPNA4,DDIT3,GSK3B,GBP5,SH3GLB1,KPNA1,KDELR2,SIX4,CDKN1A,NRP1,ARF4,MID1	down_VSAP_EC
GO:1903078	0.0697	0.986	3	19	positive regulation of protein localization to	BP	1	LRP1,PRNP,CLIP3	down_VCAV_EC
GO:0032060	0.0697	0.993	2	6	bleb assembly	BP	1	ANLN,EMP2	down_ACOR_VSMC
GO:0043584	0.0697	0.993	2	5	nose development	BP	0.905	CHD7,ALDH1A3	up_VCAV_EC
GO:0045061	0.0697	0.993	2	6	thymic T cell selection	BP	0.905	GATA3,ITPKB	up_VCAV_EC
GO:0042509	0.0697	0.998	1	17	regulation of tyrosine phosphorylation of STAT	BP	1	LYN	down_ACOR_EC
GO:0060512	0.0697	0.998	1	14	prostate gland morphogenesis	BP	1	SULF1	down_ACOR_EC
GO:0006487	0.0697	0.998	1	34	protein N-linked glycosylation	BP	1	MGAT4B	down_VPOR_EC
GO:0060509	0.0697	0.998	1	3	type I pneumocyte differentiation	BP	1	THRB	up_AFEM_EC
GO:0071493	0.0697	0.998	1	3	cellular response to UV-B	BP	1	MFAP4	up_AFEM_EC
GO:2000726	0.0697	0.998	1	3	negative regulation of cardiac muscle cell	BP	1	DLL1	up_AFEM_EC
GO:0071772	0.0697	0.998	1	50	response to BMP	BP	1	GATA5	up_VCAV_VSMC
GO:0071773	0.0697	0.998	1	50	cellular response to BMP stimulus	BP	1	GATA5	up_VCAV_VSMC
GO:0007338	0.0697	0.998	1	16	single fertilization	BP	1	HOXA9	up_VFEM_EC
GO:0048844	0.0697	0.998	1	30	artery morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0006626	0.0698	0.978	5	29	protein targeting to mitochondrion	BP	1	SREBF1,TIMM44,TOMM34,SAMM50,PMPCA	down_ACOR_VSMC
GO:2000310	0.0698	0.994	2	4	regulation of NMDA receptor activity	BP	0.905	RELN,MEF2C	up_VCAV_EC
GO:0016024	0.0698	0.998	1	3	CDP-diacylglycerol biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:0046341	0.0698	0.998	1	3	CDP-diacylglycerol metabolic process	BP	1	GPAM	up_AFEM_EC
GO:0006766	0.0698	0.998	1	16	vitamin metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0042310	0.0698	0.998	1	21	vasoconstriction	BP	1	HTR7	up_VPUL_EC
GO:0097756	0.0698	0.998	1	21	negative regulation of blood vessel diameter	BP	1	HTR7	up_VPUL_EC
GO:0007530	0.0699	0.993	2	5	sex determination	BP	1	CITED2,PTGDR	up_ACOR_VSMC
GO:0097529	0.0699	0.991	2	52	myeloid leukocyte migration	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:1900028	0.0699	0.998	1	3	negative regulation of ruffle assembly	BP	1	KANK1	up_AFEM_EC
GO:0006924	0.0699	0.998	1	3	activation-induced cell death of T cells	BP	1	GPAM	up_AFEM_EC
GO:0019336	0.0699	0.998	1	3	phenol-containing compound catabolic	BP	1	MOXD1	up_AFEM_EC
GO:0019614	0.0699	0.998	1	3	catechol-containing compound catabolic	BP	1	MOXD1	up_AFEM_EC
GO:0042420	0.0699	0.998	1	3	dopamine catabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0042424	0.0699	0.998	1	3	catecholamine catabolic process	BP	1	MOXD1	up_AFEM_EC
GO:2001214	0.0699	0.998	1	3	positive regulation of vasculogenesis	BP	1	TMEM100	up_AFEM_EC
GO:0021859	0.069952341	0.99833	1	3	pyramidal neuron differentiation	BP	1	DCLK2	up_ACOR_EC
GO:0021860	0.069952341	0.99833	1	3	pyramidal neuron development	BP	1	DCLK2	up_ACOR_EC
GO:0044272	0.07	0.975	6	35	sulfur compound biosynthetic process	BP	1	ACLY,XYLT1,ELOVL1,ELOVL6,CTH,PDHA1	down_ACOR_VSMC
GO:0050663	0.07	0.998	1	52	cytokine secretion	BP	1	TLR2	up_AFEM_VSMC

GO:0051651	0.07	0.998	1	31	maintenance of location in cell	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0097530	0.07	0.998	1	33	granulocyte migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0019883	0.0701	0.993	2	5	antigen processing and presentation of endogenous antigen	BP	1	B2M,ERAP1	up_ACOR_VSMC
GO:0006024	0.0701	0.998	1	16	glycosaminoglycan biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0019395	0.0701	0.998	1	33	fatty acid oxidation	BP	1	ETFA	down_AFEM_EC
GO:0003257	0.0701	0.998	1	3	positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	up_AFEM_EC
GO:0042104	0.0701	0.998	1	3	positive regulation of activated T cell	BP	1	GPAM	up_AFEM_EC
GO:0051446	0.0701	0.998	1	3	positive regulation of meiotic cell cycle	BP	1	OVOL1	up_AFEM_EC
GO:0051346	0.0702	0.965	12	78	negative regulation of hydrolase activity	BP	1	TNNT2,RECK,SH3RF2,CST3,SH3RF1,MARF1,PPP1R26,SPINK2,SH3BP4,PARK7,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0046104	0.0702	1	1	1	thymidine metabolic process	BP	1	TK1	down_ACOR_VSMC
GO:0046125	0.0702	1	1	1	pyrimidine deoxyribonucleoside	BP	1	TK1	down_ACOR_VSMC
GO:0007271	0.0702	0.998	1	3	synaptic transmission, cholinergic	BP	1	CHRM2	up_AFEM_EC
GO:0033600	0.0702	1	1	1	negative regulation of mammary gland epithelial	BP	0.905	GATA3	up_VCAV_EC
GO:0035799	0.0702	1	1	1	ureter maturation	BP	0.905	GATA3	up_VCAV_EC
GO:0060995	0.0702	1	1	1	cell-cell signaling involved in kidney development	BP	0.905	GATA3	up_VCAV_EC
GO:0061289	0.0702	1	1	1	Wnt signaling pathway involved in kidney	BP	0.905	GATA3	up_VCAV_EC
GO:0061290	0.0702	1	1	1	canonical Wnt signaling pathway involved in metanephric kidney	BP	0.905	GATA3	up_VCAV_EC
GO:0071442	0.0702	1	1	1	positive regulation of histone H3-K14	BP	0.905	GATA3	up_VCAV_EC
GO:0071481	0.0702	1	1	1	cellular response to X-ray	BP	0.905	GATA3	up_VCAV_EC
GO:0072204	0.0702	1	1	1	cell-cell signaling involved in metanephros	BP	0.905	GATA3	up_VCAV_EC
GO:1901536	0.0702	1	1	1	negative regulation of DNA demethylation	BP	0.905	GATA3	up_VCAV_EC
GO:1905277	0.0702	1	1	1	negative regulation of epithelial tube formation	BP	0.905	GATA3	up_VCAV_EC
GO:2000606	0.0702	1	1	1	regulation of cell proliferation involved in mesonephros	BP	0.905	GATA3	up_VCAV_EC
GO:2000607	0.0702	1	1	1	negative regulation of cell proliferation involved in mesonephros	BP	0.905	GATA3	up_VCAV_EC
GO:2000683	0.0702	1	1	1	regulation of cellular response to X-ray	BP	0.905	GATA3	up_VCAV_EC
GO:2000699	0.0702	1	1	1	fibroblast growth factor receptor signaling pathway involved in	BP	0.905	GATA3	up_VCAV_EC
GO:2000701	0.0702	1	1	1	glial cell-derived neurotrophic factor receptor signaling pathway involved in	BP	0.905	GATA3	up_VCAV_EC
GO:2000702	0.0702	1	1	1	regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud	BP	0.905	GATA3	up_VCAV_EC
GO:2000703	0.0702	1	1	1	negative regulation of fibroblast growth factor receptor signaling pathway involved in	BP	0.905	GATA3	up_VCAV_EC
GO:2000733	0.0702	1	1	1	regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in	BP	0.905	GATA3	up_VCAV_EC

GO:2000734	0.0702	1	1	1	negative regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in	BP	0.905	GATA3	up_VCAV_EC
GO:0010573	0.0702	0.998	1	9	vascular endothelial growth factor production	BP	1	C3AR1	up_VPOR_EC
GO:0010574	0.0702	0.998	1	9	regulation of vascular endothelial growth factor	BP	1	C3AR1	up_VPOR_EC
GO:0032623	0.0702	0.998	1	21	interleukin-2 production	BP	1	NR1H4	up_VPUL_EC
GO:0050663	0.0703	0.971	8	52	cytokine secretion	BP	0.905	GBP5,FERMT1,TLR4,GATA3,ARG2,ABCA1,HMGB1,NOS2	up_VCAV_EC
GO:0006278	0.0703	0.978	5	26	RNA-dependent DNA biosynthetic process	BP	1	SLC29A1,AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0007004	0.0703	0.978	5	26	telomere maintenance via telomerase	BP	1	SLC29A1,AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0031297	0.0703	0.982	4	18	replication fork processing	BP	1	RAD51,TONSL,SMARCAL1,GEN1	down_ACOR_VSMC
GO:0050768	0.0703	0.98	4	66	negative regulation of neurogenesis	BP	1	IRX3,DLL1,THRB,KANK1	up_AFEM_EC
GO:0044275	0.0703	0.987	3	10	cellular carbohydrate catabolic process	BP	1	ENOSF1,PYGM,GAA	up_ACOR_VSMC
GO:0022604	0.0703	0.985	3	122	regulation of cell morphogenesis	BP	1	ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0072498	0.0703	0.992	2	8	embryonic skeletal joint development	BP	0.874	CTNNB1,EXT1	down_VSAP_EC
GO:0150065	0.0703	0.993	2	5	regulation of deacetylase activity	BP	0.905	PRKD2,KDM5A	up_VCAV_EC
GO:0030309	0.0703	1	1	1	poly-N-acetyllactosamine metabolic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:0030311	0.0703	1	1	1	poly-N-acetyllactosamine biosynthetic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:0001843	0.0703	0.998	1	38	neural tube closure	BP	1	CITED2	down_VPOR_EC
GO:0001921	0.0703	0.998	1	3	positive regulation of receptor recycling	BP	1	BVES	up_AFEM_EC
GO:0032693	0.0703	0.998	1	3	negative regulation of interleukin-10 production	BP	1	DLL1	up_AFEM_EC
GO:0097006	0.0703	0.998	1	19	regulation of plasma lipoprotein particle levels	BP	1	NR1H4	up_APUL_EC
GO:0051239	0.070325301	0.95385	30	859	regulation of multicellular organismal process	BP	1	CDH3,NR1H4,BRSK1,PLCL1,SOX9,NDRG2,AQP1,FZD5,GNAO1,DIXDC1,NOD2,IL33,RGMA,SMAD6,PLS1,RNLS,PTGDS,PAK3,PTGER4,ARHGDIB,MAVS,FOXC2,TBX5,LRP4,CLSTN1,NRP1,AGPAT2,PRKCD,PYGO2,EFEMP1	up_ACOR_EC
GO:2000145	0.0704	0.985	3	279	regulation of cell motility	BP	1	TBX5,CCL24,ARHGEF2	up_VPUL_EC
GO:0022613	0.0704	0.991	2	208	ribonucleoprotein complex biogenesis	BP	1	EIF3M,SRSF6	down_AFEM_EC
GO:0009713	0.0704	0.993	2	5	catechol-containing compound biosynthetic	BP	1	MOXD1,PARK7	up_ACOR_VSMC
GO:0042423	0.0704	0.993	2	5	catecholamine biosynthetic process	BP	1	MOXD1,PARK7	up_ACOR_VSMC
GO:0050651	0.0704	0.998	1	3	dermatan sulfate proteoglycan biosynthetic	BP	1	CSGALNACT2	up_AFEM_EC
GO:0045617	0.0704	0.998	1	3	negative regulation of keratinocyte	BP	1	HOXA7	up_AFEM_EC
GO:0051930	0.0704	0.998	1	3	regulation of sensory perception of pain	BP	1	TMEM100	up_AFEM_EC
GO:0051931	0.0704	0.998	1	3	regulation of sensory perception	BP	1	TMEM100	up_AFEM_EC
GO:0043330	0.0704	0.998	1	16	response to exogenous dsRNA	BP	1	CAV1	up_VSAP_VSMC
GO:0035904	0.0705	0.978	5	25	aorta development	BP	0.905	ADAMTS9,CHD7,DLL4,PROX1,JAG1	up_VCAV_EC
GO:0048736	0.0705	0.98	4	66	appendage development	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0060173	0.0705	0.98	4	66	limb development	BP	1	HOXA9,HOXC10,GREM1,RECK	up_AFEM_EC
GO:0000186	0.0705	0.987	3	10	activation of MAPKK activity	BP	1	BMP4,PSEN1,MAP3K7	up_ACOR_VSMC
GO:2000737	0.0705	0.992	2	7	negative regulation of stem cell differentiation	BP	0.874	PRICKLE1,REST	down_VSAP_EC
GO:0001501	0.0705	0.991	2	178	skeletal system development	BP	1	HOXA3,CYP26B1	up_VPOR_VSMC
GO:0050767	0.0705	0.991	2	184	regulation of neurogenesis	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0045656	0.0705	0.998	1	3	negative regulation of monocyte differentiation	BP	1	HOXA7	up_AFEM_EC

GO:0072047	0.0705	0.998	1	3	proximal/distal pattern formation involved in	BP	1	IRX3	up_AFEM_EC
GO:0072081	0.0705	0.998	1	3	specification of nephron tubule identity	BP	1	IRX3	up_AFEM_EC
GO:1901605	0.0705	0.998	1	67	alpha-amino acid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0006367	0.0705	0.998	1	32	transcription initiation from RNA polymerase II	BP	1	NKX2-5	up_VPOR_VSMC
GO:0045667	0.0706	0.973	7	38	regulation of osteoblast differentiation	BP	1	SMAD6,RASSF2,BMP4,GJA1,CLSTN1,NPNT,DDR2	up_ACOR_VSMC
GO:0048844	0.0706	0.975	6	30	artery morphogenesis	BP	1	BMP4,SEC24B,CITED2,NRP1,CHD7,HPGD	up_ACOR_VSMC
GO:0030325	0.0706	0.993	2	5	adrenal gland development	BP	1	WNT11,CITED2	up_VSAP_EC
GO:0090191	0.0706	0.998	1	3	negative regulation of branching involved in ureteric bud	BP	1	GREM1	up_AFEM_EC
GO:0048592	0.0706	0.998	1	53	eye morphogenesis	BP	1	IRX5	up_AFEM_VSMC
GO:0046167	0.0706	1	1	1	glycerol-3-phosphate biosynthetic process	BP	0.905	GK5	up_VCAV_EC
GO:0035725	0.0706	0.998	1	16	sodium ion transmembrane transport	BP	1	NETO1	up_VSAP_VSMC
GO:0001780	0.0707	0.993	2	6	neutrophil homeostasis	BP	0.905	ITPKB,HMGB1	up_VCAV_EC
GO:2001243	0.0707	0.998	1	33	negative regulation of intrinsic apoptotic	BP	1	IVNS1ABP	down_AFEM_EC
GO:0051240	0.0707	1	1	489	positive regulation of multicellular organismal	BP	1	GATA5	down_AFEM_VSMC
GO:0051336	0.0707	0.999	1	251	regulation of hydrolase activity	BP	1	CST3	down_AORT_EC
GO:0043435	0.0707	1	1	1	response to corticotropin-releasing hormone	BP	0.874	NR4A1	down_VSAP_EC
GO:0071376	0.0707	1	1	1	cellular response to corticotropin-releasing	BP	0.874	NR4A1	down_VSAP_EC
GO:0060216	0.0707	0.998	1	3	definitive hemopoiesis	BP	1	HOXA9	up_AFEM_EC
GO:0043255	0.0707	0.998	1	29	regulation of carbohydrate biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0030239	0.0707	0.998	1	21	myofibril assembly	BP	1	MYBPC2	up_VPUL_EC
GO:2000736	0.0707	0.998	1	21	regulation of stem cell differentiation	BP	1	TBX5	up_VPUL_EC
GO:0032637	0.0708	0.978	5	26	interleukin-8 production	BP	0.905	PRKD2,TLR3,BCL10,NOS2,RIPK1	up_VCAV_EC
GO:0051051	0.0708	0.991	2	112	negative regulation of transport	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0051561	0.0708	0.993	2	6	positive regulation of mitochondrial calcium ion concentration	BP	0.905	MCU,ATP2A1	up_VCAV_EC
GO:0051136	0.0708	0.993	2	5	regulation of NK T cell differentiation	BP	1	ZBTB16,TGFBR2	up_VSAP_EC
GO:1904672	0.0708	0.998	1	3	regulation of somatic stem cell population	BP	1	LBH	up_AFEM_EC
GO:0001824	0.0709	0.978	5	27	blastocyst development	BP	1	GINS4,NEK2,SMARCB1,RBBP8,EMG1	down_ACOR_VSMC
GO:0051560	0.0709	0.987	3	12	mitochondrial calcium ion homeostasis	BP	0.905	PDZD8,MCU,ATP2A1	up_VCAV_EC
GO:0009117	0.0709	0.991	2	208	nucleotide metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0070233	0.0709	0.992	2	9	negative regulation of T cell apoptotic process	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0010628	0.0709	0.993	2	527	positive regulation of gene expression	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0042692	0.0709	0.991	2	105	muscle cell differentiation	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:1903044	0.0709	0.998	1	3	protein localization to membrane raft	BP	1	REEP2	up_AFEM_EC
GO:0001885	0.0709	0.998	1	19	endothelial cell development	BP	1	ARHGEF26	up_APUL_EC
GO:0043242	0.0709	0.998	1	21	negative regulation of protein complex	BP	1	ARHGEF2	up_VPUL_EC
GO:0048519	0.071	0.979	6	1554	negative regulation of biological process	BP	1	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0009206	0.071	0.977	5	39	purine ribonucleoside triphosphate biosynthetic	BP	0.874	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0006592	0.071	1	1	1	ornithine biosynthetic process	BP	0.874	ALDH18A1	down_VSAP_EC
GO:0140115	0.071	0.998	1	3	export across plasma membrane	BP	1	FXYD1	up_AFEM_EC

GO:0072507	0.071	0.998	1	103	divalent inorganic cation homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0071606	0.071	1	1	1	chemokine (C-C motif) ligand 4 production	BP	0.905	ARG2	up_VCAV_EC
GO:0071608	0.071	1	1	1	macrophage inflammatory protein-1	BP	0.905	ARG2	up_VCAV_EC
GO:0071640	0.071	1	1	1	regulation of macrophage inflammatory protein 1 alpha production	BP	0.905	ARG2	up_VCAV_EC
GO:0071641	0.071	1	1	1	negative regulation of macrophage inflammatory protein 1	BP	0.905	ARG2	up_VCAV_EC
GO:0071643	0.071	1	1	1	regulation of chemokine (C-C motif) ligand 4	BP	0.905	ARG2	up_VCAV_EC
GO:0071644	0.071	1	1	1	negative regulation of chemokine (C-C motif)	BP	0.905	ARG2	up_VCAV_EC
GO:1905076	0.071	1	1	1	regulation of interleukin-17 secretion	BP	0.905	ARG2	up_VCAV_EC
GO:1905077	0.071	1	1	1	negative regulation of interleukin-17 secretion	BP	0.905	ARG2	up_VCAV_EC
GO:1905403	0.071	1	1	1	negative regulation of activated CD8-positive, alpha-beta T cell	BP	0.905	ARG2	up_VCAV_EC
GO:2000666	0.071	1	1	1	negative regulation of interleukin-13 secretion	BP	0.905	ARG2	up_VCAV_EC
GO:0006110	0.071	0.998	1	9	regulation of glycolytic process	BP	1	FBP1	up_VPOR_EC
GO:0030811	0.071	0.998	1	9	regulation of nucleotide catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0043470	0.071	0.998	1	9	regulation of carbohydrate catabolic	BP	1	FBP1	up_VPOR_EC
GO:0032984	0.0711	0.967	10	70	protein-containing complex disassembly	BP	1	CAPG,LIMA1,STMN1,SMARCC1,EIF5A,PDXP,SMARCB1,GRWD1,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0021515	0.0711	0.992	2	9	cell differentiation in spinal cord	BP	1	LMO4,GLI3	down_VCAV_EC
GO:0044249	0.0711	1	2	1851	cellular biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0007213	0.0711	0.993	2	5	G protein-coupled acetylcholine receptor	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:0034141	0.0711	0.993	2	5	positive regulation of toll-like receptor 3 signaling	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0007034	0.0711	0.991	2	55	vacuolar transport	BP	1	HOOK3,GCC2	up_VPOR_EC
GO:2001253	0.0711	1	1	1	regulation of histone H3-K36 trimethylation	BP	0.874	IWS1	down_VSAP_EC
GO:0051901	0.0711	0.998	1	3	positive regulation of mitochondrial	BP	1	MLLT11	up_AFEM_EC
GO:1904181	0.0711	0.998	1	3	positive regulation of membrane depolarization	BP	1	MLLT11	up_AFEM_EC
GO:0060538	0.0711	0.998	1	51	skeletal muscle organ development	BP	1	BEND2	up_AFEM_VSMC
GO:0055017	0.0711	0.998	1	19	cardiac muscle tissue growth	BP	1	TBX5	up_APUL_EC
GO:0042692	0.0711	0.998	1	105	muscle cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0010939	0.0711	0.998	1	9	regulation of necrotic cell death	BP	1	ARHGEF2	up_VPOR_EC
GO:0070861	0.0711	0.998	1	9	regulation of protein exit from endoplasmic	BP	1	GCC2	up_VPOR_EC

GO:0050789	0.0712	0.942	214	3295	regulation of biological process	BP	0.874	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,CELF1,ASNS,MYH9,NR1H4,FMNL3,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,MEIS2,SGK1,ERO1A,PRKACB,PTPN14,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CBX5,CASP3,FAM49B,ENSCAFG00000003477,HYOU1,PGK1,AKAP2,WSB1,BCAR3,NUAK1,PTPN11,FSCN1,AARS,DPYSL3,LRRC8A,HOOK3,TRIB3,PGAM1,IFRD1,FARP1,TMED2,PUM3,PM20D2,FBLIM1,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,REM1,WDR1,MYO1C,PIK3C2A,CHSY1,MSN,UACA,HOXB7,KIF5B,LMAN1,HIF1A,CX3CL1,ENSCAFG00000000562,DYNLL1,SLC45A3,TUBB,IWS1,THBS2,DNAJC10,YIPF5,ACTG2,TNIK,NAA10,NXN,RGS2,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,EIF2B1,EVI2B,PVR,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,ESM1,DDX39B,ADAM17,AGRN,ACTA2,BRD2,EIF4EBP1,SKAP2,UST,PDIA4,CNOT7,CDH11,ACTR3,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,ANLN,CRYAB,STARD13,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,PTP4A1,WWC3,PDE1A,ZC3H15,IGFBP7,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,FAM162A,BACH1,CCNYL1,PLEKHG2,TLN1,EIF5,MMD	down_VSAP_EC
GO:0071214	0.0712	0.964	12	93	cellular response to abiotic stimulus	BP	0.906	LRRC8D,GATA3,FIGNL1,TMEM150C,CASP8,MAPK13,TLR3,PTGS2,BCL10,USP28,BLM,ARHGEF2	up_VCAV_EC
GO:0104004	0.0712	0.964	12	93	cellular response to environmental stimulus	BP	0.906	LRRC8D,GATA3,FIGNL1,TMEM150C,CASP8,MAPK13,TLR3,PTGS2,BCL10,USP28,BLM,ARHGEF2	up_VCAV_EC
GO:2000345	0.0712	0.993	2	5	regulation of hepatocyte proliferation	BP	1	LIMS2,SULF2	up_VSAP_EC
GO:0043039	0.0712	0.998	1	33	tRNA aminoacylation	BP	1	DARS	down_AFEM_EC
GO:0061041	0.0712	0.998	1	34	regulation of wound healing	BP	1	SRSF6	down_AFEM_EC
GO:0002248	0.0712	1	1	1	connective tissue replacement involved in inflammatory response	BP	0.874	HIF1A	down_VSAP_EC
GO:0002069	0.0712	1	1	1	columnar/cuboidal epithelial cell maturation	BP	0.874	HIF1A	down_VSAP_EC
GO:0051541	0.0712	1	1	1	elastin metabolic process	BP	0.874	HIF1A	down_VSAP_EC
GO:0060574	0.0712	1	1	1	intestinal epithelial cell maturation	BP	0.874	HIF1A	down_VSAP_EC
GO:0061030	0.0712	1	1	1	epithelial cell differentiation involved in mammary gland alveolus	BP	0.874	HIF1A	down_VSAP_EC
GO:0007021	0.0712	0.998	1	3	tubulin complex assembly	BP	1	CRYAB	up_AFEM_EC
GO:0001738	0.0712	0.998	1	27	morphogenesis of a polarized epithelium	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030216	0.0712	0.998	1	29	keratinocyte differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048640	0.0712	0.998	1	21	negative regulation of developmental growth	BP	1	TBX5	up_VPUL_EC
GO:1904659	0.071290267	0.98483	3	36	glucose transmembrane transport	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0043254	0.0713	0.961	15	164	regulation of protein complex assembly	BP	0.874	VEGFA,PTPN11,FSCN1,FBLIM1,ANKRA2,MSN,ACTR3,CTNNB1,CRYAB,APOE,TWF1,PLEKHG2,GSK3B,GBP5,CAPG	down_VSAP_EC
GO:0022029	0.0713	0.978	5	23	telencephalon cell migration	BP	1	FGF13,NRP1,PSEN1,DISC1,SUN1	up_ACOR_VSMC
GO:2001256	0.0713	0.993	2	5	regulation of store-operated calcium entry	BP	1	SARAF,STC2	up_ACOR_VSMC
GO:0050920	0.0713	0.991	2	53	regulation of chemotaxis	BP	1	C3AR1,SEMA3A	up_VPOR_EC
GO:0035624	0.0713	1	1	1	receptor transactivation	BP	0.874	ADAM17	down_VSAP_EC
GO:0051088	0.0713	1	1	1	PMA-inducible membrane protein ectodomain	BP	0.874	ADAM17	down_VSAP_EC
GO:0071403	0.0713	1	1	1	cellular response to high density lipoprotein	BP	0.874	ADAM17	down_VSAP_EC
GO:0050999	0.0713	0.998	1	9	regulation of nitric-oxide synthase activity	BP	1	ACVR2A	up_VPOR_EC
GO:2001257	0.0713	0.998	1	30	regulation of cation channel activity	BP	1	NETO1	up_VFEM_VSMC

GO:0070304	0.071310322	0.98017	4	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	FZD5,NOD2,TNFRSF19,SH3RF3	up_ACOR_EC
GO:0043549	0.0714	0.956	21	244	regulation of kinase activity	BP	0.874	VEGFA,SOCS5,ERRFI1,PTPN11,TRIB3,SESN2,TNIK,PTPN2,ADAM17,MAGED1,APOE,LYN,CCNYL1,MMD,CBLC,VLDLR,SH3GLB1,HTT,PAK2,CDKN1A,MADD	down_VSAP_EC
GO:0070663	0.0714	0.974	6	50	regulation of leukocyte proliferation	BP	0.874	CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0021782	0.0714	0.978	5	23	glial cell development	BP	1	SH3TC2,WASF3,DAG1,APP,PSEN1	up_ACOR_VSMC
GO:0002009	0.0714	0.985	3	177	morphogenesis of an epithelium	BP	1	ACVRL1,PDPN,SULF1	down_ACOR_EC
GO:0009948	0.0714	0.986	3	16	anterior/posterior axis specification	BP	0.874	TMED2,CTNNB1,DDIT3	down_VSAP_EC
GO:0045935	0.0714	1	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0051892	0.0714	1	1	1	negative regulation of cardioblast differentiation	BP	0.874	PRICKLE1	down_VSAP_EC
GO:2000690	0.0714	1	1	1	regulation of cardiac muscle cell myoblast	BP	0.874	PRICKLE1	down_VSAP_EC
GO:2000691	0.0714	1	1	1	negative regulation of cardiac muscle cell myoblast differentiation	BP	0.874	PRICKLE1	down_VSAP_EC
GO:0006813	0.071414465	0.98478	3	37	potassium ion transport	BP	1	KCNB1,ACTN2,SLC9A9	up_ACOR_EC
GO:0019755	0.071463191	0.99825	1	3	one-carbon compound transport	BP	1	AQP1	up_ACOR_EC
GO:0009790	0.0715	0.955	23	335	embryo development	BP	1	SDC4,FBN1,BMPR1A,LMO4,RECK,COL6A1,NAGLU,TBX15,HOXC4,LAMA3,SEMA3C,TEAD1,TLX2,GLI3,ZFP36L1,IFT57,LOXL3,IRX5,PRKCSH,RDH10,PCSK6,GREM1,ZBTB16	down_VCAV_EC
GO:0050877	0.0715	0.956	22	164	nervous system process	BP	1	FGF13,MBP,COCH,HRH1,LRRN4,WASF3,GLRB,GPR155,TMEM108,USP53,ABCA4,DMPK,POMK,APP,PSEN1,CHD7,CLN8,FAM107A,INSYN1,JAM3,GAA,WFS1	up_ACOR_VSMC
GO:0072657	0.0715	0.962	13	144	protein localization to membrane	BP	0.874	TRAM1,EXOC5,SRP54,MYO1C,KIF5B,SSR1,TNIK,SRPRA,AGRN,SRP72,APOE,SH3GLB1,BLZF1	down_VSAP_EC
GO:0030852	0.0715	0.992	2	6	regulation of granulocyte differentiation	BP	0.909	HCLS1,CUL4A	up_VCAV_EC
GO:0010557	0.0715	1	1	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0045667	0.0715	0.998	1	38	regulation of osteoblast differentiation	BP	1	HDAC7	down_VPOR_EC
GO:1900084	0.0715	0.998	1	3	regulation of peptidyl-tyrosine	BP	1	GREM1	up_AFEM_EC
GO:0010927	0.0715	0.998	1	28	cellular component assembly involved in	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048167	0.0715	0.998	1	28	regulation of synaptic plasticity	BP	1	NETO1	up_VFEM_VSMC
GO:0098657	0.0716	0.961	14	181	import into cell	BP	1	SNX18,LRP1,PRNP,FOLR2,CLIP3,SLC39A6,ANXA11,LRPAP1,CLTB,PARK7,CYBA,RAB31,GREM1,PACSIN3	down_VCAV_EC
GO:0010647	0.0716	0.977	5	460	positive regulation of cell communication	BP	1	ACVRL1,LYN,SULF1,STX4,NEDD4	down_ACOR_EC
GO:0060996	0.0716	0.981	4	26	dendritic spine development	BP	0.874	UBA6,APOE,PAK2,ARF4	down_VSAP_EC
GO:0048662	0.0716	0.982	4	18	negative regulation of smooth muscle cell	BP	1	PTGIR,NDRG2,CDKN1A,CLSTN1	up_ACOR_VSMC
GO:0060041	0.0716	0.985	3	41	retina development in camera-type eye	BP	1	IRX5,DLL1,THRB	up_AFEM_EC
GO:0048878	0.0716	0.985	3	283	chemical homeostasis	BP	1	HOXA3,NR1H4,NEO1	up_VPUL_EC
GO:0007266	0.0717	0.967	10	64	Rho protein signal transduction	BP	1	ARHGEF5,ARHGEF6,ABL1,CDC42EP5,CDC42EP2,F2RL1,TIAM1,DLC1,FGD4,FLOT1	up_VSAP_EC
GO:0032006	0.0717	0.968	9	52	regulation of TOR signaling	BP	1	LEP,PRKAA2,CASTOR1,UBR1,SESN3,SESN1,DDIT4,BMT2,SH3BP4	up_ACOR_VSMC
GO:1902652	0.0717	0.972	7	38	secondary alcohol metabolic process	BP	1	LEP,LCAT,ABCA1,LIPE,APP,CLN8,LMF1	up_ACOR_VSMC
GO:0010638	0.0717	0.991	2	207	positive regulation of organelle organization	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0001568	0.0717	0.999	1	252	blood vessel development	BP	1	JUP	down_VFEM_VSMC
GO:0110111	0.0717	0.998	1	17	negative regulation of animal organ	BP	1	SIX1	up_VFEM_EC
GO:0006140	0.0717	0.998	1	28	regulation of nucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC

GO:0050866	0.0718	0.974	6	48	negative regulation of cell activation	BP	0.874	SOCS5,PTPN2,APOE,LYN,SDC4,BTK	down_VSAP_EC
GO:0051094	0.0718	0.992	2	388	positive regulation of developmental process	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0002260	0.0718	0.998	1	15	lymphocyte homeostasis	BP	1	LYN	down_ACOR_EC
GO:0055072	0.0718	0.998	1	30	iron ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0015691	0.0718	1	1	1	cadmium ion transport	BP	0.91	SLC39A8	up_VCAV_EC
GO:0070574	0.0718	1	1	1	cadmium ion transmembrane transport	BP	0.91	SLC39A8	up_VCAV_EC
GO:0045604	0.0718	0.998	1	17	regulation of epidermal cell differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0050886	0.0718	0.998	1	17	endocrine process	BP	1	AVPR1A	up_VFEM_EC
GO:0045655	0.0719	0.992	2	9	regulation of monocyte differentiation	BP	1	CLSTN1,ZFP36L1	down_VCAV_EC
GO:0072073	0.0719	0.998	1	60	kidney epithelium development	BP	1	ARG2	up_AORT_VSMC
GO:0003281	0.0719	0.998	1	30	ventricular septum development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060541	0.072	0.971	7	73	respiratory system development	BP	1	ADAMTS2,BMPR1A,LOX,GLI3,LOXL3,RDH10,THRB	down_VCAV_EC
GO:0048519	0.072	0.976	7	1554	negative regulation of biological process	BP	1	CHL1,HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0048583	0.072	0.974	7	1095	regulation of response to stimulus	BP	1	NR1H4,RGS1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0046323	0.072	0.981	4	26	glucose import	BP	0.874	NR1H4,ENPP1,PTPN11,SESN2	down_VSAP_EC
GO:0042417	0.072	0.992	2	9	dopamine metabolic process	BP	1	MAOA,PARK7	down_VCAV_EC
GO:0110110	0.072	0.998	1	34	positive regulation of animal organ	BP	1	SRSF6	down_AFEM_EC
GO:0007368	0.072	0.998	1	37	determination of left/right symmetry	BP	1	CITED2	down_VPOR_EC
GO:0045597	0.072	0.999	1	253	positive regulation of cell differentiation	BP	1	GATA5	down_VFEM_VSMC
GO:0000041	0.072	0.998	1	31	transition metal ion transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0050865	0.0721	0.964	11	135	regulation of cell activation	BP	1	GPAM,PRNP,SDC4,LMO4,THY1,GLI3,ZFP36L1,BPI,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0045445	0.0721	0.981	4	27	myoblast differentiation	BP	0.874	PRICKLE1,DDIT3,REST,HIF1AN	down_VSAP_EC
GO:0032526	0.0721	0.981	4	19	response to retinoic acid	BP	0.91	TIE1,PPARG,YES1,ABCA1	up_VCAV_EC
GO:1902893	0.0721	0.981	4	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	0.91	PDGFB,BMP2,SMARCA4,HIF1A	up_VCAV_EC
GO:0007188	0.0721	0.984	3	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	CHRM2,HTR1D,PTHLH	up_AFEM_EC
GO:0035051	0.0721	0.985	3	41	cardiocyte differentiation	BP	1	DLL1,GREM1,BVES	up_AFEM_EC
GO:0001568	0.0721	0.985	3	252	blood vessel development	BP	1	HOXA3,NTRK2,HOXA1	up_APUL_EC
GO:0032102	0.0721	0.998	1	67	negative regulation of response to external	BP	1	ARG2	up_AORT_VSMC
GO:0090257	0.0721	0.998	1	52	regulation of muscle system process	BP	1	GATA5	up_VCAV_VSMC
GO:0060688	0.0721	0.998	1	29	regulation of morphogenesis of a	BP	1	SHOX2	up_VFEM_VSMC
GO:0044106	0.072131067	0.99075	2	17	cellular amine metabolic process	BP	1	NR1H4,AZIN2	up_ACOR_EC
GO:0072073	0.0722	0.968	9	60	kidney epithelium development	BP	0.91	HOXB7,PODXL,MEF2C,GATA3,MTSS1,ARG2,BMP2,JAG1,BASP1	up_VCAV_EC
GO:0043123	0.0722	0.97	8	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	MAP3K14,ABL1,F2RL1,RBCK1,MYD88,S100A4,ENSCAFG00000011993,TRADD	up_VSAP_EC
GO:0035023	0.0722	0.974	6	46	regulation of Rho protein signal transduction	BP	0.874	ARHGEF2,FARP1,APOE,PLEKHG2,NRP1,TNFAIP1	down_VSAP_EC
GO:0042325	0.0722	0.981	4	463	regulation of phosphorylation	BP	1	CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0070848	0.0722	0.985	3	193	response to growth factor	BP	1	ACVRL1,SULF1,ASPN	down_ACOR_EC
GO:0043009	0.0722	0.991	2	227	chordate embryonic development	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0018105	0.0722	0.99	2	116	peptidyl-serine phosphorylation	BP	1	PLCL1,NTRK2	up_APUL_EC
GO:0016458	0.0722	0.998	1	59	gene silencing	BP	1	ESR1	up_AORT_VSMC

GO:1903037	0.0722	0.998	1	65	regulation of leukocyte cell-cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0048486	0.0722	0.998	1	10	parasympathetic nervous system development	BP	1	SEMA3A	up_VPOR_EC
GO:0006023	0.0722	0.998	1	17	aminoglycan biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:0008654	0.0723	0.969	8	58	phospholipid biosynthetic process	BP	0.91	ADGRF5,PDGFB,SPTLC2,SAMD8,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0090128	0.0723	0.993	2	5	regulation of synapse maturation	BP	0.91	ARHGEF15,RELN	up_VCAV_EC
GO:0060606	0.0723	0.998	1	39	tube closure	BP	1	CITED2	down_VPOR_EC
GO:0046034	0.0723	0.998	1	88	ATP metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0060759	0.0723	0.998	1	37	regulation of response to cytokine stimulus	BP	1	SLIT2	up_VPUL_VSMC
GO:0046847	0.072338342	0.99071	2	17	filopodium assembly	BP	1	NRP1,PRKCD	up_ACOR_EC
GO:0032989	0.0724	0.951	33	292	cellular component morphogenesis	BP	0.91	EPHB1,TEK,IL7R,KIT,IFRD1,RELN,MEF2C,STC1,GATA3,EDN1,RAB11A,ARAP3,NEDD9,TMOD1,PPP3CA,NECTIN2,PREX2,PDZD8,PROX1,ENSCAFG00000010224,STMN1,FLNB,SNX2,FES,RAPGEF2,CREB1,FMNL3,SPTBN4,ALS2,ENSCAFG00000002015,TMOD3,ARHGEF2,ZMYM2	up_VCAV_EC
GO:0002573	0.0724	0.965	11	71	myeloid leukocyte differentiation	BP	1	HOXA7,PPARGC1B,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,TFE3,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0061326	0.0724	0.984	3	41	renal tubule development	BP	1	IRX3,DLL1,GREM1	up_AFEM_EC
GO:0072080	0.0724	0.984	3	41	nephron tubule development	BP	1	IRX3,DLL1,GREM1	up_AFEM_EC
GO:1905906	0.0724	0.993	2	5	regulation of amyloid fibril formation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0032922	0.0724	0.991	2	19	circadian regulation of gene expression	BP	1	CRY2,PPARGC1A	up_AFEM_EC
GO:0098957	0.0724	1	1	1	anterograde axonal transport of	BP	0.874	TRAK1	down_VSAP_EC
GO:0032663	0.0724	0.998	1	19	regulation of interleukin-2 production	BP	1	NR1H4	up_APUL_EC
GO:0002065	0.0724	0.998	1	37	columnar/cuboidal epithelial cell	BP	1	GATA5	up_VPUL_VSMC
GO:0023056	0.0725	0.977	5	462	positive regulation of signaling	BP	1	ACVRL1,LYN,SULF1,STX4,NEDD4	down_ACOR_EC
GO:0048666	0.0725	0.985	3	258	neuron development	BP	1	MAPK10,SLITRK5,NTRK2	up_APUL_EC
GO:0042060	0.0725	0.99	2	103	wound healing	BP	1	CAV1,F5	up_VSAP_VSMC
GO:0019827	0.0725	0.998	1	59	stem cell population maintenance	BP	1	WNT7A	up_AORT_VSMC
GO:0021545	0.0725	0.998	1	21	cranial nerve development	BP	1	HOXA3	up_VPUL_EC
GO:0120163	0.0725	0.998	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_VSAP_VSMC
GO:0019318	0.0726	0.969	8	75	hexose metabolic process	BP	0.874	ENPP1,TPI1,PGAM1,SESN2,SLC45A3,PTPN2,ATF3,GALE	down_VSAP_EC
GO:0070509	0.0726	0.981	4	21	calcium ion import	BP	0.91	PDGFB,STC1,MCU,ATP2A1	up_VCAV_EC
GO:1901655	0.0726	0.985	3	20	cellular response to ketone	BP	1	ADCY6,NR3C1,PARK7	down_VCAV_EC
GO:0007628	0.0726	0.986	3	11	adult walking behavior	BP	1	FXN,CTNS,HTRA2	up_VSAP_EC
GO:0006753	0.0726	0.991	2	211	nucleoside phosphate metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0006423	0.0726	1	1	1	cysteinyl-tRNA aminoacylation	BP	0.874	CARS	down_VSAP_EC
GO:0043122	0.0727	0.966	10	62	regulation of I-kappaB kinase/NF-kappaB signaling	BP	1	MAP3K14,ABL1,F2RL1,RBCK1,MYD88,S100A4,NLRX1,ENSCAFG00000011993,MAPKBP1,TRADD	up_VSAP_EC
GO:0044271	0.0727	0.985	4	1501	cellular nitrogen compound biosynthetic	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0007340	0.0727	0.993	2	5	acrosome reaction	BP	1	GLRB,SPINK2	up_ACOR_VSMC
GO:0080134	0.0727	0.992	2	386	regulation of response to stress	BP	1	ARG2,ESR1	up_AORT_VSMC
GO:0060341	0.0727	0.999	1	255	regulation of cellular localization	BP	1	JUP	down_VFEM_VSMC
GO:0061817	0.0727	1	1	1	endoplasmic reticulum-plasma membrane	BP	0.874	ESYT3	down_VSAP_EC
GO:0001659	0.0727	0.998	1	54	temperature homeostasis	BP	1	HOXC10	up_AFEM_VSMC

GO:0002793	0.0727	0.998	1	54	positive regulation of peptide secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0050714	0.0727	0.998	1	54	positive regulation of protein secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0071466	0.0727	0.998	1	17	cellular response to xenobiotic stimulus	BP	1	CYP26B1	up_VFEM_EC
GO:0007405	0.0727	0.998	1	21	neuroblast proliferation	BP	1	ARHGEF2	up_VPUL_EC
GO:0035137	0.0727	0.998	1	18	hindlimb morphogenesis	BP	1	PITX1	up_VSAP_VSMC
GO:0098655	0.0728	0.957	19	142	cation transmembrane transport	BP	1	ACTN2,PLCG2,KCNE3,HTR2B,PTPN3,MICU2,ITPR1,DAPK1,CACNB3,AKAP6,KCNJ4,PRKCE,CHD7,ATP6V0E1,KCNC4,FXYD1,NDUFA4L2,PARK7,SLC8A1	up_ACOR_VSMC
GO:0051271	0.0728	0.965	10	98	negative regulation of cellular component	BP	0.874	SULF1,SERPINE1,ACTN1,DPYSL3,STARD13,APOE,MMP28,STRAP,ZMYND8,NRP1	down_VSAP_EC
GO:0010762	0.0728	0.991	2	9	regulation of fibroblast migration	BP	1	SDC4,DDR2	down_VCAV_EC
GO:0001755	0.0728	0.998	1	16	neural crest cell migration	BP	1	NRP2	down_ACOR_EC
GO:0010629	0.0728	1	1	502	negative regulation of gene expression	BP	1	GATA5	down_AFEM_VSMC
GO:0002063	0.0728	0.998	1	18	chondrocyte development	BP	1	SHOX2	up_VSAP_VSMC
GO:0071895	0.072858025	0.99818	1	3	odontoblast differentiation	BP	1	DLX3	up_ACOR_EC
GO:0050896	0.0729	0.947	65	2346	response to stimulus	BP	1	CMKLR1,MT2A,LEP,LBH,CRY2,ENSCAFG00000009113,RAB20,GAS1,F5,ANGPT4,CD40,DLL1,CRYAB,CPNE7,CTSS,F3,PLXNA4,BPI,GPAM,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,SLC17A5,MFAP4,HCK,TMEM100,PLAGL2,GREM1,HTR1D,NFE2L1,FAM53B,AVPR1A,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,RECK,NR3C1,PTHLH,TBXA2R,DCUN1D3,TFPI2,BVES,LGR6,ACKR4,RAB7A,AXIN2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,DMPK,ADAM17,KANK1,TNC,ANXA11,SOD1	up_AFEM_EC
GO:0009895	0.0729	0.976	5	94	negative regulation of catabolic process	BP	1	LEP,TENT5C,CLEC16A,AXIN2,ACACB	up_AFEM_EC
GO:0048522	0.0729	0.985	4	1484	positive regulation of cellular process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:1901861	0.0729	0.984	3	41	regulation of muscle tissue development	BP	1	DLL1,GREM1,PPARGC1A	up_AFEM_EC
GO:0042493	0.0729	0.991	2	178	response to drug	BP	1	FBP1,EMX2	up_VFEM_VSMC
GO:0072329	0.0729	0.998	1	34	monocarboxylic acid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0032642	0.0729	0.998	1	22	regulation of chemokine production	BP	1	NR1H4	up_VPUL_EC
GO:0031325	0.073	0.943	88	914	positive regulation of cellular metabolic process	BP	0.91	PLK2,TEK,HCLS1,ADGRF5,KIT,SELE,PPP2R5A,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,MEF2C,ATF3,CHD7,TLR4,NLRC5,GATA3,EDN1,RALB,APLNR,RAB27A,TCF4,FOXN2,ENSCAFG00000017103,NEDD9,IRF8,PELI1,PPP3CA,YES1,SPTLC2,CASP8,MTOR,MAP3K3,BMP2,HHEX,CREM,SLK,CNOT6,PROX1,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,LDB2,JAG1,NSD1,PTGS2,MMD,RAPGEF2,PLCG2,BCL10,TAOK1,CNOT7,HMGB1,AHR,NOS2,PMAIP1,BLM,RIPK1,ITGA6,GPBP1,PDGFD,MTA2,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,JCAD,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0032386	0.073	0.962	13	137	regulation of intracellular transport	BP	0.874	PLK3,PTPN14,PTPN11,PPP1R12A,MYO1C,MSN,IWS1,YIPF5,ZPR1,CRYAB,LYN,GSK3B,CDKN1A	down_VSAP_EC
GO:0044843	0.073	0.971	7	62	cell cycle G1/S phase transition	BP	0.874	PLK3,ZPR1,EIF4EBP1,BACH1,RBBP8,INHBA,CDKN1A	down_VSAP_EC
GO:0006887	0.073	0.99	2	99	exocytosis	BP	1	LYN,STX4	down_ACOR_EC
GO:1901576	0.073	1	2	1877	organic substance biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0030166	0.073	0.99	2	19	proteoglycan biosynthetic process	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC
GO:0006023	0.073	0.997	1	17	aminoglycan biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:1904375	0.073	0.998	1	35	regulation of protein localization to cell	BP	1	GPSM2	down_AFEM_EC

GO:0120162	0.073	0.997	1	31	positive regulation of cold-induced thermogenesis	BP	1	GATM	up_VFEM_VSMC
GO:0015718	0.073	0.998	1	30	monocarboxylic acid transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:0007154	0.0731	0.969	10	1622	cell communication	BP	1	NR1H4,TBX5,MAPK10,HTR7,PLCL1,ARHGEF26,SLITRK5,NPNT,NTRK2,PDE1A	up_APUL_EC
GO:0006289	0.0731	0.974	6	35	nucleotide-excision repair	BP	1	RPA1,POLE,NEIL3,RBBP8,RAD23A,HMGN1	down_ACOR_VSMC
GO:1905477	0.0731	0.98	4	32	positive regulation of protein localization to	BP	1	LRP1,PRNP,CLIP3,AKT2	down_VCAV_EC
GO:0030856	0.0731	0.984	3	41	regulation of epithelial cell differentiation	BP	1	HOXA7,DLL1,TMEM100	up_AFEM_EC
GO:1903531	0.0731	0.984	3	41	negative regulation of secretion by cell	BP	1	LEP,CRY2,RAB7A	up_AFEM_EC
GO:0048261	0.0731	0.993	2	5	negative regulation of receptor-mediated	BP	1	ATXN2,LRPAP1	up_ACOR_VSMC
GO:0007155	0.0731	0.991	2	324	cell adhesion	BP	1	GATA5,TGFBI	up_VCAV_VSMC
GO:0061061	0.0731	0.991	2	179	muscle structure development	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0042692	0.0731	0.99	2	105	muscle cell differentiation	BP	1	STIM1,SHOX2	up_VSAP_VSMC
GO:0038190	0.0731	1	1	1	VEGF-activated neuropilin signaling pathway	BP	0.874	NRP1	down_VSAP_EC
GO:0048842	0.0731	1	1	1	positive regulation of axon extension involved in axon guidance	BP	0.874	NRP1	down_VSAP_EC
GO:0061441	0.0731	1	1	1	renal artery morphogenesis	BP	0.874	NRP1	down_VSAP_EC
GO:1902336	0.0731	1	1	1	positive regulation of retinal ganglion cell axon	BP	0.874	NRP1	down_VSAP_EC
GO:1902378	0.0731	1	1	1	VEGF-activated neuropilin signaling pathway involved in axon guidance	BP	0.874	NRP1	down_VSAP_EC
GO:1902669	0.0731	1	1	1	positive regulation of axon guidance	BP	0.874	NRP1	down_VSAP_EC
GO:1905040	0.0731	1	1	1	otic placode development	BP	0.874	NRP1	down_VSAP_EC
GO:0060560	0.0731	0.998	1	58	developmental growth involved in	BP	1	ESR1	up_AORT_VSMC
GO:0032612	0.0731	0.997	1	22	interleukin-1 production	BP	1	NR1H4	up_VPUL_EC
GO:0032008	0.0732	0.99	2	19	positive regulation of TOR signaling	BP	1	LEP,CLEC16A	up_AFEM_EC
GO:0042759	0.0732	1	1	1	long-chain fatty acid biosynthetic process	BP	1	ELOVL6	down_ACOR_VSMC
GO:0098930	0.0733	0.985	3	17	axonal transport	BP	0.874	HIF1A,TRAK1,AP3S1	down_VSAP_EC
GO:0038083	0.0733	0.985	3	16	peptidyl-tyrosine autophosphorylation	BP	0.874	VEGFA,LYN,BTK	down_VSAP_EC
GO:0051173	0.0733	0.987	3	874	positive regulation of nitrogen compound	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0045070	0.0733	0.992	2	8	positive regulation of viral genome replication	BP	0.874	CNOT7,RAD23A	down_VSAP_EC
GO:0046697	0.0733	0.993	2	5	decidualization	BP	1	CITED2,CTSB	up_ACOR_VSMC
GO:0060396	0.0733	0.993	2	5	growth hormone receptor signaling pathway	BP	1	STAT5A,PIK3R1	up_VSAP_EC
GO:0060416	0.0733	0.993	2	5	response to growth hormone	BP	1	STAT5A,PIK3R1	up_VSAP_EC
GO:0071378	0.0733	0.993	2	5	cellular response to growth hormone stimulus	BP	1	STAT5A,PIK3R1	up_VSAP_EC
GO:0043038	0.0733	0.997	1	34	amino acid activation	BP	1	DARS	down_AFEM_EC
GO:0002218	0.0733	0.998	1	53	activation of innate immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0015718	0.0733	0.997	1	30	monocarboxylic acid transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0072006	0.073330503	0.97941	4	59	nephron development	BP	1	SOX9,AQP1,FOXC2,CLSTN1	up_ACOR_EC

GO:0009893	0.0734	0.942	95	995	positive regulation of metabolic process	BP	0.91	PLK2,TEK,HCLS1,IL7R,ADGRF5,KIT,SELE,PPP2R5A,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,MEF2C,ATF3,CHD7,TIPARP,DLL4,TLR4,NLRC5,GATA3,EDN1,RALB,APLNR,RAB27A,TCF4,FOXN2,ENSCAFG00000017103,NEDD9,IRF8,PELI1,PPP3CA,YES1,SPTLC2,CASP8,MTOR,MAP3K3,BMP2,HHEX,CREM,SLK,CNOT6,PROX1,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,LDB2,JAG1,NSD1,PTGS2,MMD,RAPGEF2,PLCG2,CREB1,BCL10,TAOK1,CNOT7,GCH1,ADIPOR2,HMGB1,AHR,NOS2,PMAIP1,BLM,RIPK1,ITGA6,GPBP1,PDGFD,MTA2,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ENSCAFG00000002015,JCAD,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0006412	0.0734	0.957	18	245	translation	BP	1	UBA52,LARP6,COA1,SAMD4B,RPL23,RPL13,EIF3K,MRPL37,RPL27A,EEF2,ZFP36L1,RPL27,MRPS11,RPS27,ENSCAFG00000015122,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0051252	0.0734	0.969	9	1051	regulation of RNA metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0071214	0.0734	0.99	2	93	cellular response to abiotic stimulus	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0104004	0.0734	0.99	2	93	cellular response to environmental stimulus	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0031644	0.0734	0.99	2	19	regulation of neurological system process	BP	1	TMEM100,DMPK	up_AFEM_EC
GO:0060560	0.0734	0.99	2	58	developmental growth involved in	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0008584	0.0734	0.997	1	39	male gonad development	BP	1	CITED2	down_VPOR_EC
GO:0046546	0.0734	0.997	1	39	development of primary male sexual	BP	1	CITED2	down_VPOR_EC
GO:1900543	0.0734	0.998	1	9	negative regulation of purine nucleotide	BP	1	FBP1	up_VPOR_EC
GO:1903579	0.0734	0.998	1	9	negative regulation of ATP metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0051155	0.0734	0.997	1	18	positive regulation of striated muscle cell	BP	1	CYP26B1	up_VFEM_EC
GO:0021987	0.0734	0.998	1	37	cerebral cortex development	BP	1	SLIT2	up_VPUL_VSMC
GO:2000514	0.0735	0.986	3	13	regulation of CD4-positive, alpha-beta T cell	BP	0.91	GATA3,ARG2,HMGB1	up_VCAV_EC
GO:0060449	0.0735	0.993	2	5	bud elongation involved in lung branching	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0038066	0.0735	0.99	2	19	p38MAPK cascade	BP	1	LEP,CYLD	up_AFEM_EC
GO:0071163	0.0735	1	1	1	DNA replication preinitiation complex	BP	1	GMNN	down_ACOR_VSMC
GO:0003183	0.073508341	0.99815	1	3	mitral valve morphogenesis	BP	1	SMAD6	up_ACOR_EC
GO:0070295	0.073564911	0.99814	1	3	renal water absorption	BP	1	AQP1	up_ACOR_EC
GO:0002064	0.0736	0.968	8	71	epithelial cell development	BP	0.874	FLNB,MSN,HIF1A,ACTA2,CTNNB1,PLOD3,KLF5,MYO1E	down_VSAP_EC
GO:0048699	0.0736	0.991	2	371	generation of neurons	BP	1	HOXC10,WNT7A	up_AORT_VSMC
GO:0046427	0.0736	0.997	1	16	positive regulation of JAK-STAT cascade	BP	1	LYN	down_ACOR_EC
GO:0030505	0.0736	1	1	1	inorganic diphosphate transport	BP	0.874	ENPP1	down_VSAP_EC
GO:0035426	0.0736	1	1	1	extracellular matrix-cell signaling	BP	0.91	NTN4	up_VCAV_EC
GO:0060668	0.0736	1	1	1	regulation of branching involved in salivary gland morphogenesis by extracellular matrix-	BP	0.91	NTN4	up_VCAV_EC
GO:1901879	0.0737	0.98	4	26	regulation of protein depolymerization	BP	0.874	ARHGEF2,WDR1,CAPG,MID1	down_VSAP_EC
GO:1905207	0.0737	0.981	4	17	regulation of cardiocyte differentiation	BP	1	BMP4,TBX5,FRS2,EDN1	up_ACOR_VSMC
GO:0001708	0.0737	0.985	3	20	cell fate specification	BP	1	BMPR1A,LMO4,GLI3	down_VCAV_EC
GO:0002028	0.0737	0.99	2	19	regulation of sodium ion transport	BP	1	FXYD1,DMPK	up_AFEM_EC
GO:0034375	0.0737	0.993	2	5	high-density lipoprotein particle remodeling	BP	1	LIPC,LCAT	up_VSAP_EC

GO:0007498	0.0737	0.997	1	38	mesoderm development	BP	1	CITED2	down_VPOR_EC
GO:0007403	0.0737	1	1	1	glial cell fate determination	BP	0.874	CTNNB1	down_VSAP_EC
GO:0010908	0.0737	1	1	1	regulation of heparan sulfate proteoglycan	BP	0.874	CTNNB1	down_VSAP_EC
GO:0010909	0.0737	1	1	1	positive regulation of heparan sulfate proteoglycan biosynthetic	BP	0.874	CTNNB1	down_VSAP_EC
GO:0021781	0.0737	1	1	1	glial cell fate commitment	BP	0.874	CTNNB1	down_VSAP_EC
GO:0044334	0.0737	1	1	1	canonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal	BP	0.874	CTNNB1	down_VSAP_EC
GO:0055059	0.0737	1	1	1	asymmetric neuroblast division	BP	0.874	ARHGEF2	down_VSAP_EC
GO:0060769	0.0737	1	1	1	positive regulation of epithelial cell proliferation involved in prostate gland	BP	0.874	CTNNB1	down_VSAP_EC
GO:0060789	0.0737	1	1	1	hair follicle placode formation	BP	0.874	CTNNB1	down_VSAP_EC
GO:0061198	0.0737	1	1	1	fungiform papilla formation	BP	0.874	CTNNB1	down_VSAP_EC
GO:0061324	0.0737	1	1	1	canonical Wnt signaling pathway involved in positive regulation of cardiac outflow tract cell	BP	0.874	CTNNB1	down_VSAP_EC
GO:0072053	0.0737	1	1	1	renal inner medulla development	BP	0.874	CTNNB1	down_VSAP_EC
GO:0072054	0.0737	1	1	1	renal outer medulla development	BP	0.874	CTNNB1	down_VSAP_EC
GO:0072383	0.0737	1	1	1	plus-end-directed vesicle transport along	BP	0.874	KIF5B	down_VSAP_EC
GO:0072386	0.0737	1	1	1	plus-end-directed organelle transport along	BP	0.874	KIF5B	down_VSAP_EC
GO:1902730	0.0737	1	1	1	positive regulation of proteoglycan biosynthetic	BP	0.874	CTNNB1	down_VSAP_EC
GO:1904499	0.0737	1	1	1	regulation of chromatin-mediated maintenance of	BP	0.874	CTNNB1	down_VSAP_EC
GO:1904501	0.0737	1	1	1	positive regulation of chromatin-mediated maintenance of	BP	0.874	CTNNB1	down_VSAP_EC
GO:1904793	0.0737	1	1	1	regulation of euchromatin binding	BP	0.874	CTNNB1	down_VSAP_EC
GO:2000017	0.0737	1	1	1	positive regulation of determination of dorsal	BP	0.874	CTNNB1	down_VSAP_EC
GO:0098727	0.0737	0.998	1	60	maintenance of cell number	BP	1	WNT7A	up_AORT_VSMC
GO:1905521	0.0737	0.998	1	9	regulation of macrophage migration	BP	1	C3AR1	up_VPOR_EC
GO:0055024	0.0737	0.997	1	22	regulation of cardiac muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0032092	0.0737	0.997	1	38	positive regulation of protein binding	BP	1	HOXA3	up_VPUL_VSMC
GO:0080090	0.0738	0.982	5	1734	regulation of primary metabolic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0034765	0.0738	0.99	2	91	regulation of ion transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0014821	0.0738	0.993	2	5	phasic smooth muscle contraction	BP	1	HTR2B,EDN1	up_ACOR_VSMC
GO:0015909	0.0738	0.997	1	16	long-chain fatty acid transport	BP	1	ACSL3	down_ACOR_EC
GO:0051602	0.0738	1	1	1	response to electrical stimulus	BP	0.874	REST	down_VSAP_EC
GO:0061110	0.0738	1	1	1	dense core granule biogenesis	BP	0.874	REST	down_VSAP_EC
GO:0071257	0.0738	1	1	1	cellular response to electrical stimulus	BP	0.874	REST	down_VSAP_EC
GO:1903381	0.0738	1	1	1	regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic signaling pathway	BP	0.874	HYOU1	down_VSAP_EC
GO:1903382	0.0738	1	1	1	negative regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic	BP	0.874	HYOU1	down_VSAP_EC
GO:2000705	0.0738	1	1	1	regulation of dense core granule biogenesis	BP	0.874	REST	down_VSAP_EC

GO:2000706	0.0738	1	1	1	negative regulation of dense core granule	BP	0.874	REST	down_VSAP_EC
GO:2000740	0.0738	1	1	1	negative regulation of mesenchymal stem cell differentiation	BP	0.874	REST	down_VSAP_EC
GO:2000797	0.0738	1	1	1	regulation of amniotic stem cell differentiation	BP	0.874	REST	down_VSAP_EC
GO:2000798	0.0738	1	1	1	negative regulation of amniotic stem cell	BP	0.874	REST	down_VSAP_EC
GO:0036483	0.0738	1	1	1	neuron intrinsic apoptotic signaling pathway in response to endoplasmic	BP	0.874	HYOU1	down_VSAP_EC
GO:0097086	0.0738	1	1	1	amniotic stem cell differentiation	BP	0.874	REST	down_VSAP_EC
GO:0120163	0.073847257	0.99041	2	17	negative regulation of cold-induced	BP	1	PLCL1,FOXC2	up_ACOR_EC
GO:0051241	0.0739	0.954	23	336	negative regulation of multicellular organismal process	BP	1	DCN,PRNP,VASN,FBN1,BMPR1A,CHID1,PLCL1,ASPN,LRPAP1,THY1,TLX2,GLI3,ZFP36L1,BPI,LOXL3,SPRED1,TSC22D3,TWIST2,PRKCSH,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0040012	0.0739	0.955	21	303	regulation of locomotion	BP	1	PDGFRB,DCN,SDC4,GLIPR2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,LAMA3,TRIM8,SEMA3C,THY1,SASH1,SPRED1,TWIST2,DDR2,RAC2,FOXO3	down_VCAV_EC
GO:0031214	0.0739	0.976	5	45	biomineral tissue development	BP	1	BMPR1A,ASPN,DDR2,OMD,GREM1	down_VCAV_EC
GO:0014074	0.0739	0.977	5	26	response to purine-containing compound	BP	0.91	P2RX7,SELL,RAPGEF1,RAPGEF2,P2RX2	up_VCAV_EC
GO:0090279	0.0739	0.991	2	8	regulation of calcium ion import	BP	0.874	CTNNB1,HOMER1	down_VSAP_EC
GO:0055026	0.0739	0.993	2	5	negative regulation of cardiac muscle tissue	BP	1	TBX5,FRS2	up_ACOR_VSMC
GO:0022610	0.0739	0.991	2	326	biological adhesion	BP	1	GATA5,TGFBI	up_VCAV_VSMC
GO:0034440	0.0739	0.997	1	35	lipid oxidation	BP	1	ETFA	down_AFEM_EC
GO:0006664	0.0739	0.997	1	37	glycolipid metabolic process	BP	1	GBGT1	down_VPOR_EC
GO:1903509	0.0739	0.997	1	37	liposaccharide metabolic process	BP	1	GBGT1	down_VPOR_EC
GO:0031529	0.0739	0.997	1	20	ruffle organization	BP	1	ARHGEF26	up_APUL_EC
GO:0048246	0.0739	0.998	1	9	macrophage chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:1901631	0.0739	1	1	1	positive regulation of presynaptic membrane	BP	1	LRP4	up_VSAP_EC
GO:1903911	0.0739	1	1	1	positive regulation of receptor clustering	BP	1	LRP4	up_VSAP_EC
GO:1904395	0.0739	1	1	1	positive regulation of skeletal muscle acetylcholine-gated	BP	1	LRP4	up_VSAP_EC
GO:1904398	0.0739	1	1	1	positive regulation of neuromuscular junction development	BP	1	LRP4	up_VSAP_EC
GO:0009914	0.074	0.965	10	64	hormone transport	BP	1	LEP,TM7SF3,PRKCE,SCG5,CHD7,CCL5,RAB11B,EDN1,PFKL,PARK7	up_ACOR_VSMC
GO:0022408	0.074	0.971	7	44	negative regulation of cell-cell adhesion	BP	0.91	PODXL,PELI1,ARG2,BMP2,SWAP70,JAG1,HMGB1	up_VCAV_EC
GO:0010812	0.074	0.99	2	19	negative regulation of cell-substrate adhesion	BP	1	HOXA7,KANK1	up_AFEM_EC
GO:0007079	0.074	1	1	1	mitotic chromosome movement towards	BP	0.874	KPNB1	down_VSAP_EC
GO:0009256	0.074	1	1	1	10-formyltetrahydrofolate metabolic process	BP	0.874	ALDH1L2	down_VSAP_EC
GO:0009258	0.074	1	1	1	10-formyltetrahydrofolate catabolic process	BP	0.874	ALDH1L2	down_VSAP_EC
GO:0009397	0.074	1	1	1	folic acid-containing compound catabolic	BP	0.874	ALDH1L2	down_VSAP_EC
GO:0021764	0.074	1	1	1	amygdala development	BP	0.874	UBA6	down_VSAP_EC
GO:0042560	0.074	1	1	1	pteridine-containing compound catabolic	BP	0.874	ALDH1L2	down_VSAP_EC
GO:0051014	0.074	1	1	1	actin filament severing	BP	0.874	MYH9	down_VSAP_EC
GO:0051305	0.074	1	1	1	chromosome movement towards spindle pole	BP	0.874	KPNB1	down_VSAP_EC
GO:0097498	0.074	1	1	1	endothelial tube lumen extension	BP	0.874	STARD13	down_VSAP_EC
GO:1900756	0.074	1	1	1	protein processing in phagocytic vesicle	BP	0.874	MYH9	down_VSAP_EC

GO:1903918	0.074	1	1	1	regulation of actin filament severing	BP	0.874	MYH9	down_VSAP_EC
GO:1903919	0.074	1	1	1	negative regulation of actin filament severing	BP	0.874	MYH9	down_VSAP_EC
GO:1903921	0.074	1	1	1	regulation of protein processing in phagocytic	BP	0.874	MYH9	down_VSAP_EC
GO:1903923	0.074	1	1	1	positive regulation of protein processing in	BP	0.874	MYH9	down_VSAP_EC
GO:0001979	0.074	1	1	1	regulation of systemic arterial blood pressure by chemoreceptor signaling	BP	0.91	P2RX2	up_VCAV_EC
GO:0003027	0.074	1	1	1	regulation of systemic arterial blood pressure by carotid body	BP	0.91	P2RX2	up_VCAV_EC
GO:0003029	0.074	1	1	1	detection of hypoxic conditions in blood by carotid body	BP	0.91	P2RX2	up_VCAV_EC
GO:0002007	0.074	1	1	1	detection of hypoxic conditions in blood by	BP	0.91	P2RX2	up_VCAV_EC
GO:0048644	0.074	0.997	1	31	muscle organ morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048483	0.074	0.997	1	19	autonomic nervous system development	BP	1	SIX1	up_VFEM_EC
GO:0003158	0.074	0.997	1	38	endothelium development	BP	1	HOXB5	up_VPUL_VSMC
GO:0016571	0.0741	0.971	7	39	histone methylation	BP	0.91	IWS1,GATA3,ARID4B,NSD1,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0061098	0.0741	0.986	3	12	positive regulation of protein tyrosine kinase	BP	0.91	PDGFB,RELN,NEDD9	up_VCAV_EC
GO:0006464	0.0741	0.995	2	1162	cellular protein modification process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0036211	0.0741	0.995	2	1162	protein modification process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0072507	0.0741	0.99	2	103	divalent inorganic cation homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0060393	0.0741	0.997	1	19	regulation of pathway-restricted SMAD protein	BP	1	ACVRL1	down_ACOR_EC
GO:0060349	0.0741	0.997	1	38	bone morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0001868	0.0741	1	1	1	regulation of complement activation, lectin pathway	BP	0.874	A2M	down_VSAP_EC
GO:0001869	0.0741	1	1	1	negative regulation of complement activation, lectin pathway	BP	0.874	A2M	down_VSAP_EC
GO:0002921	0.0741	1	1	1	negative regulation of humoral immune	BP	0.874	A2M	down_VSAP_EC
GO:0007290	0.0741	1	1	1	spermatid nucleus elongation	BP	0.874	KDM3A	down_VSAP_EC
GO:0010335	0.0741	1	1	1	response to non-ionic osmotic stress	BP	0.874	PTGS2	down_VSAP_EC
GO:0031394	0.0741	1	1	1	positive regulation of prostaglandin biosynthetic process	BP	0.874	PTGS2	down_VSAP_EC
GO:0031585	0.0741	1	1	1	regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel	BP	0.874	HTT	down_VSAP_EC
GO:0031587	0.0741	1	1	1	positive regulation of inositol 1,4,5-trisphosphate-sensitive	BP	0.874	HTT	down_VSAP_EC
GO:0042297	0.0741	1	1	1	vocal learning	BP	0.874	HTT	down_VSAP_EC
GO:0045916	0.0741	1	1	1	negative regulation of complement activation	BP	0.874	A2M	down_VSAP_EC
GO:0046293	0.0741	1	1	1	formaldehyde biosynthetic process	BP	0.874	KDM3A	down_VSAP_EC
GO:0071471	0.0741	1	1	1	cellular response to non-ionic osmotic stress	BP	0.874	PTGS2	down_VSAP_EC
GO:0097402	0.0741	1	1	1	neuroblast migration	BP	0.874	PDS5B	down_VSAP_EC
GO:0098596	0.0741	1	1	1	imitative learning	BP	0.874	HTT	down_VSAP_EC
GO:0098597	0.0741	1	1	1	observational learning	BP	0.874	HTT	down_VSAP_EC
GO:0098598	0.0741	1	1	1	learned vocalization behavior or vocal learning	BP	0.874	HTT	down_VSAP_EC
GO:0140018	0.0741	1	1	1	regulation of cytoplasmic translational fidelity	BP	0.874	AARS	down_VSAP_EC
GO:1904170	0.0741	1	1	1	regulation of bleb assembly	BP	0.874	ANLN	down_VSAP_EC

GO:1904172	0.0741	1	1	1	positive regulation of bleb assembly	BP	0.874	ANLN	down_VSAP_EC
GO:1905335	0.0741	1	1	1	regulation of aggrephagy	BP	0.874	HTT	down_VSAP_EC
GO:1905337	0.0741	1	1	1	positive regulation of aggrephagy	BP	0.874	HTT	down_VSAP_EC
GO:1990034	0.0741	1	1	1	calcium ion export across plasma membrane	BP	0.874	ATP2B1	down_VSAP_EC
GO:2000258	0.0741	1	1	1	negative regulation of protein activation cascade	BP	0.874	A2M	down_VSAP_EC
GO:1903756	0.0741	1	1	1	regulation of transcription from RNA polymerase II promoter by histone	BP	0.874	ZMYND8	down_VSAP_EC
GO:1903758	0.0741	1	1	1	negative regulation of transcription from RNA polymerase II promoter by histone modification	BP	0.874	ZMYND8	down_VSAP_EC
GO:0002174	0.0741	1	1	1	mammary stem cell proliferation	BP	1	LBH	up_ACOR_VSMC
GO:1904674	0.0741	1	1	1	positive regulation of somatic stem cell	BP	1	LBH	up_ACOR_VSMC
GO:1904675	0.0741	1	1	1	regulation of somatic stem cell division	BP	1	LBH	up_ACOR_VSMC
GO:1904677	0.0741	1	1	1	positive regulation of somatic stem cell division	BP	1	LBH	up_ACOR_VSMC
GO:2000035	0.0741	1	1	1	regulation of stem cell division	BP	1	LBH	up_ACOR_VSMC
GO:2000101	0.0741	1	1	1	regulation of mammary stem cell proliferation	BP	1	LBH	up_ACOR_VSMC
GO:2000103	0.0741	1	1	1	positive regulation of mammary stem cell	BP	1	LBH	up_ACOR_VSMC
GO:0030431	0.07410108	0.99812	1	3	sleep	BP	1	PTGDS	up_ACOR_EC
GO:0048468	0.0742	0.974	6	553	cell development	BP	1	LYN,SPG11,PDPN,NRP2,SULF1,NEDD4	down_ACOR_EC
GO:0032609	0.0742	0.977	5	25	interferon-gamma production	BP	1	TLR3,ISG15,CD274,F2RL1,IL18R1	up_ACOR_VSMC
GO:0046683	0.0742	0.977	5	26	response to organophosphorus	BP	0.91	P2RX7,SELL,RAPGEF1,RAPGEF2,P2RX2	up_VCAV_EC
GO:0034660	0.0742	0.99	2	211	ncRNA metabolic process	BP	1	DARS,TSEN15	down_AFEM_EC
GO:0032462	0.0742	0.991	2	8	regulation of protein homooligomerization	BP	0.874	CRYAB,APOE	down_VSAP_EC
GO:0008283	0.0742	0.992	2	545	cell proliferation	BP	1	TGFBI,TGFBR1	down_VSAP_VSMC
GO:0000041	0.0742	0.997	1	31	transition metal ion transport	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:2001237	0.0742	0.997	1	33	negative regulation of extrinsic apoptotic	BP	1	EYA1	up_VFEM_VSMC
GO:0021644	0.0742	1	1	1	vagus nerve morphogenesis	BP	1	PLXNA4	up_VSAP_EC
GO:0021793	0.0742	1	1	1	chemorepulsion of branchiomotor axon	BP	1	PLXNA4	up_VSAP_EC
GO:0009435	0.074241256	0.99811	1	3	NAD biosynthetic process	BP	1	NMNAT2	up_ACOR_EC
GO:0002237	0.07428579	0.97525	5	85	response to molecule of bacterial origin	BP	1	NR1H4,FZD5,PTGIR,NOD2,PTGER4	up_ACOR_EC
GO:0001501	0.0743	0.955	21	178	skeletal system development	BP	1	USP1,EIF4A3,HOXA3,NAB2,INSIG1,XYLT1,MMP14,GREM1,HOXA7,HOXC10,HOXB7,POC1A,HOXC6,HOXB5,HOXC4,SGPL1,TBX15,HOXA9,SERPINH1,SIX4,AMER1	down_ACOR_VSMC
GO:0001823	0.0743	0.976	5	45	mesonephros development	BP	1	SMAD9,CLSTN1,GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:0046634	0.0743	0.977	5	24	regulation of alpha-beta T cell activation	BP	1	CD274,ZBTB16,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0051893	0.0743	0.985	3	20	regulation of focal adhesion assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0090109	0.0743	0.985	3	20	regulation of cell-substrate junction	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0090263	0.0743	0.997	1	33	positive regulation of canonical Wnt signaling	BP	1	DKK2	up_AORT_EC
GO:0001503	0.0743	0.998	1	109	ossification	BP	1	HOXA3	up_APUL_VSMC
GO:0002688	0.0743	0.997	1	34	regulation of leukocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0014855	0.0743	0.997	1	22	striated muscle cell proliferation	BP	1	TBX5	up_VPUL_EC
GO:1904427	0.0743	0.997	1	18	positive regulation of calcium ion	BP	1	STIM1	up_VSAP_VSMC

GO:0031098	0.074337919	0.97219	6	109	stress-activated protein kinase signaling cascade	BP	1	FZD5,NOD2,PAK3,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC
GO:0007169	0.0744	0.955	21	178	transmembrane receptor protein tyrosine kinase signaling pathway	BP	0.91	TEK,KIT,PDGFB,BAIAP2L1,KDR,TIPARP,RAPGEF1,GATA3,BMP2,HHEX,ANGPT2,STMN1,PRKD2,APOD,NCK1,FES,RAPGEF2,PDGFD,BMX,HIF1A,JCAD	up_VCAV_EC
GO:0032755	0.0744	0.977	5	24	positive regulation of interleukin-6 production	BP	1	TLR1,MBP,TLR3,F2RL1,NOD2	up_ACOR_VSMC
GO:0032682	0.0744	0.992	2	7	negative regulation of chemokine production	BP	0.91	ARG2,APOD	up_VCAV_EC
GO:0051249	0.0744	0.99	2	107	regulation of lymphocyte activation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0010763	0.0744	0.993	2	5	positive regulation of fibroblast migration	BP	1	DDR2,BAG4	up_VSAP_EC
GO:0031328	0.0744	1	1	512	positive regulation of cellular biosynthetic	BP	1	GATA5	down_AFEM_VSMC
GO:0006575	0.0744	0.997	1	53	cellular modified amino acid metabolic process	BP	1	ENSCAFG00000028814	up_VCAV_VSMC
GO:0021884	0.0744	0.997	1	10	forebrain neuron development	BP	1	SEMA3A	up_VPOR_EC
GO:1902904	0.0744	0.997	1	38	negative regulation of supramolecular fiber	BP	1	SLIT2	up_VPUL_VSMC
GO:0001505	0.0745	0.998	1	69	regulation of neurotransmitter levels	BP	1	WNT7A	up_AORT_VSMC
GO:0048103	0.0745	0.997	1	10	somatic stem cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:0048565	0.0745	0.997	1	38	digestive tract development	BP	1	GATA5	up_VPUL_VSMC
GO:0071605	0.07458498	0.99809	1	3	monocyte chemotactic protein-1 production	BP	1	NR1H4	up_ACOR_EC
GO:0071637	0.07458498	0.99809	1	3	regulation of monocyte chemotactic protein-1	BP	1	NR1H4	up_ACOR_EC
GO:0071638	0.07458498	0.99809	1	3	negative regulation of monocyte chemotactic	BP	1	NR1H4	up_ACOR_EC
GO:1903506	0.0746	0.941	94	977	regulation of nucleic acid-templated transcription	BP	0.91	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0009792	0.0746	0.99	2	231	embryo development ending in birth or egg	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0003006	0.0746	0.99	2	180	developmental process involved in reproduction	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0042102	0.0747	0.99	2	19	positive regulation of T cell proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0030855	0.0747	0.99	2	183	epithelial cell differentiation	BP	1	BARX1,CYP26B1	up_VPOR_VSMC
GO:0051261	0.0747	0.997	1	33	protein depolymerization	BP	1	TAOK1	up_AORT_EC
GO:0003308	0.0747	1	1	1	negative regulation of Wnt signaling pathway involved in heart	BP	0.91	BMP2	up_VCAV_EC
GO:0021984	0.0747	1	1	1	adenohypophysis development	BP	0.91	BMP2	up_VCAV_EC
GO:0035054	0.0747	1	1	1	embryonic heart tube anterior/posterior pattern specification	BP	0.91	BMP2	up_VCAV_EC
GO:0043569	0.0747	1	1	1	negative regulation of insulin-like growth factor receptor signaling	BP	0.91	BMP2	up_VCAV_EC
GO:0051040	0.0747	1	1	1	regulation of calcium-independent cell-cell	BP	0.91	BMP2	up_VCAV_EC
GO:0051042	0.0747	1	1	1	negative regulation of calcium-independent cell-	BP	0.91	BMP2	up_VCAV_EC
GO:0060129	0.0747	1	1	1	thyroid-stimulating hormone-secreting cell	BP	0.91	BMP2	up_VCAV_EC

GO:0060804	0.0747	1	1	1	positive regulation of Wnt signaling pathway by BMP signaling pathway	BP	0.91	BMP2	up_VCAV_EC
GO:0060956	0.0747	1	1	1	endocardial cell differentiation	BP	0.91	SOX18	up_VCAV_EC
GO:0003348	0.0747	1	1	1	cardiac endothelial cell differentiation	BP	0.91	SOX18	up_VCAV_EC
GO:0006021	0.0747	1	1	1	inositol biosynthetic process	BP	0.91	IMPA1	up_VCAV_EC
GO:0033566	0.0747	1	1	1	gamma-tubulin complex localization	BP	0.91	MZT1	up_VCAV_EC
GO:0060128	0.0747	1	1	1	corticotropin hormone secreting cell	BP	0.91	BMP2	up_VCAV_EC
GO:0090022	0.0747	0.997	1	9	regulation of neutrophil chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0060419	0.0747	0.997	1	22	heart growth	BP	1	TBX5	up_VPUL_EC
GO:0090611	0.074757806	0.99808	1	3	ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway	BP	1	CHMP4B	up_ACOR_EC
GO:0039689	0.074765307	0.99808	1	3	negative stranded viral RNA replication	BP	1	ATG16L2	up_ACOR_EC
GO:0048050	0.074796834	0.99808	1	3	post-embryonic eye morphogenesis	BP	1	EFEMP1	up_ACOR_EC
GO:0002312	0.0748	0.977	5	24	B cell activation involved in immune response	BP	0.91	TLR4,THOC1,SWAP70,MFNG,PLCG2	up_VCAV_EC
GO:0007162	0.0748	0.998	1	66	negative regulation of cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0061450	0.074855495	0.99808	1	3	trophoblast cell migration	BP	1	ARHGDIB	up_ACOR_EC
GO:1901163	0.074855495	0.99808	1	3	regulation of trophoblast cell migration	BP	1	ARHGDIB	up_ACOR_EC
GO:0045934	0.0749	0.947	43	407	negative regulation of nucleobase-containing compound metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,SREBF2,SMC1A,NEDD4,U2AF2,MTDH,PARPBP,NAB2,BIRC5,CAV1,TIMELESS,THRAP3,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,NOC2L,PPARD,SUV39H1,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:0060840	0.0749	0.971	7	42	artery development	BP	0.91	ADGRF5,ADAMTS9,CHD7,DLL4,PROX1,JAG1,LUZP1	up_VCAV_EC
GO:1903391	0.0749	0.98	4	21	regulation of adherens junction organization	BP	0.91	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0051881	0.0749	0.984	3	19	regulation of mitochondrial membrane	BP	1	DCN,AKT2,PARK7	down_VCAV_EC
GO:0001944	0.0749	0.999	1	263	vasculature development	BP	1	JUP	down_VFEM_VSMC
GO:0071674	0.0749	0.997	1	23	mononuclear cell migration	BP	1	CCL24	up_VPUL_EC
GO:0051155	0.0749	0.997	1	18	positive regulation of striated muscle cell	BP	1	SHOX2	up_VSAP_VSMC
GO:1900122	0.074950439	0.99807	1	3	positive regulation of receptor binding	BP	1	PLCL1	up_ACOR_EC
GO:0045595	0.075	0.98	4	469	regulation of cell differentiation	BP	1	TBX5,EVI2B,WIF1,ARHGEF2	up_VPUL_EC
GO:0045604	0.075	0.981	4	17	regulation of epidermal cell differentiation	BP	1	HOXA7,DLL1,ZFP36L1,KEAP1	up_VSAP_EC
GO:0009888	0.075	0.992	2	545	tissue development	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0008627	0.075	0.993	2	5	intrinsic apoptotic signaling pathway in response to osmotic	BP	0.91	PTGS2,ARHGEF2	up_VCAV_EC
GO:0030182	0.075	0.991	2	327	neuron differentiation	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0043009	0.075	0.99	2	227	chordate embryonic development	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0002689	0.075	0.993	2	5	negative regulation of leukocyte chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0021768	0.075	1	1	1	nucleus accumbens development	BP	0.91	ALDH1A3	up_VCAV_EC
GO:0060166	0.075	1	1	1	olfactory pit development	BP	0.91	ALDH1A3	up_VCAV_EC
GO:0032924	0.075	0.997	1	9	activin receptor signaling pathway	BP	1	ACVR2A	up_VPOR_EC
GO:0030224	0.075	0.997	1	18	monocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:1903131	0.075	0.997	1	18	mononuclear cell differentiation	BP	1	HOXA7	up_VFEM_EC

GO:0032760	0.075	0.997	1	22	positive regulation of tumor necrosis factor	BP	1	ARHGEF2	up_VPUL_EC
GO:1903557	0.075	0.997	1	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	up_VPUL_EC
GO:0051338	0.0751	0.95	31	288	regulation of transferase activity	BP	0.91	TEK,KIT,PPP2R5A,TNFAIP3,MAP3K11,PDGFB,STK10,RELN,TLR4,NLRC5,EDN1,RALB,NEDD9,MTOR,MAP3K3,BMP2,HHEX,PREX2,SLK,SH3BP5,PROX1,MADD,HMBOX1,PAK2,SH3GLB1,LDB2,MMD,RAPGEF2,BLM,RIPK1,PDGFD	up_VCAV_EC
GO:0046620	0.0751	0.973	6	30	regulation of organ growth	BP	1	FGFR2,LATS2,TBX20,TBX5,WWC2,EDN1	up_ACOR_VSMC
GO:0033108	0.0751	0.997	1	39	mitochondrial respiratory chain complex assembly	BP	1	NDUFA10	down_AFEM_EC
GO:0050921	0.0751	0.997	1	39	positive regulation of chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0051055	0.0752	0.98	4	21	negative regulation of lipid biosynthetic process	BP	0.91	PDGFB,BMP2,PROX1,ENSCAFG00000010596	up_VCAV_EC
GO:1902808	0.0752	0.985	3	12	positive regulation of cell cycle G1/S phase	BP	1	EZH2,GLI1,MTBP	down_ACOR_VSMC
GO:0009404	0.0752	0.992	2	6	toxin metabolic process	BP	1	GSTO1,CTH	down_ACOR_VSMC
GO:0071801	0.0752	0.991	2	7	regulation of podosome assembly	BP	0.884	FSCN1,MSN	down_VSAP_EC
GO:0050774	0.0752	0.992	2	6	negative regulation of dendrite morphogenesis	BP	0.91	PPP3CA,RAPGEF2	up_VCAV_EC
GO:0003012	0.0752	0.998	1	90	muscle system process	BP	1	GATA5	down_VSAP_VSMC
GO:0072593	0.0752	0.997	1	68	reactive oxygen species metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0006929	0.0752	0.997	1	10	substrate-dependent cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0006812	0.0753	0.984	3	222	cation transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:1990778	0.0753	0.99	2	91	protein localization to cell periphery	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0017015	0.0753	0.997	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	CITED2	down_VPOR_EC
GO:1903844	0.0753	0.997	1	40	regulation of cellular response to transforming growth factor beta	BP	1	CITED2	down_VPOR_EC
GO:0007507	0.07538168	0.96518	9	194	heart development	BP	1	GATA4,SOX9,PDLIM3,SMAD6,ACTN2,FOXC2,TBX5,C23H3orf58,NRP1	up_ACOR_EC
GO:0050793	0.0754	0.946	45	731	regulation of developmental process	BP	1	GPAM,NOTCH2,HSPB6,DCN,NAB2,VASN,FBN1,GLIPR2,BMPR1A,LMO4,TRPV2,NUMBL,TFE3,SYDE1,LAMA3,CLSTN1,SEMA3C,ASPN,THY1,PEX5,TLX2,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,RBM38,CDH2,LOXL3,SPRED1,RAB7B,TSC22D3,UST,TWIST2,PRKCSH,DDR2,OMD,GREM1,NAPEPLD,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC
GO:0014020	0.0754	0.997	1	41	primary neural tube formation	BP	1	CITED2	down_VPOR_EC
GO:0032649	0.0754	0.997	1	23	regulation of interferon-gamma production	BP	1	NR1H4	up_VPUL_EC
GO:0042742	0.0754	0.997	1	39	defense response to bacterium	BP	1	IL22RA1	up_VPUL_VSMC
GO:1903426	0.0754	0.997	1	17	regulation of reactive oxygen species	BP	1	CAV1	up_VSAP_VSMC
GO:0051604	0.0755	0.965	9	102	protein maturation	BP	1	ADAMTS2,RHBDL1,PCSK7,GLI3,SEC11C,A2M,PCSK6,ATOX1,LONP2	down_VCAV_EC
GO:0030101	0.0755	0.985	3	12	natural killer cell activation	BP	1	TOX,CORO1A,ELF4	down_ACOR_VSMC
GO:1903523	0.0755	0.986	3	10	negative regulation of blood circulation	BP	0.912	DOCK4,PDE4D,SPTBN4	up_VCAV_EC
GO:0009058	0.0755	1	2	1910	biosynthetic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0019369	0.0755	0.992	2	5	arachidonic acid metabolic process	BP	1	DAGLB,ENSCAFG00000023820	up_VSAP_EC
GO:0072070	0.0755	0.992	2	5	loop of Henle development	BP	1	DLL1,IRX3	up_VSAP_EC
GO:0050803	0.0755	0.997	1	55	regulation of synapse structure or activity	BP	1	SLITRK5	up_VCAV_VSMC
GO:0050807	0.0755	0.997	1	55	regulation of synapse organization	BP	1	SLITRK5	up_VCAV_VSMC
GO:0010594	0.0756	0.963	11	71	regulation of endothelial cell migration	BP	1	SLIT2,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1	up_VSAP_EC

GO:0001558	0.0756	0.964	10	101	regulation of cell growth	BP	0.887	ENPP1,IFRD1,SMARCA4,SESN2,ESM1,ADAM17,IGFBP7,INHBA,CDKN1A,NRP1	down_VSAP_EC
GO:0046847	0.0756	0.984	3	17	filopodium assembly	BP	0.887	FSCN1,DPYSL3,NRP1	down_VSAP_EC
GO:0046887	0.0756	0.997	1	18	positive regulation of hormone secretion	BP	1	STX4	down_ACOR_EC
GO:0009891	0.0756	1	1	521	positive regulation of biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0046324	0.0756	0.997	1	20	regulation of glucose import	BP	1	NR1H4	up_APUL_EC
GO:0000470	0.0756	0.997	1	9	maturation of LSU-rRNA	BP	1	RRP15	up_VPOR_EC
GO:0030166	0.0756	0.997	1	19	proteoglycan biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:0042158	0.0757	0.97	7	40	lipoprotein biosynthetic process	BP	1	LCAT,ABCA1,PIGN,PIGS,PIGG,PIK3C3,ZDHHC21	up_ACOR_VSMC
GO:0006955	0.0757	0.979	4	327	immune response	BP	1	LYN,IGF1R,IPO7,STX4	down_ACOR_EC
GO:0021675	0.0757	0.997	1	29	nerve development	BP	1	HOXA3	up_VPOR_VSMC
GO:0032635	0.075772516	0.98345	3	37	interleukin-6 production	BP	1	NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0030042	0.075777571	0.99001	2	17	actin filament depolymerization	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0030834	0.075777571	0.99001	2	17	regulation of actin filament depolymerization	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0007275	0.0758	0.941	79	1370	multicellular organism development	BP	1	ADAMTS2,NOTCH2,HSPB6,PDGFRB,SMAD9,LRP1,DCN,NAB2,NDN,ANGPT1,SDC4,VASN,FBN1,GLIPR2,KANK2,THBS3,BMPR1A,LOX,LMO4,RECK,TRPV2,ANPEP,COL6A1,NUMBL,NAGLU,CHRDL1,TBX15,AKT2,TFE3,ENSCAFG00000018277,SYDE1,HOXC4,LAMA3,CLSTN1,CSPG4,PKD1,ENSCAFG00000013404,SEMA3C,ASPN,THY1,TEAD1,HAPLN3,PEX5,TLX2,VCAN,B4GALT1,GLI3,EEF2,ZFP36L1,MYDGF,SASH1,NCDN,IFT57,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,IRX5,TSC22D3,UST,GLIS2,PRKCSH,DDR2,SHC1,RDH10,PCSK6,OMD,GREM1,CLIC4,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,SEC61A1,BRSK1	down_VCAV_EC
GO:0051493	0.0758	0.953	22	188	regulation of cytoskeleton organization	BP	1	FSCN1,SMC1A,CAPG,LIMA1,NF2,STMN1,NEK2,POC1A,RAC1,NUP62,PDXP,PLK4,IQGAP2,CDC42EP4,SMC3,STAG1,RBM14,CORO1A,ARPC1B,ARHGEF2,KIF11,GEN1	down_ACOR_VSMC
GO:0090195	0.0758	0.992	2	5	chemokine secretion	BP	1	MBP,F2RL1	up_ACOR_VSMC
GO:0001702	0.0758	0.997	1	10	gastrulation with mouth forming second	BP	1	ACVR2A	up_VPOR_EC
GO:0042509	0.0758	0.997	1	17	regulation of tyrosine phosphorylation of STAT	BP	1	CAV1	up_VSAP_VSMC
GO:0071472	0.075894645	0.99802	1	3	cellular response to salt stress	BP	1	AQP1	up_ACOR_EC
GO:0007268	0.0759	0.957	16	130	chemical synaptic transmission	BP	0.912	EPHB1,PLK2,ENSCAFG00000007112,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,SNAP23,SLC12A7,GRM8,STX11,ALS2,P2RX2	up_VCAV_EC
GO:0098916	0.0759	0.957	16	130	anterograde trans-synaptic signaling	BP	0.912	EPHB1,PLK2,ENSCAFG00000007112,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,SNAP23,SLC12A7,GRM8,STX11,ALS2,P2RX2	up_VCAV_EC
GO:0001764	0.0759	0.968	8	45	neuron migration	BP	1	GJA1,NRP1,GPM6A,TBX20,FZD3,POMK,PSEN1,DISC1	up_ACOR_VSMC
GO:0060759	0.0759	0.975	5	37	regulation of response to cytokine stimulus	BP	0.889	NR1H4,PTPN2,ADAM17,CNOT7,CDC37	down_VSAP_EC
GO:0042100	0.0759	0.98	4	19	B cell proliferation	BP	0.912	IL7R,MEF2C,TLR4,PELI1	up_VCAV_EC
GO:0032350	0.0759	0.985	3	12	regulation of hormone metabolic process	BP	0.912	GATA3,BMP2,HIF1A	up_VCAV_EC
GO:0045662	0.0759	0.991	2	8	negative regulation of myoblast differentiation	BP	0.889	PRICKLE1,DDIT3	down_VSAP_EC
GO:0008406	0.0759	0.99	2	57	gonad development	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0045137	0.0759	0.99	2	57	development of primary sexual characteristics	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0044092	0.0759	0.999	1	270	negative regulation of molecular function	BP	1	CST3	down_AORT_EC
GO:1900086	0.0759	0.999	1	2	positive regulation of peptidyl-tyrosine	BP	0.889	VEGFA	down_VSAP_EC

GO:0009889	0.076	0.939	112	1190	regulation of biosynthetic process	BP	0.912	EDNRB,HCLS1,ADGRF5,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,FAM3C,ARG2,MTOR,SAMD8,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,ENC1,CCAR1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,PTGS2,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,NOS2,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0016202	0.076	0.97	7	39	regulation of striated muscle tissue	BP	1	BMP4,FGFR2,GJA1,TBX20,TBX5,FRS2,EDN1	up_ACOR_VSMC
GO:0061035	0.076	0.976	5	24	regulation of cartilage development	BP	1	HOXA11,AXIN2,ZBTB16,RARG,SHOX2	up_VSAP_EC
GO:0070228	0.076	0.98	4	20	regulation of lymphocyte apoptotic process	BP	1	PRELID1,AURKB,ARG2,NOC2L	down_ACOR_VSMC
GO:0048731	0.076	0.988	3	1247	system development	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0051567	0.076	0.986	3	10	histone H3-K9 methylation	BP	0.912	ARID4B,KDM3A,ATRX	up_VCAV_EC
GO:0007512	0.076	0.992	2	6	adult heart development	BP	0.912	CHD7,APLNR	up_VCAV_EC
GO:0045604	0.076	0.997	1	17	regulation of epidermal cell differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0006470	0.076	0.997	1	54	protein dephosphorylation	BP	1	EYA1	up_AFEM_VSMC
GO:0045089	0.076	0.997	1	70	positive regulation of innate immune response	BP	1	ESR1	up_AORT_VSMC
GO:0009308	0.076	0.997	1	20	amine metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0050732	0.076	0.997	1	18	negative regulation of peptidyl-tyrosine	BP	1	CAV1	up_VSAP_VSMC
GO:0061299	0.076008634	0.99802	1	3	retina vasculature morphogenesis in camera-	BP	1	NRP1	up_ACOR_EC
GO:0006911	0.0761	0.985	3	11	phagocytosis, engulfment	BP	1	F2RL1,XKR8,ARHGAP12	up_VSAP_EC
GO:0050779	0.0761	0.992	2	5	RNA destabilization	BP	1	ZFP36L1,ZFP36L2	up_VSAP_EC
GO:0061157	0.0761	0.992	2	5	mRNA destabilization	BP	1	ZFP36L1,ZFP36L2	up_VSAP_EC
GO:1903792	0.0761	0.992	2	5	negative regulation of anion transport	BP	1	GABRE,OSR1	up_VSAP_EC
GO:0032880	0.0761	0.998	1	266	regulation of protein localization	BP	1	JUP	down_VFEM_VSMC
GO:0060765	0.0761	0.997	1	10	regulation of androgen receptor signaling	BP	1	RNF6	up_VPOR_EC
GO:0043154	0.0761	0.997	1	23	negative regulation of cysteine-type endopeptidase activity	BP	1	PTGER2	up_VPUL_EC
GO:0016202	0.0761	0.997	1	39	regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_VSMC
GO:0008645	0.07615329	0.98333	3	37	hexose transmembrane transport	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0015749	0.07615329	0.98333	3	37	monosaccharide transmembrane transport	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0034219	0.07615329	0.98333	3	37	carbohydrate transmembrane transport	BP	1	NR1H4,ENSCAFG00000004331,RARRES2	up_ACOR_EC
GO:0110053	0.0762	0.96	13	98	regulation of actin filament organization	BP	0.912	HCLS1,ARHGEF15,BAIAP2L1,ARHGAP28,TMOD1,MTOR,NCKAP1,IQGAP2,STMN1,SWAP70,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0046717	0.0762	0.98	4	17	acid secretion	BP	1	LEP,SLC26A7,HRH2,CFI	up_ACOR_VSMC
GO:0031098	0.0762	0.99	2	109	stress-activated protein kinase signaling cascade	BP	1	MAP2K6,CDC42EP5	up_VFEM_EC
GO:0007163	0.0762	0.997	1	60	establishment or maintenance of cell	BP	1	WNT7A	up_AORT_VSMC
GO:0003156	0.0762	0.997	1	20	regulation of animal organ formation	BP	1	TBX5	up_APUL_EC

GO:0048644	0.0762	0.997	1	31	muscle organ morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0032602	0.0762	0.997	1	23	chemokine production	BP	1	NR1H4	up_VPUL_EC
GO:0097306	0.0762	0.997	1	22	cellular response to alcohol	BP	1	PTGER2	up_VPUL_EC
GO:0032611	0.076232966	0.98992	2	17	interleukin-1 beta production	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0060759	0.07625201	0.9833	3	37	regulation of response to cytokine stimulus	BP	1	NR1H4,CCDC3,MAVS	up_ACOR_EC
GO:0032946	0.0763	0.976	5	29	positive regulation of mononuclear cell	BP	0.912	MEF2C,TLR4,PELI1,NCK1,HMGB1	up_VCAV_EC
GO:0050671	0.0763	0.976	5	29	positive regulation of lymphocyte proliferation	BP	0.912	MEF2C,TLR4,PELI1,NCK1,HMGB1	up_VCAV_EC
GO:0036010	0.0763	0.992	2	6	protein localization to endosome	BP	1	RAB35,EZR	down_ACOR_VSMC
GO:0046949	0.0763	0.992	2	6	fatty-acyl-CoA biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0035051	0.0763	0.997	1	41	cardiocyte differentiation	BP	1	CITED2	down_VPOR_EC
GO:0030334	0.0763	0.998	1	267	regulation of cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0072358	0.0763	0.998	1	268	cardiovascular system development	BP	1	JUP	down_VFEM_VSMC
GO:0070265	0.0764	0.98	4	19	necrotic cell death	BP	0.912	PELI1,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:0046887	0.0764	0.984	3	18	positive regulation of hormone secretion	BP	0.892	NR1H4,PTPN11,HIF1A	down_VSAP_EC
GO:0009651	0.0764	0.992	2	5	response to salt stress	BP	1	ZFP36L1,SLC12A6	up_VSAP_EC
GO:0048538	0.0764	0.997	1	20	thymus development	BP	1	HOXA3	up_APUL_EC
GO:2000626	0.0764	1	1	1	negative regulation of miRNA catabolic process	BP	0.912	TENT2	up_VCAV_EC
GO:2000629	0.0764	1	1	1	negative regulation of miRNA metabolic process	BP	0.912	TENT2	up_VCAV_EC
GO:0003229	0.076488134	0.98986	2	17	ventricular cardiac muscle tissue development	BP	1	FOXC2,TBX5	up_ACOR_EC
GO:0060993	0.0765	0.983	3	42	kidney morphogenesis	BP	1	IRX3,GREM1,GCNT4	up_AFEM_EC
GO:0042327	0.0765	0.984	3	289	positive regulation of phosphorylation	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0010613	0.0765	0.992	2	5	positive regulation of cardiac muscle	BP	0.912	EDN1,PPP3CA	up_VCAV_EC
GO:0014742	0.0765	0.992	2	5	positive regulation of muscle hypertrophy	BP	0.912	EDN1,PPP3CA	up_VCAV_EC
GO:0019348	0.0765	1	1	1	dolichol metabolic process	BP	1	NUS1	down_ACOR_VSMC
GO:0019408	0.0765	1	1	1	dolichol biosynthetic process	BP	1	NUS1	down_ACOR_VSMC
GO:0010628	0.0765	1	1	527	positive regulation of gene expression	BP	1	GATA5	down_AFEM_VSMC
GO:0051894	0.0765	0.997	1	10	positive regulation of focal adhesion assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0032526	0.0765	0.997	1	19	response to retinoic acid	BP	1	CYP26B1	up_VFEM_EC
GO:0009887	0.076576027	0.95911	13	314	animal organ morphogenesis	BP	1	GATA4,SOX9,AQP1,FZD5,LHX9,SMAD6,DLX3, FOXC2,TBX5,LRP4,CLSTN1,NRP1,EFEMP1	up_ACOR_EC

GO:0044238	0.0766	0.935	300	3383	primary metabolic process	BP	1	FADS2,ELK3,SCD,ACSL3,PRPSAP1,SQLE,FADS1,HMGB1,MCM6,RNPS1,LSS,SREBF1,ACLY,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,ENSCAFG00000016095,PPRC1,USP4,SF3B2,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,CTDNEP1,RAD54L,POLE,DDX23,NAB2,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,NF2,PFAS,EDC4,AURKB,NONO,MMP14,HNRNPL,TK1,CDKN2C,TOPBP1,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,RNF152,DIS3,GMNN,DHCR24,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,P	down_ACOR_VSMC
GO:0045766	0.0766	0.969	7	63	positive regulation of angiogenesis	BP	0.894	VEGFA,SERPINE1,JCAD,PIK3C2A,HIF1A,MTDH,NRP1	down_VSAP_EC
GO:0010646	0.0766	0.977	5	945	regulation of cell communication	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0006584	0.0766	0.985	3	11	catecholamine metabolic process	BP	1	MAOA,MOXD1,PARK7	up_ACOR_VSMC
GO:0009712	0.0766	0.985	3	11	catechol-containing compound metabolic	BP	1	MAOA,MOXD1,PARK7	up_ACOR_VSMC
GO:0070232	0.0766	0.985	3	13	regulation of T cell apoptotic process	BP	0.912	IL7R,ARG2,HIF1A	up_VCAV_EC
GO:0006591	0.0766	0.992	2	5	ornithine metabolic process	BP	1	HNF4A,AZIN2	up_VSAP_EC
GO:0050863	0.0766	0.997	1	69	regulation of T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0009312	0.0766	0.997	1	9	oligosaccharide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0010717	0.0766	0.997	1	32	regulation of epithelial to mesenchymal transition	BP	1	BAMBI	up_VPOR_VSMC
GO:0031331	0.076640956	0.9711	6	110	positive regulation of cellular catabolic process	BP	1	EDEM2,PIAS1,CLU,TP53INP2,RNF114,PRKCD	up_ACOR_EC
GO:0030010	0.0767	0.97	7	41	establishment of cell polarity	BP	0.912	EPHB1,FRMD4B,AMOT,FERMT1,GATA3,ZW10,FSCN1	up_VCAV_EC
GO:0090184	0.0767	0.985	3	14	positive regulation of kidney development	BP	0.912	HOXB7,PDGFB,GATA3	up_VCAV_EC
GO:0006139	0.0767	1	2	1909	nucleobase-containing compound metabolic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0002009	0.0767	0.99	2	177	morphogenesis of an epithelium	BP	1	NKX2-5,ANKRD6	up_VPOR_VSMC
GO:0031663	0.0767	0.997	1	17	lipopolysaccharide-mediated signaling	BP	1	LYN	down_ACOR_EC
GO:0009743	0.0767	0.997	1	40	response to carbohydrate	BP	1	RAB11B	down_VPOR_EC
GO:0060562	0.0768	0.956	17	120	epithelial tube morphogenesis	BP	1	SHROOM3,BMP4,FGFR2,GJA1,SEC24B,CITED2,SPINT1,LMO4,CLSTN1,NRP1,NPNT,SPINT2,TBX20,FZD3,DAG1,PSEN1,EDN1	up_ACOR_VSMC
GO:0032502	0.0768	0.974	7	1661	developmental process	BP	1	HOXC10,DKK2,HOXA9,HOXC6,SGCD,TAOK1,DUSP2	up_AORT_EC
GO:0045669	0.0768	0.976	5	24	positive regulation of osteoblast differentiation	BP	1	BMP4,GJA1,CLSTN1,NPNT,DDR2	up_ACOR_VSMC
GO:0002465	0.0768	1	1	1	peripheral tolerance induction	BP	1	CD274	up_ACOR_VSMC
GO:0002652	0.0768	1	1	1	regulation of tolerance induction dependent upon immune response	BP	1	CD274	up_ACOR_VSMC
GO:0002654	0.0768	1	1	1	positive regulation of tolerance induction dependent upon immune	BP	1	CD274	up_ACOR_VSMC
GO:0002658	0.0768	1	1	1	regulation of peripheral tolerance induction	BP	1	CD274	up_ACOR_VSMC
GO:0002660	0.0768	1	1	1	positive regulation of peripheral tolerance	BP	1	CD274	up_ACOR_VSMC
GO:0002845	0.0768	1	1	1	positive regulation of tolerance induction to	BP	1	CD274	up_ACOR_VSMC

GO:0002413	0.0768	1	1	1	tolerance induction to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0002461	0.0768	1	1	1	tolerance induction dependent upon immune	BP	1	CD274	up_ACOR_VSMC
GO:0002843	0.0768	1	1	1	regulation of tolerance induction to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:1905404	0.0768	1	1	1	positive regulation of activated CD8-positive, alpha-beta T cell	BP	1	CD274	up_ACOR_VSMC
GO:2001186	0.0768	1	1	1	negative regulation of CD8-positive, alpha-beta T cell activation	BP	1	CD274	up_ACOR_VSMC
GO:0021816	0.0768	1	1	1	extension of a leading process involved in cell motility in cerebral cortex radial glia guided	BP	0.912	ENSCAFG00000010224	up_VCAV_EC
GO:1902041	0.0768	0.997	1	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	ARHGEF2	up_VPUL_EC
GO:0050770	0.0768	0.997	1	39	regulation of axonogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0034645	0.0769	0.973	7	1546	cellular macromolecule biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11, SHOX2	up_VFEM_VSMC
GO:0032945	0.0769	0.984	3	17	negative regulation of mononuclear cell	BP	0.897	LYN,SDC4,BTK	down_VSAP_EC
GO:0050672	0.0769	0.984	3	17	negative regulation of lymphocyte proliferation	BP	0.897	LYN,SDC4,BTK	down_VSAP_EC
GO:0032094	0.0769	0.992	2	6	response to food	BP	0.912	SLC25A25,BCL10	up_VCAV_EC
GO:0035405	0.0769	1	1	1	histone-threonine phosphorylation	BP	1	HASPIN	down_ACOR_VSMC
GO:0072355	0.0769	1	1	1	histone H3-T3 phosphorylation	BP	1	HASPIN	down_ACOR_VSMC
GO:0072356	0.0769	1	1	1	chromosome passenger complex localization to	BP	1	HASPIN	down_ACOR_VSMC
GO:2000751	0.0769	1	1	1	histone H3-T3 phosphorylation involved in chromosome passenger complex localization to	BP	1	HASPIN	down_ACOR_VSMC
GO:0048639	0.0769	0.997	1	39	positive regulation of developmental growth	BP	1	TBX5	up_VPUL_VSMC
GO:0006107	0.076917604	0.99797	1	3	oxaloacetate metabolic process	BP	1	NIT2	up_ACOR_EC
GO:0051651	0.077	0.972	6	31	maintenance of location in cell	BP	1	OS9,POLR2M,DAG1,GAA,SUN1,PARK7	up_ACOR_VSMC
GO:0043552	0.077	0.985	3	11	positive regulation of phosphatidylinositol 3-kinase activity	BP	0.912	TEK,PDGFB,SH3GLB1	up_VCAV_EC
GO:0090218	0.077	0.985	3	11	positive regulation of lipid kinase activity	BP	0.912	TEK,PDGFB,SH3GLB1	up_VCAV_EC
GO:0006730	0.077	0.991	2	8	one-carbon metabolic process	BP	0.897	ALDH1L2,ENSCAFG00000008716	down_VSAP_EC
GO:0045986	0.077	0.993	2	4	negative regulation of smooth muscle	BP	0.912	DOCK4,GUCY1A1	up_VCAV_EC
GO:0043407	0.077	0.997	1	19	negative regulation of MAP kinase activity	BP	1	LYN	down_ACOR_EC
GO:1901698	0.077	0.998	1	266	response to nitrogen compound	BP	1	JUP	down_VFEM_VSMC
GO:0036376	0.077	1	1	1	sodium ion export across plasma membrane	BP	1	FXYD1	up_ACOR_VSMC
GO:1903276	0.077	1	1	1	regulation of sodium ion export across plasma	BP	1	FXYD1	up_ACOR_VSMC
GO:1903278	0.077	1	1	1	positive regulation of sodium ion export across	BP	1	FXYD1	up_ACOR_VSMC
GO:0014706	0.077	0.998	1	112	striated muscle tissue development	BP	1	TBX5	up_APUL_VSMC

GO:2001141	0.0771	0.939	94	979	regulation of RNA biosynthetic process	BP	0.912	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:2000026	0.0771	0.967	8	560	regulation of multicellular organismal development	BP	1	C3AR1,HOOK3,ARHGEF2,SEMA3A,ASPN,ACVR2A,MTDH,RNF6	up_VPOR_EC
GO:0002819	0.0771	0.969	7	44	regulation of adaptive immune response	BP	0.912	IL7R,TNFAIP3,MEF2C,GATA3,NECTIN2,THOC1,HMGB1	up_VCAV_EC
GO:1903076	0.0771	0.979	4	32	regulation of protein localization to plasma	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978	down_VCAV_EC
GO:0032330	0.0771	0.984	3	20	regulation of chondrocyte differentiation	BP	1	GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:0055067	0.0771	0.983	3	42	monovalent inorganic cation homeostasis	BP	1	RAB20,RAB7A,ATP6V0B	up_AFEM_EC
GO:0016049	0.0771	0.983	3	124	cell growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC
GO:1900003	0.0771	1	1	1	regulation of serine-type endopeptidase activity	BP	1	SPINK2	up_ACOR_VSMC
GO:1900004	0.0771	1	1	1	negative regulation of serine-type	BP	1	SPINK2	up_ACOR_VSMC
GO:1902571	0.0771	1	1	1	regulation of serine-type peptidase activity	BP	1	SPINK2	up_ACOR_VSMC
GO:1902572	0.0771	1	1	1	negative regulation of serine-type peptidase	BP	1	SPINK2	up_ACOR_VSMC
GO:0009064	0.0771	0.997	1	23	glutamine family amino acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0032079	0.077145777	0.99796	1	3	positive regulation of endodeoxyribonuclease	BP	1	PRKCD	up_ACOR_EC
GO:0051235	0.0772	0.966	8	90	maintenance of location	BP	1	FBN1,TLN2,THY1,PARK7,CYBA,ARL2BP,ENSCAFG00000017708,SOAT1	down_VCAV_EC
GO:0065008	0.0772	0.969	8	1056	regulation of biological quality	BP	1	NETO1,GATM,HOXC10,IRX5,PRR16,STIM1,CAV1,F5	up_VSAP_VSMC
GO:0009719	0.0772	0.984	3	395	response to endogenous stimulus	BP	1	FGF5,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0009792	0.0772	0.99	2	231	embryo development ending in birth or egg	BP	1	HOXA3,HOXB5	up_VPUL_VSMC
GO:0030858	0.0772	0.997	1	17	positive regulation of epithelial cell	BP	1	ACVRL1	down_ACOR_EC
GO:0060840	0.0772	0.997	1	42	artery development	BP	1	CITED2	down_VPOR_EC
GO:0015849	0.0772	0.997	1	56	organic acid transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0046942	0.0772	0.997	1	56	carboxylic acid transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0072006	0.0772	0.997	1	59	nephron development	BP	1	EYA1	up_AFEM_VSMC
GO:0010092	0.0772	0.997	1	19	specification of animal organ identity	BP	1	HOXA11	up_VSAP_VSMC
GO:0032410	0.0772	0.997	1	17	negative regulation of transporter activity	BP	1	CAV1	up_VSAP_VSMC
GO:0070265	0.0772	0.997	1	19	necrotic cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0071731	0.077249275	0.99795	1	3	response to nitric oxide	BP	1	GUCY1B1	up_ACOR_EC
GO:0071241	0.0773	0.983	3	42	cellular response to inorganic substance	BP	1	MT2A,ENSCAFG00000009113,CPNE7	up_AFEM_EC
GO:0045603	0.0773	0.992	2	5	positive regulation of endothelial cell	BP	1	BTG1,ACVRL1	up_VSAP_EC
GO:1904894	0.0773	0.997	1	17	positive regulation of STAT cascade	BP	1	LYN	down_ACOR_EC
GO:0071804	0.0773	0.997	1	31	cellular potassium ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0071805	0.0773	0.997	1	31	potassium ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0038189	0.077329312	0.99795	1	3	neuropilin signaling pathway	BP	1	NRP1	up_ACOR_EC

GO:0072525	0.0774	0.976	5	24	pyridine-containing compound biosynthetic	BP	1	NADK,GALK1,PNPO,PNP,DDIT4	up_VSAP_EC
GO:0048545	0.0774	0.978	4	68	response to steroid hormone	BP	1	LBH,CRY2,FIBIN,NR3C1	up_AFEM_EC
GO:0060337	0.0774	0.985	3	12	type I interferon signaling pathway	BP	1	IRAK1,SLC29A1,CACTIN	down_ACOR_VSMC
GO:0071357	0.0774	0.985	3	12	cellular response to type I interferon	BP	1	IRAK1,SLC29A1,CACTIN	down_ACOR_VSMC
GO:0003018	0.0774	0.983	3	42	vascular process in circulatory system	BP	1	HTR1D,AVPR1A,TBXA2R	up_AFEM_EC
GO:0050870	0.0774	0.983	3	42	positive regulation of T cell activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0051048	0.0774	0.983	3	42	negative regulation of secretion	BP	1	LEP,CRY2,RAB7A	up_AFEM_EC
GO:0048799	0.0774	0.99	2	10	animal organ maturation	BP	1	THBS3,GREM1	down_VCAV_EC
GO:2000780	0.0774	0.997	1	11	negative regulation of double-strand break	BP	1	CXHXorf57	up_VPOR_EC
GO:1904063	0.0774	0.997	1	17	negative regulation of cation transmembrane	BP	1	CAV1	up_VSAP_VSMC
GO:0033240	0.077449616	0.99794	1	3	positive regulation of cellular amine metabolic	BP	1	NR1H4	up_ACOR_EC
GO:1902531	0.077499773	0.95298	20	536	regulation of intracellular signal transduction	BP	1	NR1H4,SOX9,NDRG2,FZD5,DUSP26,NOD2,PDE4A,PAK3,TNFRSF19,ARHGDIB,MAPK8IP2,FIGNL1,LRRC15,SH3RF3,LRRC4,CLU,C23H3orf58,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0032970	0.0775	0.955	18	130	regulation of actin filament-based process	BP	1	SYNPO2L,FGF13,ARHGAP28,ACTN2,KCNE3,SYNPO2,F2RL1,JMY,NRP1,EVL,PRKCE,JUP,SSH3,EDN1,FAM107A,JAM3,INPP5K,WASL	up_ACOR_VSMC
GO:0006952	0.0775	0.96	12	319	defense response	BP	1	LEP,RAB20,CD40,F3,BPI,GPAM,HCK,CYLD,TBXA2R,NAPEPLD,CCL5,ADAM17	up_AFEM_EC
GO:0006839	0.0775	0.962	11	86	mitochondrial transport	BP	1	SREBF1,SLC25A5,TIMM44,SLC25A15,TOMM34,SAMM50,CYC1,SLC25A16,PMPCA,MRPL18,SLC25A19	down_ACOR_VSMC
GO:0009145	0.0775	0.974	5	40	purine nucleoside triphosphate biosynthetic	BP	0.902	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0034103	0.0775	0.985	3	12	regulation of tissue remodeling	BP	1	GREM1,B4GALT1,TFRC	down_ACOR_VSMC
GO:0032516	0.0775	0.991	2	8	positive regulation of phosphoprotein phosphatase activity	BP	0.902	PPP1R12A,CALM1	down_VSAP_EC
GO:0045605	0.0775	0.992	2	5	negative regulation of epidermal cell	BP	1	HOXA7,DLL1	up_VSAP_EC
GO:0072643	0.0775	0.992	2	5	interferon-gamma secretion	BP	1	ABL1,F2RL1	up_VSAP_EC
GO:0043244	0.0775	0.997	1	34	regulation of protein complex disassembly	BP	1	TAOK1	up_AORT_EC
GO:0042310	0.0775	0.997	1	21	vasoconstriction	BP	1	HTR7	up_APUL_EC
GO:0048640	0.0775	0.997	1	21	negative regulation of developmental growth	BP	1	TBX5	up_APUL_EC
GO:0097756	0.0775	0.997	1	21	negative regulation of blood vessel diameter	BP	1	HTR7	up_APUL_EC
GO:2001271	0.0775	1	1	1	negative regulation of cysteine-type endopeptidase activity involved in execution	BP	0.913	PAK2	up_VCAV_EC
GO:0051051	0.0776	0.958	14	112	negative regulation of transport	BP	1	HMGB1,SREBF1,SREBF2,NEDD4,HOXA3,SLC25A5,INSIG1,CAV1,SLC30A1,ARG2,GSTO1,EZR,CORO1A,REM1	down_ACOR_VSMC
GO:0031109	0.0776	0.972	6	36	microtubule polymerization or	BP	0.913	MZT1,STMN1,FES,TAOK1,ARHGEF2,FBXO5	up_VCAV_EC
GO:0009855	0.0776	0.983	3	42	determination of bilateral symmetry	BP	1	DLL1,GREM1,GREM2	up_AFEM_EC
GO:0048752	0.0776	0.992	2	5	semicircular canal morphogenesis	BP	0.913	CHD7,ZEB1	up_VCAV_EC
GO:0070307	0.0776	0.991	2	6	lens fiber cell development	BP	0.913	TMOD1,PROX1	up_VCAV_EC
GO:1901524	0.0776	0.992	2	5	regulation of mitophagy	BP	1	MFN2,HTRA2	up_VSAP_EC
GO:0010720	0.0776	0.989	2	110	positive regulation of cell development	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0048593	0.0776	0.997	1	41	camera-type eye morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0070586	0.0776	1	1	1	cell-cell adhesion involved in gastrulation	BP	1	MBP	up_ACOR_VSMC
GO:1904207	0.0776	1	1	1	regulation of chemokine (C-C motif) ligand 2	BP	1	MBP	up_ACOR_VSMC
GO:1904209	0.0776	1	1	1	positive regulation of chemokine (C-C motif)	BP	1	MBP	up_ACOR_VSMC

GO:0034115	0.0776	1	1	1	negative regulation of heterotypic cell-cell	BP	1	MBP	up_ACOR_VSMC
GO:0035633	0.0776	1	1	1	maintenance of permeability of blood-	BP	1	MBP	up_ACOR_VSMC
GO:0070587	0.0776	1	1	1	regulation of cell-cell adhesion involved in	BP	1	MBP	up_ACOR_VSMC
GO:2000343	0.0776	1	1	1	positive regulation of chemokine (C-X-C motif)	BP	1	MBP	up_ACOR_VSMC
GO:1990266	0.0776	0.997	1	24	neutrophil migration	BP	1	CCL24	up_VPUL_EC
GO:0031644	0.0776	0.997	1	19	regulation of neurological system process	BP	1	NETO1	up_VSAP_VSMC
GO:0071609	0.077650952	0.99793	1	3	chemokine (C-C motif) ligand 5 production	BP	1	MAVS	up_ACOR_EC
GO:0071649	0.077650952	0.99793	1	3	regulation of chemokine (C-C motif) ligand 5	BP	1	MAVS	up_ACOR_EC
GO:0043043	0.0777	0.954	18	247	peptide biosynthetic process	BP	1	UBA52,LARP6,COA1,SAMD4B,RPL23,RPL13,EIF3K,MRPL37,RPL27A,EEF2,ZFP36L1,RPL27,MRPS11,RPS27,ENSCAFG00000015122,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0007249	0.0777	0.962	11	71	I-kappaB kinase/NF-kappaB signaling	BP	1	MAP3K14,ABL1,F2RL1,RBCK1,MYD88,S100A4,NLRX1,ENSCAFG00000011993,MAPKBP1,IRAK1BP1,TRADD	up_VSAP_EC
GO:0033002	0.0777	0.965	9	55	muscle cell proliferation	BP	1	BMP4,FGFR2,PTGIR,NDRG2,CDKN1A,CLSTN1,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0046822	0.0777	0.965	9	53	regulation of nucleocytoplasmic	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,PARK7,PTPN14	up_ACOR_VSMC
GO:0050896	0.0777	0.98	6	2346	response to stimulus	BP	1	SLITRK5,CYP1A1,LIMK1,GATA5,CA2,C6	up_VCAV_VSMC
GO:0006807	0.0777	0.99	5	3221	nitrogen compound metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0043457	0.0777	0.985	3	11	regulation of cellular respiration	BP	1	PPARGC1A,BNIP3,PARK7	up_ACOR_VSMC
GO:0055082	0.0777	0.99	2	189	cellular chemical homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0000413	0.0777	1	1	1	protein peptidyl-prolyl isomerization	BP	1	PPIB	down_ACOR_VSMC
GO:1901077	0.0777	1	1	1	regulation of relaxation of muscle	BP	0.913	PDE4D	up_VCAV_EC
GO:1901078	0.0777	1	1	1	negative regulation of relaxation of muscle	BP	0.913	PDE4D	up_VCAV_EC
GO:1901897	0.0777	1	1	1	regulation of relaxation of cardiac muscle	BP	0.913	PDE4D	up_VCAV_EC
GO:1901898	0.0777	1	1	1	negative regulation of relaxation of cardiac	BP	0.913	PDE4D	up_VCAV_EC
GO:0048584	0.0778	0.944	44	592	positive regulation of response to stimulus	BP	0.903	VEGFA,SULF1,NR1H4,SERPINE1,SOCS5,JCAD,FAM49B,PTPN11,ILK,SMARCA4,PTGS2,MYO1C,CHSY1,HIF1A,TNIK,PTPN2,EIF2B1,PVR,NEO1,MTDH,ESM1,ADAM17,SKAP2,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,LYN,BNIP3,FAM162A,ATF3,GBP5,SH3GLB1,HTT,CALM1,DISC1,PAK2,A2M,INHBA,NRP1,SH3RF3,MADD,SEC13,MID1	down_VSAP_EC
GO:0072073	0.0778	0.968	7	60	kidney epithelium development	BP	0.903	ENSCAFG00000032470,ILK,HOXB7,MAGED1,CTNNB1,MYO1E,SIX4	down_VSAP_EC
GO:0045638	0.0778	0.997	1	33	negative regulation of myeloid cell	BP	1	HOXA9	up_AORT_EC
GO:0010594	0.0778	0.997	1	71	regulation of endothelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0055007	0.0778	0.997	1	31	cardiac muscle cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010092	0.0778	0.997	1	19	specification of animal organ identity	BP	1	SIX1	up_VFEM_EC
GO:0010977	0.0779	0.978	4	33	negative regulation of neuron projection	BP	1	THY1,TLX2,PRKCSH,RGMA	down_VCAV_EC
GO:0048585	0.0779	0.979	4	475	negative regulation of response to stimulus	BP	1	NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0071345	0.0779	0.983	3	210	cellular response to cytokine stimulus	BP	1	NRP2,STX4,ASPN	down_ACOR_EC
GO:0043170	0.0779	1	3	2980	macromolecule metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0051090	0.0779	0.989	2	134	regulation of DNA-binding transcription factor	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0009407	0.0779	1	1	1	toxin catabolic process	BP	1	GSTO1	down_ACOR_VSMC
GO:0006952	0.077926707	0.95826	13	319	defense response	BP	1	NR1H4,FNDC4,NOD2,IL33,TRIM8,PTGER4,MAPK8IP2,MAVS,IFIT2,CLSTN1,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0007212	0.078	0.985	3	11	dopamine receptor signaling pathway	BP	1	ADCY6,GNA14,GNAQ	up_ACOR_VSMC

GO:2000241	0.078	0.997	1	40	regulation of reproductive process	BP	1	CITED2	down_VPOR_EC
GO:1904888	0.078	0.997	1	31	cranial skeletal system development	BP	1	TBX15	up_VFEM_VSMC
GO:0048634	0.078	0.997	1	40	regulation of muscle organ development	BP	1	TBX5	up_VPUL_VSMC
GO:0032740	0.07806648	0.99791	1	3	positive regulation of interleukin-17 production	BP	1	NOD2	up_ACOR_EC
GO:0000820	0.078077209	0.99791	1	3	regulation of glutamine family amino acid	BP	1	NR1H4	up_ACOR_EC
GO:0009894	0.0781	0.951	23	277	regulation of catabolic process	BP	0.905	PRICKLE1,PLK3,SOCS5,TRIB3,PGAM1,SESN2,MSN,HIF1A,UCHL5,SMG7,MTDH,CNOT7,APOE,BNIP3,GSK3B,CDC37,SH3GLB1,HTT,ABHD5,DISC1,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0060055	0.0781	0.991	2	8	angiogenesis involved in wound healing	BP	0.905	SERPINE1,PRCP	down_VSAP_EC
GO:0007267	0.0781	0.99	2	332	cell-cell signaling	BP	1	SLITRK5,CA2	up_VCAV_VSMC
GO:0035801	0.0781	1	1	1	adrenal cortex development	BP	1	CITED2	up_ACOR_VSMC
GO:0035802	0.0781	1	1	1	adrenal cortex formation	BP	1	CITED2	up_ACOR_VSMC
GO:0048754	0.0781	0.997	1	57	branching morphogenesis of an epithelial tube	BP	1	EYA1	up_AFEM_VSMC
GO:0046503	0.0781	0.997	1	10	glycerolipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0070633	0.078106349	0.9979	1	3	transepithelial transport	BP	1	AQP1	up_ACOR_EC
GO:0070863	0.078183618	0.9979	1	3	positive regulation of protein exit from	BP	1	EDEM2	up_ACOR_EC
GO:1901701	0.0782	0.947	33	271	cellular response to oxygen-containing compound	BP	1	PTGFR,PPARGC1B,SLIT2,CDH1,ABL1,GOT1,CHRM1,OSR1,MAP3K5,PDGFD,KLF15,RARG,MGST1,STAT5A,RAB11B,PDK2,ZFP36L1,PIK3R1,ZEB1,SASH1,MYD88,CASTOR1,KCNB1,OSBPL7,RAF1,ZNF580,STX4,HTRA2,PPP3CB,NCK1,BGLAP,DDIT4,RAB11FIP2	up_VSAP_EC
GO:0042742	0.0782	0.969	7	39	defense response to bacterium	BP	1	F2RL1,PLA2G6,MYD88,MAPKBP1,CYBA,MAVS,JCHAIN	up_VSAP_EC
GO:0098739	0.0782	0.983	3	20	import across plasma membrane	BP	1	PRNP,FOLR2,SLC39A6	down_VCAV_EC
GO:0000266	0.0782	0.984	3	17	mitochondrial fission	BP	0.905	ENSCAFG00000007260,BNIP3,SLC25A46	down_VSAP_EC
GO:0043243	0.0782	0.985	3	11	positive regulation of protein complex	BP	1	ACTN2,F2RL1,BNIP3	up_ACOR_VSMC
GO:0051241	0.0782	0.99	2	336	negative regulation of multicellular organismal	BP	1	HOXC10,HOXA9	up_AFEM_VSMC
GO:0019730	0.0782	0.992	2	5	antimicrobial humoral response	BP	1	PLA2G6,JCHAIN	up_VSAP_EC
GO:0042771	0.0782	0.997	1	16	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	USP28	down_ACOR_EC
GO:0000494	0.0782	1	1	1	box C/D snoRNA 3'-end processing	BP	1	FBL	down_ACOR_VSMC
GO:1990258	0.0782	1	1	1	histone glutamine methylation	BP	1	FBL	down_ACOR_VSMC
GO:0033967	0.0782	1	1	1	box C/D snoRNA metabolic process	BP	1	FBL	down_ACOR_VSMC
GO:0034963	0.0782	1	1	1	box C/D snoRNA processing	BP	1	FBL	down_ACOR_VSMC
GO:0030879	0.0782	0.997	1	34	mammary gland development	BP	1	HOXA9	up_AORT_EC
GO:0007249	0.0782	0.997	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	ESR1	up_AORT_VSMC
GO:0051650	0.0782	0.997	1	65	establishment of vesicle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0021545	0.0782	0.997	1	21	cranial nerve development	BP	1	SIX1	up_VFEM_EC
GO:0055123	0.0782	0.997	1	40	digestive system development	BP	1	GATA5	up_VPUL_VSMC
GO:0003278	0.078236973	0.9979	1	3	apoptotic process involved in heart	BP	1	FOXC2	up_ACOR_EC
GO:0030950	0.078245193	0.9979	1	3	establishment or maintenance of actin	BP	1	AQP1	up_ACOR_EC
GO:0019627	0.078258124	0.9979	1	3	urea metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0030500	0.0783	0.975	5	25	regulation of bone mineralization	BP	1	BMP4,GJA1,ISG15,DDR2,SLC8A1	up_ACOR_VSMC
GO:0048627	0.0783	1	1	1	myoblast development	BP	1	SDC1	down_ACOR_VSMC

GO:0019064	0.0783	1	1	1	fusion of virus membrane with host plasma	BP	0.913	NECTIN2	up_VCAV_EC
GO:0030382	0.0783	1	1	1	sperm mitochondrion organization	BP	0.913	NECTIN2	up_VCAV_EC
GO:0039663	0.0783	1	1	1	membrane fusion involved in viral entry into	BP	0.913	NECTIN2	up_VCAV_EC
GO:0046814	0.0783	1	1	1	coreceptor-mediated virion attachment to host	BP	0.913	NECTIN2	up_VCAV_EC
GO:0044800	0.0783	1	1	1	multi-organism membrane fusion	BP	0.913	NECTIN2	up_VCAV_EC
GO:0044803	0.0783	1	1	1	multi-organism membrane organization	BP	0.913	NECTIN2	up_VCAV_EC
GO:1902532	0.0784	0.954	18	204	negative regulation of intracellular signal transduction	BP	0.906	ARHGEF2,NR1H4,SOCS5,HYOU1,FHL2,SESN2,PTGS2,HIF1A,PTPN2,APOE,WWC3,LYN,DDIT3,CBLC,ATF3,GSK3B,CALM1,TNFAIP1	down_VSAP_EC
GO:0007600	0.0784	0.963	10	73	sensory perception	BP	0.913	EPHB1,KIT,CHD7,HOXB8,TMEM150C,NAV2,ACPP,MMP24,SPTBN4,P2RX2	up_VCAV_EC
GO:0007160	0.0784	0.965	9	56	cell-matrix adhesion	BP	1	HOXA7,FAM107A,HOXD3,ABL1,EMP2,HPSE,PIK3R1,TIAM1,ACVRL1	up_VSAP_EC
GO:0007272	0.0784	0.972	6	31	ensheathment of neurons	BP	1	SH3TC2,MBP,WASF3,ATRN,DAG1,JAM3	up_ACOR_VSMC
GO:0008366	0.0784	0.972	6	31	axon ensheathment	BP	1	SH3TC2,MBP,WASF3,ATRN,DAG1,JAM3	up_ACOR_VSMC
GO:0034141	0.0784	0.992	2	5	positive regulation of toll-like receptor 3 signaling	BP	1	F2RL1,FLOT1	up_VSAP_EC
GO:0006119	0.0784	0.997	1	40	oxidative phosphorylation	BP	1	NDUFA10	down_AFEM_EC
GO:0033365	0.0784	0.998	1	276	protein localization to organelle	BP	1	JUP	down_VFEM_VSMC
GO:1901701	0.0784	0.998	1	271	cellular response to oxygen-containing	BP	1	JUP	down_VFEM_VSMC
GO:0032675	0.0784	0.997	1	34	regulation of interleukin-6 production	BP	1	BPI	up_AORT_EC
GO:0010634	0.0784	0.997	1	68	positive regulation of epithelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0060560	0.0784	0.997	1	58	developmental growth involved in	BP	1	LIMK1	up_VCAV_VSMC
GO:0021987	0.0784	0.997	1	37	cerebral cortex development	BP	1	EMX2	up_VFEM_VSMC
GO:0032930	0.078498869	0.99788	1	3	positive regulation of superoxide anion	BP	1	PRKCD	up_ACOR_EC
GO:0040008	0.0785	0.955	16	179	regulation of growth	BP	0.907	CELF1,ENPP1,PTPN11,IFRD1,SMARCA4,SESN2,HIF1A,ZPR1,ESM1,ADAM17,WWC3,IGFBP7,INHBA,SIX4,CDKN1A,NRP1	down_VSAP_EC
GO:0071103	0.0785	0.961	11	80	DNA conformation change	BP	0.913	PSME4,NASP,HHEX,HIST1H1A,TOP1,ASF1A,HMGB1,BLM,ATRX,HP1BP3,GINS4	up_VCAV_EC
GO:0043405	0.0785	0.964	9	85	regulation of MAP kinase activity	BP	0.907	VEGFA,PTPN11,TRIB3,TNIK,MAGED1,APOE,LYN,CBLC,MADD	down_VSAP_EC
GO:0098868	0.0785	0.985	3	11	bone growth	BP	1	RARG,DDR2,TGFBR2	up_VSAP_EC
GO:0019222	0.0785	1	2	1934	regulation of metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0051216	0.0785	0.997	1	70	cartilage development	BP	1	WNT7A	up_AORT_VSMC
GO:0048518	0.0786	0.965	11	1676	positive regulation of biological process	BP	1	EYA1,HOXA9,TOX,MAP2K6,AVPR1A,HOXB7,SIX1,MAB21L1,TIAM1,CYP26B1,CDC42EP5	up_VFEM_EC
GO:0051494	0.0786	0.969	7	44	negative regulation of cytoskeleton organization	BP	1	CAPG,LIMA1,STMN1,NEK2,RBM14,CORO1A,ARHGEF2	down_ACOR_VSMC
GO:0072376	0.0786	0.985	3	11	protein activation cascade	BP	1	KLKB1,CFD,FBLN1	up_VSAP_EC
GO:0097340	0.0786	0.991	2	6	inhibition of cysteine-type endopeptidase activity	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0097341	0.0786	0.991	2	6	zymogen inhibition	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0040034	0.0786	0.992	2	5	regulation of development,	BP	1	DLL1,GDPD5	up_VSAP_EC
GO:0002888	0.0786	0.992	2	5	positive regulation of myeloid leukocyte	BP	1	F2RL1,STX4	up_VSAP_EC
GO:2000736	0.0786	0.997	1	21	regulation of stem cell differentiation	BP	1	TBX5	up_APUL_EC
GO:0007497	0.0786	1	1	1	posterior midgut development	BP	0.913	EDNRB	up_VCAV_EC
GO:0014043	0.0786	1	1	1	negative regulation of neuron maturation	BP	0.913	EDNRB	up_VCAV_EC
GO:0035645	0.0786	1	1	1	enteric smooth muscle cell differentiation	BP	0.913	EDNRB	up_VCAV_EC
GO:0086100	0.0786	1	1	1	endothelin receptor signaling pathway	BP	0.913	EDNRB	up_VCAV_EC
GO:1903430	0.0786	1	1	1	negative regulation of cell maturation	BP	0.913	EDNRB	up_VCAV_EC

GO:1902338	0.07862149	0.99788	1	3	negative regulation of apoptotic process involved in	BP	1	FOXC2	up_ACOR_EC
GO:1904746	0.07862149	0.99788	1	3	negative regulation of apoptotic process	BP	1	FOXC2	up_ACOR_EC
GO:0045446	0.0787	0.972	6	32	endothelial cell differentiation	BP	1	BTG1,DLL1,F2RL1,ZEB1,MYD88,ACVRL1	up_VSAP_EC
GO:0042089	0.0787	0.979	4	21	cytokine biosynthetic process	BP	0.913	TLR4,GATA3,TLR3,BCL10	up_VCAV_EC
GO:0040001	0.0787	0.984	3	12	establishment of mitotic spindle localization	BP	1	ZW10,CENPA,NDC80	down_ACOR_VSMC
GO:0007193	0.0787	0.984	3	13	adenylate cyclase-inhibiting G protein-coupled receptor signaling	BP	0.913	EDN1,AKAP12,GRM8	up_VCAV_EC
GO:0060548	0.0787	0.983	3	294	negative regulation of cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:2000026	0.0787	0.991	2	560	regulation of multicellular organismal development	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0042635	0.0787	0.992	2	5	positive regulation of hair cycle	BP	1	HPSE,TRADD	up_VSAP_EC
GO:0051798	0.0787	0.992	2	5	positive regulation of hair follicle development	BP	1	HPSE,TRADD	up_VSAP_EC
GO:0070571	0.078763932	0.99787	1	3	negative regulation of neuron projection	BP	1	RGMA	up_ACOR_EC
GO:0051891	0.07877685	0.99787	1	3	positive regulation of cardioblast differentiation	BP	1	TBX5	up_ACOR_EC
GO:0009890	0.0788	0.943	44	420	negative regulation of biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,ILF3,CBX5,ATAD2,HMGA1,EIF4A3,SREBF2,SMC1A,NEDD4,MTDH,NAB2,BIRC5,INSIG1,CAV1,TIMELESS,FAM129B,AURKB,EZH2,GREM1,PLK3,HOXA7,UHRF1,GMNN,BRCA1,NOC2L,PPARD,NCL,SUV39H1,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:0031668	0.0788	0.96	12	79	cellular response to extracellular stimulus	BP	1	PRKAA2,CASTOR1,CDKN2B,GABARAPL1,CDKN1A,SESN3,PIK3C3,LAMP2,SESN1,FAM107A,BMT2,ZFYVE1	up_ACOR_VSMC
GO:1903727	0.0788	0.984	3	16	positive regulation of phospholipid metabolic	BP	0.907	NR1H4,LYN,SH3GLB1	down_VSAP_EC
GO:0002428	0.0788	1	1	1	antigen processing and presentation of peptide antigen via MHC class Ib	BP	1	B2M	up_ACOR_VSMC
GO:0002477	0.0788	1	1	1	antigen processing and presentation of exogenous peptide	BP	1	B2M	up_ACOR_VSMC
GO:0002481	0.0788	1	1	1	antigen processing and presentation of exogenous protein antigen via MHC class Ib,	BP	1	B2M	up_ACOR_VSMC
GO:0010041	0.0788	1	1	1	response to iron(III) ion	BP	1	B2M	up_ACOR_VSMC
GO:0071283	0.0788	1	1	1	cellular response to iron(III) ion	BP	1	B2M	up_ACOR_VSMC
GO:1900390	0.0788	1	1	1	regulation of iron ion import	BP	1	B2M	up_ACOR_VSMC
GO:1904435	0.0788	1	1	1	regulation of transferrin receptor binding	BP	1	B2M	up_ACOR_VSMC
GO:1904437	0.0788	1	1	1	positive regulation of transferrin receptor	BP	1	B2M	up_ACOR_VSMC
GO:0034756	0.0788	1	1	1	regulation of iron ion transport	BP	1	B2M	up_ACOR_VSMC
GO:1904432	0.0788	1	1	1	regulation of ferrous iron binding	BP	1	B2M	up_ACOR_VSMC
GO:1904434	0.0788	1	1	1	positive regulation of ferrous iron binding	BP	1	B2M	up_ACOR_VSMC
GO:0018216	0.078823351	0.99786	1	3	peptidyl-arginine methylation	BP	1	NR1H4	up_ACOR_EC
GO:0045786	0.0789	0.951	22	195	negative regulation of cell cycle	BP	0.913	PLK2,CXCL8,TNFAIP3,GATA3,BMP2,HHEX,PROX1,UHRF2,THOC1,ETAA1,USP28,TAOK1,BLM,RAD21,RAD17,SKIL,CUL4A,ZW10,ATRX,NR4A1,TOPBP1,FBXO5	up_VCAV_EC
GO:0034654	0.0789	0.965	10	1236	nucleobase-containing compound biosynthetic	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,TNRC6B,NEDD4	down_ACOR_EC
GO:0019882	0.0789	0.975	5	25	antigen processing and presentation	BP	1	CTSS,DLA88,B2M,ERAP1,TAPBPL	up_ACOR_VSMC
GO:0033559	0.0789	0.979	4	21	unsaturated fatty acid metabolic process	BP	0.913	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0003071	0.0789	0.992	2	5	renal system process involved in regulation of systemic arterial blood	BP	1	EMP2,F2RL1	up_VSAP_EC

GO:0055026	0.0789	0.992	2	5	negative regulation of cardiac muscle tissue	BP	1	DLL1,SAV1	up_VSAP_EC
GO:0071526	0.0789	0.997	1	12	semaphorin-plexin signaling pathway	BP	1	NRP2	down_ACOR_EC
GO:0009888	0.0789	1	1	545	tissue development	BP	1	GATA5	down_AFEM_VSMC
GO:0071560	0.0789	0.997	1	72	cellular response to transforming growth	BP	1	WNT7A	up_AORT_VSMC
GO:0051055	0.0789	0.997	1	21	negative regulation of lipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0070252	0.0789	0.997	1	17	actin-mediated cell contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0031115	0.07894771	0.99786	1	3	negative regulation of microtubule	BP	1	TUBB4A	up_ACOR_EC
GO:0070661	0.079	0.968	7	63	leukocyte proliferation	BP	0.909	MSN,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0006109	0.079	0.971	6	51	regulation of carbohydrate metabolic	BP	0.909	ENPP1,PGAM1,SESN2,HIF1A,SLC45A3,PTPN2	down_VSAP_EC
GO:0021879	0.079	0.997	1	15	forebrain neuron differentiation	BP	1	NRP2	down_ACOR_EC
GO:0030974	0.079	1	1	1	thiamine pyrophosphate transmembrane transport	BP	1	SLC25A19	down_ACOR_VSMC
GO:0048732	0.079	0.997	1	116	gland development	BP	1	HOXA3	up_APUL_VSMC
GO:0021772	0.079	0.997	1	11	olfactory bulb development	BP	1	SEMA3A	up_VPOR_EC
GO:0021988	0.079	0.997	1	11	olfactory lobe development	BP	1	SEMA3A	up_VPOR_EC
GO:0070527	0.079	0.997	1	10	platelet aggregation	BP	1	SLC7A11	up_VPOR_EC
GO:0002408	0.079	1	1	1	myeloid dendritic cell chemotaxis	BP	1	ARHGEF5	up_VSAP_EC
GO:1904468	0.079086013	0.99785	1	3	negative regulation of tumor necrosis factor	BP	1	NR1H4	up_ACOR_EC
GO:0006678	0.079086168	0.99785	1	3	glucosylceramide metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0032496	0.0791	0.962	10	77	response to lipopolysaccharide	BP	0.913	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,IRF8,PELI1,ABCA1,PLCG2,GCH1	up_VCAV_EC
GO:0043414	0.0791	0.962	10	70	macromolecule methylation	BP	0.913	IWS1,GATA3,ARID4B,NSD1,WTAP,MTA2,KDM3A,ATRX,ZC3H13,TET2	up_VCAV_EC
GO:0006301	0.0791	0.984	3	12	postreplication repair	BP	1	PCNA,POLH,DTL	down_ACOR_VSMC
GO:0000075	0.0791	0.989	2	91	cell cycle checkpoint	BP	1	USP28,ATRIP	down_ACOR_EC
GO:0045923	0.0791	0.99	2	8	positive regulation of fatty acid metabolic process	BP	0.909	PTGS2,SLC45A3	down_VSAP_EC
GO:0046461	0.0791	0.992	2	5	neutral lipid catabolic process	BP	1	LIPC,ABHD16A	up_VSAP_EC
GO:0046464	0.0791	0.992	2	5	acylglycerol catabolic process	BP	1	LIPC,ABHD16A	up_VSAP_EC
GO:0050727	0.0791	0.997	1	74	regulation of inflammatory response	BP	1	ESR1	up_AORT_VSMC
GO:0051051	0.0791	0.997	1	112	negative regulation of transport	BP	1	HOXA3	up_APUL_VSMC
GO:0035457	0.079182062	0.99784	1	3	cellular response to interferon-alpha	BP	1	IFIT2	up_ACOR_EC
GO:0007276	0.0792	0.955	16	130	gamete generation	BP	1	NDC1,TRIP13,CTDNEP1,FBXO5,NCAPH,POC1A,HIST1H1A,FOSL1,HMGB2,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,TTLL1	down_ACOR_VSMC
GO:0051403	0.0792	0.959	12	89	stress-activated MAPK cascade	BP	0.913	EPHB1,MAP3K11,SH2D3C,TLR4,EDN1,MAP3K3,BMP2,MAPK13,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0071559	0.0792	0.968	7	75	response to transforming growth factor beta	BP	1	SMAD9,VASN,FBN1,NR3C1,ASPN,ZFP36L1,FUT8	down_VCAV_EC
GO:0003008	0.0792	0.99	2	336	system process	BP	1	HOXC10,IRX5	up_AFEM_VSMC
GO:0009790	0.0792	0.99	2	335	embryo development	BP	1	HOXC6,C6	up_VCAV_VSMC
GO:0035909	0.0792	0.997	1	14	aorta morphogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0010812	0.0792	0.997	1	19	negative regulation of cell-substrate adhesion	BP	1	HOXA7	up_VFEM_EC
GO:0023051	0.0793	0.976	5	954	regulation of signaling	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0060441	0.0793	0.984	3	11	epithelial tube branching involved in lung	BP	1	BMP4,FGFR2,DAG1	up_ACOR_VSMC
GO:0031629	0.0793	0.99	2	8	synaptic vesicle fusion to presynaptic active zone membrane	BP	0.913	SNAP23,STX11	up_VCAV_EC

GO:0099500	0.0793	0.99	2	8	vesicle fusion to plasma membrane	BP	0.913	SNAP23,STX11	up_VCAV_EC
GO:0006071	0.0793	0.992	2	5	glycerol metabolic process	BP	1	GOT1,TKFC	up_VSAP_EC
GO:2001256	0.0793	0.992	2	5	regulation of store-operated calcium entry	BP	1	SLC8B1,CRACR2B	up_VSAP_EC
GO:0006531	0.0793	0.992	2	5	aspartate metabolic process	BP	1	GOT1,ASS1	up_VSAP_EC
GO:0034766	0.0793	0.997	1	19	negative regulation of ion transmembrane transport	BP	1	NEDD4	down_ACOR_EC
GO:0016358	0.0793	0.997	1	58	dendrite development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0016255	0.079342525	0.99784	1	3	attachment of GPI anchor to protein	BP	1	PIGS	up_ACOR_EC
GO:0008610	0.0794	0.952	19	177	lipid biosynthetic process	BP	0.913	ADGRF5,PDGFB,EDN1,PTGS1,SPTLC2,MTOR,SAMD8,BMP2,PROX1,ENSCAFG00000010596,SH3GLB1,ELOVL7,PTGS2,PLCG2,CREB1,LBR,IMPA1,PIP5K1B,ALDH1A3	up_VCAV_EC
GO:0050794	0.0794	0.964	16	3075	regulation of cellular process	BP	1	NR1H4,TBX5,MAPK10,BPI,HOXA3,PLCL1,TUBB4A,PCSK1N,ARHGEF26,LZTS1,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,PDE1A	up_APUL_EC
GO:0002683	0.0794	0.97	6	126	negative regulation of immune system process	BP	1	HOXA9,HOXA7,DLL1,BPI,GPAM,CYLD	up_AFEM_EC
GO:0050886	0.0794	0.983	3	17	endocrine process	BP	0.911	PTPN11,RAB11FIP1,INHBA	down_VSAP_EC
GO:0010468	0.0794	0.988	3	1270	regulation of gene expression	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0002437	0.0794	0.991	2	6	inflammatory response to antigenic stimulus	BP	1	HMGB1,HMGB2	down_ACOR_VSMC
GO:0006002	0.0794	0.992	2	5	fructose 6-phosphate metabolic process	BP	1	PFKM,PFKL	up_ACOR_VSMC
GO:0007389	0.0794	0.989	2	137	pattern specification process	BP	1	TBX5,HOXA3	up_VPUL_EC
GO:0006357	0.0794	1	1	547	regulation of transcription by RNA polymerase II	BP	1	GATA5	down_AFEM_VSMC
GO:0051455	0.0794	1	1	1	attachment of spindle microtubules to kinetochore involved in homologous chromosome	BP	0.914	CENPC	up_VCAV_EC
GO:0072210	0.0794	0.997	1	19	metanephric nephron development	BP	1	SALL1	up_VSAP_VSMC
GO:0045596	0.0795	0.956	14	186	negative regulation of cell differentiation	BP	1	VASN,FBN1,BMPR1A,THY1,TLX2,GLI3,ZFP36L1,LOXL3,TWIST2,PRKCSH,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0002526	0.0795	0.983	3	17	acute inflammatory response	BP	0.912	PRCP,PTGS2,A2M	down_VSAP_EC
GO:0097205	0.0795	0.984	3	12	renal filtration	BP	0.914	ADGRF5,PDGFB,CD34	up_VCAV_EC
GO:0002643	0.0795	0.992	2	5	regulation of tolerance induction	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0061004	0.0795	0.992	2	5	pattern specification involved in kidney	BP	1	OSR1,IRX3	up_VSAP_EC
GO:0072048	0.0795	0.992	2	5	renal system pattern specification	BP	1	OSR1,IRX3	up_VSAP_EC
GO:0043583	0.0795	0.997	1	59	ear development	BP	1	EYA1	up_AFEM_VSMC
GO:2001236	0.0795	0.997	1	59	regulation of extrinsic apoptotic signaling	BP	1	EYA1	up_AFEM_VSMC
GO:0051145	0.0795	0.997	1	21	smooth muscle cell differentiation	BP	1	NPNT	up_APUL_EC
GO:0003415	0.07951581	0.99783	1	3	chondrocyte hypertrophy	BP	1	SOX9	up_ACOR_EC
GO:0072513	0.079519756	0.99783	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	TBX5	up_ACOR_EC
GO:0003214	0.079564451	0.99782	1	3	cardiac left ventricle morphogenesis	BP	1	TBX5	up_ACOR_EC
GO:0060737	0.079578835	0.99782	1	3	prostate gland morphogenetic growth	BP	1	SOX9	up_ACOR_EC
GO:0001932	0.0796	0.942	49	416	regulation of protein phosphorylation	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,LATS2,PDE5A,SASH1,FGF18,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,LRRC4,PRKAG3,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC

GO:0016310	0.0796	0.944	40	641	phosphorylation	BP	1	NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,UQCR10,ASPN,THY1,ADK,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,CAMK2D,SPRED1,MAPRE3,CDKL2,DDR2,SHC1,FBH1,GREM1,BRSK1,CDK14	down_VCAV_EC
GO:0044092	0.0796	0.946	33	270	negative regulation of molecular function	BP	1	TNNT2,ARHGAP28,ACTN2,KCNE3,RECK,BMP4,EIF4A2,SH3RF2,XIRP1,LATS2,CST3,EGLN1,CDKN1A,CLSTN1,LRPAP1,SMPD1,SH3RF1,MARF1,PPP1R26,PSEN1,SPINK2,MITD1,DUSP22,DUSP26,LRRC4,B2M,DISC1,INPP5K,WFS1,SH3BP4,PARK7,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:2000145	0.0796	0.998	1	279	regulation of cell motility	BP	1	JUP	down_VFEM_VSMC
GO:0003151	0.0796	0.997	1	34	outflow tract morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0044387	0.079624361	0.99782	1	3	negative regulation of protein kinase activity by regulation of protein	BP	1	DUSP26	up_ACOR_EC
GO:1903867	0.079665132	0.99782	1	3	extraembryonic membrane development	BP	1	FZD5	up_ACOR_EC
GO:0019439	0.0797	0.953	18	150	aromatic compound catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,PDXP,AIFM1,ENSCAFG00000015189,RNASEH2C,NUDT1,EXOSC5,NUDT3	down_ACOR_VSMC
GO:0045926	0.0797	0.961	11	72	negative regulation of growth	BP	1	ENSCAFG00000009113,WNT11,HNF4A,SLIT2,SLC6A4,SAV1,MT2A,FXN,MYD88,SMARCA2,ACVRL1	up_VSAP_EC
GO:0043547	0.0797	0.989	2	61	positive regulation of GTPase activity	BP	1	ENSCAFG00000002015,ENSCAFG00000032731	up_VPOR_EC
GO:0050768	0.0797	0.997	1	66	negative regulation of neurogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0032623	0.0797	0.997	1	21	interleukin-2 production	BP	1	NR1H4	up_APUL_EC
GO:0071230	0.0797	0.997	1	23	cellular response to amino acid stimulus	BP	1	NTRK2	up_APUL_EC
GO:1901224	0.0797	0.997	1	20	positive regulation of NIK/NF-kappaB signaling	BP	1	TLR2	up_VSAP_VSMC
GO:0007200	0.079703476	0.98913	2	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	PTH1R,ACTN2	up_ACOR_EC
GO:0006930	0.079728098	0.99781	1	3	substrate-dependent cell migration, cell extension	BP	1	NRP1	up_ACOR_EC
GO:0060078	0.079777864	0.98917	2	17	regulation of postsynaptic membrane potential	BP	1	INSYN1,MAPK8IP2	up_ACOR_EC
GO:0099565	0.079777864	0.98917	2	17	chemical synaptic transmission, postsynaptic	BP	1	INSYN1,MAPK8IP2	up_ACOR_EC
GO:0043068	0.0798	0.954	16	190	positive regulation of programmed cell death	BP	0.914	CASP3,PTPN2,MAGED1,CTNNB1,LYN,BNIP3,DDIT3,FAM162A,ATF3,SH3GLB1,HTT,REST,PAK2,INHBA,CDKN1A,SPINK2	down_VSAP_EC
GO:0001944	0.0798	0.982	3	263	vasculature development	BP	1	HOXA3,NTRK2,HOXA1	up_APUL_EC
GO:0046483	0.0798	1	2	1948	heterocycle metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0002089	0.0798	0.99	2	8	lens morphogenesis in camera-type eye	BP	0.914	BCAR3,CTNNB1	down_VSAP_EC
GO:0060047	0.0798	0.997	1	57	heart contraction	BP	1	IRX5	up_AFEM_VSMC
GO:0071493	0.079819296	0.99781	1	3	cellular response to UV-B	BP	1	MFAP4	up_ACOR_EC
GO:0023021	0.079829232	0.99781	1	3	termination of signal transduction	BP	1	PRKCD	up_ACOR_EC
GO:0009650	0.079877785	0.99781	1	3	UV protection	BP	1	MFAP4	up_ACOR_EC
GO:0098609	0.0799	0.949	24	181	cell-cell adhesion	BP	1	LEP,GATA5,CD83,MBP,BMP4,PDE5A,CITED2,PKP4,CD274,LIMS2,PTPN22,NPNT,SPINT2,VCAM1,PSEN1,JUP,CDH18,PERP,DUSP22,JAM3,CELSR2,ATP2C1,BVES,PAG1	up_ACOR_VSMC
GO:0035295	0.0799	0.957	13	356	tube development	BP	1	IRX3,LEP,ANGPT4,HOXA7,DLL1,F3,THRB,TMEM100,GREM1,LUZP1,TBXA2R,PTPRB,CLIC4	up_AFEM_EC
GO:0006139	0.0799	0.971	8	1909	nucleobase-containing compound metabolic	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051094	0.0799	0.978	4	388	positive regulation of developmental process	BP	1	TOX,HOXB7,SIX1,CYP26B1	up_VFEM_EC
GO:0030947	0.0799	0.984	3	12	regulation of vascular endothelial growth factor receptor signaling	BP	0.917	HHEX,PRKD2,HIF1A	up_VCAV_EC

GO:0009719	0.0799	0.99	2	395	response to endogenous stimulus	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0036446	0.0799	1	1	1	myofibroblast differentiation	BP	1	TP53INP1	up_ACOR_VSMC
GO:0072702	0.0799	1	1	1	response to methyl methanesulfonate	BP	1	TP53INP1	up_ACOR_VSMC
GO:0072703	0.0799	1	1	1	cellular response to methyl methanesulfonate	BP	1	TP53INP1	up_ACOR_VSMC
GO:1904760	0.0799	1	1	1	regulation of myofibroblast	BP	1	TP53INP1	up_ACOR_VSMC
GO:1904761	0.0799	1	1	1	negative regulation of myofibroblast	BP	1	TP53INP1	up_ACOR_VSMC
GO:1905937	0.0799	1	1	1	negative regulation of germ cell proliferation	BP	1	PRDX4	up_ACOR_VSMC
GO:2000255	0.0799	1	1	1	negative regulation of male germ cell	BP	1	PRDX4	up_ACOR_VSMC
GO:0072073	0.0799	0.997	1	60	kidney epithelium development	BP	1	EYA1	up_AFEM_VSMC
GO:1901861	0.0799	0.997	1	41	regulation of muscle tissue development	BP	1	TBX5	up_VPUL_VSMC
GO:0009166	0.08	0.997	1	31	nucleotide catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0031110	0.08	0.997	1	24	regulation of microtubule polymerization or depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0032755	0.08	0.997	1	24	positive regulation of interleukin-6 production	BP	1	ARHGEF2	up_VPUL_EC
GO:0035051	0.08	0.997	1	41	cardiocyte differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0034111	0.080092378	0.99779	1	3	negative regulation of homotypic cell-cell	BP	1	PRKCD	up_ACOR_EC
GO:1901700	0.0801	0.944	39	364	response to oxygen-containing compound	BP	0.917	CXCL8,CALCRL,TIE1,TNFAIP3,PPARG,TNIP1,PDGFB,P2RX7,BAIAP2L1,SELL,PDE4D,MEF2C,RAPGEF1,TLR4,IRF8,PELI1,YES1,MTOR,ABCA1,MAPK13,SMARCA4,APOD,NCK1,TIMELESS,JAG1,GUCY1B1,RAPGEF2,PLCG2,CREB1,CTNNA1,GCH1,BLM,RIPK1,PDGFD,HIF1A,NR4A1,P2RX2,ZEB1,ARHGEF2	up_VCAV_EC
GO:0006796	0.0801	0.967	8	938	phosphate-containing compound metabolic	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ACSL3,MYO1D,TNRC6B,ASPN	down_ACOR_EC
GO:0032092	0.0801	0.971	6	38	positive regulation of protein binding	BP	0.917	TMEM173,MEF2C,RALB,BMP2,MFNG,RAPGEF2	up_VCAV_EC
GO:0032411	0.0801	0.975	5	24	positive regulation of transporter activity	BP	1	ACTN2,PLCG2,TCAF1,AKAP6,PARK7	up_ACOR_VSMC
GO:0042149	0.0801	0.979	4	17	cellular response to glucose starvation	BP	1	PRKAA2,SESN3,PIK3C3,SESN1	up_ACOR_VSMC
GO:0061614	0.0801	0.978	4	20	pri-miRNA transcription by RNA polymerase II	BP	0.917	PDGFB,BMP2,SMARCA4,HIF1A	up_VCAV_EC
GO:0003094	0.0801	0.984	3	11	glomerular filtration	BP	1	EMP2,SULF2,JCHAIN	up_VSAP_EC
GO:0051241	0.0801	0.99	2	336	negative regulation of multicellular organismal	BP	1	GATA5,LRRC17	up_VCAV_VSMC
GO:0032945	0.0801	0.997	1	17	negative regulation of mononuclear cell	BP	1	LYN	down_ACOR_EC
GO:0050672	0.0801	0.997	1	17	negative regulation of lymphocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0032680	0.0801	0.997	1	36	regulation of tumor necrosis factor production	BP	1	BPI	up_AORT_EC
GO:0045600	0.0801	0.997	1	21	positive regulation of fat cell differentiation	BP	1	WIF1	up_APUL_EC
GO:0060537	0.0801	0.997	1	117	muscle tissue development	BP	1	TBX5	up_APUL_VSMC
GO:0046889	0.0801	0.997	1	24	positive regulation of lipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:1903115	0.0802	0.984	3	12	regulation of actin filament-based movement	BP	1	FGF13,KCNE3,JUP	up_ACOR_VSMC
GO:0018958	0.0802	0.989	2	20	phenol-containing compound metabolic	BP	1	MOXD1,GCNT4	up_AFEM_EC
GO:0001654	0.0802	0.989	2	110	eye development	BP	1	IRX5,MAB21L1	up_VSAP_VSMC
GO:0048880	0.0802	0.989	2	110	sensory system development	BP	1	IRX5,MAB21L1	up_VSAP_VSMC
GO:0150063	0.0802	0.989	2	110	visual system development	BP	1	IRX5,MAB21L1	up_VSAP_VSMC
GO:0050795	0.0802	0.997	1	15	regulation of behavior	BP	1	HOXA1	down_ACOR_EC
GO:0033209	0.0802	0.997	1	24	tumor necrosis factor-mediated signaling	BP	1	NR1H4	up_VPUL_EC
GO:0042637	0.080220067	0.99779	1	3	catagen	BP	1	CDH3	up_ACOR_EC

GO:0051794	0.080220067	0.99779	1	3	regulation of timing of catagen	BP	1	CDH3	up_ACOR_EC
GO:0061013	0.0803	0.971	6	32	regulation of mRNA catabolic process	BP	1	AXIN2,TENT5C,ZFP36L1,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0070979	0.0803	0.984	3	13	protein K11-linked ubiquitination	BP	1	UBE2S,UBE2T,UBE2C	down_ACOR_VSMC
GO:0060676	0.0803	0.991	2	6	ureteric bud formation	BP	1	GREM1,SIX4	down_ACOR_VSMC
GO:1901137	0.0803	0.989	2	232	carbohydrate derivative biosynthetic process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0001708	0.0803	0.989	2	20	cell fate specification	BP	1	HOXC10,DLL1	up_AFEM_EC
GO:0009205	0.0803	0.997	1	98	purine ribonucleoside triphosphate metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0060419	0.0803	0.997	1	22	heart growth	BP	1	TBX5	up_APUL_EC
GO:0044344	0.0803	0.997	1	33	cellular response to fibroblast growth factor	BP	1	FGF5	up_VPOR_VSMC
GO:0071774	0.0803	0.997	1	33	response to fibroblast growth factor	BP	1	FGF5	up_VPOR_VSMC
GO:0046620	0.0803	0.997	1	30	regulation of organ growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0014902	0.0803	0.997	1	34	myotube differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0006596	0.080316726	0.99778	1	3	polyamine biosynthetic process	BP	1	AZIN2	up_ACOR_EC
GO:0009446	0.080316726	0.99778	1	3	putrescine biosynthetic process	BP	1	AZIN2	up_ACOR_EC
GO:0033387	0.080316726	0.99778	1	3	putrescine biosynthetic process from ornithine	BP	1	AZIN2	up_ACOR_EC
GO:1902713	0.080355927	0.99778	1	3	regulation of interferon-gamma secretion	BP	1	NR1H4	up_ACOR_EC
GO:0006725	0.0804	1	2	1956	cellular aromatic compound metabolic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0002639	0.0804	0.997	1	14	positive regulation of immunoglobulin	BP	1	STX4	down_ACOR_EC
GO:0042471	0.0804	0.997	1	34	ear morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0140059	0.080445053	0.99777	1	3	dendrite arborization	BP	1	NRP1	up_ACOR_EC
GO:0008283	0.0805	0.974	5	545	cell proliferation	BP	1	EYA1,SIX1,MAB21L1,TIAM1,MTSS1	up_VFEM_EC
GO:0046426	0.0805	0.983	3	20	negative regulation of JAK-STAT cascade	BP	1	DCN,BGN,ASPN	down_VCAV_EC
GO:1904893	0.0805	0.983	3	20	negative regulation of STAT cascade	BP	1	DCN,BGN,ASPN	down_VCAV_EC
GO:0045844	0.0805	0.997	1	24	positive regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0048636	0.0805	0.997	1	24	positive regulation of muscle organ	BP	1	TBX5	up_VPUL_EC
GO:0051017	0.0806	0.97	6	49	actin filament bundle assembly	BP	0.922	ACTN1,FSCN1,DPYSL3,PLS3,NRP1,TNFAIP1	down_VSAP_EC
GO:0007095	0.0806	0.984	3	11	mitotic G2 DNA damage checkpoint	BP	0.917	TAOK1,BLM,TOPBP1	up_VCAV_EC
GO:0008284	0.0806	0.989	2	238	positive regulation of cell proliferation	BP	1	HOXA3,TBX5	up_VPUL_VSMC
GO:0002687	0.0806	0.997	1	36	positive regulation of leukocyte migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0007612	0.0806	0.997	1	33	learning	BP	1	NETO1	up_VFEM_VSMC
GO:0060385	0.080644783	0.99776	1	3	axonogenesis involved in innervation	BP	1	NRP1	up_ACOR_EC
GO:0072497	0.080681767	0.99776	1	3	mesenchymal stem cell differentiation	BP	1	SOX9	up_ACOR_EC
GO:0051668	0.080689854	0.98186	3	39	localization within membrane	BP	1	CALY,AGRN,LRP4	up_ACOR_EC
GO:0030203	0.0807	0.977	4	27	glycosaminoglycan metabolic process	BP	0.923	ENSCAFG00000032470,CEMIP2,CHSY1,EXT1	down_VSAP_EC
GO:0032535	0.0807	0.982	3	128	regulation of cellular component size	BP	1	SEMA3A,TWF1,RNF6	up_VPOR_EC
GO:0006622	0.0807	0.997	1	11	protein targeting to lysosome	BP	1	GCC2	up_VPOR_EC
GO:0021869	0.080700661	0.99776	1	3	forebrain ventricular zone progenitor cell division	BP	1	DIXDC1	up_ACOR_EC
GO:0034350	0.080734633	0.99776	1	3	regulation of glial cell apoptotic process	BP	1	PRKCD	up_ACOR_EC
GO:0034351	0.080734633	0.99776	1	3	negative regulation of glial cell apoptotic process	BP	1	PRKCD	up_ACOR_EC
GO:0006685	0.080759903	0.99776	1	3	sphingomyelin catabolic process	BP	1	PRKCD	up_ACOR_EC

GO:0019221	0.0808	0.961	10	102	cytokine-mediated signaling pathway	BP	0.923	NR1H4,SOCS5,ILK,CX3CL1,PTPN2,ADAM17,CNOT7,ENSCAFG00000002015,ZC3H15,CDC37	down_VSAP_EC
GO:0033500	0.0808	0.961	10	64	carbohydrate homeostasis	BP	1	ADRA1B,LEP,PRKAA2,ERO1B,SESN3,PRKCE,RAB11B,INPP5K,WFS1,PARK7	up_ACOR_VSMC
GO:0042593	0.0808	0.961	10	64	glucose homeostasis	BP	1	ADRA1B,LEP,PRKAA2,ERO1B,SESN3,PRKCE,RAB11B,INPP5K,WFS1,PARK7	up_ACOR_VSMC
GO:0051494	0.0808	0.968	7	44	negative regulation of cytoskeleton organization	BP	0.917	ARHGAP28,TMOD1,STMN1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0042325	0.0808	0.973	5	463	regulation of phosphorylation	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0051897	0.0808	0.989	2	20	positive regulation of protein kinase B signaling	BP	1	LEP,F3	up_AFEM_EC
GO:1901184	0.0808	0.989	2	20	regulation of ERBB signaling pathway	BP	1	RAB7A,ADAM17	up_AFEM_EC
GO:0034097	0.0808	0.989	2	238	response to cytokine	BP	1	IL22RA1,SLIT2	up_VPUL_VSMC
GO:0098927	0.0808	0.997	1	17	vesicle-mediated transport between endosomal compartments	BP	1	MYO1D	down_ACOR_EC
GO:1903522	0.0808	0.997	1	58	regulation of blood circulation	BP	1	IRX5	up_AFEM_VSMC
GO:0031424	0.080839774	0.99775	1	3	keratinization	BP	1	CDH3	up_ACOR_EC
GO:0060080	0.080856613	0.99775	1	3	inhibitory postsynaptic potential	BP	1	INSYN1	up_ACOR_EC
GO:0046628	0.080863426	0.99775	1	3	positive regulation of insulin receptor signaling	BP	1	NR1H4	up_ACOR_EC
GO:0046890	0.0809	0.97	6	51	regulation of lipid biosynthetic process	BP	0.923	NR1H4,TRIB3,PTGS2,SLC45A3,APOE,REST	down_VSAP_EC
GO:0021885	0.0809	0.974	5	24	forebrain cell migration	BP	1	FGF13,NRP1,PSEN1,DISC1,SUN1	up_ACOR_VSMC
GO:0042149	0.0809	0.983	3	17	cellular response to glucose starvation	BP	0.923	ASNS,HSPA5,SESN2	down_VSAP_EC
GO:0051270	0.0809	0.982	3	296	regulation of cellular component movement	BP	1	TBX5,CCL24,ARHGEF2	up_VPUL_EC
GO:0048645	0.0809	0.997	1	33	animal organ formation	BP	1	HOXA3	up_VPOR_VSMC
GO:0048843	0.080954484	0.99775	1	3	negative regulation of axon extension involved in axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0032502	0.081	0.936	94	1661	developmental process	BP	1	ADAMTS2,GPAM,NOTCH2,HSPB6,PDGFRB,SMAD9,LRP1,DCN,NAB2,NDN,ANGPT1,PRNP,SDC4,VASN,FBN1,GLIPR2,KANK2,THBS3,BMPR1A,LOX,LMO4,EVC,RECK,TRPV2,ANPEP,COL6A1,CLIP3,NUMBL,NAGLU,CHRDL1,TBX15,AKT2,TFE3,ENSCAFG00000018277,SYDE1,HOXC4,LAMA3,CLSTN1,CSPG4,TRIM8,PKD1,PRMT6,ENSCAFG00000013404,PRELP,SEMA3C,ASPN,POLDIP2,CRISPLD2,THY1,TEAD1,HAPLN3,PEX5,TLX2,VCAN,B4GALT1,GLI3,ADAMTSL4,EEF2,ZFP36L1,MYDGF,SASH1,NCDN,RBM38,IFT57,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,A2M,IRX5,TSC22D3,UST,GLIS2,TWIST2,PRKCSH,DDR2,SHC1,RDH10,PCSK6,OMD,GREM1,NAPEPLD,CLIC4,FOXO3,SOAT1,THRB,ZBTB16,ANKRD54,RGMA,SEC61A1,BRSK1	down_VCAV_EC
GO:0042592	0.081	0.94	52	522	homeostatic process	BP	0.917	EDNRB,HCLS1,IL7R,ADGRF5,KIT,PRCP,CP,TNFAIP3,LRRC8D,ATP2B1,CD34,PDE4D,MEF2C,CHD7,TLR4,GPR4,STC1,GATA3,EDN1,APLNR,SLC39A8,LRRC8C,SLC12A7,PDZD8,ABCA1,ITPKB,STMN1,HMBOX1,SWAP70,SMARCA4,EXOC5,LDB2,PDIA5,PTGS2,PLCG2,BCL10,TAOK1,SMG7,VPS54,ADIPOR2,HMGB1,BLM,SMC5,SKIL,MCU,NR1D2,HIF1A,KDM3A,ATRX,DCP2,ATP2A1,TMOD3	up_VCAV_EC
GO:0060341	0.081	0.96	10	255	regulation of cellular localization	BP	1	LEP,KCNC4,GAS1,CRYAB,CHRM2,CAMK2A,CYLD,LRRC15,REEP2,BVES	up_AFEM_EC
GO:0009059	0.081	0.971	7	1563	macromolecule biosynthetic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060255	0.081	0.979	5	1782	regulation of macromolecule metabolic	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0060291	0.081	0.984	3	11	long-term synaptic potentiation	BP	1	FAM107A,ABL1,STX4	up_VSAP_EC
GO:0002027	0.081	0.989	2	20	regulation of heart rate	BP	1	IRX5,BVES	up_AFEM_EC
GO:0044087	0.081	0.99	2	339	regulation of cellular component biogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC

GO:0007023	0.081	1	1	1	post-chaperonin tubulin folding pathway	BP	1	TBCC	down_ACOR_VSMC
GO:2000026	0.081	1	1	560	regulation of multicellular organismal development	BP	1	GATA5	down_AFEM_VSMC
GO:0070966	0.081	1	1	1	nuclear-transcribed mRNA catabolic process, no-go	BP	0.917	CNOT6	up_VCAV_EC
GO:0048021	0.081003363	0.99774	1	3	regulation of melanin biosynthetic process	BP	1	CDH3	up_ACOR_EC
GO:1900376	0.081003363	0.99774	1	3	regulation of secondary metabolite biosynthetic	BP	1	CDH3	up_ACOR_EC
GO:0006667	0.0811	1	1	1	sphinganine metabolic process	BP	0.917	SPTLC2	up_VCAV_EC
GO:0046511	0.0811	1	1	1	sphinganine biosynthetic process	BP	0.917	SPTLC2	up_VCAV_EC
GO:0003018	0.0811	0.997	1	42	vascular process in circulatory system	BP	1	SLIT2	up_VPUL_VSMC
GO:0061438	0.081110476	0.99774	1	3	renal system vasculature morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0061439	0.081110476	0.99774	1	3	kidney vasculature morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:1901381	0.081145653	0.99773	1	3	positive regulation of potassium ion	BP	1	ACTN2	up_ACOR_EC
GO:1901361	0.0812	0.955	14	154	organic cyclic compound catabolic process	BP	0.926	ENPP1,PGK1,TPI1,PGAM1,ALDH1L2,HIF1A,ZPR1,ENTPD4,SMG7,CNOT7,ALDOC,SND1,APOE,YWHAH	down_VSAP_EC
GO:0002703	0.0812	0.965	8	47	regulation of leukocyte mediated immunity	BP	1	LEP,TP53BP1,TLR3,F2RL1,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0042559	0.0812	0.991	2	6	pteridine-containing compound biosynthetic	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0009308	0.0812	0.989	2	20	amine metabolic process	BP	1	MOXD1,NAPEPLD	up_AFEM_EC
GO:0003015	0.0812	0.997	1	58	heart process	BP	1	IRX5	up_AFEM_VSMC
GO:0035701	0.0812	1	1	1	hematopoietic stem cell migration	BP	0.917	KIT	up_VCAV_EC
GO:0036017	0.0812	1	1	1	response to erythropoietin	BP	0.917	KIT	up_VCAV_EC
GO:0036018	0.0812	1	1	1	cellular response to erythropoietin	BP	0.917	KIT	up_VCAV_EC
GO:0036215	0.0812	1	1	1	response to stem cell factor	BP	0.917	KIT	up_VCAV_EC
GO:0036216	0.0812	1	1	1	cellular response to stem cell factor stimulus	BP	0.917	KIT	up_VCAV_EC
GO:0038162	0.0812	1	1	1	erythropoietin-mediated signaling pathway	BP	0.917	KIT	up_VCAV_EC
GO:0097324	0.0812	1	1	1	melanocyte migration	BP	0.917	KIT	up_VCAV_EC
GO:0097326	0.0812	1	1	1	melanocyte adhesion	BP	0.917	KIT	up_VCAV_EC
GO:0032762	0.0812	1	1	1	mast cell cytokine production	BP	0.917	KIT	up_VCAV_EC
GO:0038109	0.0812	1	1	1	Kit signaling pathway	BP	0.917	KIT	up_VCAV_EC
GO:0034616	0.081212043	0.99773	1	3	response to laminar fluid shear stress	BP	1	SMAD6	up_ACOR_EC
GO:1902170	0.081291036	0.99773	1	3	cellular response to reactive nitrogen species	BP	1	GUCY1B1	up_ACOR_EC
GO:2000147	0.0813	0.949	22	169	positive regulation of cell motility	BP	1	TWIST2,WNT11,FAM107A,ENPP2,FGF7,ABL1,HDAC7,PDGFD,CCBE1,STAT5A,F2RL1,DDR2,PIK3R1,TIAM1,CFAP69,SASH1,ZNF580,STX4,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:1903902	0.0813	0.983	3	18	positive regulation of viral life cycle	BP	0.926	P4HB,CNOT7,RAD23A	down_VSAP_EC
GO:0010332	0.0813	0.989	2	20	response to gamma radiation	BP	1	CRYAB,DCUN1D3	up_AFEM_EC
GO:1902803	0.0813	0.989	2	20	regulation of synaptic vesicle transport	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:2000300	0.0813	0.989	2	20	regulation of synaptic vesicle exocytosis	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0001841	0.0813	0.997	1	44	neural tube formation	BP	1	CITED2	down_VPOR_EC
GO:0002028	0.0813	0.997	1	19	regulation of sodium ion transport	BP	1	NETO1	up_VSAP_VSMC
GO:0048251	0.081380936	0.99772	1	3	elastic fiber assembly	BP	1	MFAP4	up_ACOR_EC
GO:0000165	0.0814	0.95	20	236	MAPK cascade	BP	0.926	VEGFA,JCAD,PTPN11,TRIB3,ILK,TNIK,PTPN2,MAGED1,CTNNB1,APOE,LYN,CBLC,ATF3,MAPK10,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC

GO:0007507	0.0814	0.989	2	194	heart development	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:1902523	0.081464534	0.99772	1	3	positive regulation of protein K63-linked	BP	1	NOD2	up_ACOR_EC
GO:0007163	0.0815	0.967	7	60	establishment or maintenance of cell	BP	0.928	FSCN1,ILK,WDR1,MSN,UST,HTT,ARF4	down_VSAP_EC
GO:0001822	0.0815	0.972	5	98	kidney development	BP	1	IRX3,DLL1,GREM1,OVOL1,GCNT4	up_AFEM_EC
GO:0061912	0.0815	0.978	4	18	selective autophagy	BP	1	RETREG1,AMBRA1,MFN2,HTRA2	up_VSAP_EC
GO:0045471	0.0815	0.991	2	5	response to ethanol	BP	1	TP53INP1,PRKCE	up_ACOR_VSMC
GO:0060429	0.0815	0.99	2	341	epithelium development	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0007219	0.0815	0.997	1	59	Notch signaling pathway	BP	1	GATA5	up_VCAV_VSMC
GO:1905517	0.0815	0.997	1	10	macrophage migration	BP	1	C3AR1	up_VPOR_EC
GO:0090263	0.0815	0.997	1	33	positive regulation of canonical Wnt signaling	BP	1	BAMBI	up_VPOR_VSMC
GO:0030534	0.0815	0.997	1	33	adult behavior	BP	1	CHL1	up_VPOR_VSMC
GO:0003208	0.0815	0.997	1	24	cardiac ventricle morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0001657	0.0815	0.997	1	42	ureteric bud development	BP	1	SLIT2	up_VPUL_VSMC
GO:0072163	0.0815	0.997	1	42	mesonephric epithelium development	BP	1	SLIT2	up_VPUL_VSMC
GO:0072164	0.0815	0.997	1	42	mesonephric tubule development	BP	1	SLIT2	up_VPUL_VSMC
GO:0007264	0.0816	0.954	15	164	small GTPase mediated signal transduction	BP	0.928	ARHGEF2,SIPA1L1,ARHGAP31,BCAR3,FARP1,KPNB1,APOE,PLEKHG2,TAX1BP3,ARFGEF3,PAK2,CDKN1A,NRP1,TNFAIP1,MADD	down_VSAP_EC
GO:0006351	0.0816	0.964	9	1069	transcription, DNA-templated	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0001505	0.0816	0.976	4	69	regulation of neurotransmitter levels	BP	1	KCNC4,CHRM2,CAMK2A,MOXD1	up_AFEM_EC
GO:0060119	0.0816	0.989	2	10	inner ear receptor cell development	BP	1	SDC4,NAGLU	down_VCAV_EC
GO:0010763	0.0816	0.991	2	5	positive regulation of fibroblast migration	BP	1	PRKCE,DDR2	up_ACOR_VSMC
GO:0030073	0.0816	0.997	1	42	insulin secretion	BP	1	RAB11B	down_VPOR_EC
GO:0006790	0.0816	0.997	1	99	sulfur compound metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC
GO:0032609	0.0816	0.997	1	25	interferon-gamma production	BP	1	NR1H4	up_VPUL_EC
GO:0016236	0.081602566	0.97204	5	88	macroautophagy	BP	1	ATG16L2,CHMP4B,TP53INP2,VPS16,ENSCAFG00000010493	up_ACOR_EC
GO:0043123	0.0817	0.967	7	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	0.922	TLR4,PELI1,CASP8,MAP3K3,TLR3,BCL10,RIPK1	up_VCAV_EC
GO:0045646	0.0817	0.997	1	19	regulation of erythrocyte differentiation	BP	1	LYN	down_ACOR_EC
GO:0071216	0.0817	0.997	1	61	cellular response to biotic stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0006614	0.0817	0.997	1	10	SRP-dependent cotranslational protein	BP	1	SRP54	up_VPOR_EC
GO:0060600	0.081732816	0.9977	1	3	dichotomous subdivision of an epithelial terminal	BP	1	NRP1	up_ACOR_EC
GO:0060666	0.081732816	0.9977	1	3	dichotomous subdivision of terminal units involved in salivary gland	BP	1	NRP1	up_ACOR_EC
GO:0034470	0.0818	0.952	18	154	ncRNA processing	BP	1	INTS7,SRRT,NOP56,FBL,DIS3,NOC4L,RSL1D1,THUMPD2,RRP1,OSGEP,ENSCAFG00000019620,NOP14,NOP58,ENSCAFG00000015189,EMG1,RTCB,EXOSC5,NOB1	down_ACOR_VSMC
GO:0006520	0.0818	0.953	16	114	cellular amino acid metabolic process	BP	1	HNF4A,GOT1,GLUL,ADHFE1,WARS2,ALDH6A1,ABAT,BCKDHB,ENSCAFG00000016140,AZIN2,FARS2,ENSCAFG00000002977,QARS,ASS1,LARS2,IDO2	up_VSAP_EC
GO:0032103	0.0818	0.976	4	69	positive regulation of response to external	BP	1	CMKLR1,NAPEPLD,CCL5,ADAM17	up_AFEM_EC
GO:1903039	0.0818	0.981	3	43	positive regulation of leukocyte cell-cell	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0043412	0.0818	0.995	2	1225	macromolecule modification	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0009855	0.0818	0.997	1	42	determination of bilateral symmetry	BP	1	CITED2	down_VPOR_EC
GO:0010883	0.0818	0.997	1	11	regulation of lipid storage	BP	1	ABHD5	up_VPOR_EC

GO:0006941	0.0818	0.997	1	36	striated muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007260	0.0818	0.997	1	19	tyrosine phosphorylation of STAT protein	BP	1	CAV1	up_VSAP_VSMC
GO:0030111	0.0819	0.962	9	108	regulation of Wnt signaling pathway	BP	1	RECK,CLSTN1,ATP6V0C,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0031325	0.0819	0.985	3	914	positive regulation of cellular metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0030325	0.0819	0.991	2	5	adrenal gland development	BP	1	CITED2,ARID5B	up_ACOR_VSMC
GO:0044546	0.0819	0.991	2	6	NLRP3 inflammasome complex assembly	BP	0.922	GBP5,TLR4	up_VCAV_EC
GO:1900225	0.0819	0.991	2	6	regulation of NLRP3 inflammasome complex	BP	0.922	GBP5,TLR4	up_VCAV_EC
GO:0090659	0.0819	0.997	1	12	walking behavior	BP	1	SPG11	down_ACOR_EC
GO:0051456	0.0819	1	1	1	attachment of spindle microtubules to kinetochore involved in meiotic sister chromatid	BP	1	DSN1	down_ACOR_VSMC
GO:0009199	0.0819	0.997	1	100	ribonucleoside triphosphate metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0060819	0.0819	1	1	1	inactivation of X chromosome by genetic	BP	1	PCGF5	up_ACOR_VSMC
GO:0014855	0.0819	0.997	1	22	striated muscle cell proliferation	BP	1	TBX5	up_APUL_EC
GO:0033627	0.0819	0.997	1	22	cell adhesion mediated by integrin	BP	1	NPNT	up_APUL_EC
GO:0009225	0.0819	0.997	1	10	nucleotide-sugar metabolic process	BP	1	GNPNAT1	up_VPOR_EC
GO:0001655	0.082	0.954	15	116	urogenital system development	BP	0.922	HOXB7,PDGFB,PODXL,MEF2C,TIPARP,GPR4,GATA3,MTSS1,ODC1,ARG2,BMP2,PROX1,JAG1,BASP1,ITGA6	up_VCAV_EC
GO:0032388	0.082	0.969	6	62	positive regulation of intracellular transport	BP	1	PRNP,ENSCAFG00000014978,AKT2,SCP2,GLI3,MAVS	down_VCAV_EC
GO:0031086	0.082	0.991	2	5	nuclear-transcribed mRNA catabolic process, deadenylation-	BP	1	PNRC1,DCP1B	up_ACOR_VSMC
GO:0031087	0.082	0.991	2	5	deadenylation-independent decapping of nuclear-transcribed mRNA	BP	1	PNRC1,DCP1B	up_ACOR_VSMC
GO:0002682	0.082	0.989	2	343	regulation of immune system process	BP	1	TLR2,HOXA9	up_AFEM_VSMC
GO:0015786	0.082	1	1	1	UDP-glucose transmembrane transport	BP	1	SLC35C2	down_ACOR_VSMC
GO:0046101	0.082	1	1	1	hypoxanthine biosynthetic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0006551	0.082	1	1	1	leucine metabolic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0009082	0.082	1	1	1	branched-chain amino acid biosynthetic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0009098	0.082	1	1	1	leucine biosynthetic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0009099	0.082	1	1	1	valine biosynthetic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0046100	0.082	1	1	1	hypoxanthine metabolic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0009126	0.082	0.997	1	100	purine nucleoside monophosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0009167	0.082	0.997	1	100	purine ribonucleoside monophosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0010212	0.082	0.997	1	60	response to ionizing radiation	BP	1	EYA1	up_AFEM_VSMC
GO:0048706	0.082	0.997	1	59	embryonic skeletal system development	BP	1	HOXC6	up_VCAV_VSMC
GO:0045980	0.082	0.997	1	10	negative regulation of nucleotide metabolic	BP	1	FBP1	up_VPOR_EC
GO:0071347	0.082	0.997	1	25	cellular response to interleukin-1	BP	1	CCL24	up_VPUL_EC
GO:0021766	0.082	0.997	1	20	hippocampus development	BP	1	EMX2	up_VSAP_VSMC
GO:0021824	0.082018822	0.99768	1	3	cerebral cortex tangential migration using cell-axon interactions	BP	1	NRP1	up_ACOR_EC
GO:0021828	0.082018822	0.99768	1	3	gonadotrophin-releasing hormone neuronal migration to the	BP	1	NRP1	up_ACOR_EC

GO:0021856	0.082018822	0.99768	1	3	hypothalamic tangential migration using cell-axon interactions	BP	1	NRP1	up_ACOR_EC
GO:0021886	0.082018822	0.99768	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	up_ACOR_EC
GO:0021888	0.082018822	0.99768	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	up_ACOR_EC
GO:0021979	0.082018822	0.99768	1	3	hypothalamus cell differentiation	BP	1	NRP1	up_ACOR_EC
GO:0035290	0.082018822	0.99768	1	3	trunk segmentation	BP	1	NRP1	up_ACOR_EC
GO:0036484	0.082018822	0.99768	1	3	trunk neural crest cell migration	BP	1	NRP1	up_ACOR_EC
GO:0036486	0.082018822	0.99768	1	3	ventral trunk neural crest cell migration	BP	1	NRP1	up_ACOR_EC
GO:0097490	0.082018822	0.99768	1	3	sympathetic neuron projection extension	BP	1	NRP1	up_ACOR_EC
GO:0097491	0.082018822	0.99768	1	3	sympathetic neuron projection guidance	BP	1	NRP1	up_ACOR_EC
GO:1901166	0.082018822	0.99768	1	3	neural crest cell migration involved in autonomic nervous system	BP	1	NRP1	up_ACOR_EC
GO:1903375	0.082018822	0.99768	1	3	facioacoustic ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0010721	0.0821	0.964	8	73	negative regulation of cell development	BP	0.933	DPYSL3,HOOK3,IFRD1,CTNNB1,APOE,REST,NRP1,YWHAH	down_VSAP_EC
GO:0007166	0.0821	0.974	5	686	cell surface receptor signaling pathway	BP	1	NR1H4,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0006959	0.0821	0.982	3	21	humoral immune response	BP	1	CFD,TFE3,A2M	down_VCAV_EC
GO:0009799	0.0821	0.981	3	43	specification of symmetry	BP	1	DLL1,GREM1,GREM2	up_AFEM_EC
GO:0006692	0.0821	0.984	3	11	prostanoid metabolic process	BP	1	PTGES,ABHD16A,HPGD	up_VSAP_EC
GO:0006693	0.0821	0.984	3	11	prostaglandin metabolic process	BP	1	PTGES,ABHD16A,HPGD	up_VSAP_EC
GO:1900024	0.0821	0.997	1	16	regulation of substrate adhesion-dependent cell	BP	1	PDPN	down_ACOR_EC
GO:0030218	0.0821	0.997	1	42	erythrocyte differentiation	BP	1	CITED2	down_VPOR_EC
GO:0031109	0.0821	0.997	1	36	microtubule polymerization or	BP	1	TAOK1	up_AORT_EC
GO:0006936	0.0821	0.997	1	74	muscle contraction	BP	1	ARG2	up_AORT_VSMC
GO:0050928	0.0821	1	1	1	negative regulation of positive chemotaxis	BP	0.922	ANGPT2	up_VCAV_EC
GO:0014812	0.0821	0.997	1	21	muscle cell migration	BP	1	SIX1	up_VFEM_EC
GO:0051781	0.0821	0.997	1	18	positive regulation of cell division	BP	1	FGF5	up_VSAP_VSMC
GO:0010468	0.0822	0.972	6	1270	regulation of gene expression	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051250	0.0822	0.973	5	38	negative regulation of lymphocyte activation	BP	0.933	SOCS5,PTPN2,LYN,SDC4,BTK	down_VSAP_EC
GO:0042737	0.0822	0.978	4	18	drug catabolic process	BP	1	MAOA,FMO4,MOXD1,CAT	up_ACOR_VSMC
GO:0033059	0.0822	0.983	3	12	cellular pigmentation	BP	0.922	RAB11A,RAB27A,SHROOM2	up_VCAV_EC
GO:0034724	0.0822	0.983	3	12	DNA replication-independent nucleosome	BP	0.922	NASP,ASF1A,ATRX	up_VCAV_EC
GO:0045638	0.0822	0.997	1	33	negative regulation of myeloid cell	BP	1	HOXA9	up_VFEM_VSMC
GO:0007613	0.0822	0.997	1	20	memory	BP	1	NETO1	up_VSAP_VSMC
GO:0043161	0.0823	0.954	15	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	0.934	PRICKLE1,PLK3,SOCS5,HSP90B1,TRIB3,DNAJC10,UCHL5,SPOPL,DNAJB9,DDIT3,GSK3B,SPOP,RAD23A,USP14,TNFAIP1	down_VSAP_EC
GO:0035137	0.0823	0.978	4	18	hindlimb morphogenesis	BP	1	OSR2,OSR1,ZBTB16,RARG	up_VSAP_EC
GO:0070838	0.0823	0.988	2	96	divalent metal ion transport	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0051130	0.0823	0.989	2	342	positive regulation of cellular component	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0072676	0.0823	0.997	1	25	lymphocyte migration	BP	1	CCL24	up_VPUL_EC
GO:1904016	0.0823	1	1	1	response to Thyroglobulin triiodothyronine	BP	1	NCOA2	up_VSAP_EC

GO:1904017	0.0823	1	1	1	cellular response to Thyroglobulin	BP	1	NCOA2	up_VSAP_EC
GO:1990791	0.082313577	0.99767	1	3	dorsal root ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0021648	0.08238223	0.99766	1	3	vestibulocochlear nerve morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0097105	0.082382502	0.99766	1	3	presynaptic membrane assembly	BP	1	LRP4	up_ACOR_EC
GO:0032880	0.0824	0.944	33	266	regulation of protein localization	BP	1	EXPH5,SH3TC2,TLR1,ACTN2,LEP,HTR2B,TCAF1,MBP,PRKAA2,FERMT1,BMP4,TM7SF3,CD274,AR,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,DAG1,PARP9,PSEN1,JUP,CCL5,RAB11B,NOD2,SCAMP5,INPP5K,PFKL,WASL,PARK7,PTPN14	up_ACOR_VSMC
GO:0048592	0.0824	0.964	8	53	eye morphogenesis	BP	0.924	EPHB1,PROX1,TSPAN12,JAG1,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0071359	0.0824	0.984	3	11	cellular response to dsRNA	BP	1	PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0051050	0.0824	0.981	3	235	positive regulation of transport	BP	1	STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:1903055	0.0824	0.991	2	6	positive regulation of extracellular matrix	BP	1	FSCN1,COLGALT1	down_ACOR_VSMC
GO:0003139	0.0824	0.991	2	5	secondary heart field specification	BP	1	BMP4,SMARCD3	up_ACOR_VSMC
GO:0010872	0.0824	0.998	1	2	regulation of cholesterol esterification	BP	0.934	APOE	down_VSAP_EC
GO:0032612	0.0824	0.997	1	22	interleukin-1 production	BP	1	NR1H4	up_APUL_EC
GO:0060411	0.0824	0.997	1	33	cardiac septum morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032835	0.0824	0.997	1	21	glomerulus development	BP	1	MTSS1	up_VFEM_EC
GO:0030879	0.0824	0.997	1	34	mammary gland development	BP	1	HOXA9	up_VFEM_VSMC
GO:0099537	0.0825	0.953	16	131	trans-synaptic signaling	BP	0.924	EPHB1,PLK2,ENSCAFG00000007112,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,SNAP23,SLC12A7,GRM8,STX11,ALS2,P2RX2	up_VCAV_EC
GO:0097659	0.0825	0.964	9	1072	nucleic acid-templated transcription	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0048025	0.0825	0.991	2	6	negative regulation of mRNA splicing, via	BP	1	RNPS1,U2AF2	down_ACOR_VSMC
GO:0018209	0.0825	0.988	2	125	peptidyl-serine modification	BP	1	PLCL1,NTRK2	up_APUL_EC
GO:0051546	0.0825	0.991	2	6	keratinocyte migration	BP	0.924	FERMT1,MTOR	up_VCAV_EC
GO:0045216	0.0825	0.997	1	44	cell-cell junction organization	BP	1	HDAC7	down_VPOR_EC
GO:0006897	0.0826	0.965	7	158	endocytosis	BP	1	LEP,RAB20,DLL1,GREM1,ICAM5,RAB7A,ANXA11	up_AFEM_EC
GO:0007369	0.0826	0.997	1	63	gastrulation	BP	1	EYA1	up_AFEM_VSMC
GO:1900026	0.0826	0.997	1	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0050729	0.0826	0.997	1	25	positive regulation of inflammatory response	BP	1	CCL24	up_VPUL_EC
GO:0009653	0.0827	0.961	10	773	anatomical structure morphogenesis	BP	1	C3AR1,PTK7,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,MTDH,RNF6	up_VPOR_EC
GO:0046661	0.0827	0.967	7	45	male sex differentiation	BP	1	SF1,DHCR24,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC
GO:0031323	0.0827	0.979	5	1788	regulation of cellular metabolic process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0042743	0.0827	0.991	2	5	hydrogen peroxide metabolic process	BP	1	CAT,PARK7	up_ACOR_VSMC
GO:0070664	0.0827	0.997	1	18	negative regulation of leukocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0032677	0.0827	0.997	1	22	regulation of interleukin-8 production	BP	1	BPI	up_APUL_EC
GO:0045927	0.0827	0.997	1	61	positive regulation of growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0001554	0.0827	1	1	1	luteolysis	BP	1	SLIT2	up_VSAP_EC
GO:0010593	0.0827	1	1	1	negative regulation of lamellipodium assembly	BP	1	SLIT2	up_VSAP_EC
GO:0021823	0.0827	1	1	1	cerebral cortex tangential migration using cell-cell interactions	BP	1	SLIT2	up_VSAP_EC

GO:0021827	0.0827	1	1	1	postnatal olfactory bulb interneuron migration	BP	1	SLIT2	up_VSAP_EC
GO:0021836	0.0827	1	1	1	chemorepulsion involved in postnatal olfactory bulb interneuron migration	BP	1	SLIT2	up_VSAP_EC
GO:0021966	0.0827	1	1	1	corticospinal neuron axon guidance	BP	1	SLIT2	up_VSAP_EC
GO:0021972	0.0827	1	1	1	corticospinal neuron axon guidance through spinal	BP	1	SLIT2	up_VSAP_EC
GO:0035385	0.0827	1	1	1	Roundabout signaling pathway	BP	1	SLIT2	up_VSAP_EC
GO:0050924	0.0827	1	1	1	positive regulation of negative chemotaxis	BP	1	SLIT2	up_VSAP_EC
GO:0050929	0.0827	1	1	1	induction of negative chemotaxis	BP	1	SLIT2	up_VSAP_EC
GO:0051414	0.0827	1	1	1	response to cortisol	BP	1	SLIT2	up_VSAP_EC
GO:0061364	0.0827	1	1	1	apoptotic process involved in luteolysis	BP	1	SLIT2	up_VSAP_EC
GO:0070099	0.0827	1	1	1	regulation of chemokine-mediated signaling	BP	1	SLIT2	up_VSAP_EC
GO:0070100	0.0827	1	1	1	negative regulation of chemokine-mediated	BP	1	SLIT2	up_VSAP_EC
GO:0071670	0.0827	1	1	1	smooth muscle cell chemotaxis	BP	1	SLIT2	up_VSAP_EC
GO:0071671	0.0827	1	1	1	regulation of smooth muscle cell chemotaxis	BP	1	SLIT2	up_VSAP_EC
GO:0071672	0.0827	1	1	1	negative regulation of smooth muscle cell	BP	1	SLIT2	up_VSAP_EC
GO:0090260	0.0827	1	1	1	negative regulation of retinal ganglion cell axon	BP	1	SLIT2	up_VSAP_EC
GO:0006366	0.0828	0.938	59	583	transcription by RNA polymerase II	BP	0.926	EDNRB,HCLS1,FLI1,PPARG,TNIP1,PDGFB,TMEM173,MEF2C,ATF3,CHD7,DLL4,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,ENSCAFG00000017103,IRF8,SOX18,PPP3CA,YES1,ELF4,BMP2,HMG20A,HHEX,CREM,PROX1,ARID4B,HMBOX1,PRKD2,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,JAG1,TCERG1,CTDSPL2,CNOT7,HMGB1,AHR,RIPK1,ITGA6,SKIL,MTA2,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ARID5A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0043062	0.0828	0.955	14	99	extracellular structure organization	BP	1	LIPC,ABL1,CTSS,ADAMTSL4,RECK,DDR2,SULF2,LOX,ECM2,LCAT,FBLN1,FLOT1,DPT,SOAT1	up_VSAP_EC
GO:0032774	0.0828	0.964	9	1073	RNA biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0031032	0.0828	0.966	7	61	actomyosin structure organization	BP	0.936	ACTN1,WDR1,ENSCAFG00000017326,SIX4,NRP1,TNFAIP1,MYBPC2	down_VSAP_EC
GO:0018195	0.0828	0.991	2	6	peptidyl-arginine modification	BP	1	PRMT1,PRMT5	down_ACOR_VSMC
GO:0071539	0.0828	0.99	2	8	protein localization to centrosome	BP	0.936	HOOK3,GSK3B	down_VSAP_EC
GO:1905508	0.0828	0.99	2	8	protein localization to microtubule organizing	BP	0.936	HOOK3,GSK3B	down_VSAP_EC
GO:0007595	0.0828	0.991	2	6	lactation	BP	0.926	CREB1,HIF1A	up_VCAV_EC
GO:0021798	0.0828	0.998	1	2	forebrain dorsal/ventral pattern formation	BP	1	GLI3	down_VCAV_EC
GO:0035441	0.0828	0.998	1	2	cell migration involved in vasculogenesis	BP	1	PDGFRB	down_VCAV_EC
GO:1903555	0.0828	0.997	1	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	BPI	up_AORT_EC
GO:0071333	0.0828	0.997	1	25	cellular response to glucose stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0042327	0.082830342	0.95641	12	289	positive regulation of phosphorylation	BP	1	SOX9,ENSCAFG00000004331,FZD5,NOD2,PAK3,TNFRSF19,MAVS,LRP4,SH3RF3,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0021559	0.082874666	0.99763	1	3	trigeminal nerve development	BP	1	NRP1	up_ACOR_EC
GO:0021636	0.082874666	0.99763	1	3	trigeminal nerve morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0021637	0.082874666	0.99763	1	3	trigeminal nerve structural organization	BP	1	NRP1	up_ACOR_EC
GO:0021785	0.082874666	0.99763	1	3	branchiomotor neuron axon guidance	BP	1	NRP1	up_ACOR_EC
GO:1902287	0.082874666	0.99763	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	NRP1	up_ACOR_EC

GO:0071222	0.0829	0.966	7	46	cellular response to lipopolysaccharide	BP	0.926	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,IRF8,ABCA1	up_VCAV_EC
GO:0045833	0.0829	0.977	4	29	negative regulation of lipid metabolic process	BP	0.937	NR1H4,TRIB3,APOE,REST	down_VSAP_EC
GO:0022008	0.0829	0.982	3	406	neurogenesis	BP	1	CHL1,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0046426	0.0829	0.997	1	20	negative regulation of JAK-STAT cascade	BP	1	ASPN	down_ACOR_EC
GO:1904893	0.0829	0.997	1	20	negative regulation of STAT cascade	BP	1	ASPN	down_ACOR_EC
GO:1904628	0.0829	1	1	1	cellular response to phorbol 13-acetate 12-	BP	1	CDK4	down_ACOR_VSMC
GO:1904627	0.0829	1	1	1	response to phorbol 13-acetate 12-myristate	BP	1	CDK4	down_ACOR_VSMC
GO:0061478	0.0829	0.998	1	2	response to platelet aggregation inhibitor	BP	1	ADCY6	down_VCAV_EC
GO:1904321	0.0829	0.998	1	2	response to forskolin	BP	1	ADCY6	down_VCAV_EC
GO:1904322	0.0829	0.998	1	2	cellular response to forskolin	BP	1	ADCY6	down_VCAV_EC
GO:0002757	0.0829	0.997	1	78	immune response-activating signal	BP	1	ESR1	up_AORT_VSMC
GO:0048511	0.0829	0.997	1	72	rhythmic process	BP	1	ESR1	up_AORT_VSMC
GO:0090101	0.0829	0.997	1	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	BAMBI	up_VPOR_VSMC
GO:0051249	0.083	0.961	9	107	regulation of lymphocyte activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,ZFP36L1,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0010604	0.083	0.985	3	919	positive regulation of macromolecule metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0050691	0.083	0.983	3	11	regulation of defense response to virus by host	BP	1	RNF216,PQBP1,MAVS	up_VSAP_EC
GO:0038179	0.083	0.989	2	10	neurotrophin signaling pathway	BP	1	NDN,AKT1S1	down_VCAV_EC
GO:0030595	0.083	0.988	2	57	leukocyte chemotaxis	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0043985	0.083	1	1	1	histone H4-R3 methylation	BP	1	PRMT1	down_ACOR_VSMC
GO:0022904	0.083	0.997	1	43	respiratory electron transport chain	BP	1	NDUFA10	down_AFEM_EC
GO:0045944	0.083	0.998	1	287	positive regulation of transcription by RNA polymerase II	BP	1	GATA5	down_VFEM_VSMC
GO:0045956	0.083	1	1	1	positive regulation of calcium ion-dependent	BP	1	SCAMP5	up_ACOR_VSMC
GO:0045637	0.083	0.997	1	73	regulation of myeloid cell differentiation	BP	1	HOXA9	up_AORT_VSMC
GO:0051648	0.083	0.997	1	69	vesicle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0072329	0.083	0.997	1	34	monocarboxylic acid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0035307	0.083044283	0.98841	2	18	positive regulation of protein	BP	1	DUSP26,PRKCD	up_ACOR_EC
GO:0000904	0.0831	0.981	3	181	cell morphogenesis involved in differentiation	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0031111	0.0831	0.983	3	11	negative regulation of microtubule polymerization or	BP	1	FGF13,MID1,TUBB4A	up_ACOR_VSMC
GO:0010896	0.0831	1	1	1	regulation of triglyceride catabolic process	BP	1	ABHD5	down_ACOR_VSMC
GO:0010898	0.0831	1	1	1	positive regulation of triglyceride catabolic	BP	1	ABHD5	down_ACOR_VSMC
GO:0009953	0.0831	0.997	1	34	dorsal/ventral pattern formation	BP	1	HOXA11	up_VFEM_VSMC
GO:0019218	0.0831	0.997	1	25	regulation of steroid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0060982	0.083125298	0.99762	1	3	coronary artery morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0051271	0.0832	0.971	5	98	negative regulation of cellular component	BP	1	ANGPT4,HOXA7,RECK,TBXA2R,KANK1	up_AFEM_EC
GO:0051150	0.0832	0.983	3	13	regulation of smooth muscle cell differentiation	BP	0.928	KIT,PDGFB,ZEB1	up_VCAV_EC
GO:0055074	0.0832	0.988	2	95	calcium ion homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:1903034	0.0832	0.997	1	40	regulation of response to wounding	BP	1	SRSF6	down_AFEM_EC
GO:0006694	0.0832	0.997	1	42	steroid biosynthetic process	BP	1	HSD3B7	down_VPOR_EC

GO:2000224	0.0832	1	1	1	regulation of testosterone biosynthetic process	BP	1	DKKL1	up_ACOR_VSMC
GO:2000225	0.0832	1	1	1	negative regulation of testosterone biosynthetic	BP	1	DKKL1	up_ACOR_VSMC
GO:0061370	0.0832	1	1	1	testosterone biosynthetic process	BP	1	DKKL1	up_ACOR_VSMC
GO:0051249	0.0833	0.953	15	107	regulation of lymphocyte activation	BP	1	CD274,TBC1D10C,ABL1,ZBTB16,TOX,STAT6,ZFP36L1,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0032488	0.0833	0.991	2	5	Cdc42 protein signal transduction	BP	1	ABCA1,NRP1	up_ACOR_VSMC
GO:0032489	0.0833	0.991	2	5	regulation of Cdc42 protein signal	BP	1	ABCA1,NRP1	up_ACOR_VSMC
GO:0002507	0.0833	0.99	2	7	tolerance induction	BP	0.929	TNFAIP3,HMGB1	up_VCAV_EC
GO:0000022	0.0833	1	1	1	mitotic spindle elongation	BP	1	AURKB	down_ACOR_VSMC
GO:0051256	0.0833	1	1	1	mitotic spindle midzone assembly	BP	1	AURKB	down_ACOR_VSMC
GO:0043062	0.0833	0.997	1	99	extracellular structure organization	BP	1	TGFBI	down_VSAP_VSMC
GO:0055024	0.0833	0.997	1	22	regulation of cardiac muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0032259	0.0834	0.96	10	71	methylation	BP	0.929	IWS1,GATA3,ARID4B,NSD1,WTAP,MTA2,KDM3A,ATRX,ZC3H13,TET2	up_VCAV_EC
GO:0050810	0.0834	0.982	3	17	regulation of steroid biosynthetic process	BP	0.941	NR1H4,APOE,REST	down_VSAP_EC
GO:0007026	0.0834	0.99	2	8	negative regulation of microtubule	BP	0.941	ARHGEF2,MID1	down_VSAP_EC
GO:0060333	0.0834	0.99	2	8	interferon-gamma-mediated signaling	BP	0.941	PTPN2,CDC37	down_VSAP_EC
GO:0007056	0.0834	1	1	1	spindle assembly involved in female meiosis	BP	1	FBXO5	down_ACOR_VSMC
GO:0007057	0.0834	1	1	1	spindle assembly involved in female meiosis I	BP	1	FBXO5	down_ACOR_VSMC
GO:1905319	0.0834	1	1	1	mesenchymal stem cell migration	BP	1	FBXO5	down_ACOR_VSMC
GO:1905320	0.0834	1	1	1	regulation of mesenchymal stem cell	BP	1	FBXO5	down_ACOR_VSMC
GO:1905322	0.0834	1	1	1	positive regulation of mesenchymal stem cell	BP	1	FBXO5	down_ACOR_VSMC
GO:0031032	0.0834	0.997	1	61	actomyosin structure organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0003170	0.0834	0.997	1	25	heart valve development	BP	1	TBX5	up_VPUL_EC
GO:1903364	0.083459916	0.9755	4	61	positive regulation of cellular protein catabolic	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0040013	0.0835	0.959	10	100	negative regulation of locomotion	BP	0.941	SULF1,SERPINE1,DPYSL3,PTPN2,STARD13,APOE,MMP28,STRAP,ZMYND8,NRP1	down_VSAP_EC
GO:0033572	0.0835	0.991	2	5	transferrin transport	BP	1	RAB11B,LMTK2	up_ACOR_VSMC
GO:0002682	0.0835	0.989	2	343	regulation of immune system process	BP	1	LRRC17,C6	up_VCAV_VSMC
GO:0060978	0.0835	0.998	1	2	angiogenesis involved in coronary vascular	BP	1	PDGFRB	down_VCAV_EC
GO:0003073	0.0835	0.997	1	20	regulation of systemic arterial blood pressure	BP	1	AVPR1A	up_VFEM_EC
GO:0048771	0.0835	0.997	1	43	tissue remodeling	BP	1	HOXA3	up_VPUL_VSMC
GO:0015722	0.0835	1	1	1	canalicular bile acid transport	BP	1	ABCB11	up_VSAP_EC
GO:0045727	0.0836	0.966	7	40	positive regulation of translation	BP	1	PRR16,PYM1,EEF2,LARP6,RPUSD4,EIF3D,NCK1	up_VSAP_EC
GO:0001894	0.0836	0.968	6	49	tissue homeostasis	BP	0.941	PTPN11,EXOC5,CTNNB1,TFRC,STRAP,HOMER1	down_VSAP_EC
GO:0046916	0.0836	0.997	1	35	cellular transition metal ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0032642	0.0836	0.997	1	22	regulation of chemokine production	BP	1	NR1H4	up_APUL_EC
GO:0032621	0.0836	1	1	1	interleukin-18 production	BP	0.929	GBP5	up_VCAV_EC
GO:0072616	0.0836	1	1	1	interleukin-18 secretion	BP	0.929	GBP5	up_VCAV_EC
GO:0071526	0.0836	0.997	1	12	semaphorin-plexin signaling pathway	BP	1	SEMA3A	up_VPOR_EC
GO:0043407	0.0836	0.997	1	19	negative regulation of MAP kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0046626	0.083678674	0.98827	2	18	regulation of insulin receptor signaling	BP	1	NR1H4,PRKCD	up_ACOR_EC

GO:0070664	0.0837	0.982	3	18	negative regulation of leukocyte proliferation	BP	0.941	LYN,SDC4,BTK	down_VSAP_EC
GO:0032653	0.0837	0.983	3	11	regulation of interleukin-10 production	BP	1	CD274,DLL1,CD83	up_VSAP_EC
GO:1902622	0.0837	0.983	3	11	regulation of neutrophil migration	BP	1	C5AR2,SLIT2,MYD88	up_VSAP_EC
GO:0008626	0.0837	1	1	1	granzyme-mediated apoptotic signaling	BP	1	BNIP3	up_ACOR_VSMC
GO:0061138	0.0837	0.997	1	73	morphogenesis of a branching epithelium	BP	1	ESR1	up_AORT_VSMC
GO:0046785	0.0837	0.997	1	23	microtubule polymerization	BP	1	TUBB4A	up_APUL_EC
GO:0045332	0.0837	1	1	1	phospholipid translocation	BP	0.929	ATP8A1	up_VCAV_EC
GO:0061091	0.0837	1	1	1	regulation of phospholipid translocation	BP	0.929	ATP8A1	up_VCAV_EC
GO:0061092	0.0837	1	1	1	positive regulation of phospholipid	BP	0.929	ATP8A1	up_VCAV_EC
GO:1901019	0.0837	0.997	1	20	regulation of calcium ion transmembrane transporter activity	BP	1	STIM1	up_VSAP_VSMC
GO:1903707	0.0838	0.964	8	48	negative regulation of hemopoiesis	BP	1	HOXA7,HOXA9,DLL1,ZBTB16,ZFP36L1,PIK3R1,MYC,FBXO7	up_VSAP_EC
GO:0001912	0.0838	0.989	2	9	positive regulation of leukocyte mediated	BP	0.941	FAM49B,PVR	down_VSAP_EC
GO:0046184	0.0838	0.99	2	6	aldehyde biosynthetic process	BP	0.929	BMP2,KDM3A	up_VCAV_EC
GO:0030224	0.0838	0.997	1	18	monocyte differentiation	BP	1	HOXA7	down_ACOR_EC
GO:1903131	0.0838	0.997	1	18	mononuclear cell differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0018395	0.0838	1	1	1	peptidyl-lysine hydroxylation to 5-	BP	1	JMJD6	down_ACOR_VSMC
GO:0009799	0.0838	0.997	1	43	specification of symmetry	BP	1	CITED2	down_VPOR_EC
GO:0002438	0.0838	1	1	1	acute inflammatory response to antigenic	BP	1	PARK7	up_ACOR_VSMC
GO:0002866	0.0838	1	1	1	positive regulation of acute inflammatory response to antigenic	BP	1	PARK7	up_ACOR_VSMC
GO:0009441	0.0838	1	1	1	glycolate metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0010273	0.0838	1	1	1	detoxification of copper ion	BP	1	PARK7	up_ACOR_VSMC
GO:0018323	0.0838	1	1	1	enzyme active site formation via L-cysteine	BP	1	PARK7	up_ACOR_VSMC
GO:0033860	0.0838	1	1	1	regulation of NAD(P)H oxidase activity	BP	1	PARK7	up_ACOR_VSMC
GO:0033864	0.0838	1	1	1	positive regulation of NAD(P)H oxidase activity	BP	1	PARK7	up_ACOR_VSMC
GO:0036471	0.0838	1	1	1	cellular response to glyoxal	BP	1	PARK7	up_ACOR_VSMC
GO:0036482	0.0838	1	1	1	neuron intrinsic apoptotic signaling pathway in response to hydrogen	BP	1	PARK7	up_ACOR_VSMC
GO:0036525	0.0838	1	1	1	protein deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0036526	0.0838	1	1	1	peptidyl-cysteine deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0036527	0.0838	1	1	1	peptidyl-arginine deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0036528	0.0838	1	1	1	peptidyl-lysine deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0036529	0.0838	1	1	1	protein deglycation, glyoxal removal	BP	1	PARK7	up_ACOR_VSMC
GO:0036530	0.0838	1	1	1	protein deglycation, methylglyoxal removal	BP	1	PARK7	up_ACOR_VSMC
GO:0036531	0.0838	1	1	1	glutathione deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0046295	0.0838	1	1	1	glycolate biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0046826	0.0838	1	1	1	negative regulation of protein export from	BP	1	PARK7	up_ACOR_VSMC
GO:0002863	0.0838	1	1	1	positive regulation of inflammatory response to antigenic stimulus	BP	1	PARK7	up_ACOR_VSMC
GO:0002864	0.0838	1	1	1	regulation of acute inflammatory response to	BP	1	PARK7	up_ACOR_VSMC
GO:0050787	0.0838	1	1	1	detoxification of mercury ion	BP	1	PARK7	up_ACOR_VSMC

GO:0060081	0.0838	1	1	1	membrane hyperpolarization	BP	1	PARK7	up_ACOR_VSMC
GO:0061687	0.0838	1	1	1	detoxification of inorganic compound	BP	1	PARK7	up_ACOR_VSMC
GO:0090086	0.0838	1	1	1	negative regulation of protein deubiquitination	BP	1	PARK7	up_ACOR_VSMC
GO:0097238	0.0838	1	1	1	cellular response to methylglyoxal	BP	1	PARK7	up_ACOR_VSMC
GO:0097501	0.0838	1	1	1	stress response to metal ion	BP	1	PARK7	up_ACOR_VSMC
GO:0106044	0.0838	1	1	1	guanine deglycation	BP	1	PARK7	up_ACOR_VSMC
GO:0106045	0.0838	1	1	1	guanine deglycation, methylglyoxal removal	BP	1	PARK7	up_ACOR_VSMC
GO:0106046	0.0838	1	1	1	guanine deglycation, glyoxal removal	BP	1	PARK7	up_ACOR_VSMC
GO:0140041	0.0838	1	1	1	cellular detoxification of methylglyoxal	BP	1	PARK7	up_ACOR_VSMC
GO:1901671	0.0838	1	1	1	positive regulation of superoxide dismutase	BP	1	PARK7	up_ACOR_VSMC
GO:1902958	0.0838	1	1	1	positive regulation of mitochondrial electron transport, NADH to	BP	1	PARK7	up_ACOR_VSMC
GO:1903094	0.0838	1	1	1	negative regulation of protein K48-linked	BP	1	PARK7	up_ACOR_VSMC
GO:1903122	0.0838	1	1	1	negative regulation of TRAIL-activated apoptotic signaling pathway	BP	1	PARK7	up_ACOR_VSMC
GO:1903167	0.0838	1	1	1	regulation of pyrroline-5-carboxylate reductase	BP	1	PARK7	up_ACOR_VSMC
GO:1903168	0.0838	1	1	1	positive regulation of pyrroline-5-carboxylate	BP	1	PARK7	up_ACOR_VSMC
GO:1903184	0.0838	1	1	1	L-dopa metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903185	0.0838	1	1	1	L-dopa biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903189	0.0838	1	1	1	glyoxal metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903195	0.0838	1	1	1	regulation of L-dopa biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903197	0.0838	1	1	1	positive regulation of L-dopa biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903383	0.0838	1	1	1	regulation of hydrogen peroxide-induced neuron intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:1903384	0.0838	1	1	1	negative regulation of hydrogen peroxide-induced neuron intrinsic	BP	1	PARK7	up_ACOR_VSMC
GO:1903750	0.0838	1	1	1	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	PARK7	up_ACOR_VSMC
GO:1903751	0.0838	1	1	1	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	PARK7	up_ACOR_VSMC
GO:1904833	0.0838	1	1	1	positive regulation of removal of superoxide	BP	1	PARK7	up_ACOR_VSMC
GO:1905258	0.0838	1	1	1	regulation of nitrosative stress-induced intrinsic apoptotic signaling	BP	1	PARK7	up_ACOR_VSMC
GO:1905259	0.0838	1	1	1	negative regulation of nitrosative stress-induced intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:1990169	0.0838	1	1	1	stress response to copper ion	BP	1	PARK7	up_ACOR_VSMC
GO:2000152	0.0838	1	1	1	regulation of ubiquitin-specific protease activity	BP	1	PARK7	up_ACOR_VSMC
GO:2000157	0.0838	1	1	1	negative regulation of ubiquitin-specific	BP	1	PARK7	up_ACOR_VSMC
GO:2000277	0.0838	1	1	1	positive regulation of oxidative phosphorylation uncoupler activity	BP	1	PARK7	up_ACOR_VSMC
GO:2000284	0.0838	1	1	1	positive regulation of cellular amino acid	BP	1	PARK7	up_ACOR_VSMC
GO:1901863	0.0838	0.997	1	25	positive regulation of muscle tissue	BP	1	TBX5	up_VPUL_EC

GO:0010604	0.0839	0.934	88	919	positive regulation of macromolecule metabolic process	BP	0.929	PLK2,TEK,HCLS1,IL7R,KIT,SELE,PPP2R5A,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,MEF2C,ATF3,CHD7,TIPARP,DLL4,TLR4,NLRC5,GATA3,EDN1,RALB,APLNR,RAB27A,TCF4,FOXN2,ENSCAFG00000017103,NEDD9,IRF8,PELI1,PPP3CA,YES1,CASP8,MTOR,MAP3K3,BMP2,HHEX,CREM,SLK,CNOT6,PROX1,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,LDB2,JAG1,NSD1,PTGS2,MMD,RAPGEF2,PLCG2,BCL10,TAOK1,CNOT7,HMGB1,AHR,PMAIP1,BLM,RIPK1,ITGA6,GPBP1,PDGFD,MTA2,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,ENSCAFG00000002015,JCAD,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0043086	0.0839	0.947	22	170	negative regulation of catalytic activity	BP	1	TNNT2,RECK,BMP4,EIF4A2,SH3RF2,LATS2,CST3,CDKN1A,SMPD1,SH3RF1,MARF1,PPP1R26,PSEN1,SPINK2,DUSP22,DUSP26,LRRC4,INPP5K,SH3BP4,PARK7,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:1902532	0.0839	0.981	3	204	negative regulation of intracellular signal	BP	1	LYN,IGF1R,ASPN	down_ACOR_EC
GO:0060193	0.0839	0.983	3	11	positive regulation of lipase activity	BP	1	HTR2B,FGFR2,LMF1	up_ACOR_VSMC
GO:0072511	0.0839	0.988	2	97	divalent inorganic cation transport	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0007260	0.0839	0.997	1	19	tyrosine phosphorylation of STAT protein	BP	1	LYN	down_ACOR_EC
GO:0002840	0.0839	1	1	1	regulation of T cell mediated immune	BP	1	HMGB1	down_ACOR_VSMC
GO:0017055	0.0839	1	1	1	negative regulation of RNA polymerase II transcriptional	BP	1	HMGB1	down_ACOR_VSMC
GO:0032072	0.0839	1	1	1	regulation of restriction endodeoxyribonuclease	BP	1	HMGB1	down_ACOR_VSMC
GO:0032425	0.0839	1	1	1	positive regulation of mismatch repair	BP	1	HMGB1	down_ACOR_VSMC
GO:0002424	0.0839	1	1	1	T cell mediated immune response to tumor cell	BP	1	HMGB1	down_ACOR_VSMC
GO:2000425	0.0839	1	1	1	regulation of apoptotic cell clearance	BP	1	HMGB1	down_ACOR_VSMC
GO:2000426	0.0839	1	1	1	negative regulation of apoptotic cell clearance	BP	1	HMGB1	down_ACOR_VSMC
GO:0009791	0.083971817	0.98083	3	38	post-embryonic development	BP	1	FZD5,PYGO2,EFEMP1	up_ACOR_EC
GO:0061387	0.084	0.977	4	18	regulation of extent of cell growth	BP	1	ABL1,PLXNA4,DPYSL2,TTL	up_VSAP_EC
GO:0007566	0.084	0.989	2	10	embryo implantation	BP	1	RECK,SYDE1	down_VCAV_EC
GO:1903126	0.084	1	1	1	negative regulation of centriole-centriole	BP	1	NEK2	down_ACOR_VSMC
GO:0030856	0.084	0.997	1	41	regulation of epithelial cell differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0034067	0.084	0.997	1	11	protein localization to Golgi apparatus	BP	1	GCC2	up_VPOR_EC
GO:0021555	0.084	1	1	1	midbrain-hindbrain boundary morphogenesis	BP	1	KDM2B	up_VSAP_EC
GO:0021592	0.084	1	1	1	fourth ventricle development	BP	1	KDM2B	up_VSAP_EC
GO:0021993	0.084	1	1	1	initiation of neural tube closure	BP	1	KDM2B	up_VSAP_EC
GO:0070544	0.084	1	1	1	histone H3-K36 demethylation	BP	1	KDM2B	up_VSAP_EC
GO:0007266	0.0840082	0.97524	4	64	Rho protein signal transduction	BP	1	PAK3,ARHGDIB,NRP1,ARHGEF26	up_ACOR_EC
GO:0015980	0.0841	0.953	15	106	energy derivation by oxidation of organic compounds	BP	1	DLST,C1QTNF2,COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,PHKA2,FXN,NDUFS2,PASK,MTFR1L,IDH1,IDH3A,ENSCAFG00000006639,NDUFV1	up_VSAP_EC
GO:0023052	0.0841	0.97	7	1602	signaling	BP	1	FGF5,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:1902904	0.0841	0.972	5	38	negative regulation of supramolecular fiber	BP	0.941	ARHGEF2,CRYAB,TWF1,CAPG,MID1	down_VSAP_EC
GO:0050873	0.0841	0.982	3	18	brown fat cell differentiation	BP	0.941	ERO1A,PTGS2,BNIP3	down_VSAP_EC
GO:0003400	0.0841	1	1	1	regulation of COPII vesicle coating	BP	1	PREB	down_ACOR_VSMC
GO:1905661	0.0841	1	1	1	regulation of telomerase RNA reverse transcriptase	BP	1	HNRNPD	down_ACOR_VSMC

GO:1905663	0.0841	1	1	1	positive regulation of telomerase RNA reverse	BP	1	HNRNPD	down_ACOR_VSMC
GO:0090113	0.0841	1	1	1	regulation of ER to Golgi vesicle-mediated transport by GTP	BP	1	PREB	down_ACOR_VSMC
GO:0017198	0.0841	0.998	1	2	N-terminal peptidyl-serine acetylation	BP	0.941	NAA10	down_VSAP_EC
GO:0018002	0.0841	0.998	1	2	N-terminal peptidyl-glutamic acid acetylation	BP	0.941	NAA10	down_VSAP_EC
GO:0030920	0.0841	0.998	1	2	peptidyl-serine acetylation	BP	0.941	NAA10	down_VSAP_EC
GO:0050922	0.0841	0.997	1	11	negative regulation of chemotaxis	BP	1	SEMA3A	up_VPOR_EC
GO:0043281	0.0842	0.963	8	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	HMGB1,BIRC5,PDCD2,DHCR24,CYCS,ENSCAFG00000005299,AIFM1,DELE1	down_ACOR_VSMC
GO:0060389	0.0842	0.997	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	ACVRL1	down_ACOR_EC
GO:0097724	0.0842	1	1	1	sperm flagellum movement	BP	1	TTLL1	down_ACOR_VSMC
GO:0046900	0.0842	1	1	1	tetrahydrofolylpolyglutamate metabolic process	BP	1	GGH	down_ACOR_VSMC
GO:1905419	0.0842	1	1	1	sperm flagellum movement involved in flagellated sperm motility	BP	1	TTLL1	down_ACOR_VSMC
GO:0051270	0.0842	0.998	1	296	regulation of cellular component movement	BP	1	JUP	down_VFEM_VSMC
GO:0009144	0.0842	0.997	1	103	purine nucleoside triphosphate metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0032635	0.0842	0.997	1	37	interleukin-6 production	BP	1	BPI	up_AORT_EC
GO:1903391	0.0843	0.981	3	21	regulation of adherens junction organization	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0039019	0.0843	0.998	1	2	pronephric nephron development	BP	1	SEC61A1	down_VCAV_EC
GO:1900223	0.0843	0.998	1	2	positive regulation of amyloid-beta clearance	BP	1	LRP1	down_VCAV_EC
GO:1904352	0.0843	0.998	1	2	positive regulation of protein catabolic process	BP	1	LRP1	down_VCAV_EC
GO:1905167	0.0843	0.998	1	2	positive regulation of lysosomal protein	BP	1	LRP1	down_VCAV_EC
GO:0065004	0.0843	0.997	1	81	protein-DNA complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0048666	0.0844	0.958	10	258	neuron development	BP	1	IRX5,LEP,PLXNA4,NEFH,THRB,LGI4,CAMK2A,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0090090	0.0844	0.981	3	44	negative regulation of canonical Wnt signaling	BP	1	GREM1,CYLD,AXIN2	up_AFEM_EC
GO:0022407	0.0844	0.988	2	96	regulation of cell-cell adhesion	BP	1	LYN,PDPN	down_ACOR_EC
GO:1903825	0.0844	0.997	1	17	organic acid transmembrane transport	BP	1	PDPN	down_ACOR_EC
GO:1905039	0.0844	0.997	1	17	carboxylic acid transmembrane transport	BP	1	PDPN	down_ACOR_EC
GO:0007130	0.0844	1	1	1	synaptonemal complex assembly	BP	1	TRIP13	down_ACOR_VSMC
GO:0070561	0.0844	0.998	1	2	vitamin D receptor signaling pathway	BP	1	KANK2	down_VCAV_EC
GO:0070562	0.0844	0.998	1	2	regulation of vitamin D receptor signaling	BP	1	KANK2	down_VCAV_EC
GO:0071305	0.0844	0.998	1	2	cellular response to vitamin D	BP	1	KANK2	down_VCAV_EC
GO:0009161	0.0844	0.997	1	103	ribonucleoside monophosphate	BP	1	AK5	down_VSAP_VSMC
GO:1903977	0.0844	1	1	1	positive regulation of glial cell migration	BP	1	CRKL	up_ACOR_VSMC
GO:2000649	0.0845	0.983	3	11	regulation of sodium ion transmembrane transporter activity	BP	1	OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0006012	0.0845	0.99	2	6	galactose metabolic process	BP	1	B4GALT1,GALE	down_ACOR_VSMC
GO:0072592	0.0845	1	1	1	oxygen metabolic process	BP	1	LIPT2	up_ACOR_VSMC
GO:2000374	0.0845	1	1	1	regulation of oxygen metabolic process	BP	1	LIPT2	up_ACOR_VSMC
GO:2000376	0.0845	1	1	1	positive regulation of oxygen metabolic process	BP	1	LIPT2	up_ACOR_VSMC
GO:0043500	0.0845	0.997	1	21	muscle adaptation	BP	1	GATM	up_VSAP_VSMC

GO:0042326	0.0846	0.948	21	163	negative regulation of phosphorylation	BP	1	SMAD6,RASSF2,BMP4,LATS2,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,PTPN22,SMPD1,DAG1,PSEN1,SYNJ2BP,DUSP22,DUSP26,LRRC4,DDIT4,INPP5K,PARK7,CRKL	up_ACOR_VSMC
GO:0006935	0.0846	0.95	17	143	chemotaxis	BP	0.933	EPHB1,EDNRB,KIT,CXCL8,CXCR4,DOCK4,AMOT,PDGFB,RELN,PDE4D,GATA3,MMP28,ANGPT2,PRKD2,SWAP70,FES,HMGB1	up_VCAV_EC
GO:0042330	0.0846	0.95	17	143	taxis	BP	0.933	EPHB1,EDNRB,KIT,CXCL8,CXCR4,DOCK4,AMOT,PDGFB,RELN,PDE4D,GATA3,MMP28,ANGPT2,PRKD2,SWAP70,FES,HMGB1	up_VCAV_EC
GO:0045637	0.0846	0.958	11	73	regulation of myeloid cell differentiation	BP	1	HOXA7,HOXA9,PPARGC1B,DLL1,ANKRD54,ZBTB16,RARG,ZFP36L1,PIK3R1,MYC,TFE3	up_VSAP_EC
GO:0061217	0.0846	0.982	3	13	regulation of mesonephros	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0035709	0.0846	1	1	1	memory T cell activation	BP	1	FAM49B	down_ACOR_VSMC
GO:0046167	0.0846	1	1	1	glycerol-3-phosphate biosynthetic process	BP	1	GK5	down_ACOR_VSMC
GO:2000567	0.0846	1	1	1	regulation of memory T cell activation	BP	1	FAM49B	down_ACOR_VSMC
GO:2000568	0.0846	1	1	1	positive regulation of memory T cell activation	BP	1	FAM49B	down_ACOR_VSMC
GO:0006366	0.0846	1	1	583	transcription by RNA polymerase II	BP	1	GATA5	down_AFEM_VSMC
GO:0046661	0.0846	0.997	1	45	male sex differentiation	BP	1	CITED2	down_VPOR_EC
GO:0021700	0.0846	0.997	1	65	developmental maturation	BP	1	IRX5	up_AFEM_VSMC
GO:0048538	0.0846	0.997	1	20	thymus development	BP	1	SIX1	up_VFEM_EC
GO:0048747	0.0846	0.997	1	20	muscle fiber development	BP	1	SHOX2	up_VSAP_VSMC
GO:0034198	0.0847	0.976	4	27	cellular response to amino acid starvation	BP	0.945	SESN2,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:1990928	0.0847	0.976	4	27	response to amino acid starvation	BP	0.945	SESN2,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0051716	0.0847	1	2	2001	cellular response to stimulus	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071606	0.0847	1	1	1	chemokine (C-C motif) ligand 4 production	BP	1	ARG2	down_ACOR_VSMC
GO:0071608	0.0847	1	1	1	macrophage inflammatory protein-1	BP	1	ARG2	down_ACOR_VSMC
GO:0071640	0.0847	1	1	1	regulation of macrophage inflammatory protein 1 alpha production	BP	1	ARG2	down_ACOR_VSMC
GO:0071641	0.0847	1	1	1	negative regulation of macrophage inflammatory protein 1	BP	1	ARG2	down_ACOR_VSMC
GO:0071643	0.0847	1	1	1	regulation of chemokine (C-C motif) ligand 4	BP	1	ARG2	down_ACOR_VSMC
GO:0071644	0.0847	1	1	1	negative regulation of chemokine (C-C motif)	BP	1	ARG2	down_ACOR_VSMC
GO:1905076	0.0847	1	1	1	regulation of interleukin-17 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:1905077	0.0847	1	1	1	negative regulation of interleukin-17 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:1905403	0.0847	1	1	1	negative regulation of activated CD8-positive, alpha-beta T cell	BP	1	ARG2	down_ACOR_VSMC
GO:2000666	0.0847	1	1	1	negative regulation of interleukin-13 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:0033633	0.0847	1	1	1	negative regulation of cell-cell adhesion mediated by	BP	0.933	SWAP70	up_VCAV_EC
GO:1902309	0.0847	1	1	1	negative regulation of peptidyl-serine	BP	0.933	SWAP70	up_VCAV_EC
GO:0034766	0.0847	0.997	1	19	negative regulation of ion transmembrane transport	BP	1	CAV1	up_VSAP_VSMC
GO:0034614	0.084728206	0.98056	3	39	cellular response to reactive oxygen species	BP	1	AQP1,GUCY1B1,PRKCD	up_ACOR_EC
GO:0018958	0.0848	0.977	4	20	phenol-containing compound metabolic	BP	0.933	GATA3,SNCAIP,RAPGEF2,GCH1	up_VCAV_EC
GO:0070601	0.0848	0.99	2	6	centromeric sister chromatid cohesion	BP	1	SGO1,SGO2	down_ACOR_VSMC
GO:0002327	0.0848	0.991	2	5	immature B cell differentiation	BP	0.933	KIT,ATP11C	up_VCAV_EC
GO:2000807	0.0848	0.998	1	2	regulation of synaptic vesicle clustering	BP	1	CDH2	down_VCAV_EC
GO:2000809	0.0848	0.998	1	2	positive regulation of synaptic vesicle clustering	BP	1	CDH2	down_VCAV_EC

GO:0000578	0.0849	0.983	3	11	embryonic axis specification	BP	1	SMAD6,FRS2,PCSK6	up_ACOR_VSMC
GO:0043412	0.085	0.931	112	1225	macromolecule modification	BP	0.933	EPHB1,PLK2,TEK,HCLS1,ST8SIA6,KIT,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,PDE4D,IWS1,MEF2C,ATF3,TIPARP,RAPGEF1,TLR4,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,ZDHHC22,NEDD9,PELI1,YES1,ENSCAFG00000010893,EPHB4,B3GNT5,MTOR,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,ENSCAFG00000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,TLR3,MFNG,NCK1,ESCO1,TRMT9B,DPH5,VHL,OTUD4,WSB1,PARP4,FES,NSD1,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,HMGB1,NOS2,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,WTAP,MTA2,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,KDM3A,LMTK2,ATRX,ZC3H13,ZDHHC6,IVNS1ABP,JCAD,TET2,ARHGEF2,CDON	up_VCAV_EC
GO:0070059	0.085	0.972	5	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	1	ITPR1,SERINC3,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0048538	0.085	0.997	1	20	thymus development	BP	1	HOXA3	down_ACOR_EC
GO:0009992	0.085	1	1	1	cellular water homeostasis	BP	1	ANXA7	down_ACOR_VSMC
GO:0032361	0.085	1	1	1	pyridoxal phosphate catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0042365	0.085	1	1	1	water-soluble vitamin catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0042820	0.085	1	1	1	vitamin B6 catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0071579	0.085	1	1	1	regulation of zinc ion transport	BP	1	SLC30A1	down_ACOR_VSMC
GO:0071580	0.085	1	1	1	regulation of zinc ion transmembrane transport	BP	1	SLC30A1	down_ACOR_VSMC
GO:0071581	0.085	1	1	1	regulation of zinc ion transmembrane import	BP	1	SLC30A1	down_ACOR_VSMC
GO:0071582	0.085	1	1	1	negative regulation of zinc ion transport	BP	1	SLC30A1	down_ACOR_VSMC
GO:0071583	0.085	1	1	1	negative regulation of zinc ion transmembrane	BP	1	SLC30A1	down_ACOR_VSMC
GO:0071584	0.085	1	1	1	negative regulation of zinc ion transmembrane	BP	1	SLC30A1	down_ACOR_VSMC
GO:0090281	0.085	1	1	1	negative regulation of calcium ion import	BP	1	SLC30A1	down_ACOR_VSMC
GO:1902298	0.085	1	1	1	cell cycle DNA replication maintenance of fidelity	BP	1	RAD51	down_ACOR_VSMC
GO:1904026	0.085	1	1	1	regulation of collagen fibril organization	BP	1	COLGALT1	down_ACOR_VSMC
GO:1904028	0.085	1	1	1	positive regulation of collagen fibril	BP	1	COLGALT1	down_ACOR_VSMC
GO:1990426	0.085	1	1	1	mitotic recombination-dependent replication	BP	1	RAD51	down_ACOR_VSMC
GO:1990505	0.085	1	1	1	mitotic DNA replication maintenance of fidelity	BP	1	RAD51	down_ACOR_VSMC
GO:0005988	0.085	1	1	1	lactose metabolic process	BP	1	B4GALT1	down_ACOR_VSMC
GO:0005989	0.085	1	1	1	lactose biosynthetic process	BP	1	B4GALT1	down_ACOR_VSMC
GO:0016480	0.085	1	1	1	negative regulation of transcription by RNA polymerase III	BP	1	NAB2	down_ACOR_VSMC
GO:0031247	0.085	1	1	1	actin rod assembly	BP	1	PDXP	down_ACOR_VSMC
GO:0045578	0.085	1	1	1	negative regulation of B cell differentiation	BP	1	HMGB3	down_ACOR_VSMC
GO:0060057	0.085	1	1	1	apoptotic process involved in mammary	BP	1	B4GALT1	down_ACOR_VSMC
GO:0060058	0.085	1	1	1	positive regulation of apoptotic process involved in mammary	BP	1	B4GALT1	down_ACOR_VSMC
GO:0061386	0.085	1	1	1	closure of optic fissure	BP	1	PHACTR4	down_ACOR_VSMC
GO:0070084	0.085	1	1	1	protein initiator methionine removal	BP	1	METAP2	down_ACOR_VSMC

GO:1903519	0.085	1	1	1	regulation of mammary gland involution	BP	1	B4GALT1	down_ACOR_VSMC
GO:1903521	0.085	1	1	1	positive regulation of mammary gland	BP	1	B4GALT1	down_ACOR_VSMC
GO:2001247	0.085	1	1	1	positive regulation of phosphatidylcholine biosynthetic process	BP	1	ACSL3	down_ACOR_VSMC
GO:1902904	0.085	0.997	1	38	negative regulation of supramolecular fiber	BP	1	TAOK1	up_AORT_EC
GO:1903393	0.085	0.997	1	11	positive regulation of adherens junction	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0031929	0.0851	0.959	10	62	TOR signaling	BP	1	LEP,PRKAA2,CASTOR1,UBR1,SESN3,SESN1,DDIT4,DISC1,BMT2,SH3BP4	up_ACOR_VSMC
GO:0006633	0.0851	0.968	6	38	fatty acid biosynthetic process	BP	1	SCD,INSIG1,BRCA1,ELOVL1,ELOVL6,LIPC	down_ACOR_VSMC
GO:0090316	0.0851	0.971	5	48	positive regulation of intracellular protein	BP	1	PRNP,ENSCAFG00000014978,AKT2,GLI3,MAVS	down_VCAV_EC
GO:0032675	0.0851	0.975	4	34	regulation of interleukin-6 production	BP	1	BPI,CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0003229	0.0851	0.977	4	17	ventricular cardiac muscle tissue development	BP	1	TNNT2,FGFR2,TBX5,CHD7	up_ACOR_VSMC
GO:0044091	0.0851	0.989	2	10	membrane biogenesis	BP	1	CLIP3,CDH2	down_VCAV_EC
GO:0046823	0.0851	0.99	2	6	negative regulation of nucleocytoplasmic	BP	1	FERMT1,PARK7	up_ACOR_VSMC
GO:0032796	0.0851	1	1	1	uropod organization	BP	1	CORO1A	down_ACOR_VSMC
GO:0009123	0.0851	0.997	1	104	nucleoside monophosphate	BP	1	AK5	down_VSAP_VSMC
GO:0060193	0.0851	0.997	1	11	positive regulation of lipase activity	BP	1	ABHD5	up_VPOR_EC
GO:0042136	0.0851	0.997	1	21	neurotransmitter biosynthetic process	BP	1	CAV1	up_VSAP_VSMC
GO:0044403	0.085139747	0.96698	6	116	symbiont process	BP	1	ATG16L2,AQP1,TRIM8,MAVS,LRRC15,CHMP4B	up_ACOR_EC
GO:2001233	0.0852	0.95	17	149	regulation of apoptotic signaling pathway	BP	0.933	TNFAIP3,ATF3,FIGNL1,MADD,PAK2,SH3GLB1,NCK1,PTGS2,BCL10,CTNNA1,PMAIP1,RIPK1,ITGA6,SKIL,HIF1A,IVNS1ABP,ARHGEF2	up_VCAV_EC
GO:0042107	0.0852	0.976	4	22	cytokine metabolic process	BP	0.933	TLR4,GATA3,TLR3,BCL10	up_VCAV_EC
GO:1903829	0.0852	0.988	2	91	positive regulation of cellular protein	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0032954	0.0852	1	1	1	regulation of cytokinetic process	BP	1	NUP62	down_ACOR_VSMC
GO:1902412	0.0852	1	1	1	regulation of mitotic cytokinesis	BP	1	NUP62	down_ACOR_VSMC
GO:1903438	0.0852	1	1	1	positive regulation of mitotic cytokinetic	BP	1	NUP62	down_ACOR_VSMC
GO:0021816	0.0852	1	1	1	extension of a leading process involved in cell motility in cerebral cortex radial glia guided	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:1903436	0.0852	1	1	1	regulation of mitotic cytokinetic process	BP	1	NUP62	down_ACOR_VSMC
GO:1903490	0.0852	1	1	1	positive regulation of mitotic cytokinesis	BP	1	NUP62	down_ACOR_VSMC
GO:0048584	0.0852	1	1	592	positive regulation of response to stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0032414	0.0852	0.997	1	21	positive regulation of ion transmembrane transporter activity	BP	1	STIM1	up_VSAP_VSMC
GO:0034762	0.0853	0.958	10	122	regulation of transmembrane transport	BP	1	PRNP,FXYD1,CLIP3,ENSCAFG00000014978,AKT2,CACNB3,THY1,PARK7,CYBA,CLIC4	down_VCAV_EC
GO:1902600	0.0853	0.972	5	31	proton transmembrane transport	BP	1	NNT,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0002902	0.0853	0.99	2	6	regulation of B cell apoptotic process	BP	1	AURKB,NOC2L	down_ACOR_VSMC
GO:0030097	0.0853	0.988	2	244	hemopoiesis	BP	1	TMEM176A,TMEM176B	up_VPUL_VSMC
GO:0006696	0.0853	1	1	1	ergosterol biosynthetic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0044107	0.0853	1	1	1	cellular alcohol metabolic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0061519	0.0853	1	1	1	macrophage homeostasis	BP	1	BAP1	down_ACOR_VSMC
GO:0008204	0.0853	1	1	1	ergosterol metabolic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0044108	0.0853	1	1	1	cellular alcohol biosynthetic process	BP	1	FDFT1	down_ACOR_VSMC

GO:0045338	0.0853	1	1	1	farnesyl diphosphate metabolic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0002764	0.0853	0.997	1	80	immune response-regulating signaling	BP	1	ESR1	up_AORT_VSMC
GO:0034765	0.0854	0.962	8	91	regulation of ion transmembrane transport	BP	1	PRNP,FXYD1,AKT2,CACNB3,THY1,PARK7,CYBA,CLIC4	down_VCAV_EC
GO:0061572	0.0854	0.968	6	50	actin filament bundle organization	BP	0.951	ACTN1,FSCN1,DPYSL3,PLS3,NRP1,TNFAIP1	down_VSAP_EC
GO:0060563	0.0854	0.977	4	18	neuroepithelial cell differentiation	BP	1	WNT11,ABL1,DLL1,DLX3	up_VSAP_EC
GO:0042474	0.0854	0.983	3	11	middle ear morphogenesis	BP	1	OSR2,INSIG2,OSR1	up_VSAP_EC
GO:0090659	0.0854	0.982	3	12	walking behavior	BP	1	FXN,CTNS,HTRA2	up_VSAP_EC
GO:0032070	0.0854	0.99	2	6	regulation of deoxyribonuclease	BP	1	HMGB1,PCNA	down_ACOR_VSMC
GO:1901360	0.0854	1	2	2016	organic cyclic compound metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0034312	0.0854	0.989	2	8	diol biosynthetic process	BP	0.933	SPTLC2,GCH1	up_VCAV_EC
GO:0021691	0.0854	1	1	1	cerebellar Purkinje cell layer maturation	BP	1	ARCN1	down_ACOR_VSMC
GO:0035239	0.0854	0.998	1	299	tube morphogenesis	BP	1	JUP	down_VFEM_VSMC
GO:1990569	0.0854	1	1	1	UDP-N-acetylglucosamine transmembrane transport	BP	0.933	SLC35A3	up_VCAV_EC
GO:0031111	0.0854	0.997	1	11	negative regulation of microtubule polymerization or	BP	1	ARHGEF2	up_VPOR_EC
GO:0050770	0.0854	0.997	1	39	regulation of axonogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0008064	0.0855	0.959	10	72	regulation of actin polymerization or	BP	0.933	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,SWAP70,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0030832	0.0855	0.959	10	72	regulation of actin filament length	BP	0.933	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,SWAP70,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0016239	0.0855	0.976	4	20	positive regulation of macroautophagy	BP	0.933	RALB,SPTLC2,SH3GLB1,HIF1A	up_VCAV_EC
GO:0040012	0.0855	0.981	3	303	regulation of locomotion	BP	1	TBX5,CCL24,ARHGEF2	up_VPUL_EC
GO:0051447	0.0855	0.99	2	6	negative regulation of meiotic cell cycle	BP	1	FBXO5,TTK	down_ACOR_VSMC
GO:0016558	0.0855	0.989	2	10	protein import into peroxisome matrix	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0035986	0.0855	1	1	1	senescence-associated heterochromatin focus	BP	1	HMGA1	down_ACOR_VSMC
GO:0090402	0.0855	1	1	1	oncogene-induced cell senescence	BP	1	HMGA1	down_ACOR_VSMC
GO:0009064	0.0855	0.997	1	23	glutamine family amino acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:1902042	0.0855	0.997	1	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	ARHGEF2	up_VPOR_EC
GO:2001169	0.0855	0.997	1	11	regulation of ATP biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0003156	0.0855	0.997	1	20	regulation of animal organ formation	BP	1	HOXA11	up_VSAP_VSMC
GO:0051272	0.0856	0.946	22	170	positive regulation of cellular component movement	BP	1	TWIST2,WNT11,FAM107A,ENPP2,FGF7,ABL1,HDAC7,PDGFD,CCBE1,STAT5A,F2RL1,DDR2,PIK3R1,TIAM1,CFAP69,SASH1,ZNF580,STX4,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0033500	0.0856	0.959	10	64	carbohydrate homeostasis	BP	1	HNF4A,SLC8B1,RAB11B,PDK2,PIK3R1,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0042593	0.0856	0.959	10	64	glucose homeostasis	BP	1	HNF4A,SLC8B1,RAB11B,PDK2,PIK3R1,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0043406	0.0856	0.96	9	62	positive regulation of MAP kinase activity	BP	0.933	KIT,MAP3K11,PDGFB,TLR4,EDN1,BMP2,MADD,RIPK1,PDGFD	up_VCAV_EC
GO:0019322	0.0856	1	1	1	pentose biosynthetic process	BP	1	PGD	down_ACOR_VSMC
GO:0009628	0.0856	0.998	1	302	response to abiotic stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0071559	0.0856	0.997	1	75	response to transforming growth factor beta	BP	1	WNT7A	up_AORT_VSMC
GO:0021846	0.0856	0.997	1	11	cell proliferation in forebrain	BP	1	HOOK3	up_VPOR_EC
GO:0051494	0.0856	0.997	1	44	negative regulation of cytoskeleton organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0090288	0.0856	0.997	1	44	negative regulation of cellular response to growth factor stimulus	BP	1	SLIT2	up_VPUL_VSMC

GO:0008584	0.085699529	0.98025	3	39	male gonad development	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:0046546	0.085699529	0.98025	3	39	development of primary male sexual	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:0090288	0.0857	0.98	3	44	negative regulation of cellular response to growth factor stimulus	BP	1	GREM1,GREM2,ADAM17	up_AFEM_EC
GO:0046636	0.0857	0.989	2	10	negative regulation of alpha-beta T cell	BP	1	GLI3,LOXL3	down_VCAV_EC
GO:0010613	0.0857	0.991	2	5	positive regulation of cardiac muscle	BP	1	PDE5A,EDN1	up_ACOR_VSMC
GO:0014742	0.0857	0.991	2	5	positive regulation of muscle hypertrophy	BP	1	PDE5A,EDN1	up_ACOR_VSMC
GO:0002155	0.0857	1	1	1	regulation of thyroid hormone mediated	BP	0.933	PRCP	up_VCAV_EC
GO:0002254	0.0857	1	1	1	kinin cascade	BP	0.933	PRCP	up_VCAV_EC
GO:0002353	0.0857	1	1	1	plasma kallikrein-kinin cascade	BP	0.933	PRCP	up_VCAV_EC
GO:0090207	0.0857	0.997	1	11	regulation of triglyceride metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0016052	0.0857	0.997	1	34	carbohydrate catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0010464	0.0857	0.997	1	21	regulation of mesenchymal cell	BP	1	SHOX2	up_VSAP_VSMC
GO:2000576	0.085730656	0.99716	1	4	positive regulation of microtubule motor	BP	1	DYNC1I1	up_ACOR_EC
GO:2000580	0.085730656	0.99716	1	4	regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNC1I1	up_ACOR_EC
GO:2000582	0.085730656	0.99716	1	4	positive regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNC1I1	up_ACOR_EC
GO:0019438	0.0858	0.961	10	1258	aromatic compound biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,TNRC6B,NEDD4	down_ACOR_EC
GO:0048706	0.0858	0.987	2	59	embryonic skeletal system development	BP	1	HOXA3,ACVR2A	up_VPOR_EC
GO:0048732	0.0858	0.987	2	116	gland development	BP	1	HOXA9,SIX1	up_VFEM_EC
GO:0032269	0.0858	0.998	1	306	negative regulation of cellular protein metabolic	BP	1	CST3	down_AORT_EC
GO:0038167	0.0858	1	1	1	epidermal growth factor receptor signaling pathway via positive regulation of NF-kappaB	BP	1	RASSF2	up_ACOR_VSMC
GO:0038168	0.0858	1	1	1	epidermal growth factor receptor signaling pathway via I-kappaB	BP	1	RASSF2	up_ACOR_VSMC
GO:0045738	0.0858	0.997	1	12	negative regulation of DNA repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0010648	0.0859	0.937	48	407	negative regulation of cell communication	BP	1	SMAD6,LEP,LBH,HTR2B,RASSF2,PRKAA2,MLLT3,FERMT1,BMP4,ELF1,CASTOR1,LATS2,ZNRF3,AR,PTGIR,NDRG2,ITPR1,F2RL1,DAPK1,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,RGS2,DAG1,PSEN1,SYNJ2BP,WWC2,DUSP22,SESN1,DUSP26,LRRC4,DDIT4,HERPUD1,INPP5K,BMT2,PFKL,WFS1,SH3BP4,PARK7	up_ACOR_VSMC
GO:0048634	0.0859	0.965	7	40	regulation of muscle organ development	BP	1	BMP4,FGFR2,GJA1,TBX20,TBX5,FRS2,EDN1	up_ACOR_VSMC
GO:0009201	0.0859	0.971	5	41	ribonucleoside triphosphate biosynthetic	BP	0.956	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0051147	0.0859	0.98	3	44	regulation of muscle cell differentiation	BP	1	DLL1,GREM1,DMPK	up_AFEM_EC
GO:0003156	0.0859	0.996	1	20	regulation of animal organ formation	BP	1	SULF1	down_ACOR_EC
GO:0040018	0.086	0.983	3	11	positive regulation of multicellular organism	BP	0.933	CHD7,CREB1,SPTBN4	up_VCAV_EC
GO:0046320	0.086	0.989	2	10	regulation of fatty acid oxidation	BP	1	AKT2,LONP2	down_VCAV_EC
GO:0010575	0.086	0.989	2	8	positive regulation of vascular endothelial growth factor production	BP	0.957	SULF1,HIF1A	down_VSAP_EC
GO:0014010	0.086	1	1	1	Schwann cell proliferation	BP	1	NF2	down_ACOR_VSMC
GO:0043535	0.086	0.997	1	45	regulation of blood vessel endothelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0043648	0.086	0.996	1	26	dicarboxylic acid metabolic process	BP	1	NR1H4	up_VPUL_EC

GO:0071326	0.086	0.996	1	26	cellular response to monosaccharide stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0071331	0.086	0.996	1	26	cellular response to hexose stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0010563	0.086081228	0.95915	9	203	negative regulation of phosphorus metabolic	BP	1	PKIB,NDRG2,DUSP26,SMAD6,LRRC15,LRRC4,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0045936	0.086081228	0.95915	9	203	negative regulation of phosphate metabolic	BP	1	PKIB,NDRG2,DUSP26,SMAD6,LRRC15,LRRC4,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0051271	0.0861	0.953	14	98	negative regulation of cellular component movement	BP	1	KCNE3,TCAF1,RECK,TP53INP1,NRP1,EVL,SPINT2,TBX5,DAG1,SEMA6D,SYNJ2BP,JUP,DUSP22,WASL	up_ACOR_VSMC
GO:0018272	0.0861	1	1	1	protein-pyridoxal-5-phosphate linkage via peptidyl-N6-pyridoxal	BP	1	CTH	down_ACOR_VSMC
GO:0018352	0.0861	1	1	1	protein-pyridoxal-5-phosphate linkage	BP	1	CTH	down_ACOR_VSMC
GO:0019343	0.0861	1	1	1	cysteine biosynthetic process via cystathionine	BP	1	CTH	down_ACOR_VSMC
GO:0019344	0.0861	1	1	1	cysteine biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0019346	0.0861	1	1	1	transsulfuration	BP	1	CTH	down_ACOR_VSMC
GO:0035887	0.0861	1	1	1	aortic smooth muscle cell differentiation	BP	1	CTH	down_ACOR_VSMC
GO:0071266	0.0861	1	1	1	'de novo' L-methionine biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:1904829	0.0861	1	1	1	regulation of aortic smooth muscle cell	BP	1	CTH	down_ACOR_VSMC
GO:1904831	0.0861	1	1	1	positive regulation of aortic smooth muscle cell	BP	1	CTH	down_ACOR_VSMC
GO:0009092	0.0861	1	1	1	homoserine metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0044524	0.0861	1	1	1	protein sulfhydration	BP	1	CTH	down_ACOR_VSMC
GO:0006537	0.0861	0.998	1	2	glutamate biosynthetic process	BP	1	GLS2	down_VCAV_EC
GO:0010769	0.0861	0.997	1	69	regulation of cell morphogenesis involved	BP	1	WNT7A	up_AORT_VSMC
GO:0008063	0.0861	1	1	1	Toll signaling pathway	BP	0.933	PELI1	up_VCAV_EC
GO:0097298	0.0861	1	1	1	regulation of nucleus size	BP	0.933	HP1BP3	up_VCAV_EC
GO:0050921	0.0861	0.996	1	39	positive regulation of chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0032088	0.0861	0.996	1	26	negative regulation of NF-kappaB transcription	BP	1	NR1H4	up_VPUL_EC
GO:0018130	0.0862	0.961	10	1261	heterocycle biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,TNRC6B,NEDD4	down_ACOR_EC
GO:0033628	0.0862	0.982	3	14	regulation of cell adhesion mediated by integrin	BP	0.933	PODXL,FERMT1,SWAP70	up_VCAV_EC
GO:0098581	0.0862	0.991	2	5	detection of external biotic stimulus	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0048667	0.0862	0.987	2	140	cell morphogenesis involved in neuron	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0055081	0.0862	0.996	1	17	anion homeostasis	BP	1	HOXA3	down_ACOR_EC
GO:0050679	0.0862	0.997	1	62	positive regulation of epithelial cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0003151	0.0862	0.996	1	34	outflow tract morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0046323	0.0862	0.996	1	26	glucose import	BP	1	NR1H4	up_VPUL_EC
GO:0010648	0.0863	0.938	42	407	negative regulation of cell communication	BP	0.933	CXCL8,TNFAIP3,TNIP1,PDE4D,FERMT1,ATF3,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,APLNR,ARAP3,HOMER3,EGFL7,FIGNL1,CASP8,MTOR,BMP2,HHEX,PREX2,GDPD5,RIOK3,STMN1,MCC,SMARCA4,APOD,NCK1,OTUD4,PTGS2,CTDSPL2,CTNNA1,CNOT7,RIPK1,ITGA6,RGS2,SKIL,HIF1A,TNFAIP1,IVNS1ABP,ARHGEF2,PEAR1	up_VCAV_EC
GO:0048709	0.0863	0.981	3	17	oligodendrocyte differentiation	BP	0.958	SLC45A3,EIF2B1,CTNNB1	down_VSAP_EC
GO:0097028	0.0863	0.982	3	11	dendritic cell differentiation	BP	1	F2RL1,BATF2,TGFBR2	up_VSAP_EC
GO:0048661	0.0863	0.996	1	17	positive regulation of smooth muscle cell	BP	1	SULF1	down_ACOR_EC
GO:0040012	0.0863	0.998	1	303	regulation of locomotion	BP	1	JUP	down_VFEM_VSMC
GO:2000346	0.0863	1	1	1	negative regulation of hepatocyte proliferation	BP	1	LIMS2	up_ACOR_VSMC

GO:0006865	0.0863	0.996	1	23	amino acid transport	BP	1	NTRK2	up_APUL_EC
GO:0010464	0.0863	0.996	1	21	regulation of mesenchymal cell	BP	1	SIX1	up_VFEM_EC
GO:0007033	0.0864	0.955	12	82	vacuole organization	BP	1	FEZ1,ABCA1,TP53INP1,GABARAPL1,PSEN1,PIK3C3,CLN8,AKTIP,ATG16L2,GAA,FEZ2,ACP2	up_ACOR_VSMC
GO:0046637	0.0864	0.976	4	18	regulation of alpha-beta T cell differentiation	BP	1	ZBTB16,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0045776	0.0864	0.99	2	6	negative regulation of blood pressure	BP	0.933	PRCP,NOS2	up_VCAV_EC
GO:0030282	0.0864	0.996	1	37	bone mineralization	BP	1	HOXA3	up_VPOR_VSMC
GO:0048588	0.0864	0.996	1	44	developmental cell growth	BP	1	SLIT2	up_VPUL_VSMC
GO:1903900	0.086450791	0.97998	3	40	regulation of viral life cycle	BP	1	TRIM8,MAVS,CHMP4B	up_ACOR_EC
GO:0009187	0.0865	0.983	3	10	cyclic nucleotide metabolic process	BP	0.933	NPR1,GUCY1A1,GUCY1B1	up_VCAV_EC
GO:0014037	0.0865	0.988	2	10	Schwann cell differentiation	BP	1	NAB2,AKT2	down_VCAV_EC
GO:0032924	0.0865	0.989	2	9	activin receptor signaling pathway	BP	0.96	TGFBR1,INHBA	down_VSAP_EC
GO:1901097	0.0865	0.998	1	2	negative regulation of autophagosome	BP	1	CLEC16A	down_VCAV_EC
GO:0045580	0.0865	0.996	1	35	regulation of T cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0042310	0.0865	0.996	1	21	vasoconstriction	BP	1	AVPR1A	up_VFEM_EC
GO:0097756	0.0865	0.996	1	21	negative regulation of blood vessel diameter	BP	1	AVPR1A	up_VFEM_EC
GO:0010996	0.086569656	0.99741	1	3	response to auditory stimulus	BP	1	USP53	up_ACOR_EC
GO:0030334	0.0866	0.94	33	267	regulation of cell migration	BP	1	VEGFD,LGR6,TCAF1,RECK,BMP4,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,EVL,TBX5,PRKCE,DAG1,APP,LAMA3,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,FAM107A,JAM3,WASL,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0045597	0.0866	0.946	21	253	positive regulation of cell differentiation	BP	0.96	ARHGEF2,SERPINE1,SOCS5,DPYSL3,ILK,PTGS2,HIF1A,EVI2B,CTNNB1,ENSCAFG00000002015,APOE,KLF5,LYN,MMD,VLDLR,REST,PRMT1,DISC1,INHBA,HIF1AN,NRP1	down_VSAP_EC
GO:0060255	0.0866	0.958	13	1782	regulation of macromolecule metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,SULF1,ELK3,HOXA1,ASPN,NEDD4	down_ACOR_EC
GO:0034330	0.0866	0.956	11	80	cell junction organization	BP	0.933	TEK,PRKCH,OCLN,RAPGEF1,TJP1,SLK,APOD,RAPGEF2,CTNNA1,ENSCAFG00000002015,FSCN1	up_VCAV_EC
GO:0014015	0.0866	0.982	3	11	positive regulation of gliogenesis	BP	1	ZNF365,APP,CRKL	up_ACOR_VSMC
GO:0007265	0.0866	0.987	2	121	Ras protein signal transduction	BP	1	TIAM1,CDC42EP5	up_VFEM_EC
GO:0002155	0.0866	1	1	1	regulation of thyroid hormone mediated	BP	1	PRCP	down_ACOR_VSMC
GO:0002353	0.0866	1	1	1	plasma kallikrein-kinin cascade	BP	1	PRCP	down_ACOR_VSMC
GO:0002254	0.0866	1	1	1	kinin cascade	BP	1	PRCP	down_ACOR_VSMC
GO:0051145	0.0866	0.996	1	21	smooth muscle cell differentiation	BP	1	SIX1	up_VFEM_EC
GO:0110110	0.0866	0.996	1	34	positive regulation of animal organ	BP	1	HOXA11	up_VFEM_VSMC
GO:1901879	0.0866	0.996	1	26	regulation of protein depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0098742	0.0866	0.996	1	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5	up_VPUL_VSMC
GO:0060041	0.0867	0.965	7	41	retina development in camera-type eye	BP	1	THRB,CDON,IRX5,DLL1,RARG,CLCN2,ACVRL1	up_VSAP_EC
GO:0010611	0.0867	0.982	3	11	regulation of cardiac muscle hypertrophy	BP	1	GATA5,PDE5A,EDN1	up_ACOR_VSMC
GO:0014743	0.0867	0.982	3	11	regulation of muscle hypertrophy	BP	1	GATA5,PDE5A,EDN1	up_ACOR_VSMC
GO:0050708	0.0867	0.987	2	101	regulation of protein secretion	BP	1	LYN,STX4	down_ACOR_EC
GO:0009744	0.0867	1	1	1	response to sucrose	BP	0.933	CALCRL	up_VCAV_EC
GO:0034285	0.0867	1	1	1	response to disaccharide	BP	0.933	CALCRL	up_VCAV_EC

GO:0071324	0.0867	1	1	1	cellular response to disaccharide stimulus	BP	0.933	CALCRL	up_VCAV_EC
GO:0071329	0.0867	1	1	1	cellular response to sucrose stimulus	BP	0.933	CALCRL	up_VCAV_EC
GO:0097646	0.0867	1	1	1	calcitonin family receptor signaling pathway	BP	0.933	CALCRL	up_VCAV_EC
GO:1990408	0.0867	1	1	1	calcitonin gene-related peptide receptor signaling	BP	0.933	CALCRL	up_VCAV_EC
GO:1990410	0.0867	1	1	1	adrenomedullin receptor signaling pathway	BP	0.933	CALCRL	up_VCAV_EC
GO:0051963	0.0867	0.996	1	26	regulation of synapse assembly	BP	1	FLRT3	up_VPUL_EC
GO:0032210	0.0868	0.976	4	20	regulation of telomere maintenance via	BP	1	AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:1904356	0.0868	0.976	4	20	regulation of telomere maintenance via telomere lengthening	BP	1	AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0055081	0.0868	0.981	3	17	anion homeostasis	BP	0.961	NR1H4,ENPP1,APOE	down_VSAP_EC
GO:0007339	0.0868	0.99	2	6	binding of sperm to zona pellucida	BP	1	B4GALT1,CCT4	down_ACOR_VSMC
GO:0035036	0.0868	0.99	2	6	sperm-egg recognition	BP	1	B4GALT1,CCT4	down_ACOR_VSMC
GO:0035455	0.0868	0.99	2	6	response to interferon-alpha	BP	0.933	MX2,GATA3	up_VCAV_EC
GO:0071621	0.0868	0.996	1	27	granulocyte chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0007155	0.0869	0.938	40	324	cell adhesion	BP	1	SMAD6,ACTN2,LEP,GATA5,CD83,MBP,FERMT1,BMP4,PDE5A,CITED2,PKP4,CD274,TINAGL1,LIMS2,NRP1,PTPN22,NPNT,SPINT2,VCAM1,PRKCE,RND1,ECM2,LAMA3,PSEN1,JUP,CDH18,PERP,DUSP22,NID1,DUSP26,FAM107A,JAM3,IGFBP7,CELSR2,ATP2C1,DOCK5,BVES,RREB1,PAG1,CRKL	up_ACOR_VSMC
GO:0009605	0.0869	0.948	18	538	response to external stimulus	BP	1	CMKLR1,LEP,CRY2,CD40,PLXNA4,BPI,GPAM,CHRM2,SLC17A5,CLEC16A,POSTN,TBXA2R,ACKR4,ACACB,NAPEPLD,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0030224	0.0869	0.976	4	18	monocyte differentiation	BP	1	HOXA7,ZFP36L1,MYC,PIR	up_VSAP_EC
GO:1903131	0.0869	0.976	4	18	mononuclear cell differentiation	BP	1	HOXA7,ZFP36L1,MYC,PIR	up_VSAP_EC
GO:0006623	0.0869	0.996	1	16	protein targeting to vacuole	BP	1	NEDD4	down_ACOR_EC
GO:1900041	0.0869	1	1	1	negative regulation of interleukin-2 secretion	BP	1	EZR	down_ACOR_VSMC
GO:0032640	0.0869	0.996	1	39	tumor necrosis factor production	BP	1	BPI	up_AORT_EC
GO:0001823	0.0869	0.996	1	45	mesonephros development	BP	1	SLIT2	up_VPUL_VSMC
GO:0032474	0.0869	1	1	1	otolith morphogenesis	BP	1	LRIG3	up_VSAP_EC
GO:0046426	0.0869	0.996	1	20	negative regulation of JAK-STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:1904893	0.0869	0.996	1	20	negative regulation of STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0000288	0.087	0.971	5	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	EXOSC7,ZFP36L1,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0001568	0.087	0.988	2	252	blood vessel development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0022008	0.087	0.989	2	406	neurogenesis	BP	1	HOXC10,WNT7A	up_AORT_VSMC
GO:0006413	0.087	0.996	1	42	translational initiation	BP	1	EIF3M	down_AFEM_EC
GO:0051961	0.087	0.997	1	73	negative regulation of nervous system	BP	1	WNT7A	up_AORT_VSMC
GO:0043467	0.087	0.996	1	35	regulation of generation of precursor metabolites	BP	1	FBP1	up_VFEM_VSMC
GO:1901292	0.087	0.996	1	34	nucleoside phosphate catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0048813	0.08709393	0.97979	3	39	dendrite morphogenesis	BP	1	PAK3,MAPK8IP2,NRP1	up_ACOR_EC
GO:0046883	0.0871	0.962	8	49	regulation of hormone secretion	BP	1	LEP,TM7SF3,PRKCE,SCG5,CHD7,CCL5,EDN1,PFKL	up_ACOR_VSMC
GO:0071216	0.0871	0.964	7	61	cellular response to biotic stimulus	BP	0.963	NR1H4,HSPA5,SERPINE1,MTDH,LYN,DDIT3,GSK3B	down_VSAP_EC
GO:0051049	0.0871	0.971	5	479	regulation of transport	BP	1	LYN,HOXA3,ACSL3,STX4,NEDD4	down_ACOR_EC

GO:0031347	0.0871	0.987	2	144	regulation of defense response	BP	1	NR1H4,CCL24	up_VPUL_EC
GO:0060364	0.0871	0.998	1	2	frontal suture morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0002040	0.0871	0.996	1	46	sprouting angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0003208	0.0871	0.996	1	24	cardiac ventricle morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0045766	0.0871	0.997	1	63	positive regulation of angiogenesis	BP	1	C6	up_VCAV_VSMC
GO:0022900	0.0872	0.996	1	46	electron transport chain	BP	1	NDUFA10	down_AFEM_EC
GO:0032602	0.0872	0.996	1	23	chemokine production	BP	1	NR1H4	up_APUL_EC
GO:0062014	0.0872	0.996	1	35	negative regulation of small molecule metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0006955	0.0873	0.938	39	327	immune response	BP	1	TLR1,SMAD6,PLCG2,LEP,CD83,COCH,TP53BP1,MX1,ELF1,TLR3,ISG15,CD274,CTSS,TINAGL1,BLNK,F2RL1,HRH2,DAPK1,C1S,EDA,TNFSF10,PTPN22,EVL,C7,PRKCE,PARP9,APP,PSEN1,CCL5,DUSP22,NOD2,DLA88,JAM3,B2M,SERINC3,TNFRSF11B,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0032504	0.0873	0.948	18	152	multicellular organism reproduction	BP	1	ACSL4,NDC1,TRIP13,CTDNEP1,FBXO5,NCAPH,POC1A,B4GALT1,HIST1H1A,FOSL1,HMGB2,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,TTLL1	down_ACOR_VSMC
GO:0048609	0.0873	0.948	18	152	multicellular organismal reproductive process	BP	1	ACSL4,NDC1,TRIP13,CTDNEP1,FBXO5,NCAPH,POC1A,B4GALT1,HIST1H1A,FOSL1,HMGB2,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,TTLL1	down_ACOR_VSMC
GO:0001780	0.0873	0.99	2	6	neutrophil homeostasis	BP	1	HMGB1,PIK3CD	down_ACOR_VSMC
GO:1904716	0.0873	1	1	1	positive regulation of chaperone-mediated	BP	1	PLK3	down_ACOR_VSMC
GO:2000777	0.0873	1	1	1	positive regulation of proteasomal ubiquitin-dependent protein catabolic process involved	BP	1	PLK3	down_ACOR_VSMC
GO:0007159	0.0873	0.997	1	79	leukocyte cell-cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0042391	0.0873	0.997	1	81	regulation of membrane potential	BP	1	WNT7A	up_AORT_VSMC
GO:0006406	0.0874	0.971	5	27	mRNA export from nucleus	BP	0.933	IWS1,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0071427	0.0874	0.971	5	27	mRNA-containing ribonucleoprotein complex export from	BP	0.933	IWS1,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0002755	0.0874	0.99	2	6	MyD88-dependent toll-like receptor signaling	BP	0.933	TNIP1,TLR4	up_VCAV_EC
GO:0034101	0.0874	0.996	1	45	erythrocyte homeostasis	BP	1	CITED2	down_VPOR_EC
GO:0032649	0.0874	0.996	1	23	regulation of interferon-gamma production	BP	1	NR1H4	up_APUL_EC
GO:0071108	0.0875	0.982	3	11	protein K48-linked deubiquitination	BP	0.933	TNFAIP3,OTUD4,USP37	up_VCAV_EC
GO:0010591	0.0875	0.982	3	12	regulation of lamellipodium assembly	BP	0.933	MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0016477	0.0875	0.981	3	426	cell migration	BP	1	CHL1,BAMBI,C3AR1	up_VPOR_VSMC
GO:0010742	0.0875	0.99	2	6	macrophage derived foam cell differentiation	BP	0.933	PRKCH,PPARG	up_VCAV_EC
GO:0090077	0.0875	0.99	2	6	foam cell differentiation	BP	0.933	PRKCH,PPARG	up_VCAV_EC
GO:0044419	0.08750821	0.96582	6	117	interspecies interaction between organisms	BP	1	ATG16L2,AQP1,TRIM8,MAVS,LRRC15,CHMP4B	up_ACOR_EC
GO:0009987	0.0876	0.964	29	5086	cellular process	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,ACSL4,SPG11,PDPN,NRP2,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,IPO7,RPSA,ATRIP,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,STX4,MYO1D,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0001822	0.0876	0.957	10	98	kidney development	BP	0.967	SULF1,ENSCAFG00000032470,ILK,HOXB7,ACTA2,MAGED1,CTNNB1,MYO1E,SIX4,NRP1	down_VSAP_EC
GO:0044773	0.0876	0.971	5	28	mitotic DNA damage checkpoint	BP	1	CDK1,CASP2,FANCI,TOPBP1,CLSPN	down_ACOR_VSMC
GO:0050869	0.0876	0.989	2	8	negative regulation of B cell activation	BP	0.967	LYN,BTK	down_VSAP_EC
GO:0003163	0.0876	1	1	1	sinoatrial node development	BP	1	BVES	up_ACOR_VSMC

GO:0060921	0.0876	1	1	1	sinoatrial node cell differentiation	BP	1	BVES	up_ACOR_VSMC
GO:0060931	0.0876	1	1	1	sinoatrial node cell development	BP	1	BVES	up_ACOR_VSMC
GO:0042539	0.0876	1	1	1	hypotonic salinity response	BP	1	SLC12A6	up_VSAP_EC
GO:0071477	0.0876	1	1	1	cellular hypotonic salinity response	BP	1	SLC12A6	up_VSAP_EC
GO:0003002	0.087657417	0.96574	6	118	regionalization	BP	1	FZD5,SMAD6,FOXC2,LRP4,CLSTN1,NRP1	up_ACOR_EC
GO:0001866	0.0877	1	1	1	NK T cell proliferation	BP	1	ELF4	down_ACOR_VSMC
GO:0007052	0.0877	0.996	1	42	mitotic spindle organization	BP	1	GPSM2	down_AFEM_EC
GO:0035262	0.0877	1	1	1	gonad morphogenesis	BP	1	LHX9	up_ACOR_VSMC
GO:0008584	0.0877	0.996	1	39	male gonad development	BP	1	HOXA9	up_AORT_EC
GO:0046546	0.0877	0.996	1	39	development of primary male sexual	BP	1	HOXA9	up_AORT_EC
GO:0001570	0.0877	0.996	1	37	vasculogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0014855	0.0877	0.996	1	22	striated muscle cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0046580	0.0878	0.976	4	18	negative regulation of Ras protein signal	BP	0.933	RAPGEF1,ARAP3,STMN1,TNFAIP1	up_VCAV_EC
GO:0010835	0.0878	0.99	2	6	regulation of protein ADP-ribosylation	BP	1	PUM3,TINF2	down_ACOR_VSMC
GO:0048537	0.0878	1	1	1	mucosal-associated lymphoid tissue	BP	1	TOX	down_ACOR_VSMC
GO:0048541	0.0878	1	1	1	Peyer's patch development	BP	1	TOX	down_ACOR_VSMC
GO:1901293	0.0878	0.997	1	106	nucleoside phosphate biosynthetic process	BP	1	AK5	down_VSAP_VSMC
GO:0090360	0.0878	1	1	1	platelet-derived growth factor production	BP	1	NDRG2	up_ACOR_VSMC
GO:0090361	0.0878	1	1	1	regulation of platelet-derived growth factor	BP	1	NDRG2	up_ACOR_VSMC
GO:0008217	0.0878	0.996	1	38	regulation of blood pressure	BP	1	LNPEP	up_AORT_EC
GO:0045088	0.0878	0.997	1	81	regulation of innate immune response	BP	1	ESR1	up_AORT_VSMC
GO:0031529	0.0878	0.996	1	20	ruffle organization	BP	1	CAV1	up_VSAP_VSMC
GO:0008654	0.0879	0.959	9	58	phospholipid biosynthetic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,CHPT1,PIGN,PIGS,PIGG,CRLS1	up_ACOR_VSMC
GO:1904377	0.0879	0.98	3	21	positive regulation of protein localization to cell	BP	1	LRP1,PRNP,CLIP3	down_VCAV_EC
GO:0045661	0.0879	0.981	3	18	regulation of myoblast differentiation	BP	0.969	PRICKLE1,DDIT3,HIF1AN	down_VSAP_EC
GO:0003413	0.0879	0.99	2	6	chondrocyte differentiation involved in endochondral bone	BP	1	POC1A,SERPINH1	down_ACOR_VSMC
GO:0051098	0.0879	0.987	2	129	regulation of binding	BP	1	HOXA3,PLCL1	up_APUL_EC
GO:0060009	0.0879	0.99	2	5	Sertoli cell development	BP	0.933	ARID4B,ATRX	up_VCAV_EC
GO:0034394	0.0879	0.996	1	19	protein localization to cell surface	BP	1	STX4	down_ACOR_EC
GO:1902749	0.0879	0.996	1	39	regulation of cell cycle G2/M phase transition	BP	1	TAOK1	up_AORT_EC
GO:0046889	0.0879	0.996	1	24	positive regulation of lipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0048565	0.0879	0.996	1	38	digestive tract development	BP	1	SHOX2	up_VFEM_VSMC
GO:0043331	0.0879	0.996	1	20	response to dsRNA	BP	1	CAV1	up_VSAP_VSMC
GO:0010596	0.088	0.987	2	21	negative regulation of endothelial cell migration	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:0071417	0.088	0.987	2	142	cellular response to organonitrogen	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:1902510	0.088	1	1	1	regulation of apoptotic DNA fragmentation	BP	1	AIFM1	down_ACOR_VSMC
GO:1903624	0.088	1	1	1	regulation of DNA catabolic process	BP	1	AIFM1	down_ACOR_VSMC
GO:0038034	0.088	0.996	1	21	signal transduction in absence of ligand	BP	1	EYA1	up_VFEM_EC
GO:0097192	0.088	0.996	1	21	extrinsic apoptotic signaling pathway in	BP	1	EYA1	up_VFEM_EC

GO:0006469	0.0881	0.961	8	78	negative regulation of protein kinase activity	BP	0.97	SOCS5,ERRFI1,TRIB3,PTPN2,APOE,LYN,CBLC,CDKN1A	down_VSAP_EC
GO:0006893	0.0881	0.996	1	20	Golgi to plasma membrane transport	BP	1	ACSL3	down_ACOR_EC
GO:1903034	0.088195945	0.9794	3	40	regulation of response to wounding	BP	1	RGMA,FOXC2,PRKCD	up_ACOR_EC
GO:0030509	0.0882	0.97	5	47	BMP signaling pathway	BP	1	SMAD9,FBN1,CHRDL1,GREM1,RGMA	down_VCAV_EC
GO:1905340	0.0882	1	1	1	regulation of protein localization to	BP	1	NDC80	down_ACOR_VSMC
GO:1905342	0.0882	1	1	1	positive regulation of protein localization to	BP	1	NDC80	down_ACOR_VSMC
GO:0031110	0.0882	0.996	1	24	regulation of microtubule polymerization or depolymerization	BP	1	TUBB4A	up_APUL_EC
GO:0007411	0.0882	0.996	1	45	axon guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:0097485	0.0882	0.996	1	45	neuron projection guidance	BP	1	SLIT2	up_VPUL_VSMC
GO:0072210	0.088247192	0.98719	2	19	metanephric nephron development	BP	1	SOX9,AQP1	up_ACOR_EC
GO:0071363	0.0883	0.945	21	188	cellular response to growth factor stimulus	BP	0.933	CXCL8,PDGFB,MEF2C,FERMT1,DLL4,RAPGEF1,GATA3,SMAD1,YES1,BMP2,HHEX,PRKD2,RAPGEF2,CTDSPL2,CREB1,RIPK1,SKIL,HIF1A,ENSCAFG00000002015,JCAD,ZEB1	up_VCAV_EC
GO:0002064	0.0883	0.955	11	71	epithelial cell development	BP	1	EXPH5,SHROOM3,BMP4,GJA1,ATRX,SEC24B,ARHGEF26,F2RL1,SPINT2,FRS2,FOSL2	up_ACOR_VSMC
GO:0032507	0.0883	0.98	3	18	maintenance of protein location in cell	BP	0.97	HSPA5,TLN1,KDELR2	down_VSAP_EC
GO:0035924	0.0883	0.987	2	21	cellular response to vascular endothelial growth factor stimulus	BP	1	GAS1,DLL1	up_AFEM_EC
GO:0055065	0.0883	0.987	2	145	metal ion homeostasis	BP	1	HOXA3,NEO1	up_VPUL_EC
GO:0001658	0.0883	0.996	1	24	branching involved in ureteric bud	BP	1	NPNT	up_APUL_EC
GO:0062013	0.0883	0.996	1	27	positive regulation of small molecule metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0008306	0.0883	0.996	1	21	associative learning	BP	1	NETO1	up_VSAP_VSMC
GO:0032880	0.0884	0.944	22	266	regulation of protein localization	BP	0.97	NR1H4,PLK3,PTPN14,PTPN11,SESN2,MYO1C,MSN,KIF5B,HIF1A,IWS1,ZPR1,CTNNB1,LYN,MMD,GSK3B,SH3GLB1,TAX1BP3,REST,RAB11FIP1,SIX4,CDKN1A,RHBDF2	down_VSAP_EC
GO:0006511	0.0884	0.945	21	253	ubiquitin-dependent protein catabolic process	BP	0.97	PRICKLE1,PLK3,SOCS5,HSP90B1,TRIB3,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,USP48,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,USP14,TNFAIP1	down_VSAP_EC
GO:0007154	0.0884	0.968	7	1622	cell communication	BP	1	FGF5,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0097581	0.0884	0.971	5	26	lamellipodium organization	BP	1	WASF3,ENPP2,SLIT2,FGD4,NCK1	up_VSAP_EC
GO:0060571	0.0884	0.981	3	13	morphogenesis of an epithelial fold	BP	0.933	HHEX,HIF1A,LUZP1	up_VCAV_EC
GO:0001782	0.0884	0.989	2	8	B cell homeostasis	BP	0.97	HIF1A,LYN	down_VSAP_EC
GO:2000574	0.0884	0.989	2	6	regulation of microtubule motor activity	BP	1	DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:0010721	0.0884	0.997	1	73	negative regulation of cell development	BP	1	WNT7A	up_AORT_VSMC
GO:0042632	0.0884	0.996	1	27	cholesterol homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0051270	0.0885	0.938	36	296	regulation of cellular component movement	BP	1	FGF13,VEGFD,LGR6,KCNE3,TCAF1,RECK,BMP4,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,EVL,SPINT2,TBX5,PRKCE,DAG1,APP,LAMA3,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,FAM107A,JAM3,WASL,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0051336	0.0885	0.94	31	251	regulation of hydrolase activity	BP	1	TNNT2,HTR2B,USP6NL,MBP,RECK,EVI5L,FGFR2,SCARB2,SH3RF2,PKP4,CHN2,CST3,F2RL1,DAPK1,NPNT,SH3RF1,MARF1,PPP1R26,SGSM2,SPINK2,CCL5,PERP,DYNC1I2,SBF2,SH3BP4,DYNC1I1,PARK7,GPATCH2,ZFYVE1,BVES,LMF1	up_ACOR_VSMC
GO:0010565	0.0885	0.97	5	40	regulation of cellular ketone metabolic process	BP	0.971	NR1H4,TRIB3,PTGS2,SLC45A3,REST	down_VSAP_EC
GO:0060671	0.0885	1	1	1	epithelial cell differentiation involved in embryonic placenta	BP	1	SPINT2	up_ACOR_VSMC

GO:0060672	0.0885	1	1	1	epithelial cell morphogenesis involved	BP	1	SPINT2	up_ACOR_VSMC
GO:1902083	0.0885	1	1	1	negative regulation of peptidyl-cysteine S-	BP	1	OXR1	up_ACOR_VSMC
GO:2000169	0.0885	1	1	1	regulation of peptidyl-cysteine S-nitrosylation	BP	1	OXR1	up_ACOR_VSMC
GO:0042891	0.0885	1	1	1	antibiotic transport	BP	0.933	RALBP1	up_VCAV_EC
GO:1900753	0.0885	1	1	1	doxorubicin transport	BP	0.933	RALBP1	up_VCAV_EC
GO:1901656	0.0885	1	1	1	glycoside transport	BP	0.933	RALBP1	up_VCAV_EC
GO:0007275	0.0886	0.926	147	1370	multicellular organism development	BP	1	EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,LBH,AFF3,GATA5,GATA4,CD83,ANGPT1,EPYC,HTR2B,RASSF2,MBP,PRDX4,RECK,SHROOM3,FEZ1,MLLT3,ITM2C,FERMT1,BMP4,LNPK,TBX18,FGFR2,TP53BP1,GJA1,ATRX,TLR3,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,CITED2,SPINT1,GLRB,ISG15,ACSL6,ZNRF3,CD274,ZNF365,SASH1,LMO4,TMEM108,FGF18,FAM210B,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,EBF4,ZMYM2,ITPR1,LIMS2,ANKRD1,F2RL1,CAMK2D,CTSB,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,GPM6A,CHD2,ULK2,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,PTGDR,TBX20,BBX,TBX5,FZD3,FRS2,CPAMD8,RND1,DAG1,POMK,APP,LAMA3,PSEN1,SEMA6D,TGFBR1,PCSK6,SYNJ2BP,CHD7,JUP,SPINK2,SIPA1L1,DDR2,CLN8,FOSL2,PERP,PSKH1,RTKN2,SIAH1,SSH3,C10H2orf49,EDN1,NID1,HPGD,ARID5B,ASAP1,DMC1,SERPINB5,JAM3,B2M,DISC1,AP2B1,TNFRSF11B,TACC1,GAA,ATXN10,FEZ2,SUN1,INPP5K,CNOT4,LHX9,WFS1,WDR48,WASL,ACP2,ERAP1,ID3,SLC8A1,TEAD1,ENSCAFG00000003530,IL18R1,BVES,RREB1,ZDHHC21,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0007163	0.0886	0.959	9	60	establishment or maintenance of cell	BP	0.933	EPHB1,TEK,FRMD4B,AMOT,FERMT1,GATA3,CTNNA1,ZW10,FSCN1	up_VCAV_EC
GO:0002295	0.0886	0.99	2	5	T-helper cell lineage commitment	BP	0.933	IL6,MTOR	up_VCAV_EC
GO:0002363	0.0886	0.99	2	5	alpha-beta T cell lineage commitment	BP	0.933	IL6,MTOR	up_VCAV_EC
GO:0043373	0.0886	0.99	2	5	CD4-positive, alpha-beta T cell lineage commitment	BP	0.933	IL6,MTOR	up_VCAV_EC
GO:0007195	0.0886	1	1	1	adenylate cyclase-inhibiting dopamine receptor signaling	BP	1	PRMT5	down_ACOR_VSMC
GO:0019918	0.0886	1	1	1	peptidyl-arginine methylation, to	BP	1	PRMT5	down_ACOR_VSMC
GO:0035246	0.0886	1	1	1	peptidyl-arginine N-methylation	BP	1	PRMT5	down_ACOR_VSMC
GO:0035247	0.0886	1	1	1	peptidyl-arginine omega-N-methylation	BP	1	PRMT5	down_ACOR_VSMC
GO:1904990	0.0886	1	1	1	regulation of adenylate cyclase-inhibiting dopamine receptor	BP	1	PRMT5	down_ACOR_VSMC
GO:1904992	0.0886	1	1	1	positive regulation of adenylate cyclase-inhibiting dopamine	BP	1	PRMT5	down_ACOR_VSMC
GO:0051248	0.0886	0.998	1	316	negative regulation of protein metabolic process	BP	1	CST3	down_AORT_EC
GO:2000117	0.0886	0.996	1	27	negative regulation of cysteine-type	BP	1	PTGER2	up_VPUL_EC

GO:0006355	0.0887	0.929	93	974	regulation of transcription, DNA-templated	BP	0.933	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0052027	0.0887	1	1	1	modulation by symbiont of host signal transduction	BP	0.933	TNIP1	up_VCAV_EC
GO:0085032	0.0887	1	1	1	modulation by symbiont of host I-kappaB kinase/NF-kappaB	BP	0.933	TNIP1	up_VCAV_EC
GO:0022409	0.0888	0.961	8	56	positive regulation of cell-cell adhesion	BP	0.933	IL7R,PODXL,GATA3,ITPKB,NCK1,BCL10,HMGB1,ITGA6	up_VCAV_EC
GO:0006812	0.0888	0.979	3	222	cation transport	BP	1	LYN,HOXA3,NEDD4	down_ACOR_EC
GO:0031333	0.0888	0.996	1	46	negative regulation of protein complex assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0032677	0.0888	0.996	1	22	regulation of interleukin-8 production	BP	1	TLR2	up_VSAP_VSMC
GO:0010155	0.088845327	0.99694	1	4	regulation of proton transport	BP	1	PM20D1	up_ACOR_EC
GO:0060348	0.0889	0.963	7	78	bone development	BP	1	NOTCH2,SMAD9,NAB2,FBN1,THBS3,GLI3,GREM1	down_VCAV_EC
GO:0040013	0.0889	0.969	5	100	negative regulation of locomotion	BP	1	ANGPT4,HOXA7,RECK,TBXA2R,KANK1	up_AFEM_EC
GO:0032228	0.0889	0.988	2	8	regulation of synaptic transmission, GABAergic	BP	0.974	KIF5B,PLCL1	down_VSAP_EC
GO:0036363	0.0889	1	1	1	transforming growth factor beta activation	BP	1	SLC29A1	down_ACOR_VSMC
GO:1901388	0.0889	1	1	1	regulation of transforming growth factor beta	BP	1	SLC29A1	down_ACOR_VSMC
GO:1901389	0.0889	1	1	1	negative regulation of transforming growth factor beta activation	BP	1	SLC29A1	down_ACOR_VSMC
GO:1905323	0.0889	1	1	1	telomerase holoenzyme complex assembly	BP	1	SLC29A1	down_ACOR_VSMC
GO:0007178	0.0889	0.997	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	TGFBR1	down_VSAP_VSMC
GO:0003334	0.0889	0.997	1	4	keratinocyte development	BP	1	FOSL2	up_AFEM_EC
GO:0035637	0.0889	0.996	1	21	multicellular organismal signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0045861	0.089	0.973	4	71	negative regulation of proteolysis	BP	1	GAS1,CRYAB,CLEC16A,RECK	up_AFEM_EC
GO:0010033	0.089	0.982	3	772	response to organic substance	BP	1	CYP1A1,GATA5,CA2	up_VCAV_VSMC
GO:0035162	0.089	0.988	2	8	embryonic hemopoiesis	BP	0.974	HIF1A,SH2B3	down_VSAP_EC
GO:0031345	0.089	0.996	1	46	negative regulation of cell projection organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0002040	0.089	0.996	1	46	sprouting angiogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:1903901	0.08903468	0.98701	2	19	negative regulation of viral life cycle	BP	1	TRIM8,MAVS	up_ACOR_EC
GO:2000377	0.0891	0.969	5	41	regulation of reactive oxygen species metabolic	BP	0.975	PRCP,HIF1A,BNIP3,CDKN1A,ARF4	down_VSAP_EC
GO:0030500	0.0891	0.971	5	25	regulation of bone mineralization	BP	1	OSR2,OSR1,DDR2,OMD,BGLAP	up_VSAP_EC
GO:0001738	0.0891	0.974	4	27	morphogenesis of a polarized epithelium	BP	0.975	PTK7,EXOC5,WDR1,MSN	down_VSAP_EC
GO:0031297	0.0891	0.975	4	18	replication fork processing	BP	0.933	THOC1,ETAA1,BLM,ATRX	up_VCAV_EC
GO:0050873	0.0891	0.975	4	18	brown fat cell differentiation	BP	1	NAPEPLD,EBF2,ARL4A,ALDH6A1	up_VSAP_EC
GO:0033314	0.0891	0.989	2	6	mitotic DNA replication checkpoint	BP	1	TOPBP1,CLSPN	down_ACOR_VSMC

GO:0070493	0.0891	0.989	2	6	thrombin-activated receptor signaling	BP	1	STMN1,IQGAP2	down_ACOR_VSMC
GO:0032877	0.0891	1	1	1	positive regulation of DNA endoreduplication	BP	1	E2F8	down_ACOR_VSMC
GO:0033301	0.0891	1	1	1	cell cycle comprising mitosis without	BP	1	E2F8	down_ACOR_VSMC
GO:0033865	0.0891	0.996	1	43	nucleoside bisphosphate metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0033875	0.0891	0.996	1	43	ribonucleoside bisphosphate metabolic	BP	1	SUCLG2	down_AFEM_EC
GO:0034032	0.0891	0.996	1	43	purine nucleoside bisphosphate metabolic	BP	1	SUCLG2	down_AFEM_EC
GO:0043624	0.0891	0.996	1	39	cellular protein complex disassembly	BP	1	TAOK1	up_AORT_EC
GO:0048762	0.0892	0.962	7	77	mesenchymal cell differentiation	BP	1	VASN,GLIPR2,BMPR1A,SEMA3C,LOXL3,RDH10,GREM1	down_VCAV_EC
GO:0097305	0.0892	0.967	6	31	response to alcohol	BP	1	PRKAA2,TP53INP1,ADCY6,PTGDR,PRKCE,JUP	up_ACOR_VSMC
GO:0022008	0.0892	0.974	4	406	neurogenesis	BP	1	EMX2,HOXC10,IRX5,SHOX2	up_VSAP_VSMC
GO:0009887	0.0892	0.998	1	314	animal organ morphogenesis	BP	1	GATA5	down_VFEM_VSMC
GO:1902285	0.0892	0.997	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	PLXNA4	up_AFEM_EC
GO:0051098	0.0892	0.997	1	129	regulation of binding	BP	1	HOXA3	up_APUL_VSMC
GO:0009743	0.089273988	0.97905	3	40	response to carbohydrate	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0019219	0.0893	0.928	110	1151	regulation of nucleobase-containing compound metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,SRSF2,MED17,U2AF2,SLC29A1,MTDH,HEY1,PARPBP,SRRT,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,HNRNPL,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,SF3B4,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,E2F8,TFRC,PPARD,YBX3,HNRNPF,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,RBM17,HOXA10,ERF,TCERG1,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,MIS18A,HMGN1,CCT4,SIX4,SF3A1,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:0046483	0.0893	0.966	8	1948	heterocycle metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:1903146	0.0893	0.98	3	17	regulation of autophagy of mitochondrion	BP	0.976	HIF1A,CDC37,HTT	down_VSAP_EC
GO:0006614	0.0893	0.988	2	10	SRP-dependent cotranslational protein	BP	1	SSR3,SEC61B	down_VCAV_EC
GO:0022607	0.0894	0.929	90	969	cellular component assembly	BP	0.933	EPHB1,PLK2,TEK,HCLS1,GBP5,SELP,KIT,PRKCH,ARHGEF15,CDA,MX2,PODXL,BAIAP2L1,VWF,LAMC2,OCLN,MEF2C,RAPGEF1,TLR4,EDN1,RAB11A,RALB,SMAD1,SNCAIP,IRF8,SNAP91,ARHGAP28,TMOD1,NASP,NECTIN2,MTOR,ACPP,SNAP23,LRRC8C,TJP1,LNX2,CAV2,SLK,SCAF11,CNOT6,ABCA1,NCKAP1,MZT1,RIOK3,PROX1,IQGAP2,ENSCAFG00000010224,STMN1,SNX2,SH3GLB1,SWAP70,APOD,CENPC,NCK1,KCNJ2,EXOC5,FES,HIST1H1A,EHD4,RAPGEF2,BCL10,SENP6,PAN3,PRPF39,CTNNA1,CNOT7,GCH1,ASF1A,HMGB1,PMAIP1,ARPC5L,BLM,RIPK1,LSM14A,ITGA6,MCU,ZW10,IQUB,ATRX,HAUS3,ALDH1A3,HP1BP3,ENSCAFG00000002015,P2RX2,TNFAIP1,SPATA6,TMOD3,FSCN1,FBXO5,SASS6	up_VCAV_EC
GO:0060560	0.0894	0.958	9	58	developmental growth involved in	BP	1	WNT11,SLIT2,ABL1,PLXNA4,RARG,DPYSL2,TTL,ULK1,TGFBR2	up_VSAP_EC
GO:0048260	0.0894	0.981	3	15	positive regulation of receptor-mediated	BP	0.933	SELE,HIST1H1A,PLCG2	up_VCAV_EC
GO:0006954	0.0894	0.987	2	147	inflammatory response	BP	1	NR1H4,CCL24	up_VPUL_EC
GO:0051852	0.0894	1	1	1	disruption by host of symbiont cells	BP	1	F2RL1	up_ACOR_VSMC

GO:0051873	0.0894	1	1	1	killing by host of symbiont cells	BP	1	F2RL1	up_ACOR_VSMC
GO:0070942	0.0894	1	1	1	neutrophil mediated cytotoxicity	BP	1	F2RL1	up_ACOR_VSMC
GO:0070943	0.0894	1	1	1	neutrophil mediated killing of symbiont cell	BP	1	F2RL1	up_ACOR_VSMC
GO:0070944	0.0894	1	1	1	neutrophil mediated killing of bacterium	BP	1	F2RL1	up_ACOR_VSMC
GO:0070945	0.0894	1	1	1	neutrophil mediated killing of gram-negative	BP	1	F2RL1	up_ACOR_VSMC
GO:0070948	0.0894	1	1	1	regulation of neutrophil mediated cytotoxicity	BP	1	F2RL1	up_ACOR_VSMC
GO:0070949	0.0894	1	1	1	regulation of neutrophil mediated killing of	BP	1	F2RL1	up_ACOR_VSMC
GO:0070950	0.0894	1	1	1	regulation of neutrophil mediated killing of	BP	1	F2RL1	up_ACOR_VSMC
GO:0070951	0.0894	1	1	1	regulation of neutrophil mediated killing of gram-	BP	1	F2RL1	up_ACOR_VSMC
GO:0070960	0.0894	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_ACOR_VSMC
GO:0070962	0.0894	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_ACOR_VSMC
GO:0070963	0.0894	1	1	1	positive regulation of neutrophil mediated killing of gram-negative	BP	1	F2RL1	up_ACOR_VSMC
GO:0090198	0.0894	1	1	1	negative regulation of chemokine secretion	BP	1	F2RL1	up_ACOR_VSMC
GO:0097029	0.0894	1	1	1	mature conventional dendritic cell	BP	1	F2RL1	up_ACOR_VSMC
GO:1900135	0.0894	1	1	1	positive regulation of renin secretion into blood	BP	1	F2RL1	up_ACOR_VSMC
GO:0070961	0.0894	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_ACOR_VSMC
GO:0003100	0.0894	1	1	1	regulation of systemic arterial blood pressure by	BP	0.933	EDN1	up_VCAV_EC
GO:0003298	0.0894	1	1	1	physiological muscle hypertrophy	BP	0.933	EDN1	up_VCAV_EC
GO:0003301	0.0894	1	1	1	physiological cardiac muscle hypertrophy	BP	0.933	EDN1	up_VCAV_EC
GO:0031583	0.0894	1	1	1	phospholipase D-activating G protein-coupled receptor signaling	BP	0.933	EDN1	up_VCAV_EC
GO:0035812	0.0894	1	1	1	renal sodium excretion	BP	0.933	EDN1	up_VCAV_EC
GO:0035813	0.0894	1	1	1	regulation of renal sodium excretion	BP	0.933	EDN1	up_VCAV_EC
GO:0035815	0.0894	1	1	1	positive regulation of renal sodium excretion	BP	0.933	EDN1	up_VCAV_EC
GO:0042313	0.0894	1	1	1	protein kinase C deactivation	BP	0.933	EDN1	up_VCAV_EC
GO:0043179	0.0894	1	1	1	rhythmic excitation	BP	0.933	EDN1	up_VCAV_EC
GO:0051771	0.0894	1	1	1	negative regulation of nitric-oxide synthase	BP	0.933	EDN1	up_VCAV_EC
GO:0060024	0.0894	1	1	1	rhythmic synaptic transmission	BP	0.933	EDN1	up_VCAV_EC
GO:0060584	0.0894	1	1	1	regulation of prostaglandin-	BP	0.933	EDN1	up_VCAV_EC
GO:0060585	0.0894	1	1	1	positive regulation of prostaglandin-endoperoxide synthase	BP	0.933	EDN1	up_VCAV_EC
GO:0061049	0.0894	1	1	1	cell growth involved in cardiac muscle cell	BP	0.933	EDN1	up_VCAV_EC
GO:0061050	0.0894	1	1	1	regulation of cell growth involved in cardiac muscle cell development	BP	0.933	EDN1	up_VCAV_EC
GO:0061051	0.0894	1	1	1	positive regulation of cell growth involved in cardiac muscle cell development	BP	0.933	EDN1	up_VCAV_EC
GO:0060349	0.0894	0.996	1	38	bone morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0016241	0.0895	0.963	7	41	regulation of macroautophagy	BP	1	MFN2,POLDIP2,PIP4K2B,UBQLN2,HTRA2,HMOX1,NPRL3	up_VSAP_EC
GO:1904062	0.0895	0.965	6	62	regulation of cation transmembrane transport	BP	1	PRNP,FXYD1,CACNB3,THY1,PARK7,CYBA	down_VCAV_EC
GO:0006412	0.0895	0.987	2	245	translation	BP	1	DARS,EIF3M	down_AFEM_EC
GO:0045600	0.0895	0.987	2	21	positive regulation of fat cell differentiation	BP	1	CMKLR1,NAPEPLD	up_AFEM_EC

GO:0003223	0.0895	0.998	1	2	ventricular compact myocardium	BP	1	BMPR1A	down_VCAV_EC
GO:0001697	0.0895	1	1	1	histamine-induced gastric acid secretion	BP	1	HRH2	up_ACOR_VSMC
GO:0006679	0.0895	1	1	1	glucosylceramide biosynthetic process	BP	1	UGCG	up_ACOR_VSMC
GO:0021563	0.0895	0.997	1	4	glossopharyngeal nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0045669	0.0895	0.996	1	24	positive regulation of osteoblast differentiation	BP	1	NPNT	up_APUL_EC
GO:0016477	0.0896	0.934	50	426	cell migration	BP	1	FGF13,VEGFD,LGR6,HTR2B,TCAF1,ZRANB1,RECK,FERMT1,BMP4,GJA1,HRH1,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,GPM6A,EVL,TBX20,TBX5,PRKCE,FZD3,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,ARID5B,FAM107A,JAM3,DISC1,SUN1,WASL,DOCK5,ENSCAFG00000029553,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0060693	0.0896	0.989	2	6	regulation of branching involved in salivary gland	BP	0.934	NTN4,BTBD7	up_VCAV_EC
GO:0001568	0.0896	0.987	2	252	blood vessel development	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:0003137	0.0896	1	1	1	Notch signaling pathway involved in heart	BP	1	GATA5	up_ACOR_VSMC
GO:0061999	0.0896	1	1	1	regulation of cardiac endothelial to	BP	1	GATA5	up_ACOR_VSMC
GO:0062000	0.0896	1	1	1	positive regulation of cardiac endothelial to mesenchymal transition	BP	1	GATA5	up_ACOR_VSMC
GO:0090381	0.0896	1	1	1	regulation of heart induction	BP	1	GATA5	up_ACOR_VSMC
GO:1901321	0.0896	1	1	1	positive regulation of heart induction	BP	1	GATA5	up_ACOR_VSMC
GO:0035480	0.0896	1	1	1	regulation of Notch signaling pathway involved in heart	BP	1	GATA5	up_ACOR_VSMC
GO:0035481	0.0896	1	1	1	positive regulation of Notch signaling pathway involved in heart	BP	1	GATA5	up_ACOR_VSMC
GO:0071706	0.0896	0.996	1	40	tumor necrosis factor superfamily cytokine	BP	1	BPI	up_AORT_EC
GO:0008202	0.0896	0.996	1	80	steroid metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0033209	0.0896	0.996	1	24	tumor necrosis factor-mediated signaling	BP	1	NR1H4	up_APUL_EC
GO:0030510	0.0896	0.996	1	27	regulation of BMP signaling pathway	BP	1	NEO1	up_VPUL_EC
GO:0040011	0.0897	0.938	32	505	locomotion	BP	1	PDGFRB,DCN,NDN,SDC4,GLIPR2,KANK2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,HSD3B7,LAMA3,CSPG4,TRIM8,SEMA3C,THY1,PEX5,B4GALT1,GLI3,SASH1,CDH2,FUT8,SPRED1,SPNS1,TWIST2,DDR2,GREM1,RAC2,FOXO3	down_VCAV_EC
GO:0090066	0.0897	0.962	7	162	regulation of anatomical structure size	BP	1	PRR16,PLXNA4,HTR1D,AVPR1A,TBXA2R,CDC42EP5,KANK1	up_AFEM_EC
GO:0042254	0.0897	0.979	3	128	ribosome biogenesis	BP	1	RSL24D1,RPL10L,RRP15	up_VPOR_EC
GO:0032660	0.0897	0.989	2	7	regulation of interleukin-17 production	BP	0.935	TLR4,ARG2	up_VCAV_EC
GO:1901533	0.0897	1	1	1	negative regulation of hematopoietic progenitor cell differentiation	BP	1	HSPA9	down_ACOR_VSMC
GO:1902037	0.0897	1	1	1	negative regulation of hematopoietic stem cell differentiation	BP	1	HSPA9	down_ACOR_VSMC
GO:0042489	0.0897	1	1	1	negative regulation of odontogenesis of dentin-containing tooth	BP	1	TNFRSF11B	up_ACOR_VSMC
GO:1900046	0.0897	0.996	1	21	regulation of hemostasis	BP	1	CAV1	up_VSAP_VSMC
GO:0030193	0.0897	0.996	1	21	regulation of blood coagulation	BP	1	CAV1	up_VSAP_VSMC
GO:0032436	0.08975112	0.97889	3	40	positive regulation of proteasomal ubiquitin-dependent protein	BP	1	PIAS1,CLU,RNF114	up_ACOR_EC
GO:0001525	0.0898	0.951	13	173	angiogenesis	BP	1	HSPB6,PDGFRB,DCN,ANGPT1,ANPEP,THY1,B4GALT1,MYDGF,SASH1,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC

GO:0051960	0.0898	0.973	4	216	regulation of nervous system development	BP	1	HOOK3,ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0070887	0.0898	0.982	3	775	cellular response to chemical stimulus	BP	1	CYP1A1,GATA5,CA2	up_VCAV_VSMC
GO:0009141	0.0898	0.997	1	110	nucleoside triphosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0048841	0.0898	0.997	1	4	regulation of axon extension involved in	BP	1	PLXNA4	up_AFEM_EC
GO:0045844	0.0898	0.996	1	24	positive regulation of striated muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0048636	0.0898	0.996	1	24	positive regulation of muscle organ	BP	1	TBX5	up_APUL_EC
GO:2000009	0.089811381	0.99687	1	4	negative regulation of protein localization to cell	BP	1	ACTN2	up_ACOR_EC
GO:0061448	0.089817182	0.96835	5	89	connective tissue development	BP	1	NR1H4,SOX9,PTH1R,FOXC2,EFEMP1	up_ACOR_EC
GO:0048639	0.089888664	0.97886	3	39	positive regulation of developmental growth	BP	1	PLS1,TBX5,NRP1	up_ACOR_EC
GO:1903707	0.0899	0.969	5	48	negative regulation of hemopoiesis	BP	1	FBN1,GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0060045	0.0899	0.981	3	11	positive regulation of cardiac muscle cell	BP	1	FGFR2,TBX20,TBX5	up_ACOR_VSMC
GO:0045876	0.0899	0.989	2	6	positive regulation of sister chromatid cohesion	BP	0.936	SMC5,RAD21	up_VCAV_EC
GO:1904772	0.0899	1	1	1	response to tetrachloromethane	BP	1	EZH2	down_ACOR_VSMC
GO:0036333	0.0899	1	1	1	hepatocyte homeostasis	BP	1	EZH2	down_ACOR_VSMC
GO:0001763	0.0899	0.996	1	78	morphogenesis of a branching structure	BP	1	ESR1	up_AORT_VSMC
GO:0035306	0.0899	0.996	1	24	positive regulation of dephosphorylation	BP	1	NPNT	up_APUL_EC
GO:0051668	0.0899	0.996	1	39	localization within membrane	BP	1	NETO1	up_VFEM_VSMC
GO:0045664	0.089995275	0.96159	7	144	regulation of neuron differentiation	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0050866	0.09	0.969	5	48	negative regulation of cell activation	BP	1	PRNP,SDC4,GLI3,BPI,LOXL3	down_VCAV_EC
GO:1903169	0.09	0.973	4	34	regulation of calcium ion transmembrane transport	BP	1	PRNP,CACNB3,THY1,CYBA	down_VCAV_EC
GO:0006122	0.09	0.989	2	7	mitochondrial electron transport, ubiquinol to	BP	1	CYCS,CYC1	down_ACOR_VSMC
GO:0003231	0.09	0.996	1	48	cardiac ventricle development	BP	1	CITED2	down_VPOR_EC
GO:0007210	0.09	1	1	1	serotonin receptor signaling pathway	BP	1	HTR2B	up_ACOR_VSMC
GO:0014827	0.09	1	1	1	intestine smooth muscle contraction	BP	1	HTR2B	up_ACOR_VSMC
GO:0071502	0.09	1	1	1	cellular response to temperature stimulus	BP	1	HTR2B	up_ACOR_VSMC
GO:0110026	0.09	1	1	1	regulation of DNA strand resection involved in replication fork processing	BP	1	ZNF365	up_ACOR_VSMC
GO:0010513	0.09	1	1	1	positive regulation of phosphatidylinositol biosynthetic process	BP	1	HTR2B	up_ACOR_VSMC
GO:0006954	0.09000216	0.96157	7	147	inflammatory response	BP	1	NR1H4,FNDC4,NOD2,IL33,PTGER4,CLSTN1,RARRES2	up_ACOR_EC
GO:0042594	0.0901	0.956	10	64	response to starvation	BP	1	PRKAA2,GABARAPL1,CDKN1A,ULK2,SESN3,PIK3C3,LAMP2,SESN1,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0070229	0.0901	0.981	3	13	negative regulation of lymphocyte apoptotic	BP	1	AURKB,ARG2,NOC2L	down_ACOR_VSMC
GO:0046133	0.0901	0.998	1	2	pyrimidine ribonucleoside catabolic process	BP	0.98	ENTPD4	down_VSAP_EC
GO:0046135	0.0901	0.998	1	2	pyrimidine nucleoside catabolic process	BP	0.98	ENTPD4	down_VSAP_EC
GO:0001866	0.0901	1	1	1	NK T cell proliferation	BP	0.937	ELF4	up_VCAV_EC
GO:0071248	0.0901	0.996	1	35	cellular response to metal ion	BP	1	FBP1	up_VFEM_VSMC
GO:0045597	0.0902	0.987	2	253	positive regulation of cell differentiation	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0003279	0.0902	0.996	1	48	cardiac septum development	BP	1	CITED2	down_VPOR_EC
GO:0032104	0.0902	0.997	1	4	regulation of response to extracellular stimulus	BP	1	LEP	up_AFEM_EC
GO:0032107	0.0902	0.997	1	4	regulation of response to nutrient levels	BP	1	LEP	up_AFEM_EC
GO:0061298	0.0903	0.988	2	8	retina vasculature development in camera-	BP	0.98	HIF1A,NRP1	down_VSAP_EC

GO:0047484	0.0903	0.99	2	5	regulation of response to osmotic stress	BP	0.938	PTGS2,ARHGEF2	up_VCAV_EC
GO:0061724	0.0903	0.997	1	4	lipophagy	BP	1	RAB7A	up_AFEM_EC
GO:2000392	0.0903	0.997	1	4	regulation of lamellipodium	BP	1	KANK1	up_AFEM_EC
GO:0008543	0.0903	0.996	1	27	fibroblast growth factor receptor signaling	BP	1	FLRT3	up_VPUL_EC
GO:0034220	0.0904	0.949	14	188	ion transmembrane transport	BP	1	PRNP,FOLR2,FXYD1,AKT2,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SCARA5,CYBA,ARHGAP1,CLIC4	down_VCAV_EC
GO:0007605	0.0904	0.97	5	27	sensory perception of sound	BP	0.938	KIT,CHD7,NAV2,SPTBN4,P2RX2	up_VCAV_EC
GO:0042108	0.0904	0.98	3	14	positive regulation of cytokine biosynthetic	BP	0.938	TLR4,TLR3,BCL10	up_VCAV_EC
GO:0002523	0.0904	1	1	1	leukocyte migration involved in inflammatory	BP	1	JAM3	up_ACOR_VSMC
GO:0061740	0.0904	1	1	1	protein targeting to lysosome involved in chaperone-mediated	BP	1	LAMP2	up_ACOR_VSMC
GO:0071211	0.0904	1	1	1	protein targeting to vacuole involved in	BP	1	LAMP2	up_ACOR_VSMC
GO:0090138	0.0904	1	1	1	regulation of actin cytoskeleton organization	BP	1	JAM3	up_ACOR_VSMC
GO:0007368	0.0904	0.996	1	37	determination of left/right symmetry	BP	1	NKX2-5	up_VPOR_VSMC
GO:0033500	0.0905	0.962	7	64	carbohydrate homeostasis	BP	0.98	NR1H4,PTPN11,PRCP,SMARCA4,SESN2,HIF1A,PTPN2	down_VSAP_EC
GO:0042593	0.0905	0.962	7	64	glucose homeostasis	BP	0.98	NR1H4,PTPN11,PRCP,SMARCA4,SESN2,HIF1A,PTPN2	down_VSAP_EC
GO:2000106	0.0905	0.97	5	29	regulation of leukocyte apoptotic process	BP	1	PRELID1,AURKB,ARG2,NOC2L,PIK3CD	down_ACOR_VSMC
GO:0019216	0.0905	0.986	2	101	regulation of lipid metabolic process	BP	1	LYN,ACSL3	down_ACOR_EC
GO:0033210	0.0905	0.997	1	4	leptin-mediated signaling pathway	BP	1	LEP	up_AFEM_EC
GO:0044320	0.0905	0.997	1	4	cellular response to leptin stimulus	BP	1	LEP	up_AFEM_EC
GO:0021954	0.0905	0.996	1	26	central nervous system neuron development	BP	1	NTRK2	up_APUL_EC
GO:0009636	0.0905	0.996	1	66	response to toxic substance	BP	1	CYP1A1	up_VCAV_VSMC
GO:1902622	0.0905	0.996	1	11	regulation of neutrophil migration	BP	1	C3AR1	up_VPOR_EC
GO:0007018	0.0906	0.954	11	82	microtubule-based movement	BP	1	KIF2A,CFAP298,CENPE,KIF22,TRAK1,KIF4A,KIF15,KIF11,TTLL1,KIF21B,KIF24	down_ACOR_VSMC
GO:0021543	0.0906	0.965	6	49	pallium development	BP	0.98	HIF1A,UBA6,CTNNB1,GSK3B,DISC1,NRP1	down_VSAP_EC
GO:0035304	0.0906	0.974	4	29	regulation of protein dephosphorylation	BP	0.98	NUAK1,PPP1R12A,HTT,CALM1	down_VSAP_EC
GO:0061549	0.0906	0.99	2	5	sympathetic ganglion development	BP	1	NRP1,FZD3	up_ACOR_VSMC
GO:0070228	0.0906	0.996	1	20	regulation of lymphocyte apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0002313	0.0906	0.997	1	4	mature B cell differentiation involved in	BP	1	DLL1	up_AFEM_EC
GO:0002335	0.0906	0.997	1	4	mature B cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:1903510	0.0906	0.996	1	22	mucopolysaccharide metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0031349	0.090605566	0.96798	5	90	positive regulation of defense response	BP	1	NR1H4,NOD2,IL33,PTGER4,MAVS	up_ACOR_EC
GO:0051893	0.090650158	0.98658	2	20	regulation of focal adhesion assembly	BP	1	ARHGAP6,NRP1	up_ACOR_EC
GO:0090109	0.090650158	0.98658	2	20	regulation of cell-substrate junction	BP	1	ARHGAP6,NRP1	up_ACOR_EC
GO:0000904	0.0907	0.942	24	181	cell morphogenesis involved in differentiation	BP	1	EPYC,FEZ1,FGFR2,SEC24B,LATS2,ZNF365,ARHGEF26,NRP1,ULK2,UNC5B,SPINT2,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL,DOCK5,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0007492	0.0907	0.974	4	27	endoderm development	BP	0.98	CTNNB1,EXT1,INHBA,COL12A1	down_VSAP_EC
GO:0050777	0.0907	0.974	4	28	negative regulation of immune response	BP	0.98	SOCS5,PTPN2,CNOT7,A2M	down_VSAP_EC
GO:0042761	0.0907	0.989	2	7	very long-chain fatty acid biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0048704	0.0907	0.996	1	46	embryonic skeletal system morphogenesis	BP	1	TBX15	down_VPOR_EC
GO:0015732	0.0907	0.997	1	4	prostaglandin transport	BP	1	LEP	up_AFEM_EC

GO:0003170	0.0907	0.996	1	25	heart valve development	BP	1	TBX5	up_APUL_EC
GO:0043200	0.0907	0.996	1	26	response to amino acid	BP	1	NTRK2	up_APUL_EC
GO:0048738	0.090714758	0.97256	4	64	cardiac muscle tissue development	BP	1	ACTN2,FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0090169	0.0908	0.981	3	13	regulation of spindle assembly	BP	1	SMC1A,SMC3,STAG1	down_ACOR_VSMC
GO:0001568	0.0908	0.979	3	252	blood vessel development	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0043043	0.0908	0.987	2	247	peptide biosynthetic process	BP	1	DARS,EIF3M	down_AFEM_EC
GO:1900017	0.0908	0.989	2	6	positive regulation of cytokine production involved in inflammatory	BP	0.938	GBP5,TLR4	up_VCAV_EC
GO:0043484	0.0908	0.996	1	43	regulation of RNA splicing	BP	1	SRSF6	down_AFEM_EC
GO:0070836	0.0908	0.998	1	2	caveola assembly	BP	0.938	CAV2	up_VCAV_EC
GO:0019362	0.0908	0.996	1	35	pyridine nucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046496	0.0908	0.996	1	35	nicotinamide nucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043535	0.0909	0.978	3	45	regulation of blood vessel endothelial cell migration	BP	1	ANGPT4,TBXA2R,ADAM17	up_AFEM_EC
GO:0046325	0.0909	0.997	1	4	negative regulation of glucose import	BP	1	LEP	up_AFEM_EC
GO:0043112	0.091	0.96	8	57	receptor metabolic process	BP	0.938	SELE,CXCL8,CALCRL,EDN1,PLCG2,HIF1A,ALS2,LMTK2	up_VCAV_EC
GO:0021987	0.091	0.969	5	37	cerebral cortex development	BP	0.982	HIF1A,CTNNB1,GSK3B,DISC1,NRP1	down_VSAP_EC
GO:0051051	0.091	0.986	2	112	negative regulation of transport	BP	1	HOXA3,NEDD4	down_ACOR_EC
GO:0046467	0.091	0.996	1	45	membrane lipid biosynthetic process	BP	1	GBGT1	down_VPOR_EC
GO:0000122	0.091	0.997	1	218	negative regulation of transcription by RNA polymerase II	BP	1	MOSPD1	down_VFEM_EC
GO:0002583	0.091	1	1	1	regulation of antigen processing and presentation of peptide	BP	1	TAPBPL	up_ACOR_VSMC
GO:0002584	0.091	1	1	1	negative regulation of antigen processing and presentation of peptide	BP	1	TAPBPL	up_ACOR_VSMC
GO:0002589	0.091	1	1	1	regulation of antigen processing and presentation of peptide	BP	1	TAPBPL	up_ACOR_VSMC
GO:0002590	0.091	1	1	1	negative regulation of antigen processing and presentation of peptide	BP	1	TAPBPL	up_ACOR_VSMC
GO:0021527	0.091	1	1	1	spinal cord association neuron differentiation	BP	1	LMO4	up_ACOR_VSMC
GO:0044241	0.091	0.997	1	4	lipid digestion	BP	1	LEP	up_AFEM_EC
GO:0045793	0.091	0.997	1	4	positive regulation of cell size	BP	1	PRR16	up_AFEM_EC
GO:0043031	0.091	0.997	1	4	negative regulation of macrophage activation	BP	1	BPI	up_AFEM_EC
GO:0090304	0.0911	0.957	11	1694	nucleic acid metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0070887	0.0911	0.956	10	775	cellular response to chemical stimulus	BP	1	C3AR1,ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0006725	0.0911	0.965	8	1956	cellular aromatic compound metabolic	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042594	0.0911	0.962	7	64	response to starvation	BP	0.983	ASNS,HSPA5,SESN2,DDIT3,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0001910	0.0911	0.981	3	12	regulation of leukocyte mediated cytotoxicity	BP	1	LEP,F2RL1,B2M	up_ACOR_VSMC
GO:0006740	0.0911	1	1	1	NADPH regeneration	BP	1	NNT	down_ACOR_VSMC
GO:0044057	0.0911	0.996	1	110	regulation of system process	BP	1	GATA5	down_VSAP_VSMC
GO:0010643	0.0911	1	1	1	cell communication by chemical coupling	BP	1	GJA1	up_ACOR_VSMC
GO:0060156	0.0911	1	1	1	milk ejection reflex	BP	1	GJA1	up_ACOR_VSMC
GO:1903753	0.0911	0.997	1	4	negative regulation of p38MAPK cascade	BP	1	CYLD	up_AFEM_EC

GO:2000647	0.0911	0.997	1	4	negative regulation of stem cell proliferation	BP	1	OVOL1	up_AFEM_EC
GO:0043271	0.0911	0.996	1	28	negative regulation of ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0023057	0.0912	0.934	42	409	negative regulation of signaling	BP	0.938	CXCL8,TNFAIP3,TNIP1,PDE4D,FERMT1,ATF3,DLL4,RAPGEF1,TLR4,NLRC5,GATA3,APLNR,ARAP3,HOMER3,EGFL7,FIGNL1,CASP8,MTOR,BMP2,HHEX,PREX2,GDPD5,RIOK3,STMN1,MCC,SMARCA4,APOD,NCK1,OTUD4,PTGS2,CTDSPL2,CTNNA1,CNOT7,RIPK1,ITGA6,RGS2,SKIL,HIF1A,TNFAIP1,IVNS1ABP,ARHGEF2,PEAR1	up_VCAV_EC
GO:0007160	0.0912	0.957	9	56	cell-matrix adhesion	BP	1	ACTN2,FERMT1,NRP1,NPNT,JUP,DUSP22,NID1,FAM107A,JAM3	up_ACOR_VSMC
GO:0045879	0.0912	0.987	2	10	negative regulation of smoothened signaling	BP	1	GLI3,GLIS2	down_VCAV_EC
GO:2000765	0.0912	0.989	2	6	regulation of cytoplasmic translation	BP	0.938	NCK1,DPH5	up_VCAV_EC
GO:0008015	0.0912	0.986	2	120	blood circulation	BP	1	MAP2K6,AVPR1A	up_VFEM_EC
GO:0072132	0.0912	0.996	1	23	mesenchyme morphogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0070970	0.0912	0.997	1	4	interleukin-2 secretion	BP	1	GPAM	up_AFEM_EC
GO:0002194	0.0912	1	1	1	hepatocyte cell migration	BP	0.938	PROX1	up_VCAV_EC
GO:0061114	0.0912	1	1	1	branching involved in pancreas morphogenesis	BP	0.938	PROX1	up_VCAV_EC
GO:0090425	0.0912	1	1	1	acinar cell differentiation	BP	0.938	PROX1	up_VCAV_EC
GO:2000977	0.0912	1	1	1	regulation of forebrain neuron differentiation	BP	0.938	PROX1	up_VCAV_EC
GO:2000979	0.0912	1	1	1	positive regulation of forebrain neuron	BP	0.938	PROX1	up_VCAV_EC
GO:0060414	0.0912	1	1	1	aorta smooth muscle tissue morphogenesis	BP	0.938	PROX1	up_VCAV_EC
GO:0060849	0.0912	1	1	1	regulation of transcription involved in lymphatic endothelial cell fate	BP	0.938	PROX1	up_VCAV_EC
GO:0002694	0.0913	0.946	17	126	regulation of leukocyte activation	BP	1	CD274,TBC1D10C,ABL1,ZBTB16,TOX,STAT6,F2RL1,ZFP36L1,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,STX4,NCK1,TGFBR2	up_VSAP_EC
GO:1901888	0.0913	0.973	4	29	regulation of cell junction assembly	BP	0.983	VEGFA,MYO1C,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0007063	0.0913	0.981	3	12	regulation of sister chromatid cohesion	BP	0.938	SMC5,RAD21,ATRX	up_VCAV_EC
GO:0090110	0.0913	0.988	2	8	cargo loading into COPII-coated vesicle	BP	0.983	SEC24D,SEC13	down_VSAP_EC
GO:0035459	0.0913	0.988	2	8	cargo loading into vesicle	BP	0.983	SEC24D,SEC13	down_VSAP_EC
GO:0042754	0.0913	0.997	1	4	negative regulation of circadian rhythm	BP	1	CRY2	up_AFEM_EC
GO:1900119	0.0913	0.997	1	4	positive regulation of execution phase of	BP	1	FAP	up_AFEM_EC
GO:0023057	0.0914	0.933	48	409	negative regulation of signaling	BP	1	SMAD6,LEP,LBH,HTR2B,RASSF2,PRKAA2,MLLT3,FERMT1,BMP4,ELF1,CASTOR1,LATS2,ZNRF3,AR,PTGIR,NDRG2,ITPR1,F2RL1,DAPK1,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,RGS2,DAG1,PSEN1,SYNJ2BP,WWC2,DUSP22,SESN1,DUSP26,LRRC4,DDIT4,HERPUD1,INPP5K,BMT2,PFKL,WFS1,SH3BP4,PARK7	up_ACOR_VSMC
GO:0099536	0.0914	0.947	16	133	synaptic signaling	BP	0.938	EPHB1,PLK2,ENSCAFG00000007112,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,SNAP23,SLC12A7,GRM8,STX11,ALS2,P2RX2	up_VCAV_EC
GO:0002700	0.0914	0.962	7	40	regulation of production of molecular mediator of immune response	BP	1	TP53BP1,TLR3,F2RL1,PTPN22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0043030	0.0914	0.981	3	12	regulation of macrophage activation	BP	0.938	ADGRF5,TLR4,CD200	up_VCAV_EC
GO:0043117	0.0914	1	1	1	positive regulation of vascular permeability	BP	1	TRPV4	down_ACOR_VSMC
GO:0001867	0.0914	0.998	1	2	complement activation, lectin pathway	BP	1	A2M	down_VCAV_EC
GO:0051775	0.0914	0.998	1	2	response to redox state	BP	1	VASN	down_VCAV_EC
GO:0007617	0.0914	0.997	1	4	mating behavior	BP	1	THRB	up_AFEM_EC

GO:0009309	0.0914	0.997	1	4	amine biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0042401	0.0914	0.997	1	4	cellular biogenic amine biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0045742	0.0914	0.997	1	4	positive regulation of epidermal growth factor receptor signaling	BP	1	ADAM17	up_AFEM_EC
GO:1904683	0.0914	0.997	1	4	regulation of metalloendopeptidase	BP	1	RECK	up_AFEM_EC
GO:0001704	0.0914	0.996	1	43	formation of primary germ layer	BP	1	DUSP2	up_AORT_EC
GO:0090630	0.0914	0.996	1	23	activation of GTPase activity	BP	1	TIAM1	up_VFEM_EC
GO:0019915	0.0914	0.996	1	22	lipid storage	BP	1	CAV1	up_VSAP_VSMC
GO:0042310	0.0914	0.996	1	21	vasoconstriction	BP	1	CAV1	up_VSAP_VSMC
GO:0097756	0.0914	0.996	1	21	negative regulation of blood vessel diameter	BP	1	CAV1	up_VSAP_VSMC
GO:0032231	0.0915	0.966	6	32	regulation of actin filament bundle assembly	BP	1	SYNPO2L,ARHGAP28,SYNPO2,NRP1,EVL,INPP5K	up_ACOR_VSMC
GO:0045056	0.0915	0.99	2	5	transcytosis	BP	1	LRPAP1,RAB11B	up_ACOR_VSMC
GO:0030949	0.0915	0.989	2	6	positive regulation of vascular endothelial growth factor receptor	BP	0.938	PRKD2,HIF1A	up_VCAV_EC
GO:0071310	0.0915	1	1	634	cellular response to organic substance	BP	1	GATA5	down_AFEM_VSMC
GO:0099171	0.0915	1	1	1	presynaptic modulation of chemical synaptic	BP	1	FBXL20	up_ACOR_VSMC
GO:0099575	0.0915	1	1	1	regulation of protein catabolic process at presynapse, modulating	BP	1	FBXL20	up_ACOR_VSMC
GO:1905208	0.0915	0.997	1	4	negative regulation of cardiocyte differentiation	BP	1	DLL1	up_AFEM_EC
GO:0034446	0.0915	0.996	1	23	substrate adhesion-dependent cell spreading	BP	1	RADIL	up_VFEM_EC
GO:0006813	0.0915	0.996	1	37	potassium ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0032677	0.0916	0.979	3	22	regulation of interleukin-8 production	BP	1	PARK7,BPI,MAVS	down_VCAV_EC
GO:0046777	0.0916	0.986	2	86	protein autophosphorylation	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0071495	0.0916	0.987	2	365	cellular response to endogenous stimulus	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0001993	0.0916	1	1	1	regulation of systemic arterial blood pressure by norepinephrine-norepinephrine-epinephrine	BP	1	ADRA1B	up_ACOR_VSMC
GO:0001994	0.0916	1	1	1	vasoconstriction involved in regulation of systemic	BP	1	ADRA1B	up_ACOR_VSMC
GO:0003321	0.0916	1	1	1	positive regulation of blood pressure by epinephrine-norepinephrine-epinephrine	BP	1	ADRA1B	up_ACOR_VSMC
GO:0009952	0.0916	0.996	1	66	anterior/posterior pattern specification	BP	1	HOXC6	up_VCAV_VSMC
GO:0055092	0.0916	0.996	1	28	sterol homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0016561	0.0916	1	1	1	protein import into peroxisome matrix,	BP	1	PEX6	up_VSAP_EC
GO:0032103	0.0917	0.957	9	69	positive regulation of response to external	BP	0.939	GBP5,CXCL8,PDGFB,TLR4,PRKD2,SWAP70,TLR3,PTGS2,HMGB1	up_VCAV_EC
GO:0051924	0.0917	0.964	6	53	regulation of calcium ion transport	BP	0.985	REM1,CTNNB1,LYN,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0043551	0.0917	0.996	1	17	regulation of phosphatidylinositol 3-	BP	1	LYN	down_ACOR_EC
GO:0042661	0.0917	0.998	1	2	regulation of mesodermal cell fate specification	BP	1	BMPR1A	down_VCAV_EC
GO:0048369	0.0917	0.998	1	2	lateral mesoderm morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0048370	0.0917	0.998	1	2	lateral mesoderm formation	BP	1	BMPR1A	down_VCAV_EC
GO:0048371	0.0917	0.998	1	2	lateral mesodermal cell differentiation	BP	1	BMPR1A	down_VCAV_EC
GO:0048372	0.0917	0.998	1	2	lateral mesodermal cell fate commitment	BP	1	BMPR1A	down_VCAV_EC
GO:0048377	0.0917	0.998	1	2	lateral mesodermal cell fate specification	BP	1	BMPR1A	down_VCAV_EC

GO:0048378	0.0917	0.998	1	2	regulation of lateral mesodermal cell fate	BP	1	BMPR1A	down_VCAV_EC
GO:1905770	0.0917	0.998	1	2	regulation of mesodermal cell differentiation	BP	1	BMPR1A	down_VCAV_EC
GO:1905902	0.0917	0.998	1	2	regulation of mesoderm formation	BP	1	BMPR1A	down_VCAV_EC
GO:0034349	0.0917	0.997	1	4	glial cell apoptotic process	BP	1	DLL1	up_AFEM_EC
GO:0046321	0.0917	0.997	1	4	positive regulation of fatty acid oxidation	BP	1	PPARGC1A	up_AFEM_EC
GO:0048505	0.0917	0.997	1	4	regulation of timing of cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:1900025	0.0917	0.997	1	4	negative regulation of substrate adhesion-dependent cell spreading	BP	1	KANK1	up_AFEM_EC
GO:0030154	0.0918	0.964	7	1040	cell differentiation	BP	1	TBX5,MAPK10,ARHGEF26,SLITRK5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0043651	0.0918	1	1	1	linoleic acid metabolic process	BP	1	CYP2J2	up_ACOR_VSMC
GO:0090107	0.0918	1	1	1	regulation of high-density lipoprotein particle	BP	1	LCAT	up_ACOR_VSMC
GO:0034505	0.0918	0.997	1	4	tooth mineralization	BP	1	CNNM4	up_AFEM_EC
GO:0099173	0.0919	0.962	7	40	postsynapse organization	BP	1	GLRB,ZNF365,TMEM108,EGLN1,NRP1,LRRC4,WASL	up_ACOR_VSMC
GO:0060393	0.0919	0.979	3	19	regulation of pathway-restricted SMAD protein	BP	0.986	SNX25,STRAP,INHBA	down_VSAP_EC
GO:0033316	0.0919	1	1	1	meiotic spindle assembly checkpoint	BP	1	TTK	down_ACOR_VSMC
GO:0044779	0.0919	1	1	1	meiotic spindle checkpoint	BP	1	TTK	down_ACOR_VSMC
GO:0044785	0.0919	1	1	1	metaphase/anaphase transition of meiotic cell	BP	1	TTK	down_ACOR_VSMC
GO:1902102	0.0919	1	1	1	regulation of metaphase/anaphase transition of meiotic cell	BP	1	TTK	down_ACOR_VSMC
GO:1902103	0.0919	1	1	1	negative regulation of metaphase/anaphase transition of meiotic cell	BP	1	TTK	down_ACOR_VSMC
GO:1903096	0.0919	1	1	1	protein localization to meiotic spindle midzone	BP	1	TTK	down_ACOR_VSMC
GO:1905132	0.0919	1	1	1	regulation of meiotic chromosome separation	BP	1	TTK	down_ACOR_VSMC
GO:1905133	0.0919	1	1	1	negative regulation of meiotic chromosome	BP	1	TTK	down_ACOR_VSMC
GO:1905359	0.0919	1	1	1	protein localization to meiotic spindle	BP	1	TTK	down_ACOR_VSMC
GO:0030072	0.0919	0.996	1	48	peptide hormone secretion	BP	1	RAB11B	down_VPOR_EC
GO:0010715	0.0919	0.997	1	4	regulation of extracellular matrix disassembly	BP	1	FAP	up_AFEM_EC
GO:0044058	0.0919	0.997	1	4	regulation of digestive system process	BP	1	LEP	up_AFEM_EC
GO:0046337	0.0919	0.997	1	4	phosphatidylethanolamine metabolic process	BP	1	NAPEPLD	up_AFEM_EC
GO:2000831	0.0919	0.997	1	4	regulation of steroid hormone secretion	BP	1	CRY2	up_AFEM_EC
GO:0072507	0.092	0.954	10	103	divalent inorganic cation homeostasis	BP	0.986	SLC39A7,ERO1A,ATP2B1,TMTC2,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0000956	0.092	0.959	8	55	nuclear-transcribed mRNA catabolic process	BP	1	RNPS1,EIF4A3,EDC3,THRAP3,EDC4,SMG9,ENSCAFG00000015189,EXOSC5	down_ACOR_VSMC
GO:0051094	0.092	0.964	6	388	positive regulation of developmental process	BP	1	C3AR1,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,MTDH	up_VPOR_EC
GO:0033314	0.092	0.989	2	6	mitotic DNA replication checkpoint	BP	0.942	RAD17,TOPBP1	up_VCAV_EC
GO:2001233	0.092	0.986	2	149	regulation of apoptotic signaling pathway	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0014850	0.092	0.997	1	4	response to muscle activity	BP	1	PPARGC1A	up_AFEM_EC
GO:0030502	0.092	0.997	1	4	negative regulation of bone mineralization	BP	1	GREM1	up_AFEM_EC
GO:0051923	0.092	0.997	1	4	sulfation	BP	1	TPST2	up_AFEM_EC
GO:2001135	0.092	0.997	1	4	regulation of endocytic recycling	BP	1	BVES	up_AFEM_EC
GO:0050806	0.092	0.996	1	25	positive regulation of synaptic transmission	BP	1	NTRK2	up_APUL_EC
GO:0021510	0.092	0.996	1	23	spinal cord development	BP	1	HOXC10	up_VFEM_EC

GO:0006754	0.092	0.996	1	36	ATP biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0035115	0.0921	0.98	3	12	embryonic forelimb morphogenesis	BP	1	RECK,LNPK,TBX5	up_ACOR_VSMC
GO:0007220	0.0921	0.997	1	4	Notch receptor processing	BP	1	ADAM17	up_AFEM_EC
GO:0014819	0.0921	0.997	1	4	regulation of skeletal muscle contraction	BP	1	DMPK	up_AFEM_EC
GO:0042118	0.0921	0.997	1	4	endothelial cell activation	BP	1	HOXA9	up_AFEM_EC
GO:0060839	0.0921	0.997	1	4	endothelial cell fate commitment	BP	1	DLL1	up_AFEM_EC
GO:0072148	0.0921	0.997	1	4	epithelial cell fate commitment	BP	1	DLL1	up_AFEM_EC
GO:0040029	0.0921	0.996	1	74	regulation of gene expression, epigenetic	BP	1	ESR1	up_AORT_VSMC
GO:0010906	0.0921	0.996	1	38	regulation of glucose metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0055065	0.0922	0.949	13	145	metal ion homeostasis	BP	0.987	SLC39A7,ERO1A,ATP2B1,TMTC2,HIF1A,NEO1,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0071706	0.0922	0.962	7	40	tumor necrosis factor superfamily cytokine	BP	1	TLR1,LEP,TLR3,CD274,PTPN22,APP,NOD2	up_ACOR_VSMC
GO:1903432	0.0922	0.974	4	18	regulation of TORC1 signaling	BP	1	CASTOR1,SESN3,SESN1,BMT2	up_ACOR_VSMC
GO:0021517	0.0922	0.98	3	12	ventral spinal cord development	BP	0.942	RELN,DLL4,GDPD5	up_VCAV_EC
GO:1901532	0.0922	0.989	2	6	regulation of hematopoietic progenitor	BP	1	HSPA9,PDCD2	down_ACOR_VSMC
GO:0032530	0.0922	0.989	2	6	regulation of microvillus organization	BP	1	FSCN1,EZR	down_ACOR_VSMC
GO:0034105	0.0922	0.989	2	6	positive regulation of tissue remodeling	BP	1	B4GALT1,TFRC	down_ACOR_VSMC
GO:0018198	0.0922	0.987	2	10	peptidyl-cysteine modification	BP	1	CLIP3,PARK7	down_VCAV_EC
GO:0001913	0.0922	0.987	2	10	T cell mediated cytotoxicity	BP	0.987	FAM49B,PVR	down_VSAP_EC
GO:0010768	0.0922	1	1	1	negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage	BP	1	NEDD4	down_ACOR_VSMC
GO:0019089	0.0922	1	1	1	transmission of virus	BP	1	NEDD4	down_ACOR_VSMC
GO:0044007	0.0922	1	1	1	dissemination or transmission of symbiont	BP	1	NEDD4	down_ACOR_VSMC
GO:0044111	0.0922	1	1	1	development involved in symbiotic interaction	BP	1	NEDD4	down_ACOR_VSMC
GO:0051821	0.0922	1	1	1	dissemination or transmission of organism from other organism	BP	1	NEDD4	down_ACOR_VSMC
GO:0098957	0.0922	1	1	1	anterograde axonal transport of	BP	1	TRAK1	down_ACOR_VSMC
GO:0051562	0.0922	1	1	1	negative regulation of mitochondrial calcium ion concentration	BP	1	MICU2	up_ACOR_VSMC
GO:0003256	0.0922	0.997	1	4	regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	up_AFEM_EC
GO:0002332	0.0922	1	1	1	transitional stage B cell differentiation	BP	1	ABL1	up_VSAP_EC
GO:0002333	0.0922	1	1	1	transitional one stage B cell differentiation	BP	1	ABL1	up_VSAP_EC
GO:0010519	0.0922	1	1	1	negative regulation of phospholipase activity	BP	1	ABL1	up_VSAP_EC
GO:0090135	0.0922	1	1	1	actin filament branching	BP	1	ABL1	up_VSAP_EC
GO:1900042	0.0922	1	1	1	positive regulation of interleukin-2 secretion	BP	1	ABL1	up_VSAP_EC
GO:1900275	0.0922	1	1	1	negative regulation of phospholipase C activity	BP	1	ABL1	up_VSAP_EC
GO:1902715	0.0922	1	1	1	positive regulation of interferon-gamma	BP	1	ABL1	up_VSAP_EC
GO:1904529	0.0922	1	1	1	regulation of actin filament binding	BP	1	ABL1	up_VSAP_EC
GO:1904531	0.0922	1	1	1	positive regulation of actin filament binding	BP	1	ABL1	up_VSAP_EC
GO:1904616	0.0922	1	1	1	regulation of actin binding	BP	1	ABL1	up_VSAP_EC

GO:1904618	0.0922	1	1	1	positive regulation of actin binding	BP	1	ABL1	up_VSAP_EC
GO:1905244	0.0922	1	1	1	regulation of modification of synaptic structure	BP	1	ABL1	up_VSAP_EC
GO:0048639	0.0923	0.962	7	39	positive regulation of developmental growth	BP	1	LEP,FGFR2,NRP1,TBX20,TBX5,CHD7,EDN1	up_ACOR_VSMC
GO:0003198	0.0923	0.997	1	4	epithelial to mesenchymal transition involved in endocardial cushion	BP	1	TMEM100	up_AFEM_EC
GO:1903147	0.0923	0.997	1	4	negative regulation of autophagy of	BP	1	CLEC16A	up_AFEM_EC
GO:0090673	0.0923	1	1	1	endothelial cell-matrix adhesion	BP	0.943	ADAMTS9	up_VCAV_EC
GO:0009165	0.0924	0.95	13	104	nucleotide biosynthetic process	BP	1	PRPSAP1,ACLY,RRM1,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0070374	0.0924	0.959	8	57	positive regulation of ERK1 and ERK2 cascade	BP	0.943	TEK,PDGFB,TLR4,BMP2,PRKD2,RAPGEF2,HMGB1,PDGFD	up_VCAV_EC
GO:0070665	0.0924	0.969	5	31	positive regulation of leukocyte proliferation	BP	0.943	MEF2C,TLR4,PELI1,NCK1,HMGB1	up_VCAV_EC
GO:0050848	0.0924	0.973	4	30	regulation of calcium-mediated signaling	BP	0.987	FHL2,GSK3B,HTT,CALM1	down_VSAP_EC
GO:1901379	0.0924	0.98	3	12	regulation of potassium ion transmembrane	BP	1	ACTN2,KCNE3,AKAP6	up_ACOR_VSMC
GO:0003007	0.0924	0.986	2	94	heart morphogenesis	BP	1	ACVRL1,NRP2	down_ACOR_EC
GO:2000479	0.0924	0.988	2	8	regulation of cAMP-dependent protein kinase	BP	0.987	SESN2,HTT	down_VSAP_EC
GO:0007089	0.0924	1	1	1	traversing start control point of mitotic cell cycle	BP	1	MTBP	down_ACOR_VSMC
GO:0051309	0.0924	1	1	1	female meiosis chromosome separation	BP	1	NCAPH	down_ACOR_VSMC
GO:0038166	0.0924	0.997	1	4	angiotensin-activated signaling pathway	BP	1	CAMK2A	up_AFEM_EC
GO:0010827	0.0924	0.996	1	28	regulation of glucose transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0050709	0.0924	0.996	1	28	negative regulation of protein secretion	BP	1	NR1H4	up_VPUL_EC
GO:0010604	0.0925	0.963	7	919	positive regulation of macromolecule metabolic	BP	1	HOXA11,HOXA9,SALL1,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0001775	0.0925	0.986	2	219	cell activation	BP	1	HOXA9,BPI	up_AORT_EC
GO:0051893	0.0925	0.996	1	20	regulation of focal adhesion assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0090109	0.0925	0.996	1	20	regulation of cell-substrate junction	BP	1	ACVRL1	down_ACOR_EC
GO:0090336	0.0925	0.997	1	4	positive regulation of brown fat cell	BP	1	NAPEPLD	up_AFEM_EC
GO:1901228	0.0925	0.997	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GREM1	up_AFEM_EC
GO:0010769	0.0925	0.996	1	69	regulation of cell morphogenesis involved	BP	1	LIMK1	up_VCAV_VSMC
GO:0021730	0.0925	1	1	1	trigeminal sensory nucleus development	BP	1	NFIB	up_VSAP_EC
GO:0021740	0.0925	1	1	1	principal sensory nucleus of trigeminal nerve	BP	1	NFIB	up_VSAP_EC
GO:0061141	0.0925	1	1	1	lung ciliated cell differentiation	BP	1	NFIB	up_VSAP_EC
GO:2000790	0.0925	1	1	1	regulation of mesenchymal cell proliferation involved in	BP	1	NFIB	up_VSAP_EC
GO:2000791	0.0925	1	1	1	negative regulation of mesenchymal cell proliferation involved in	BP	1	NFIB	up_VSAP_EC
GO:2000795	0.0925	1	1	1	negative regulation of epithelial cell proliferation involved in lung	BP	1	NFIB	up_VSAP_EC
GO:0051341	0.0925	0.996	1	22	regulation of oxidoreductase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0051403	0.092543726	0.9671	5	89	stress-activated MAPK cascade	BP	1	FZD5,NOD2,TNFRSF19,MAPK8IP2,SH3RF3	up_ACOR_EC
GO:0044249	0.0926	0.954	13	1851	cellular biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,TNRC6B,NEDD4	down_ACOR_EC
GO:0009893	0.0926	0.97	5	995	positive regulation of metabolic process	BP	1	EYA1,GATM,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060078	0.0926	0.974	4	17	regulation of postsynaptic membrane potential	BP	1	TMEM108,DMPK,APP,INSYN1	up_ACOR_VSMC

GO:0099565	0.0926	0.974	4	17	chemical synaptic transmission, postsynaptic	BP	1	TMEM108,DMPK,APP,INSYN1	up_ACOR_VSMC
GO:0009225	0.0926	0.987	2	10	nucleotide-sugar metabolic process	BP	1	GFPT2,FUT8	down_VCAV_EC
GO:0003013	0.0926	0.986	2	121	circulatory system process	BP	1	MAP2K6,AVPR1A	up_VFEM_EC
GO:0034769	0.0926	1	1	1	basement membrane disassembly	BP	1	CTSS	up_ACOR_VSMC
GO:0030854	0.0926	0.997	1	4	positive regulation of granulocyte	BP	1	EVI2B	up_AFEM_EC
GO:0035630	0.0926	0.997	1	4	bone mineralization involved in bone	BP	1	GREM1	up_AFEM_EC
GO:0060219	0.0926	0.997	1	4	camera-type eye photoreceptor cell	BP	1	THRB	up_AFEM_EC
GO:0071333	0.0926	0.996	1	25	cellular response to glucose stimulus	BP	1	NR1H4	up_APUL_EC
GO:0010866	0.0927	0.989	2	6	regulation of triglyceride biosynthetic process	BP	1	SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0072376	0.0927	0.987	2	11	protein activation cascade	BP	1	CFD,A2M	down_VCAV_EC
GO:0071498	0.0927	0.988	2	8	cellular response to fluid shear stress	BP	0.989	SOCS5,PTGS2	down_VSAP_EC
GO:0033147	0.0927	0.997	1	4	negative regulation of intracellular estrogen receptor signaling	BP	1	LBH	up_AFEM_EC
GO:2001212	0.0927	0.997	1	4	regulation of vasculogenesis	BP	1	TMEM100	up_AFEM_EC
GO:0038044	0.0927	1	1	1	transforming growth factor-beta secretion	BP	0.944	FERMT1	up_VCAV_EC
GO:2001201	0.0927	1	1	1	regulation of transforming growth factor-beta	BP	0.944	FERMT1	up_VCAV_EC
GO:2001203	0.0927	1	1	1	positive regulation of transforming growth factor-beta secretion	BP	0.944	FERMT1	up_VCAV_EC
GO:0051886	0.0927	1	1	1	negative regulation of timing of anagen	BP	0.944	FERMT1	up_VCAV_EC
GO:0045666	0.0927	0.996	1	68	positive regulation of neuron differentiation	BP	1	LIMK1	up_VCAV_VSMC
GO:0006937	0.0927	0.996	1	40	regulation of muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0019682	0.0928	0.987	2	10	glyceraldehyde-3-phosphate metabolic	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0071674	0.0928	0.996	1	23	mononuclear cell migration	BP	1	LYN	down_ACOR_EC
GO:0050655	0.0928	0.997	1	4	dermatan sulfate proteoglycan metabolic	BP	1	CSGALNACT2	up_AFEM_EC
GO:0015693	0.0928	0.997	1	4	magnesium ion transport	BP	1	NIPAL1	up_AFEM_EC
GO:0042742	0.0928	0.996	1	39	defense response to bacterium	BP	1	BPI	up_AORT_EC
GO:0051270	0.092834212	0.95018	12	296	regulation of cellular component movement	BP	1	SOX9,AQP1,SEMA6D,ZMYND8,MMP28,PTGER4,ARHGDIB,FOXC2,LRRC15,TBX5,RARRES2,NRP1	up_ACOR_EC
GO:0008610	0.092878276	0.95745	8	177	lipid biosynthetic process	BP	1	NR1H4,THNSL2,CCDC3,PTGDS,CHPT1,PIGS,AGPAT2,PRKCD	up_ACOR_EC
GO:0001933	0.0929	0.943	19	146	negative regulation of protein phosphorylation	BP	1	SMAD6,RASSF2,BMP4,LATS2,NDRG2,F2RL1,FAM129A,CDKN1A,PTPN22,SMPD1,DAG1,PSEN1,SYNJ2BP,DUSP22,DUSP26,LRRC4,INPP5K,PARK7,CRKL	up_ACOR_VSMC
GO:0006643	0.0929	0.954	10	68	membrane lipid metabolic process	BP	1	PIGN,PIGS,UGCG,PIGG,ORMDL3,SMPD1,CLN8,SERINC3,NEU3,SERINC1	up_ACOR_VSMC
GO:0097755	0.0929	0.98	3	12	positive regulation of blood vessel diameter	BP	0.945	DOCK4,GUCY1A1,NOS2	up_VCAV_EC
GO:0007442	0.0929	0.998	1	2	hindgut morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0031666	0.0929	0.998	1	2	positive regulation of lipopolysaccharide-mediated signaling	BP	1	SASH1	down_VCAV_EC
GO:0042478	0.0929	0.998	1	2	regulation of eye photoreceptor cell	BP	1	THRB	down_VCAV_EC
GO:0061218	0.0929	0.997	1	4	negative regulation of mesonephros	BP	1	GREM1	up_AFEM_EC
GO:1901857	0.0929	0.997	1	4	positive regulation of cellular respiration	BP	1	PPARGC1A	up_AFEM_EC
GO:0097150	0.0929	0.996	1	13	neuronal stem cell population maintenance	BP	1	HOOK3	up_VPOR_EC
GO:0070293	0.092925084	0.99665	1	4	renal absorption	BP	1	AQP1	up_ACOR_EC

GO:0031401	0.092947167	0.94758	14	358	positive regulation of protein modification process	BP	1	SOX9,ENSCAFG00000004331,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0006732	0.093	0.947	15	107	coenzyme metabolic process	BP	1	ACSM3,ACACB,NADK,ENSCAFG00000013986,COQ9,PDK2,GALK1,MOCOS,PCBD1,ACSS2,MVK,PNPO,DCAKD,PNP,DDIT4	up_VSAP_EC
GO:0006403	0.093	0.956	9	64	RNA localization	BP	1	DDX39A,RAN,FBL,NUP62,NUP188,DDX39B,NOP58,MRPL18,CCT4	down_ACOR_VSMC
GO:0002824	0.093	0.973	4	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	0.992	SOCS5,FAM49B,PVR,TFRC	down_VSAP_EC
GO:0045765	0.093	0.986	2	105	regulation of angiogenesis	BP	1	ACVRL1,SULF1	down_ACOR_EC
GO:0097006	0.093	0.996	1	19	regulation of plasma lipoprotein particle levels	BP	1	ACSL3	down_ACOR_EC
GO:0055059	0.093	1	1	1	asymmetric neuroblast division	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0045216	0.093	0.996	1	44	cell-cell junction organization	BP	1	FSCN1	down_AFEM_EC
GO:0021775	0.093	0.998	1	2	smoothened signaling pathway involved in ventral spinal cord	BP	1	GLI3	down_VCAV_EC
GO:0021776	0.093	0.998	1	2	smoothened signaling pathway involved in spinal cord motor neuron cell	BP	1	GLI3	down_VCAV_EC
GO:0060573	0.093	0.998	1	2	cell fate specification involved in pattern	BP	1	GLI3	down_VCAV_EC
GO:0021521	0.093	0.998	1	2	ventral spinal cord interneuron specification	BP	1	GLI3	down_VCAV_EC
GO:1904684	0.093	0.998	1	2	negative regulation of metalloendopeptidase	BP	1	RECK	down_VCAV_EC
GO:1905049	0.093	0.998	1	2	negative regulation of metallopeptidase activity	BP	1	RECK	down_VCAV_EC
GO:0007500	0.093	1	1	1	mesodermal cell fate determination	BP	1	BMP4	up_ACOR_VSMC
GO:0035990	0.093	1	1	1	tendon cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0035992	0.093	1	1	1	tendon formation	BP	1	BMP4	up_ACOR_VSMC
GO:0060503	0.093	1	1	1	bud dilation involved in lung branching	BP	1	BMP4	up_ACOR_VSMC
GO:0061149	0.093	1	1	1	BMP signaling pathway involved in ureter	BP	1	BMP4	up_ACOR_VSMC
GO:0061150	0.093	1	1	1	renal system segmentation	BP	1	BMP4	up_ACOR_VSMC
GO:0061151	0.093	1	1	1	BMP signaling pathway involved in renal system	BP	1	BMP4	up_ACOR_VSMC
GO:0061155	0.093	1	1	1	pulmonary artery endothelial tube	BP	1	BMP4	up_ACOR_VSMC
GO:0061216	0.093	1	1	1	regulation of transcription from RNA polymerase II promoter involved in mesonephros	BP	1	BMP4	up_ACOR_VSMC
GO:0071893	0.093	1	1	1	BMP signaling pathway involved in nephric duct	BP	1	BMP4	up_ACOR_VSMC
GO:0072096	0.093	1	1	1	negative regulation of branch elongation involved in ureteric bud	BP	1	BMP4	up_ACOR_VSMC
GO:0072097	0.093	1	1	1	negative regulation of branch elongation involved in ureteric bud branching by BMP	BP	1	BMP4	up_ACOR_VSMC
GO:0072099	0.093	1	1	1	anterior/posterior pattern specification involved in ureteric bud development	BP	1	BMP4	up_ACOR_VSMC
GO:0072100	0.093	1	1	1	specification of ureteric bud anterior/posterior	BP	1	BMP4	up_ACOR_VSMC
GO:0072101	0.093	1	1	1	specification of ureteric bud anterior/posterior symmetry by BMP	BP	1	BMP4	up_ACOR_VSMC
GO:0072192	0.093	1	1	1	ureter epithelial cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0072197	0.093	1	1	1	ureter morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0072200	0.093	1	1	1	negative regulation of mesenchymal cell proliferation involved in	BP	1	BMP4	up_ACOR_VSMC

GO:1901964	0.093	1	1	1	positive regulation of cell proliferation involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:2000005	0.093	1	1	1	negative regulation of metanephric S-shaped body morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:2000006	0.093	1	1	1	regulation of metanephric comma-shaped body	BP	1	BMP4	up_ACOR_VSMC
GO:2000007	0.093	1	1	1	negative regulation of metanephric comma-shaped body	BP	1	BMP4	up_ACOR_VSMC
GO:2000137	0.093	1	1	1	negative regulation of cell proliferation involved in heart morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0048390	0.093	1	1	1	intermediate mesoderm morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0048391	0.093	1	1	1	intermediate mesoderm formation	BP	1	BMP4	up_ACOR_VSMC
GO:0048392	0.093	1	1	1	intermediate mesodermal cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0055018	0.093	1	1	1	regulation of cardiac muscle fiber development	BP	1	BMP4	up_ACOR_VSMC
GO:0055020	0.093	1	1	1	positive regulation of cardiac muscle fiber	BP	1	BMP4	up_ACOR_VSMC
GO:0060235	0.093	1	1	1	lens induction in camera-type eye	BP	1	BMP4	up_ACOR_VSMC
GO:2000004	0.093	1	1	1	regulation of metanephric S-shaped body	BP	1	BMP4	up_ACOR_VSMC
GO:0051668	0.093	0.996	1	39	localization within membrane	BP	1	LHFPL4	up_VPOR_VSMC
GO:0003231	0.093	0.996	1	48	cardiac ventricle development	BP	1	TBX5	up_VPUL_VSMC
GO:0003279	0.093	0.996	1	48	cardiac septum development	BP	1	TBX5	up_VPUL_VSMC
GO:0030070	0.0931	1	1	1	insulin processing	BP	1	ERO1B	up_ACOR_VSMC
GO:1901142	0.0931	1	1	1	insulin metabolic process	BP	1	ERO1B	up_ACOR_VSMC
GO:0022615	0.0931	0.997	1	4	protein to membrane docking	BP	1	RAB7A	up_AFEM_EC
GO:0046533	0.0931	0.997	1	4	negative regulation of photoreceptor cell	BP	1	THRB	up_AFEM_EC
GO:0002274	0.0931	0.996	1	40	myeloid leukocyte activation	BP	1	BPI	up_AORT_EC
GO:0021510	0.0931	0.996	1	23	spinal cord development	BP	1	HOXC10	up_VSAP_VSMC
GO:0032642	0.0931	0.996	1	22	regulation of chemokine production	BP	1	TLR2	up_VSAP_VSMC
GO:0001818	0.093158591	0.97155	4	65	negative regulation of cytokine production	BP	1	CDH3,NR1H4,NDRG2,PTGER4	up_ACOR_EC
GO:0050852	0.0932	0.969	5	26	T cell receptor signaling pathway	BP	1	PLCG2,ELF1,PTPN22,PSEN1,DUSP22	up_ACOR_VSMC
GO:1904353	0.0932	0.98	3	13	regulation of telomere capping	BP	1	HNRNPD,AURKB,NEK2	down_ACOR_VSMC
GO:0071788	0.0932	1	1	1	endoplasmic reticulum tubular network	BP	1	LNPK	up_ACOR_VSMC
GO:1902307	0.0932	0.997	1	4	positive regulation of sodium ion	BP	1	FXYD1	up_AFEM_EC
GO:0055123	0.0932	0.996	1	40	digestive system development	BP	1	SHOX2	up_VFEM_VSMC
GO:0022610	0.0933	0.933	40	326	biological adhesion	BP	1	SMAD6,ACTN2,LEP,GATA5,CD83,MBP,FERMT1,BMP4,PDE5A,CITED2,PKP4,CD274,TINAGL1,LIMS2,NRP1,PTPN22,NPNT,SPINT2,VCAM1,PRKCE,RND1,ECM2,LAMA3,PSEN1,JUP,CDH18,PERP,DUSP22,NID1,DUSP26,FAM107A,JAM3,IGFBP7,CELSR2,ATP2C1,DOCK5,BVES,RREB1,PAG1,CRKL	up_ACOR_VSMC
GO:0006807	0.0933	0.968	10	3221	nitrogen compound metabolic process	BP	1	IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0048010	0.0933	0.973	4	20	vascular endothelial growth factor receptor	BP	0.948	KDR,HHEX,PRKD2,HIF1A	up_VCAV_EC
GO:0045893	0.0933	0.972	4	413	positive regulation of transcription, DNA-	BP	1	HOXA11,HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:0032879	0.0933	0.989	2	767	regulation of localization	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0048699	0.0933	0.987	2	371	generation of neurons	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0003062	0.0933	1	1	1	regulation of heart rate by chemical signal	BP	1	SREBF1	down_ACOR_VSMC

GO:0009786	0.0933	1	1	1	regulation of asymmetric cell division	BP	1	ASPM	down_ACOR_VSMC
GO:0060032	0.0933	1	1	1	notochord regression	BP	1	GLI1	down_ACOR_VSMC
GO:0045004	0.0933	1	1	1	DNA replication proofreading	BP	1	POLE	down_ACOR_VSMC
GO:0045769	0.0933	1	1	1	negative regulation of asymmetric cell division	BP	1	ASPM	down_ACOR_VSMC
GO:1904170	0.0933	1	1	1	regulation of bleb assembly	BP	1	ANLN	down_ACOR_VSMC
GO:1904172	0.0933	1	1	1	positive regulation of bleb assembly	BP	1	ANLN	down_ACOR_VSMC
GO:0010746	0.0933	0.998	1	2	regulation of plasma membrane long-chain	BP	1	AKT2	down_VCAV_EC
GO:0010748	0.0933	0.998	1	2	negative regulation of plasma membrane long-chain fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:0015911	0.0933	0.998	1	2	plasma membrane long-chain fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:1902001	0.0933	0.998	1	2	fatty acid transmembrane transport	BP	1	AKT2	down_VCAV_EC
GO:2000192	0.0933	0.998	1	2	negative regulation of fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:0071375	0.0933	0.996	1	68	cellular response to peptide hormone stimulus	BP	1	CA2	up_VCAV_VSMC
GO:0000722	0.0934	0.989	2	6	telomere maintenance via recombination	BP	1	RAD51,SMC6	down_ACOR_VSMC
GO:0021861	0.0934	0.998	1	2	forebrain radial glial cell differentiation	BP	1	GLI3	down_VCAV_EC
GO:0061709	0.0934	0.998	1	2	reticulophagy	BP	1	RETREG1	down_VCAV_EC
GO:0048701	0.0934	0.996	1	25	embryonic cranial skeleton morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:1901863	0.0934	0.996	1	25	positive regulation of muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0043269	0.0934	0.996	1	135	regulation of ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0072593	0.0934	0.996	1	68	reactive oxygen species metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0060633	0.093470578	0.99661	1	4	negative regulation of transcription initiation from RNA polymerase II	BP	1	CLSTN1	up_ACOR_EC
GO:2000143	0.093470578	0.99661	1	4	negative regulation of DNA-templated	BP	1	CLSTN1	up_ACOR_EC
GO:0051093	0.0935	0.935	33	273	negative regulation of developmental process	BP	1	THRB,HOXA7,TWIST2,HOXA9,AXIN2,LIMS2,SLIT2,SLC6A4,ABL1,HDAC7,DLL1,EPN2,OSR1,SAV1,ZBTB16,RARG,ZFP36L1,FXN,PIK3R1,MYC,IRX3,ZEB1,TBXA2R,RTN4RL1,LRP4,ZADH2,FBXO7,LIMD1,FBLN1,ZFP36L2,NFIB,ACVRL1,LBH	up_VSAP_EC
GO:0043408	0.0935	0.943	18	211	regulation of MAPK cascade	BP	0.996	VEGFA,JCAD,PTPN11,TRIB3,TNIK,PTPN2,MAGED1,CTNNB1,APOE,LYN,CBLC,ATF3,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0010257	0.0935	0.969	5	25	NADH dehydrogenase complex assembly	BP	1	NDUFS7,DMAC2,NDUFAF3,NDUFB10,COA1	up_VSAP_EC
GO:0032981	0.0935	0.969	5	25	mitochondrial respiratory chain complex I assembly	BP	1	NDUFS7,DMAC2,NDUFAF3,NDUFB10,COA1	up_VSAP_EC
GO:0001944	0.0935	0.986	2	263	vasculature development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0002028	0.0935	0.996	1	19	regulation of sodium ion transport	BP	1	NEDD4	down_ACOR_EC
GO:0035581	0.0935	0.998	1	2	sequestering of extracellular ligand from	BP	1	FBN1	down_VCAV_EC
GO:0043383	0.0935	0.998	1	2	negative T cell selection	BP	1	GLI3	down_VCAV_EC
GO:0051595	0.0935	0.998	1	2	response to methylglyoxal	BP	1	PARK7	down_VCAV_EC
GO:1900115	0.0935	0.998	1	2	extracellular regulation of signal transduction	BP	1	FBN1	down_VCAV_EC
GO:1900116	0.0935	0.998	1	2	extracellular negative regulation of signal	BP	1	FBN1	down_VCAV_EC
GO:1901668	0.0935	0.998	1	2	regulation of superoxide dismutase activity	BP	1	PARK7	down_VCAV_EC
GO:1902177	0.0935	0.998	1	2	positive regulation of oxidative stress-induced intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:1905874	0.0935	0.998	1	2	regulation of postsynaptic density organization	BP	1	CDH2	down_VCAV_EC

GO:0038086	0.0935	0.998	1	2	VEGF-activated platelet-derived growth factor receptor signaling	BP	1	PDGFRB	down_VCAV_EC
GO:0038091	0.0935	0.998	1	2	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor	BP	1	PDGFRB	down_VCAV_EC
GO:0045060	0.0935	0.998	1	2	negative thymic T cell selection	BP	1	GLI3	down_VCAV_EC
GO:1902897	0.0935	0.998	1	2	regulation of postsynaptic density protein 95	BP	1	CDH2	down_VCAV_EC
GO:2000282	0.0935	0.998	1	2	regulation of cellular amino acid biosynthetic	BP	1	PARK7	down_VCAV_EC
GO:0010927	0.0935	0.996	1	28	cellular component assembly involved in	BP	1	MYBPC2	up_VPUL_EC
GO:0051649	0.0936	0.964	6	630	establishment of localization in cell	BP	1	LYN,SPG11,IPO7,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0045646	0.0936	0.973	4	19	regulation of erythrocyte differentiation	BP	1	ISG15,FAM210B,P4HTM,B2M	up_ACOR_VSMC
GO:0046633	0.0936	0.988	2	7	alpha-beta T cell proliferation	BP	0.948	ARG2,ELF4	up_VCAV_EC
GO:0031334	0.0936	0.996	1	84	positive regulation of protein complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0032768	0.0936	0.996	1	12	regulation of monooxygenase activity	BP	1	ACVR2A	up_VPOR_EC
GO:0055117	0.0936	0.996	1	21	regulation of cardiac muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0097191	0.0937	0.957	8	79	extrinsic apoptotic signaling pathway	BP	0.997	ARHGEF2,SERPINE1,ATF3,HTT,PAK2,INHBA,NRP1,MADD	down_VSAP_EC
GO:0010721	0.0937	0.971	4	73	negative regulation of cell development	BP	1	IRX3,DLL1,THRB,KANK1	up_AFEM_EC
GO:0036445	0.0937	0.988	2	6	neuronal stem cell division	BP	1	ASPM,ARHGEF2	down_ACOR_VSMC
GO:0055057	0.0937	0.988	2	6	neuroblast division	BP	1	ASPM,ARHGEF2	down_ACOR_VSMC
GO:0009617	0.0937	0.986	2	133	response to bacterium	BP	1	NR1H4,BPI	up_APUL_EC
GO:0098722	0.0937	0.998	1	2	asymmetric stem cell division	BP	1	ZBTB16	down_VCAV_EC
GO:0006886	0.0937	0.998	1	332	intracellular protein transport	BP	1	JUP	down_VFEM_VSMC
GO:1903576	0.0937	1	1	1	response to L-arginine	BP	1	CASTOR1	up_ACOR_VSMC
GO:1903577	0.0937	1	1	1	cellular response to L-arginine	BP	1	CASTOR1	up_ACOR_VSMC
GO:0019218	0.0937	0.996	1	25	regulation of steroid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0021872	0.093732133	0.98591	2	19	forebrain generation of neurons	BP	1	DCLK2,NRP1	up_ACOR_EC
GO:0007389	0.0938	0.944	18	137	pattern specification process	BP	1	SMAD6,GATA5,MLLT3,BMP4,FGFR2,GJA1,CITED2,CLSTN1,NRP1,SMARCD3,TBX20,TBX5,FRS2,PSEN1,PCSK6,PSKH1,EDN1,CRKL	up_ACOR_VSMC
GO:2000177	0.0938	0.973	4	26	regulation of neural precursor cell	BP	0.997	ILK,HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0031076	0.0938	0.979	3	14	embryonic camera-type eye development	BP	0.948	PROX1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0090176	0.0938	0.998	1	2	microtubule cytoskeleton organization involved in establishment of planar	BP	1	BRSK1	down_VCAV_EC
GO:0007519	0.0938	0.996	1	49	skeletal muscle tissue development	BP	1	CITED2	down_VPOR_EC
GO:0002713	0.0938	1	1	1	negative regulation of B cell mediated immunity	BP	0.948	THOC1	up_VCAV_EC
GO:0045829	0.0938	1	1	1	negative regulation of isotype switching	BP	0.948	THOC1	up_VCAV_EC
GO:0048297	0.0938	1	1	1	negative regulation of isotype switching to IgA	BP	0.948	THOC1	up_VCAV_EC
GO:0002890	0.0938	1	1	1	negative regulation of immunoglobulin mediated immune	BP	0.948	THOC1	up_VCAV_EC
GO:0090067	0.0938	1	1	1	regulation of thalamus size	BP	1	SLC6A4	up_VSAP_EC
GO:0032456	0.0939	0.973	4	19	endocytic recycling	BP	1	ACTN2,RAB11B,LMTK2,BVES	up_ACOR_VSMC
GO:0051961	0.0939	0.971	4	73	negative regulation of nervous system	BP	1	IRX3,DLL1,THRB,KANK1	up_AFEM_EC
GO:0030032	0.0939	0.973	4	19	lamellipodium assembly	BP	1	WASF3,SLIT2,FGD4,NCK1	up_VSAP_EC
GO:0051960	0.0939	0.986	2	216	regulation of nervous system development	BP	1	EYA1,SHOX2	up_VFEM_VSMC

GO:0002036	0.0939	1	1	1	regulation of L-glutamate import across plasma	BP	1	PSEN1	up_ACOR_VSMC
GO:0002038	0.0939	1	1	1	positive regulation of L-glutamate import across	BP	1	PSEN1	up_ACOR_VSMC
GO:0015871	0.0939	1	1	1	choline transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0051582	0.0939	1	1	1	positive regulation of neurotransmitter uptake	BP	1	PSEN1	up_ACOR_VSMC
GO:1904797	0.0939	1	1	1	negative regulation of core promoter binding	BP	1	PSEN1	up_ACOR_VSMC
GO:0010958	0.0939	1	1	1	regulation of amino acid import across plasma	BP	1	PSEN1	up_ACOR_VSMC
GO:0016080	0.0939	1	1	1	synaptic vesicle targeting	BP	1	PSEN1	up_ACOR_VSMC
GO:0021870	0.0939	1	1	1	Cajal-Retzius cell differentiation	BP	1	PSEN1	up_ACOR_VSMC
GO:0098629	0.0939	1	1	1	trans-Golgi network membrane organization	BP	1	AZIN2	up_ACOR_VSMC
GO:0006796	0.094	0.966	6	938	phosphate-containing compound metabolic	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0043949	0.094	0.98	3	13	regulation of cAMP-mediated signaling	BP	0.948	PDE4D,APLNR,RAPGEF2	up_VCAV_EC
GO:0002528	0.094	0.998	1	2	regulation of vascular permeability involved in acute inflammatory	BP	1	CLSTN1	down_VCAV_EC
GO:0036306	0.094	1	1	1	embryonic heart tube elongation	BP	1	TBX20	up_ACOR_VSMC
GO:1900477	0.094	1	1	1	negative regulation of G1/S transition of mitotic cell cycle by negative regulation of transcription from RNA polymerase II	BP	1	NACC2	up_ACOR_VSMC
GO:1903996	0.094	1	1	1	negative regulation of non-membrane spanning protein tyrosine kinase	BP	1	DUSP22	up_ACOR_VSMC
GO:0021524	0.094	1	1	1	visceral motor neuron differentiation	BP	1	TBX20	up_ACOR_VSMC
GO:0042985	0.094	1	1	1	negative regulation of amyloid precursor protein biosynthetic process	BP	1	ITM2C	up_ACOR_VSMC
GO:0051685	0.094	1	1	1	maintenance of ER location	BP	1	POLR2M	up_ACOR_VSMC
GO:0003290	0.094	1	1	1	atrial septum secundum morphogenesis	BP	1	GATA4	up_ACOR_VSMC
GO:1901373	0.094	1	1	1	lipid hydroperoxide transport	BP	1	SCP2	up_ACOR_VSMC
GO:1902310	0.094	1	1	1	positive regulation of peptidyl-serine	BP	1	DUSP26	up_ACOR_VSMC
GO:0043542	0.094	0.996	1	86	endothelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0036289	0.094	1	1	1	peptidyl-serine autophosphorylation	BP	0.948	RIPK1	up_VCAV_EC
GO:0060545	0.094	1	1	1	positive regulation of necroptotic process	BP	0.948	RIPK1	up_VCAV_EC
GO:0070926	0.094	1	1	1	regulation of ATP:ADP antiporter activity	BP	0.948	RIPK1	up_VCAV_EC
GO:1905206	0.094	1	1	1	positive regulation of hydrogen peroxide-	BP	0.948	RIPK1	up_VCAV_EC
GO:2001040	0.094	1	1	1	positive regulation of cellular response to drug	BP	0.948	RIPK1	up_VCAV_EC
GO:0033138	0.094	0.996	1	28	positive regulation of peptidyl-serine	BP	1	PTGER2	up_VPUL_EC
GO:0065007	0.0941	0.93	92	3499	biological regulation	BP	1	HOXA9,CMKLR1,MT2A,IRX3,IRX5,HOXC10,HOXA10,LEP,KCNC4,LBH,PRR16,CRY2,ENSCAFG00000009113,RAB20,GAS1,F5,ANGPT4,HOXA7,CD40,DLL1,CRYAB,KCND1,F3,PLXNA4,BPI,GPAM,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,TWIST2,MAB21L1,THRB,LGI4,MYO1D,MFAP4,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,HTR1D,NFE2L1,OVOL1,FAM53B,AVPR1A,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,FXYD1,LRRC15,FAM13A,MYBL1,RECK,NR3C1,PTHLH,TBXA2R,EVI2B,MOXD1,DCUN1D3,CNNM4,TFPI2,REEP2,EAF1,BVES,LGR6,RAB7A,AXIN2,YEATS2,ATP6V0B,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,CLIC4,AGPAT2,GCNT4,FOSL2,KANK1,TNC	up_AFEM_EC

GO:0051050	0.0941	0.936	29	235	positive regulation of transport	BP	1	EXPH5,TLR1,ACTN2,PLCG2,LEP,HTR2B,TCAF1,MBP,FERMT1,TM7SF3,ABCA1,CD274,ANKRD1,F2RL1,AKAP6,PTPN22,SCP2,PRKCE,PSEN1,JUP,EDN1,NOD2,B2M,FXYD1,SCAMP5,INPP5K,WFS1,AZIN2,PARK7	up_ACOR_VSMC
GO:0006811	0.0941	0.949	12	330	ion transport	BP	1	LEP,KCNC4,KCND1,SLC17A5,ATP6V1B2,SLC6A6,CAMK2A,FXYD1,ATP6V0B,NIPAL1,DMPK,CLIC4	up_AFEM_EC
GO:0007623	0.0941	0.958	8	55	circadian rhythm	BP	0.948	PPARG,PROX1,ENSCAFG00000010596,TIMELESS,TOP1,CREB1,NR1D2,KDM5A	up_VCAV_EC
GO:0030073	0.0941	0.961	7	42	insulin secretion	BP	1	LEP,TM7SF3,PRKCE,CCL5,RAB11B,PFKL,PARK7	up_ACOR_VSMC
GO:0006937	0.0941	0.964	6	40	regulation of muscle contraction	BP	0.948	DOCK4,PDE4D,STC1,GUCY1A1,KCNJ2,ATP2A1	up_VCAV_EC
GO:0048846	0.0941	0.988	2	6	axon extension involved in axon guidance	BP	1	SLIT2,PLXNA4	up_VSAP_EC
GO:1902284	0.0941	0.988	2	6	neuron projection extension involved in neuron projection	BP	1	SLIT2,PLXNA4	up_VSAP_EC
GO:1904528	0.0941	0.998	1	2	positive regulation of microtubule binding	BP	1	MAPRE3	down_VCAV_EC
GO:0032103	0.0941	0.996	1	69	positive regulation of response to external	BP	1	TLR2	up_AFEM_VSMC
GO:0030308	0.0941	0.996	1	49	negative regulation of cell growth	BP	1	SLIT2	up_VPUL_VSMC
GO:1900454	0.0941	1	1	1	positive regulation of long-term synaptic depression	BP	1	KCNB1	up_VSAP_EC
GO:0040007	0.0942	0.935	33	276	growth	BP	1	HOXA11,ENSCAFG00000009113,WNT11,HNF4A,FAM107A,ACACB,SLIT2,SLC6A4,FGF7,ABL1,DLL1,SAV1,PLXNA4,RARG,DDR2,ZFP36L1,MT2A,FXN,GAS1,MYD88,LRP4,DPYSL2,WISP2,KDM2B,IGFBP6,TAF8,TTL,SMARCA2,ACVRL1,HTRA2,ULK1,TGFBR2,LATS2	up_VSAP_EC
GO:0048522	0.0942	0.957	10	1484	positive regulation of cellular process	BP	1	HOXA11,HOXA9,NETO1,SALL1,MAB21L1,PRR16,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0045766	0.0942	0.985	2	63	positive regulation of angiogenesis	BP	1	C3AR1,MTDH	up_VPOR_EC
GO:1905953	0.0942	0.996	1	12	negative regulation of lipid localization	BP	1	ABHD5	up_VPOR_EC
GO:0002011	0.0942	0.996	1	28	morphogenesis of an epithelial sheet	BP	1	FLRT3	up_VPUL_EC
GO:0007043	0.0942	0.996	1	28	cell-cell junction assembly	BP	1	NR1H4	up_VPUL_EC
GO:0048289	0.0942	1	1	1	isotype switching to IgE isotypes	BP	1	STAT6	up_VSAP_EC
GO:0048293	0.0942	1	1	1	regulation of isotype switching to IgE isotypes	BP	1	STAT6	up_VSAP_EC
GO:0048295	0.0942	1	1	1	positive regulation of isotype switching to IgE	BP	1	STAT6	up_VSAP_EC
GO:0060711	0.0942	0.996	1	21	labyrinthine layer development	BP	1	GJB5	up_VSAP_VSMC
GO:0035690	0.0943	0.95	12	91	cellular response to drug	BP	0.949	TNFAIP3,PDGFB,MEF2C,PPP3CA,MAPK13,TIMELESS,GUCY1B1,CTNNA1,BLM,RIPK1,ATRX,ARHGEF2	up_VCAV_EC
GO:0006888	0.0943	0.996	1	49	ER to Golgi vesicle-mediated transport	BP	1	ERGIC1	down_VPOR_EC
GO:1902959	0.0943	0.998	1	2	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein	BP	0.998	LYN	down_VSAP_EC
GO:1902961	0.0943	0.998	1	2	positive regulation of aspartic-type endopeptidase activity involved in amyloid	BP	0.998	LYN	down_VSAP_EC
GO:1905245	0.0943	0.998	1	2	regulation of aspartic-type peptidase activity	BP	0.998	LYN	down_VSAP_EC
GO:1905247	0.0943	0.998	1	2	positive regulation of aspartic-type peptidase	BP	0.998	LYN	down_VSAP_EC
GO:0009750	0.0943	1	1	1	response to fructose	BP	1	SLC2A5	up_ACOR_VSMC
GO:0015755	0.0943	1	1	1	fructose transmembrane transport	BP	1	SLC2A5	up_ACOR_VSMC
GO:0032445	0.0943	1	1	1	fructose import	BP	1	SLC2A5	up_ACOR_VSMC
GO:0071332	0.0943	1	1	1	cellular response to fructose stimulus	BP	1	SLC2A5	up_ACOR_VSMC
GO:0098704	0.0943	1	1	1	carbohydrate import across plasma membrane	BP	1	SLC2A5	up_ACOR_VSMC
GO:1900259	0.0943	1	1	1	regulation of RNA-directed 5'-3' RNA	BP	1	EIF4A2	up_ACOR_VSMC

GO:1900260	0.0943	1	1	1	negative regulation of RNA-directed 5'-3' RNA polymerase activity	BP	1	EIF4A2	up_ACOR_VSMC
GO:1990539	0.0943	1	1	1	fructose import across plasma membrane	BP	1	SLC2A5	up_ACOR_VSMC
GO:0090407	0.094371837	0.95662	8	177	organophosphate biosynthetic process	BP	1	NR1H4,NMNAT2,GUCY1B1,CHPT1,PIGS,AK7,ALDOC,AGPAT2	up_ACOR_EC
GO:0031326	0.0944	0.923	110	1176	regulation of cellular biosynthetic process	BP	0.949	EDNRB,HCLS1,ADGRF5,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,FAM3C,MTOR,SAMD8,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,ENC1,CCAR1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,PTGS2,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,NOS2,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0031325	0.0944	0.927	65	914	positive regulation of cellular metabolic process	BP	0.998	ARHGEF2,PRICKLE1,VEGFA,MYH9,NR1H4,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,MSN,HIF1A,SLC45A3,TNIK,ZPR1,PTPN2,YES1,PEG3,MTDH,DDX39B,ADAM17,CNOT7,MAGED1,CTNNB1,TFRC,APOE,KLF5,LYN,BNIP3,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,SH3GLB1,HTT,REST,ABHD5,CALM1,DISC1,RAD23A,PAK2,INHBA,NR4A1,CDKN1A,TMTC3,NRP1,SH3RF3,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0001933	0.0944	0.948	13	146	negative regulation of protein phosphorylation	BP	0.998	SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,DNAJC10,PTPN2,APOE,LYN,STRAP,CBLC,ATF3,CDKN1A	down_VSAP_EC
GO:0060485	0.0944	0.957	8	93	mesenchyme development	BP	1	VASN,GLIPR2,BMPR1A,SEMA3C,ZFP36L1,LOXL3,RDH10,GREM1	down_VCAV_EC
GO:0031667	0.0944	0.966	5	102	response to nutrient levels	BP	1	LEP,CLEC16A,POSTN,ACACB,PPARGC1A	up_AFEM_EC
GO:0032507	0.0944	0.973	4	18	maintenance of protein location in cell	BP	1	OS9,DAG1,SUN1,PARK7	up_ACOR_VSMC
GO:0120036	0.0944	0.987	2	373	plasma membrane bounded cell projection	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0030850	0.0944	0.996	1	20	prostate gland development	BP	1	SULF1	down_ACOR_EC
GO:0060046	0.0944	0.998	1	2	regulation of acrosome reaction	BP	0.998	SPINK2	down_VSAP_EC
GO:0030329	0.0944	1	1	1	prenylcysteine metabolic process	BP	1	PCYOX1	up_ACOR_VSMC
GO:0015739	0.0944	1	1	1	sialic acid transport	BP	1	SLC17A5	up_ACOR_VSMC
GO:0030328	0.0944	1	1	1	prenylcysteine catabolic process	BP	1	PCYOX1	up_ACOR_VSMC
GO:0070555	0.0944	0.996	1	29	response to interleukin-1	BP	1	CCL24	up_VPUL_EC
GO:0010562	0.0945	0.94	21	312	positive regulation of phosphorus metabolic process	BP	1	NOTCH2,PDGFRB,PRNP,GLIPR2,BMPR1A,LMO4,CLIP3,AKT2,CSPG4,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0045937	0.0945	0.94	21	312	positive regulation of phosphate metabolic process	BP	1	NOTCH2,PDGFRB,PRNP,GLIPR2,BMPR1A,LMO4,CLIP3,AKT2,CSPG4,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0007019	0.0945	0.979	3	13	microtubule depolymerization	BP	1	STMN1,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0031643	0.0945	1	1	1	positive regulation of myelination	BP	1	WASF3	up_ACOR_VSMC

GO:1901575	0.0946	0.93	47	643	organic substance catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,ENPP1,SNX25,PGK1,TPI1,TRIB3,PGAM1,ALDH1L2,SESN2,CEMIP2,MSN,SEL1L,HIF1A,USP12,DNAJC10,UBA6,ZPR1,ENTPD4,UCHL5,SPOPL,PLCL1,SMG7,CNOT7,DNAJB9,ALDOC,SND1,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,GALE,ABHD5,SPOP,DISC1,RAD23A,TMTC3,USP14,YWHAH,TNFAIP1	down_VSAP_EC
GO:0042100	0.0946	0.996	1	19	B cell proliferation	BP	1	LYN	down_ACOR_EC
GO:1900063	0.0946	0.998	1	2	regulation of peroxisome organization	BP	1	MAVS	down_VCAV_EC
GO:0090090	0.0946	0.996	1	44	negative regulation of canonical Wnt signaling	BP	1	DKK2	up_AORT_EC
GO:0019751	0.0947	0.964	6	33	polyol metabolic process	BP	1	GOT1,INPP5E,PPIP5K1,GALK1,PCBD1,TKFC	up_VSAP_EC
GO:1902680	0.0947	0.972	4	415	positive regulation of RNA biosynthetic process	BP	1	HOXA11,HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:1903508	0.0947	0.972	4	415	positive regulation of nucleic acid-templated	BP	1	HOXA11,HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:0003206	0.0947	0.996	1	51	cardiac chamber morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0032609	0.0947	0.996	1	25	interferon-gamma production	BP	1	NR1H4	up_APUL_EC
GO:0014859	0.0947	1	1	1	negative regulation of skeletal muscle cell	BP	0.949	EPHB1	up_VCAV_EC
GO:1902723	0.0947	1	1	1	negative regulation of skeletal muscle satellite	BP	0.949	EPHB1	up_VCAV_EC
GO:0007597	0.0947	1	1	1	blood coagulation, intrinsic pathway	BP	0.949	KLKB1	up_VCAV_EC
GO:0051919	0.0947	1	1	1	positive regulation of fibrinolysis	BP	0.949	KLKB1	up_VCAV_EC
GO:0060696	0.094717513	0.99651	1	4	regulation of phospholipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0061326	0.094739956	0.97718	3	41	renal tubule development	BP	1	SOX9,AQP1,CLSTN1	up_ACOR_EC
GO:0072080	0.094739956	0.97718	3	41	nephron tubule development	BP	1	SOX9,AQP1,CLSTN1	up_ACOR_EC
GO:0072224	0.094762481	0.99651	1	4	metanephric glomerulus development	BP	1	AQP1	up_ACOR_EC
GO:0072239	0.094762481	0.99651	1	4	metanephric glomerulus vasculature development	BP	1	AQP1	up_ACOR_EC
GO:0060249	0.0948	0.947	14	110	anatomical structure homeostasis	BP	0.949	ADGRF5,CD34,TLR4,HMBOX1,EXOC5,LDB2,TAOK1,SMG7,VPS54,BLM,SMC5,HIF1A,ATRX,DCP2	up_VCAV_EC
GO:0003300	0.0948	0.973	4	18	cardiac muscle hypertrophy	BP	1	GATA5,HTR2B,PDE5A,EDN1	up_ACOR_VSMC
GO:0014896	0.0948	0.973	4	18	muscle hypertrophy	BP	1	GATA5,HTR2B,PDE5A,EDN1	up_ACOR_VSMC
GO:0014897	0.0948	0.973	4	18	striated muscle hypertrophy	BP	1	GATA5,HTR2B,PDE5A,EDN1	up_ACOR_VSMC
GO:0002791	0.0948	0.985	2	104	regulation of peptide secretion	BP	1	LYN,STX4	down_ACOR_EC
GO:0045964	0.0948	0.998	1	2	positive regulation of dopamine metabolic	BP	1	PARK7	down_VCAV_EC
GO:1903179	0.0948	0.998	1	2	regulation of dopamine biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:1903181	0.0948	0.998	1	2	positive regulation of dopamine biosynthetic	BP	1	PARK7	down_VCAV_EC
GO:0045915	0.0948	0.998	1	2	positive regulation of catecholamine metabolic	BP	1	PARK7	down_VCAV_EC
GO:0032330	0.094812102	0.9856	2	20	regulation of chondrocyte differentiation	BP	1	SOX9,EFEMP1	up_ACOR_EC
GO:0048732	0.0949	0.945	16	116	gland development	BP	1	LBH,BMP4,FGFR2,GJA1,CITED2,LMO4,LIMS2,NRP1,FRS2,DAG1,PSEN1,ARID5B,SERPINB5,RREB1,ZDHHC21,CRKL	up_ACOR_VSMC
GO:0002694	0.0949	0.952	10	126	regulation of leukocyte activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,ZFP36L1,BPI,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0045600	0.0949	0.978	3	21	positive regulation of fat cell differentiation	BP	1	ZFP36L1,NAPEPLD,ZBTB16	down_VCAV_EC
GO:0007605	0.0949	0.996	1	27	sensory perception of sound	BP	1	HOXA1	up_APUL_EC
GO:0016202	0.0949	0.996	1	39	regulation of striated muscle tissue	BP	1	SHOX2	up_VFEM_VSMC
GO:0060840	0.0949	0.996	1	42	artery development	BP	1	EYA1	up_VFEM_VSMC
GO:0045833	0.0949	0.996	1	29	negative regulation of lipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0045844	0.0949	0.996	1	24	positive regulation of striated muscle tissue	BP	1	SHOX2	up_VSAP_VSMC

GO:0048636	0.0949	0.996	1	24	positive regulation of muscle organ	BP	1	SHOX2	up_VSAP_VSMC
GO:0006644	0.095	0.945	16	118	phospholipid metabolic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,CHPT1,PIGN,PIGS,PLPP2,PIGG,SMPD1,CRLS1,CLN8,SERINC3,SERINC1,CFI,INPP5K	up_ACOR_VSMC
GO:0051640	0.095	0.945	15	174	organelle localization	BP	1	MYH9,SHROOM2,EXOC5,HOOK3,MYO1C,KIF5B,HIF1A,TRAK1,CTNNB1,KPNB1,LYN,GSK3B,HTT,AP3S1,ESYT3	down_VSAP_EC
GO:0061138	0.095	0.951	11	73	morphogenesis of a branching epithelium	BP	1	BMP4,FGFR2,SPINT1,CLSTN1,NRP1,NPNT,SPINT2,TBX20,FRS2,DAG1,EDN1	up_ACOR_VSMC
GO:0042110	0.095	0.954	9	109	T cell activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,ZFP36L1,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0045637	0.095	0.971	4	73	regulation of myeloid cell differentiation	BP	1	HOXA9,HOXA7,DLL1,EVI2B	up_AFEM_EC
GO:0042127	0.095	0.978	3	452	regulation of cell proliferation	BP	1	HOXA3,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0019915	0.095	0.985	2	22	lipid storage	BP	1	CRY2,ACACB	up_AFEM_EC
GO:1903391	0.095	0.996	1	21	regulation of adherens junction organization	BP	1	ACVRL1	down_ACOR_EC
GO:1903093	0.095	0.998	1	2	regulation of protein K48-linked deubiquitination	BP	1	PARK7	down_VCAV_EC
GO:0003218	0.095	1	1	1	cardiac left ventricle formation	BP	1	TBX5	up_ACOR_VSMC
GO:0048593	0.095008718	0.97708	3	41	camera-type eye morphogenesis	BP	1	SOX9,AQP1,FZD5	up_ACOR_EC
GO:0000209	0.0951	0.95	12	83	protein polyubiquitination	BP	1	SKP2,SASH1,KLHL20,MARCH5,PTPN22,UBE2H,RNF24,RNF19A,SHPRH,NOD2,RNF181,DZIP3	up_ACOR_VSMC
GO:0055024	0.0951	0.985	2	22	regulation of cardiac muscle tissue	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0010507	0.0951	0.996	1	26	negative regulation of autophagy	BP	1	LZTS1	up_APUL_EC
GO:1904018	0.0951	0.996	1	69	positive regulation of vasculature development	BP	1	C6	up_VCAV_VSMC
GO:0048562	0.0952	0.966	5	102	embryonic organ morphogenesis	BP	1	TBX15,IRX5,HOXA7,DLL1,HOXA6	up_AFEM_EC
GO:0032526	0.0952	0.996	1	19	response to retinoic acid	BP	1	LYN	down_ACOR_EC
GO:0071322	0.0952	0.996	1	29	cellular response to carbohydrate stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0051246	0.0953	0.929	50	832	regulation of protein metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,LRP1,DCN,PRNP,GLIPR2,BGN,LARP6,BMPR1A,RECK,CLIP3,AKT1S1,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,PLCL1,CSPG4,PRMT6,ASPN,EIF3K,THY1,NECAB3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,ARL2BP,IFT57,MAVS,CDH2,GSDME,SPRED1,A2M,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,PACSIN3,EIF4EBP1	down_VCAV_EC
GO:0015893	0.0953	0.968	5	26	drug transport	BP	1	TCN2,PSEN1,CLN8,EDN1,PARK7	up_ACOR_VSMC
GO:0002040	0.0953	0.977	3	46	sprouting angiogenesis	BP	1	DLL1,GREM1,TBXA2R	up_AFEM_EC
GO:0010907	0.0953	0.987	2	10	positive regulation of glucose metabolic process	BP	1	SLC45A3,PTPN2	down_VSAP_EC
GO:0071156	0.0954	0.972	4	21	regulation of cell cycle arrest	BP	1	SLC29A1,CASP2,CDK4,BRCA1	down_ACOR_VSMC
GO:0006925	0.0954	0.988	2	6	inflammatory cell apoptotic process	BP	0.953	MEF2C,ITPKB	up_VCAV_EC
GO:0016556	0.0954	0.988	2	7	mRNA modification	BP	0.954	WTAP,ZC3H13	up_VCAV_EC
GO:0061053	0.0954	0.996	1	24	somite development	BP	1	SIX1	up_VFEM_EC
GO:1903531	0.095421936	0.97694	3	41	negative regulation of secretion by cell	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:0009071	0.095475794	0.99646	1	4	serine family amino acid catabolic process	BP	1	THNSL2	up_ACOR_EC
GO:0007179	0.0955	0.955	9	57	transforming growth factor beta receptor	BP	1	SMAD6,FERMT1,CITED2,CDKN2B,NPNT,FUT8,TGFBR1,DUSP22,HPGD	up_ACOR_VSMC
GO:0040018	0.0955	0.986	2	11	positive regulation of multicellular organism	BP	1	GPAM,PEX5	down_VCAV_EC
GO:0050926	0.0955	0.988	2	6	regulation of positive chemotaxis	BP	1	VEGFD,F2RL1	up_ACOR_VSMC
GO:0021953	0.0955	0.996	1	49	central nervous system neuron differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0021885	0.0955	0.996	1	24	forebrain cell migration	BP	1	EMX2	up_VSAP_VSMC
GO:0033692	0.0956	0.996	1	20	cellular polysaccharide biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC

GO:1903377	0.0956	0.998	1	2	negative regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:0062028	0.0956	1	1	1	regulation of stress granule assembly	BP	1	PRKAA2	up_ACOR_VSMC
GO:1904428	0.0956	1	1	1	negative regulation of tubulin deacetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0042592	0.0957	0.931	39	522	homeostatic process	BP	1	P4HB,SLC39A7,NR1H4,ENSCAFG00000013214,ERO1A,ENPP1,CASP3,ENSCAFG00000003477,PTPN11,EXOC5,ATP2B1,LRRC8A,PRCP,SMARCA4,SESN2,PTGS2,TMTC2,HIF1A,DNAJC10,NXN,PTPN2,NEO1,PLCL1,SMG7,PDIA4,CTNNB1,TFRC,APOE,LYN,STRAP,DDIT3,CLCN3,HTT,PRMT1,CALM1,DISC1,INHBA,KDM3A,HOMER1	down_VSAP_EC
GO:2000145	0.0957	0.933	34	279	regulation of cell motility	BP	1	VEGFD,LGR6,TCAF1,RECK,BMP4,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,EVL,SPINT2,TBX5,PRKCE,DAG1,APP,LAMA3,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,FAM107A,JAM3,WASL,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0006355	0.0957	0.981	3	974	regulation of transcription, DNA-	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0072015	0.0957	0.989	2	5	glomerular visceral epithelial cell	BP	0.954	PODXL,JAG1	up_VCAV_EC
GO:0072310	0.0957	0.989	2	5	glomerular epithelial cell development	BP	0.954	PODXL,JAG1	up_VCAV_EC
GO:1904424	0.0957	0.988	2	6	regulation of GTP binding	BP	0.954	ARHGAP28,STMN1	up_VCAV_EC
GO:1902430	0.0957	0.998	1	2	negative regulation of amyloid-beta formation	BP	1	APOE	down_VSAP_EC
GO:1902992	0.0957	0.998	1	2	negative regulation of amyloid precursor protein catabolic process	BP	1	APOE	down_VSAP_EC
GO:0002792	0.0957	0.996	1	29	negative regulation of peptide secretion	BP	1	NR1H4	up_VPUL_EC
GO:0021543	0.0957	0.996	1	49	pallium development	BP	1	SLIT2	up_VPUL_VSMC
GO:0045089	0.0958	0.996	1	70	positive regulation of innate immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0001678	0.0958	0.996	1	29	cellular glucose homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0061734	0.0958	1	1	1	parkin-mediated stimulation of mitophagy in response to	BP	1	MFN2	up_VSAP_EC
GO:1901605	0.0959	0.953	10	67	alpha-amino acid metabolic process	BP	1	PRDX4,ENSCAFG00000002977,NIT2,ERO1B,EGLN1,P4HA1,SARDH,AZIN2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0001818	0.0959	0.953	10	65	negative regulation of cytokine production	BP	1	WNT11,CD274,C5AR2,HDAC7,DLL1,ANXA4,F2RL1,NLRX1,CD83,MAPKBP1	up_VSAP_EC
GO:0006022	0.0959	0.971	4	29	aminoglycan metabolic process	BP	1	ENSCAFG00000032470,CEMIP2,CHSY1,EXT1	down_VSAP_EC
GO:0071772	0.0959	0.996	1	50	response to BMP	BP	1	GATA5	up_VPUL_VSMC
GO:0071773	0.0959	0.996	1	50	cellular response to BMP stimulus	BP	1	GATA5	up_VPUL_VSMC
GO:0072507	0.096	0.985	2	103	divalent inorganic cation homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0050892	0.096	0.988	2	6	intestinal absorption	BP	1	LIMA1,EZR	down_ACOR_VSMC
GO:0002063	0.096	0.996	1	18	chondrocyte development	BP	1	SULF1	down_ACOR_EC
GO:0050804	0.096	0.996	1	87	modulation of chemical synaptic transmission	BP	1	WNT7A	up_AORT_VSMC
GO:0099177	0.096	0.996	1	87	regulation of trans-synaptic signaling	BP	1	WNT7A	up_AORT_VSMC
GO:0042060	0.0961	0.952	10	103	wound healing	BP	1	SERPINE1,IFRD1,PRCP,HIF1A,ADAM17,APOE,LYN,SLC7A11,ITGB3,SDC4	down_VSAP_EC
GO:0001654	0.0961	0.954	9	110	eye development	BP	1	PDGFRB,FBN1,NAGLU,CHRDL1,THY1,GLI3,IRX5,RDH10,THRB	down_VCAV_EC
GO:0048880	0.0961	0.954	9	110	sensory system development	BP	1	PDGFRB,FBN1,NAGLU,CHRDL1,THY1,GLI3,IRX5,RDH10,THRB	down_VCAV_EC
GO:0150063	0.0961	0.954	9	110	visual system development	BP	1	PDGFRB,FBN1,NAGLU,CHRDL1,THY1,GLI3,IRX5,RDH10,THRB	down_VCAV_EC
GO:2001234	0.0961	0.956	8	75	negative regulation of apoptotic signaling	BP	1	ARHGEF2,SERPINE1,HYOU1,PTGS2,HIF1A,CTNNB1,HTT,NRP1	down_VSAP_EC
GO:0030030	0.0961	0.986	2	377	cell projection organization	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0006478	0.0961	1	1	1	peptidyl-tyrosine sulfation	BP	1	TPST2	up_ACOR_VSMC

GO:0007249	0.0961	0.996	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0046533	0.096175766	0.9964	1	4	negative regulation of photoreceptor cell	BP	1	SOX9	up_ACOR_EC
GO:0051336	0.0962	0.936	27	251	regulation of hydrolase activity	BP	0.959	SELE,AMOT,FGD6,MEF2C,RAPGEF1,CASP8,MTOR,BMP2,CHN2,PPP1R2,IQGAP2,PAK2,PRKD2,PTGS2,RAPGEF2,BCL10,HMGB1,TBC1D1,PMAIP1,ITGA6,KDM5A,ALS2,ENSCAFG00000002015,FKBP15,PSMB9,RABGAP1,USP6NL	up_VCAV_EC
GO:0061462	0.0962	0.996	1	15	protein localization to lysosome	BP	1	NEDD4	down_ACOR_EC
GO:0071326	0.0962	0.996	1	26	cellular response to monosaccharide stimulus	BP	1	NR1H4	up_APUL_EC
GO:0071331	0.0962	0.996	1	26	cellular response to hexose stimulus	BP	1	NR1H4	up_APUL_EC
GO:0043524	0.0962	0.996	1	39	negative regulation of neuron apoptotic process	BP	1	CHL1	up_VPOR_VSMC
GO:0007190	0.0962	1	1	1	activation of adenylate cyclase activity	BP	1	RAF1	up_VSAP_EC
GO:0071550	0.0962	1	1	1	death-inducing signaling complex assembly	BP	1	RAF1	up_VSAP_EC
GO:0007162	0.0963	0.954	9	66	negative regulation of cell adhesion	BP	0.96	PODXL,PELI1,ARG2,BMP2,ANGPT2,SWAP70,APOD,JAG1,HMGB1	up_VCAV_EC
GO:0045599	0.0963	0.978	3	19	negative regulation of fat cell differentiation	BP	1	ENPP1,TRIB3,DDIT3	down_VSAP_EC
GO:0007275	0.0963	0.984	3	1370	multicellular organism development	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0072710	0.0963	0.988	2	6	response to hydroxyurea	BP	1	RAD51,TIMELESS	down_ACOR_VSMC
GO:0097329	0.0963	0.988	2	6	response to antimetabolite	BP	1	RAD51,TIMELESS	down_ACOR_VSMC
GO:0050678	0.0963	0.996	1	117	regulation of epithelial cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:1905123	0.0963	1	1	1	regulation of glucosylceramidase	BP	1	SCARB2	up_ACOR_VSMC
GO:0060445	0.0963	0.996	1	13	branching involved in salivary gland	BP	1	SEMA3A	up_VPOR_EC
GO:0072524	0.0963	0.996	1	37	pyridine-containing compound metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0006083	0.0963	1	1	1	acetate metabolic process	BP	1	ACSS2	up_VSAP_EC
GO:0006208	0.0963	1	1	1	pyrimidine nucleobase catabolic process	BP	1	ALDH6A1	up_VSAP_EC
GO:0006210	0.0963	1	1	1	thymine catabolic process	BP	1	ALDH6A1	up_VSAP_EC
GO:0019427	0.0963	1	1	1	acetyl-CoA biosynthetic process from acetate	BP	1	ACSS2	up_VSAP_EC
GO:0019859	0.0963	1	1	1	thymine metabolic process	BP	1	ALDH6A1	up_VSAP_EC
GO:0038161	0.0963	1	1	1	prolactin signaling pathway	BP	1	CREBRF	up_VSAP_EC
GO:0043402	0.0963	1	1	1	glucocorticoid mediated signaling pathway	BP	1	CREBRF	up_VSAP_EC
GO:1900169	0.0963	1	1	1	regulation of glucocorticoid mediated	BP	1	CREBRF	up_VSAP_EC
GO:1900170	0.0963	1	1	1	negative regulation of glucocorticoid mediated signaling pathway	BP	1	CREBRF	up_VSAP_EC
GO:1902211	0.0963	1	1	1	regulation of prolactin signaling pathway	BP	1	CREBRF	up_VSAP_EC
GO:1902213	0.0963	1	1	1	positive regulation of prolactin signaling	BP	1	CREBRF	up_VSAP_EC
GO:0032268	0.0964	0.929	47	778	regulation of cellular protein metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,LRP1,DCN,PRNP,GLIPR2,BGN,LARP6,BMPR1A,RECK,CLIP3,AKT1S1,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,PLCL1,CSPG4,PRMT6,ASPN,EIF3K,THY1,PARK7,EEF2,ZFP36L1,MYDGF,SASH1,CLEC16A,ARL2BP,IFT57,MAVS,CDH2,GSDME,SPRED1,A2M,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,PACSIN3,EIF4EBP1	down_VCAV_EC
GO:0043297	0.0964	0.978	3	17	apical junction assembly	BP	1	WDR1,MYO1C,CTNNB1	down_VSAP_EC
GO:1903506	0.0964	0.981	3	977	regulation of nucleic acid-templated transcription	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0072358	0.0964	0.986	2	268	cardiovascular system development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0060575	0.0964	0.987	2	9	intestinal epithelial cell differentiation	BP	1	HIF1A,KLF5	down_VSAP_EC

GO:0001944	0.0964	0.986	2	263	vasculature development	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:1903899	0.0964	0.998	1	2	positive regulation of PERK-mediated unfolded protein response	BP	1	PTPN2	down_VSAP_EC
GO:0032637	0.0964	0.996	1	26	interleukin-8 production	BP	1	BPI	up_APUL_EC
GO:1900076	0.0964	0.996	1	29	regulation of cellular response to insulin	BP	1	NR1H4	up_VPUL_EC
GO:0007597	0.0964	1	1	1	blood coagulation, intrinsic pathway	BP	1	KLKB1	up_VSAP_EC
GO:0051919	0.0964	1	1	1	positive regulation of fibrinolysis	BP	1	KLKB1	up_VSAP_EC
GO:0019538	0.0965	0.923	97	1713	protein metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,CFD,PRNP,UBA52,GLIPR2,BGN,LARP6,COA1,BMPR1A,KRTCAP2,VKORC1,RECK,CLIP3,NUMBL,AKT1S1,TIMP2,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,HR,RPL23,RPL13,PCSK7,PLCL1,DDOST,CSPG4,PRMT6,GFPT2,ASPN,PIGS,HS3ST3B1,EIF3K,THY1,NECAB3,RNF216,WDR45,MRPL37,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RNPEP,RPL27,COPS7A,ARL2BP,IFT57,MAVS,MRPS11,CDH2,LOXL3,GSDME,CAMK2D,RPS27,FUT8,SPRED1,A2M,SEC61B,MAPRE3,CDKL2,HM13,PRKCSH,DDR2,SHC1,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,FBH1,GREM1,RPN2,KLHL29,ATOX1,LONP2,FOXO3,SOAT1,PACSIN3,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0009968	0.0965	0.929	46	392	negative regulation of signal transduction	BP	1	SMAD6,LBH,HTR2B,RASSF2,PRKAA2,MLLT3,FERMT1,BMP4,ELF1,CASTOR1,LATS2,ZNRF3,AR,PTGIR,NDRG2,ITPR1,F2RL1,DAPK1,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,RGS2,DAG1,PSEN1,SYNJ2BP,WWC2,DUSP22,SESN1,DUSP26,LRRC4,DDIT4,HERPUD1,INPP5K,BMT2,WFS1,SH3BP4,PARK7	up_ACOR_VSMC
GO:0090314	0.0965	0.986	2	11	positive regulation of protein targeting to	BP	1	PRNP,AKT2	down_VCAV_EC
GO:0045844	0.0965	0.996	1	24	positive regulation of striated muscle tissue	BP	1	CYP26B1	up_VFEM_EC
GO:0048636	0.0965	0.996	1	24	positive regulation of muscle organ	BP	1	CYP26B1	up_VFEM_EC
GO:0048634	0.0965	0.996	1	40	regulation of muscle organ development	BP	1	SHOX2	up_VFEM_VSMC
GO:0042044	0.0966	0.988	2	6	fluid transport	BP	1	ITPR1,INPP5K	up_ACOR_VSMC
GO:0030512	0.0966	0.996	1	24	negative regulation of transforming growth factor beta receptor	BP	1	CAV1	up_VSAP_VSMC
GO:1903845	0.0966	0.996	1	24	negative regulation of cellular response to transforming growth	BP	1	CAV1	up_VSAP_VSMC
GO:1903391	0.09664098	0.98511	2	21	regulation of adherens junction organization	BP	1	ARHGAP6,NRP1	up_ACOR_EC
GO:0050864	0.0967	0.963	6	36	regulation of B cell activation	BP	0.961	TNFAIP3,MEF2C,TLR4,PELI1,THOC1,ATP11C	up_VCAV_EC
GO:0043407	0.0967	0.978	3	19	negative regulation of MAP kinase activity	BP	1	APOE,LYN,CBLC	down_VSAP_EC
GO:2001141	0.0967	0.981	3	979	regulation of RNA biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0071300	0.0967	0.979	3	12	cellular response to retinoic acid	BP	1	OSR1,RARG,HTRA2	up_VSAP_EC
GO:0001914	0.0967	0.987	2	8	regulation of T cell mediated cytotoxicity	BP	0.961	IL7R,NECTIN2	up_VCAV_EC
GO:0031349	0.0967	0.996	1	90	positive regulation of defense response	BP	1	ESR1	up_AORT_VSMC
GO:0032602	0.0967	0.996	1	23	chemokine production	BP	1	TLR2	up_VSAP_VSMC
GO:0009314	0.0968	0.942	17	143	response to radiation	BP	1	USP1,HMGCR,SMC1A,NEDD4,INTS7,RAD54L,RAD51,AURKB,TOPBP1,MAP3K20,PLK3,PCNA,NOC2L,POLH,DTL,CDC25A,HMGN1	down_ACOR_VSMC
GO:1901362	0.0968	0.955	10	1293	organic cyclic compound biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,TNRC6B,NEDD4	down_ACOR_EC
GO:0014033	0.0968	0.967	5	30	neural crest cell differentiation	BP	0.961	EDNRB,MEF2C,EDN1,JAG1,HIF1A	up_VCAV_EC
GO:0033046	0.0968	0.972	4	21	negative regulation of sister chromatid	BP	0.961	RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC

GO:0033048	0.0968	0.972	4	21	negative regulation of mitotic sister chromatid	BP	0.961	RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0051985	0.0968	0.972	4	21	negative regulation of chromosome segregation	BP	0.961	RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0071825	0.0968	0.979	3	12	protein-lipid complex subunit organization	BP	1	LIPC,LCAT,SOAT1	up_VSAP_EC
GO:0071827	0.0968	0.979	3	12	plasma lipoprotein particle organization	BP	1	LIPC,LCAT,SOAT1	up_VSAP_EC
GO:1903778	0.0968	0.998	1	2	protein localization to vacuolar membrane	BP	1	SH3GLB1	down_VSAP_EC
GO:0050905	0.0968	0.996	1	26	neuromuscular process	BP	1	HOXA1	up_APUL_EC
GO:0002573	0.0968	0.996	1	71	myeloid leukocyte differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0001974	0.0968	0.996	1	13	blood vessel remodeling	BP	1	HOXA3	up_VPOR_EC
GO:0001757	0.0968	1	1	1	somite specification	BP	1	DLL1	up_VSAP_EC
GO:0002085	0.0968	1	1	1	inhibition of neuroepithelial cell	BP	1	DLL1	up_VSAP_EC
GO:0007386	0.0968	1	1	1	compartment pattern specification	BP	1	DLL1	up_VSAP_EC
GO:0014807	0.0968	1	1	1	regulation of somitogenesis	BP	1	DLL1	up_VSAP_EC
GO:0021688	0.0968	1	1	1	cerebellar molecular layer formation	BP	1	DLL1	up_VSAP_EC
GO:0021693	0.0968	1	1	1	cerebellar Purkinje cell layer structural	BP	1	DLL1	up_VSAP_EC
GO:0021698	0.0968	1	1	1	cerebellar cortex structural organization	BP	1	DLL1	up_VSAP_EC
GO:0045168	0.0968	1	1	1	cell-cell signaling involved in cell fate commitment	BP	1	DLL1	up_VSAP_EC
GO:0045608	0.0968	1	1	1	negative regulation of inner ear auditory receptor cell	BP	1	DLL1	up_VSAP_EC
GO:0045632	0.0968	1	1	1	negative regulation of mechanoreceptor	BP	1	DLL1	up_VSAP_EC
GO:0046331	0.0968	1	1	1	lateral inhibition	BP	1	DLL1	up_VSAP_EC
GO:0048630	0.0968	1	1	1	skeletal muscle tissue growth	BP	1	DLL1	up_VSAP_EC
GO:0048631	0.0968	1	1	1	regulation of skeletal muscle tissue growth	BP	1	DLL1	up_VSAP_EC
GO:0048633	0.0968	1	1	1	positive regulation of skeletal muscle tissue	BP	1	DLL1	up_VSAP_EC
GO:0060853	0.0968	1	1	1	Notch signaling pathway involved in arterial endothelial cell fate	BP	1	DLL1	up_VSAP_EC
GO:0097102	0.0968	1	1	1	endothelial tip cell fate specification	BP	1	DLL1	up_VSAP_EC
GO:2000981	0.0968	1	1	1	negative regulation of inner ear receptor cell	BP	1	DLL1	up_VSAP_EC
GO:0009308	0.096821377	0.98512	2	20	amine metabolic process	BP	1	NR1H4,AZIN2	up_ACOR_EC
GO:0046426	0.096870147	0.98511	2	20	negative regulation of JAK-STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:1904893	0.096870147	0.98511	2	20	negative regulation of STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:0003161	0.0969	0.988	2	6	cardiac conduction system development	BP	1	TBX5,BVES	up_ACOR_VSMC
GO:0007571	0.0969	1	1	1	age-dependent general metabolic decline	BP	1	CLN8	up_ACOR_VSMC
GO:0051935	0.0969	1	1	1	glutamate reuptake	BP	1	CLN8	up_ACOR_VSMC
GO:0001306	0.0969	1	1	1	age-dependent response to oxidative stress	BP	1	CLN8	up_ACOR_VSMC
GO:0021523	0.0969	1	1	1	somatic motor neuron differentiation	BP	1	CLN8	up_ACOR_VSMC
GO:0051933	0.0969	1	1	1	amino acid neurotransmitter	BP	1	CLN8	up_ACOR_VSMC
GO:1903672	0.096938297	0.98509	2	20	positive regulation of sprouting angiogenesis	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0038166	0.096972227	0.99634	1	4	angiotensin-activated signaling pathway	BP	1	ACTN2	up_ACOR_EC

GO:0030154	0.097	0.921	111	1040	cell differentiation	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,NAPEPLD,TWIST2,HOXA9,CDON,WNT11,HNF4A,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,RADIL,PPARGC1B,GJB5,IRX5,SLIT2,ZHX3,HOXD3,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,OSR1,MAP3K5,ADAMTSL4,WARS2,SAV1,KLF15,ANXA4,PLXNA4,ARL4A,RILPL2,ANKRD54,ZBTB16,TOX,ALDH6A1,RARG,STAT6,PATZ1,PLPP3,GTF3C5,F2RL1,DLX3,GLIS2,DDR2,ZFP36L1,PIK3R1,TIAM1,GAS1,BATF2,MYC,IRX3,ZEB1,SULF2,SHOX2,EEF2,RTN4RL1,HOXC10,MYD88,TFE3,LRP4,DPYSL2,GDPD5,ZADH2,DAGLB,HPS4,FRMD6,CLCN2,E2F4,FBXO7,NTN4,LIMD1,CDK9,CD83,NR2F6,FBLN1,ZFP36L2,PLEKHB2,RAF1,PNP,TAF8,NFIB,CYB5D2,CDNF,ANPEP,PQBP1,TTL,ACVRL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,MAP2K2,TGFBR2,CITED2,OGN,PIR,LBH,KEAP1,SOAT1,LATS2	up_VSAP_EC
GO:0050878	0.097	0.95	11	75	regulation of body fluid levels	BP	1	HNF4A,KLKB1,EMP2,CHRM1,PDGFD,HPSE,CLDN1,F2RL1,HPS4,FBLN1,CYBA	up_VSAP_EC
GO:0019229	0.097	0.979	3	12	regulation of vasoconstriction	BP	1	CHRM1,TBXA2R,AGTR1	up_VSAP_EC
GO:0060429	0.097	0.998	1	341	epithelium development	BP	1	GATA5	down_VFEM_VSMC
GO:1901135	0.0971	0.935	26	390	carbohydrate derivative metabolic process	BP	1	GPAM,DCN,ADCY6,KRTCAP2,CHID1,H6PD,DDOST,NT5C2,PGLS,ATP5MC1,GFPT2,UQCR10,PIGS,NECAB3,ADK,B4GALT1,PARK7,AMPD2,FUT8,ENSCAFG00000017708,ACSS2,PRKCSH,PCSK6,RPN2,SOAT1,ACAT1	down_VCAV_EC
GO:1901361	0.0971	0.941	18	154	organic cyclic compound catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,FEN1,RNASEH2B,SMG9,DIS3,FASTKD3,PDXP,AIFM1,ENSCAFG00000015189,RNASEH2C,NUDT1,EXOSC5,NUDT3	down_ACOR_VSMC
GO:0060284	0.0971	0.944	15	212	regulation of cell development	BP	1	NOTCH2,FBN1,BMPR1A,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,CDH2,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0034248	0.0971	0.951	10	125	regulation of cellular amide metabolic process	BP	1	PRNP,LARP6,SAMD4B,EIF3K,EEF2,ZFP36L1,ORMDL3,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0030335	0.0971	0.958	7	165	positive regulation of cell migration	BP	1	CMKLR1,ANGPT4,TWIST2,LRRC15,LGR6,CCL5,ADAM17	up_AFEM_EC
GO:0035556	0.0971	0.964	6	845	intracellular signal transduction	BP	1	NR1H4,MAPK10,PLCL1,ARHGEF26,NPNT,NTRK2	up_APUL_EC
GO:0046173	0.0971	0.972	4	19	polyol biosynthetic process	BP	1	PLCG2,PCBD1,PPIP5K1,PTS	up_ACOR_VSMC
GO:0010596	0.0971	0.995	1	21	negative regulation of endothelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:1902743	0.0971	0.996	1	16	regulation of lamellipodium	BP	1	PDPN	down_ACOR_EC
GO:0003002	0.0971	0.996	1	118	regionalization	BP	1	GATA5	down_VSAP_VSMC
GO:0021537	0.0971	0.996	1	73	telencephalon development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0048537	0.0971	1	1	1	mucosal-associated lymphoid tissue	BP	1	TOX	up_VSAP_EC
GO:0048541	0.0971	1	1	1	Peyer's patch development	BP	1	TOX	up_VSAP_EC
GO:0006468	0.0972	0.925	62	544	protein phosphorylation	BP	1	FGF13,ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,CDC7,HTR2B,RASSF2,MBP,PRKAA2,BMP4,FGFR2,TLR3,SH3RF2,LATS2,PDE5A,SASH1,FGF18,NDRG2,CDKN2B,GRK7,F2RL1,FAM129A,CAMK2D,DAPK1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,PIK3C3,CCL5,DDR2,PSKH1,DUSP22,EDN1,AKTIP,DUSP26,NOD2,LRRC4,LMTK2,PRKAG3,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,CRKL,CDKL2	up_ACOR_VSMC
GO:0050906	0.0972	0.979	3	13	detection of stimulus involved in sensory	BP	0.964	EPHB1,KIT,MMP24	up_VCAV_EC
GO:0009611	0.0972	0.985	2	122	response to wounding	BP	1	CAV1,F5	up_VSAP_VSMC
GO:0050684	0.0972	0.996	1	46	regulation of mRNA processing	BP	1	SRSF6	down_AFEM_EC
GO:0140074	0.0972	0.998	1	2	cardiac endothelial to mesenchymal transition	BP	1	SEMA3C	down_VCAV_EC
GO:0003150	0.0972	1	1	1	muscular septum morphogenesis	BP	1	FZD1	up_VSAP_EC
GO:0035425	0.0972	1	1	1	autocrine signaling	BP	1	FZD1	up_VSAP_EC

GO:0044338	0.0972	1	1	1	canonical Wnt signaling pathway involved in mesenchymal stem cell	BP	1	FZD1	up_VSAP_EC
GO:0060022	0.0972	1	1	1	hard palate development	BP	1	FZD1	up_VSAP_EC
GO:0045834	0.09728099	0.9763	3	41	positive regulation of lipid metabolic process	BP	1	NR1H4,CCDC3,PRKCD	up_ACOR_EC
GO:2000317	0.0973	0.998	1	2	negative regulation of T-helper 17 type immune	BP	1	LOXL3	down_VCAV_EC
GO:2000319	0.0973	0.998	1	2	regulation of T-helper 17 cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:2000320	0.0973	0.998	1	2	negative regulation of T-helper 17 cell	BP	1	LOXL3	down_VCAV_EC
GO:0034334	0.0973	0.998	1	2	adherens junction maintenance	BP	1	RASSF8	down_VCAV_EC
GO:2000316	0.0973	0.998	1	2	regulation of T-helper 17 type immune response	BP	1	LOXL3	down_VCAV_EC
GO:0043648	0.0973	0.995	1	26	dicarboxylic acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0046462	0.0973	1	1	1	monoacylglycerol metabolic process	BP	1	ABHD16A	up_VSAP_EC
GO:0052651	0.0973	1	1	1	monoacylglycerol catabolic process	BP	1	ABHD16A	up_VSAP_EC
GO:1901523	0.0973	1	1	1	icosanoid catabolic process	BP	1	ABHD16A	up_VSAP_EC
GO:1905344	0.0973	1	1	1	prostaglandin catabolic process	BP	1	ABHD16A	up_VSAP_EC
GO:0019538	0.097353617	0.9285	53	1713	protein metabolic process	BP	1	C7,NR1H4,BRSK1,PLCL1,PKIB,SOX9,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,IFI6,DUSP26,NOD2,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,CLU,CHMP4B,TP53INP2,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,HM13,PRKCD,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0051293	0.0974	0.978	3	13	establishment of spindle localization	BP	1	ZW10,CENPA,NDC80	down_ACOR_VSMC
GO:0045869	0.0974	1	1	1	negative regulation of single stranded viral RNA replication via double stranded DNA	BP	1	INPP5K	up_ACOR_VSMC
GO:2000466	0.0974	1	1	1	negative regulation of glycogen (starch) synthase	BP	1	INPP5K	up_ACOR_VSMC
GO:2001151	0.0974	1	1	1	regulation of renal water transport	BP	1	INPP5K	up_ACOR_VSMC
GO:2001153	0.0974	1	1	1	positive regulation of renal water transport	BP	1	INPP5K	up_ACOR_VSMC
GO:0007019	0.0974	0.996	1	13	microtubule depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0048536	0.0974	0.996	1	12	spleen development	BP	1	BARX1	up_VPOR_EC
GO:0035850	0.0974	0.995	1	25	epithelial cell differentiation involved in	BP	1	MTSS1	up_VFEM_EC
GO:0051262	0.0974	0.995	1	40	protein tetramerization	BP	1	FBP1	up_VFEM_VSMC
GO:0007624	0.0974	1	1	1	ultradian rhythm	BP	1	ENOX1	up_VSAP_EC
GO:0010638	0.0975	0.937	23	207	positive regulation of organelle organization	BP	1	FSCN1,SREBF1,HNRNPD,SDC1,BIRC5,NF2,AURKB,NEK2,FEN1,POC1A,BRCA1,RAC1,NUP62,PDXP,PLK4,IQGAP2,CDC42EP4,ENSCAFG00000005299,CORO1A,ARPC1B,TADA2A,UBE2C,CCT4	down_ACOR_VSMC
GO:0060537	0.0975	0.943	16	117	muscle tissue development	BP	1	TNNT2,ACTN2,BMP4,FGFR2,GJA1,PPARGC1A,CITED2,NEBL,ANKRD1,EGLN1,TBX20,TBX5,FRS2,CHD7,EDN1,BVES	up_ACOR_VSMC
GO:0002685	0.0975	0.961	6	55	regulation of leukocyte migration	BP	1	VEGFA,SERPINE1,MSN,ADAM17,MMP28,LYN	down_VSAP_EC
GO:0010811	0.0975	0.97	4	36	positive regulation of cell-substrate adhesion	BP	1	FBLN2,THY1,EDIL3,ECM2	down_VCAV_EC
GO:0051642	0.0975	0.978	3	13	centrosome localization	BP	1	EZR,ASPM,CEP83	down_ACOR_VSMC
GO:0061842	0.0975	0.978	3	13	microtubule organizing center localization	BP	1	EZR,ASPM,CEP83	down_ACOR_VSMC
GO:0060343	0.0975	0.986	2	11	trabecula formation	BP	1	THBS3,GREM1	down_VCAV_EC
GO:0051899	0.0975	0.995	1	22	membrane depolarization	BP	1	CAV1	up_VSAP_VSMC

GO:0003174	0.097575049	0.9963	1	4	mitral valve development	BP	1	SMAD6	up_ACOR_EC
GO:0051279	0.0976	0.977	3	19	regulation of release of sequestered calcium ion into cytosol	BP	1	LYN,HTT,CALM1	down_VSAP_EC
GO:0051494	0.0976	0.995	1	44	negative regulation of cytoskeleton organization	BP	1	TAOK1	up_AORT_EC
GO:0032088	0.0976	0.995	1	26	negative regulation of NF-kappaB transcription	BP	1	NR1H4	up_APUL_EC
GO:0046323	0.0976	0.995	1	26	glucose import	BP	1	NR1H4	up_APUL_EC
GO:0030258	0.0976	0.996	1	71	lipid modification	BP	1	CYP1A1	up_VCAV_VSMC
GO:0010862	0.0976	0.996	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	ACVR2A	up_VPOR_EC
GO:1901317	0.0976	1	1	1	regulation of flagellated sperm motility	BP	1	CFAP69	up_VSAP_EC
GO:1902093	0.0976	1	1	1	positive regulation of flagellated sperm motility	BP	1	CFAP69	up_VSAP_EC
GO:1905516	0.0976	1	1	1	positive regulation of fertilization	BP	1	CFAP69	up_VSAP_EC
GO:0010605	0.0977	0.926	54	745	negative regulation of macromolecule metabolic process	BP	1	PRICKLE1,NR1H4,PLK3,SERPINE1,SOCS5,ETV6,ENPP1,ERRFI1,SNX25,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,DNAJC10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,PEG3,SMG7,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,APOE,WWC3,KLF5,LYN,STRAP,DDIT3,CBLC,ATF3,VLDLR,REST,ZMYND8,EIF2S1,CDYL,PAK2,LRRTM2,A2M,HIF1AN,SIX4,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:0043588	0.0977	0.97	4	74	skin development	BP	1	HOXA7,DLL1,OVOL1,FOSL2	up_AFEM_EC
GO:0002833	0.0977	0.979	3	12	positive regulation of response to biotic	BP	1	CD274,SASH1,F2RL1	up_ACOR_VSMC
GO:0071310	0.0977	0.988	2	634	cellular response to organic substance	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0032000	0.0977	0.997	1	2	positive regulation of fatty acid beta-oxidation	BP	1	AKT2	down_VCAV_EC
GO:0017145	0.0977	0.996	1	13	stem cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:0032411	0.0977	0.995	1	24	positive regulation of transporter activity	BP	1	STIM1	up_VSAP_VSMC
GO:0008152	0.0978	0.967	11	3714	metabolic process	BP	1	ETFA,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15	down_AFEM_EC
GO:0002262	0.0978	0.961	6	54	myeloid cell homeostasis	BP	1	CASP3,HIF1A,PTPN2,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0006793	0.0978	0.964	6	948	phosphorus metabolic process	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0002709	0.0978	0.972	4	19	regulation of T cell mediated immunity	BP	1	DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0060538	0.0978	0.995	1	51	skeletal muscle organ development	BP	1	CITED2	down_VPOR_EC
GO:2000027	0.0978	0.996	1	72	regulation of animal organ morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0043568	0.097868676	0.99627	1	4	positive regulation of insulin-like growth factor receptor signaling	BP	1	CDH3	up_ACOR_EC
GO:0071310	0.0979	0.924	71	634	cellular response to organic substance	BP	1	SMAD6,ACTN2,IFNGR1,LEP,LBH,GATA5,SKP2,PRKAA2,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,EIF4A2,MED14,CASTOR1,LATS2,CITED2,TP53INP1,AR,SASH1,SLC2A5,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,ANKRD1,F2RL1,DAPK1,CTSB,AKAP6,CREBRF,NRP1,UBR1,PTPN22,NPNT,EVL,APLP1,PTGDR,SESN3,CCDC3,PRKCE,FRS2,AGRN,FUT8,PARP9,APP,PSEN1,TGFBR1,JUP,CCL5,NR3C1,DUSP22,RAB11B,HPGD,NOD2,LRRC4,ARID5B,FAM107A,DDIT4,ENSCAFG00000018360,HERPUD1,GNAQ,INPP5K,WFS1,DZIP3,SH3BP4,PARK7,STC2,CRKL	up_ACOR_VSMC
GO:1904375	0.0979	0.97	4	35	regulation of protein localization to cell	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978	down_VCAV_EC
GO:0007260	0.0979	0.977	3	19	tyrosine phosphorylation of STAT protein	BP	1	PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0048592	0.0979	0.995	1	53	eye morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0006613	0.0979	0.996	1	12	cotranslational protein targeting to membrane	BP	1	SRP54	up_VPOR_EC

GO:1900186	0.0979	1	1	1	negative regulation of clathrin-dependent	BP	1	UBQLN2	up_VSAP_EC
GO:1904020	0.0979	1	1	1	regulation of G protein-coupled receptor	BP	1	UBQLN2	up_VSAP_EC
GO:1904021	0.0979	1	1	1	negative regulation of G protein-coupled receptor	BP	1	UBQLN2	up_VSAP_EC
GO:0016125	0.098	0.959	7	41	sterol metabolic process	BP	1	LEP,LCAT,ABCA1,LIPE,APP,CLN8,LMF1	up_ACOR_VSMC
GO:0048812	0.098	0.985	2	151	neuron projection morphogenesis	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0042472	0.098	0.995	1	27	inner ear morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0010868	0.098	1	1	1	negative regulation of triglyceride biosynthetic	BP	0.969	ENSCAFG00000010596	up_VCAV_EC
GO:1902905	0.098	0.996	1	72	positive regulation of supramolecular fiber	BP	1	LIMK1	up_VCAV_VSMC
GO:0055072	0.098	0.995	1	30	iron ion homeostasis	BP	1	NEO1	up_VPUL_EC
GO:0030326	0.098	0.995	1	51	embryonic limb morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0035113	0.098	0.995	1	51	embryonic appendage morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0032755	0.098	0.995	1	24	positive regulation of interleukin-6 production	BP	1	TLR2	up_VSAP_VSMC
GO:0007423	0.0981	0.94	18	155	sensory organ development	BP	0.969	EPHB1,ARHGEF15,CHD7,DLL4,GATA3,EDN1,TMOD1,BMP2,PROX1,TSPAN12,SMARCA4,SLC25A25,JAG1,SKIL,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0010970	0.0981	0.956	8	48	transport along microtubule	BP	1	RHOT1,TMEM108,IFT43,APP,DYNC1I2,SUN1,DYNC1I1,ENSCAFG00000013536	up_ACOR_VSMC
GO:0001890	0.0981	0.956	8	51	placenta development	BP	1	LEP,FGFR2,CITED2,SPINT1,CTSB,EGLN1,ENSCAFG00000006238,SPINT2	up_ACOR_VSMC
GO:0099111	0.0981	0.956	8	48	microtubule-based transport	BP	1	RHOT1,TMEM108,IFT43,APP,DYNC1I2,SUN1,DYNC1I1,ENSCAFG00000013536	up_ACOR_VSMC
GO:0007215	0.0981	0.978	3	13	glutamate receptor signaling pathway	BP	0.969	RELN,MEF2C,GRM8	up_VCAV_EC
GO:0097205	0.0981	0.979	3	12	renal filtration	BP	1	EMP2,SULF2,JCHAIN	up_VSAP_EC
GO:0034641	0.0981	1	2	2171	cellular nitrogen compound metabolic	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071800	0.0981	0.987	2	8	podosome assembly	BP	1	FSCN1,MSN	down_VSAP_EC
GO:1901165	0.0981	0.997	1	2	positive regulation of trophoblast cell migration	BP	1	SYDE1	down_VCAV_EC
GO:1903984	0.0981	0.997	1	2	positive regulation of TRAIL-activated apoptotic signaling pathway	BP	1	ATF3	down_VSAP_EC
GO:0009966	0.0982	0.921	95	868	regulation of signal transduction	BP	1	SH3TC2,ADRA1B,TLR1,SMAD6,LGR6,LEP,LBH,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,ABCA1,ELF1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,ZNRF3,AR,PTGIR,SASH1,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ITPR1,LIMS2,ANKRD1,F2RL1,DAPK1,BNIP3,CRLF3,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,DMPK,NPNT,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,FRS2,RGS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,SIPA1L1,CCL5,WWC2,DUSP22,SIAH1,EDN1,SESN1,DUSP26,NOD2,LRRC4,DDIT4,DISC1,SH3RF3,SERINC3,USP20,HERPUD1,MAP3K7,INPP5K,BMT2,WFS1,SH3BP4,ENSCAFG00000029553,PARK7,IL18R1,CRKL	up_ACOR_VSMC
GO:0051049	0.0982	0.927	47	479	regulation of transport	BP	0.969	HCLS1,SELE,ATP8A1,MX2,PDGFB,TMEM173,RELN,PDE4D,IWS1,MEF2C,FERMT1,CHD7,TLR4,STC1,GATA3,EDN1,RAB11A,APLNR,RAB27A,CTTNBP2NL,SNCAIP,PPP3CA,YES1,ARG2,BMP2K,RSC1A1,ABCA1,KCNJ3,SH3GLB1,APOD,KCNJ2,CD200,FES,HIST1H1A,PLCG2,CTDSPL2,CREB1,GCC2,HMGB1,TBC1D1,SPTBN4,RIPK1,MCU,DNAJC13,HIF1A,RABGAP1,USP6NL	up_VCAV_EC
GO:0034121	0.0982	0.995	1	22	regulation of toll-like receptor signaling	BP	1	LYN	down_ACOR_EC
GO:0006063	0.0982	1	1	1	uronic acid metabolic process	BP	1	PRKCE	up_ACOR_VSMC
GO:0019585	0.0982	1	1	1	glucuronate metabolic process	BP	1	PRKCE	up_ACOR_VSMC

GO:0030473	0.0982	1	1	1	nuclear migration along microtubule	BP	1	SUN1	up_ACOR_VSMC
GO:0043578	0.0982	1	1	1	nuclear matrix organization	BP	1	SUN1	up_ACOR_VSMC
GO:0070197	0.0982	1	1	1	meiotic attachment of telomere to nuclear	BP	1	SUN1	up_ACOR_VSMC
GO:0090286	0.0982	1	1	1	cytoskeletal anchoring at nuclear membrane	BP	1	SUN1	up_ACOR_VSMC
GO:0090292	0.0982	1	1	1	nuclear matrix anchoring at nuclear membrane	BP	1	SUN1	up_ACOR_VSMC
GO:0097240	0.0982	1	1	1	chromosome attachment to the nuclear envelope	BP	1	SUN1	up_ACOR_VSMC
GO:2001029	0.0982	1	1	1	regulation of cellular glucuronidation	BP	1	PRKCE	up_ACOR_VSMC
GO:2001031	0.0982	1	1	1	positive regulation of cellular glucuronidation	BP	1	PRKCE	up_ACOR_VSMC
GO:0021817	0.0982	1	1	1	nucleokinesis involved in cell motility in cerebral cortex radial glia guided	BP	1	SUN1	up_ACOR_VSMC
GO:0035668	0.0982	1	1	1	TRAM-dependent toll-like receptor signaling	BP	1	PRKCE	up_ACOR_VSMC
GO:0035669	0.0982	1	1	1	TRAM-dependent toll-like receptor 4 signaling	BP	1	PRKCE	up_ACOR_VSMC
GO:0044821	0.0982	1	1	1	meiotic telomere tethering at nuclear	BP	1	SUN1	up_ACOR_VSMC
GO:0052695	0.0982	1	1	1	cellular glucuronidation	BP	1	PRKCE	up_ACOR_VSMC
GO:0045637	0.0982	0.996	1	73	regulation of myeloid cell differentiation	BP	1	HOXA9	up_AFEM_VSMC
GO:0006114	0.0982	1	1	1	glycerol biosynthetic process	BP	1	GOT1	up_VSAP_EC
GO:0006532	0.0982	1	1	1	aspartate biosynthetic process	BP	1	GOT1	up_VSAP_EC
GO:0019401	0.0982	1	1	1	alditol biosynthetic process	BP	1	GOT1	up_VSAP_EC
GO:0019550	0.0982	1	1	1	glutamate catabolic process to aspartate	BP	1	GOT1	up_VSAP_EC
GO:0019551	0.0982	1	1	1	glutamate catabolic process to 2-oxoglutarate	BP	1	GOT1	up_VSAP_EC
GO:0048812	0.0983	0.944	14	151	neuron projection morphogenesis	BP	1	SIPA1L1,SGK1,PTPN11,IFRD1,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0046165	0.0983	0.962	6	42	alcohol biosynthetic process	BP	0.969	SPTLC2,BMP2,ITPKB,PLCG2,GCH1,IMPA1	up_VCAV_EC
GO:0048813	0.0983	0.965	5	39	dendrite morphogenesis	BP	1	SIPA1L1,TNIK,VLDLR,NRP1,YWHAH	down_VSAP_EC
GO:0070885	0.0983	0.986	2	9	negative regulation of calcineurin-NFAT signaling	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:0106057	0.0983	0.986	2	9	negative regulation of calcineurin-mediated	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:0097195	0.0983	1	1	1	pilomotor reflex	BP	1	NPNT	up_ACOR_VSMC
GO:0061138	0.0983	0.996	1	73	morphogenesis of a branching epithelium	BP	1	EYA1	up_AFEM_VSMC
GO:0031346	0.0983	0.996	1	73	positive regulation of cell projection organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0002514	0.0983	1	1	1	B cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0002649	0.0983	1	1	1	regulation of tolerance induction to self antigen	BP	1	TGFBR2	up_VSAP_EC
GO:0002651	0.0983	1	1	1	positive regulation of tolerance induction to self	BP	1	TGFBR2	up_VSAP_EC
GO:0002661	0.0983	1	1	1	regulation of B cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0002663	0.0983	1	1	1	positive regulation of B cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0010310	0.0983	1	1	1	regulation of hydrogen peroxide metabolic	BP	1	ZNF205	up_VSAP_EC
GO:0010726	0.0983	1	1	1	positive regulation of hydrogen peroxide	BP	1	ZNF205	up_VSAP_EC
GO:0010728	0.0983	1	1	1	regulation of hydrogen peroxide biosynthetic	BP	1	ZNF205	up_VSAP_EC
GO:0010729	0.0983	1	1	1	positive regulation of hydrogen peroxide	BP	1	ZNF205	up_VSAP_EC
GO:0030167	0.0983	1	1	1	proteoglycan catabolic process	BP	1	HPSE	up_VSAP_EC
GO:0030200	0.0983	1	1	1	heparan sulfate proteoglycan catabolic	BP	1	HPSE	up_VSAP_EC
GO:0042128	0.0983	1	1	1	nitrate assimilation	BP	1	SUOX	up_VSAP_EC

GO:0042986	0.0983	1	1	1	positive regulation of amyloid precursor protein biosynthetic process	BP	1	SOAT1	up_VSAP_EC
GO:0062042	0.0983	1	1	1	regulation of cardiac epithelial to mesenchymal	BP	1	TGFBR2	up_VSAP_EC
GO:0062043	0.0983	1	1	1	positive regulation of cardiac epithelial to mesenchymal transition	BP	1	TGFBR2	up_VSAP_EC
GO:1905005	0.0983	1	1	1	regulation of epithelial to mesenchymal transition involved in endocardial	BP	1	TGFBR2	up_VSAP_EC
GO:1905007	0.0983	1	1	1	positive regulation of epithelial to mesenchymal transition involved in	BP	1	TGFBR2	up_VSAP_EC
GO:1905317	0.0983	1	1	1	inferior endocardial cushion morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:1990086	0.0983	1	1	1	lens fiber cell apoptotic process	BP	1	TGFBR2	up_VSAP_EC
GO:1990428	0.0983	1	1	1	miRNA transport	BP	1	TGFBR2	up_VSAP_EC
GO:2000563	0.0983	1	1	1	positive regulation of CD4-positive, alpha-beta T cell proliferation	BP	1	TGFBR2	up_VSAP_EC
GO:1901863	0.0983	0.995	1	25	positive regulation of muscle tissue	BP	1	SHOX2	up_VSAP_VSMC
GO:0051171	0.0984	0.953	11	1697	regulation of nitrogen compound metabolic	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0044342	0.0984	0.987	2	7	type B pancreatic cell proliferation	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0034091	0.0984	0.988	2	6	regulation of maintenance of sister chromatid	BP	0.969	SMC5,ATRX	up_VCAV_EC
GO:0034182	0.0984	0.988	2	6	regulation of maintenance of mitotic sister chromatid	BP	0.969	SMC5,ATRX	up_VCAV_EC
GO:0055123	0.0984	0.995	1	40	digestive system development	BP	1	BARX1	up_VPOR_VSMC
GO:0003281	0.0984	0.995	1	30	ventricular septum development	BP	1	TBX5	up_VPUL_EC
GO:0001819	0.098439234	0.96033	6	120	positive regulation of cytokine production	BP	1	FZD5,NOD2,IL33,PTGER4,MAVS,AGPAT2	up_ACOR_EC
GO:1901033	0.0985	0.997	1	2	positive regulation of response to reactive	BP	1	PARK7	down_VCAV_EC
GO:0008625	0.0985	0.995	1	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	ARHGEF2	up_VPUL_EC
GO:0021675	0.0985	0.995	1	29	nerve development	BP	1	HOXA3	up_VPUL_EC
GO:0033227	0.0985	1	1	1	dsRNA transport	BP	1	FLOT1	up_VSAP_EC
GO:1904924	0.0985	1	1	1	negative regulation of mitophagy in response to mitochondrial	BP	1	HTRA2	up_VSAP_EC
GO:0071612	0.0985	1	1	1	IP-10 production	BP	1	MAVS	up_VSAP_EC
GO:0071651	0.0985	1	1	1	positive regulation of chemokine (C-C motif)	BP	1	MAVS	up_VSAP_EC
GO:0071658	0.0985	1	1	1	regulation of IP-10 production	BP	1	MAVS	up_VSAP_EC
GO:0071660	0.0985	1	1	1	positive regulation of IP-10 production	BP	1	MAVS	up_VSAP_EC
GO:1902902	0.098578665	0.99622	1	4	negative regulation of autophagosome assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0008406	0.0986	0.953	9	57	gonad development	BP	1	GATA4,PRDX4,ATRX,CITED2,SPINK2,ARID5B,DMC1,LHX9,WDR48	up_ACOR_VSMC
GO:0045137	0.0986	0.953	9	57	development of primary sexual characteristics	BP	1	GATA4,PRDX4,ATRX,CITED2,SPINK2,ARID5B,DMC1,LHX9,WDR48	up_ACOR_VSMC
GO:0006807	0.0986	1	3	3221	nitrogen compound metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:2000036	0.0986	0.978	3	12	regulation of stem cell population maintenance	BP	1	SAV1,KDM2B,LBH	up_VSAP_EC
GO:0046640	0.0986	0.987	2	6	regulation of alpha-beta T cell proliferation	BP	1	CD274,PTPN22	up_ACOR_VSMC
GO:0010595	0.0986	0.995	1	52	positive regulation of endothelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0061302	0.0986	0.997	1	2	smooth muscle cell-matrix adhesion	BP	1	SERPINE1	down_VSAP_EC
GO:2000097	0.0986	0.997	1	2	regulation of smooth muscle cell-matrix	BP	1	SERPINE1	down_VSAP_EC
GO:2000098	0.0986	0.997	1	2	negative regulation of smooth muscle cell-matrix	BP	1	SERPINE1	down_VSAP_EC

GO:0006589	0.0986	1	1	1	octopamine biosynthetic process	BP	1	MOXD1	up_ACOR_VSMC
GO:0046333	0.0986	1	1	1	octopamine metabolic process	BP	1	MOXD1	up_ACOR_VSMC
GO:0051091	0.0986	0.996	1	87	positive regulation of DNA-binding transcription factor activity	BP	1	ESR1	up_AORT_VSMC
GO:0006957	0.0986	1	1	1	complement activation, alternative pathway	BP	1	CFD	up_VSAP_EC
GO:0007619	0.0986	1	1	1	courtship behavior	BP	1	THRB	up_VSAP_EC
GO:0007621	0.0986	1	1	1	negative regulation of female receptivity	BP	1	THRB	up_VSAP_EC
GO:0008050	0.0986	1	1	1	female courtship behavior	BP	1	THRB	up_VSAP_EC
GO:0031643	0.0986	1	1	1	positive regulation of myelination	BP	1	WASF3	up_VSAP_EC
GO:0033299	0.0986	1	1	1	secretion of lysosomal enzymes	BP	1	NAGPA	up_VSAP_EC
GO:0042480	0.0986	1	1	1	negative regulation of eye photoreceptor cell	BP	1	THRB	up_VSAP_EC
GO:0045924	0.0986	1	1	1	regulation of female receptivity	BP	1	THRB	up_VSAP_EC
GO:0060180	0.0986	1	1	1	female mating behavior	BP	1	THRB	up_VSAP_EC
GO:0070782	0.0986	1	1	1	phosphatidylserine exposure on apoptotic cell	BP	1	XKR8	up_VSAP_EC
GO:0097474	0.0986	1	1	1	retinal cone cell apoptotic process	BP	1	THRB	up_VSAP_EC
GO:0106064	0.0986	1	1	1	regulation of cobalamin metabolic process	BP	1	CLYBL	up_VSAP_EC
GO:1901401	0.0986	1	1	1	regulation of tetrapyrrole metabolic process	BP	1	CLYBL	up_VSAP_EC
GO:1902068	0.0986	1	1	1	regulation of sphingolipid mediated signaling	BP	1	PLPP3	up_VSAP_EC
GO:1903576	0.0986	1	1	1	response to L-arginine	BP	1	CASTOR1	up_VSAP_EC
GO:1903577	0.0986	1	1	1	cellular response to L-arginine	BP	1	CASTOR1	up_VSAP_EC
GO:1903837	0.0986	1	1	1	regulation of mRNA 3'-UTR binding	BP	1	CDK9	up_VSAP_EC
GO:1903839	0.0986	1	1	1	positive regulation of mRNA 3'-UTR binding	BP	1	CDK9	up_VSAP_EC
GO:2001226	0.0986	1	1	1	negative regulation of chloride transport	BP	1	GABRE	up_VSAP_EC
GO:0098629	0.0986	1	1	1	trans-Golgi network membrane organization	BP	1	AZIN2	up_VSAP_EC
GO:0071280	0.098663517	0.99621	1	4	cellular response to copper ion	BP	1	AQP1	up_ACOR_EC
GO:1901701	0.0987	0.932	30	271	cellular response to oxygen-containing compound	BP	0.969	CXCL8,CALCRL,TNFAIP3,PPARG,TNIP1,PDGFB,BAIAP2L1,PDE4D,MEF2C,RAPGEF1,TLR4,IRF8,YES1,MTOR,ABCA1,MAPK13,SMARCA4,NCK1,TIMELESS,GUCY1B1,RAPGEF2,CTNNA1,GCH1,BLM,RIPK1,PDGFD,HIF1A,NR4A1,ZEB1,ARHGEF2	up_VCAV_EC
GO:0051607	0.0987	0.953	9	58	defense response to virus	BP	1	MX1,TLR3,ISG15,F2RL1,BNIP3,PTPN22,PARP9,DDIT4,SERINC3	up_ACOR_VSMC
GO:0010804	0.0987	0.987	2	6	negative regulation of tumor necrosis factor-mediated signaling	BP	1	F2RL1,CCDC3	up_ACOR_VSMC
GO:0030166	0.0987	0.995	1	19	proteoglycan biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0071470	0.0987	0.995	1	13	cellular response to osmotic stress	BP	1	ARHGEF2	up_VPOR_EC
GO:0003206	0.0987	0.995	1	51	cardiac chamber morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0006145	0.0987	1	1	1	purine nucleobase catabolic process	BP	1	GDA	up_VSAP_EC
GO:0006147	0.0987	1	1	1	guanine catabolic process	BP	1	GDA	up_VSAP_EC
GO:0006539	0.0987	1	1	1	glutamate catabolic process via 2-oxoglutarate	BP	1	ADHFE1	up_VSAP_EC
GO:0035426	0.0987	1	1	1	extracellular matrix-cell signaling	BP	1	NTN4	up_VSAP_EC
GO:0046098	0.0987	1	1	1	guanine metabolic process	BP	1	GDA	up_VSAP_EC
GO:0060040	0.0987	1	1	1	retinal bipolar neuron differentiation	BP	1	IRX5	up_VSAP_EC

GO:0060668	0.0987	1	1	1	regulation of branching involved in salivary gland morphogenesis by extracellular matrix-	BP	1	NTN4	up_VSAP_EC
GO:2001144	0.0987	1	1	1	regulation of phosphatidylinositol-3,4,5-trisphosphate 5-	BP	1	BAG4	up_VSAP_EC
GO:2001145	0.0987	1	1	1	negative regulation of phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase activity	BP	1	BAG4	up_VSAP_EC
GO:0034769	0.0987	1	1	1	basement membrane disassembly	BP	1	CTSS	up_VSAP_EC
GO:0072008	0.098719431	0.99621	1	4	glomerular mesangial cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0072144	0.098719431	0.99621	1	4	glomerular mesangial cell development	BP	1	FOXC2	up_ACOR_EC
GO:0060767	0.098797999	0.9962	1	4	epithelial cell proliferation involved in prostate gland development	BP	1	SOX9	up_ACOR_EC
GO:0048518	0.0988	0.964	7	1676	positive regulation of biological process	BP	1	FGF5,HOXA3,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0002694	0.0988	0.984	2	126	regulation of leukocyte activation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0003186	0.0988	0.997	1	2	tricuspid valve morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0002253	0.0988	0.996	1	92	activation of immune response	BP	1	ESR1	up_AORT_VSMC
GO:0061448	0.0988	0.996	1	89	connective tissue development	BP	1	WNT7A	up_AORT_VSMC
GO:1901861	0.0988	0.995	1	41	regulation of muscle tissue development	BP	1	SHOX2	up_VFEM_VSMC
GO:0097529	0.0988	0.995	1	52	myeloid leukocyte migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0000053	0.0988	1	1	1	argininosuccinate metabolic process	BP	1	ASS1	up_VSAP_EC
GO:0000101	0.0988	1	1	1	sulfur amino acid transport	BP	1	CTNS	up_VSAP_EC
GO:0002174	0.0988	1	1	1	mammary stem cell proliferation	BP	1	LBH	up_VSAP_EC
GO:0002238	0.0988	1	1	1	response to molecule of fungal origin	BP	1	MYD88	up_VSAP_EC
GO:0002413	0.0988	1	1	1	tolerance induction to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0002461	0.0988	1	1	1	tolerance induction dependent upon immune	BP	1	CD274	up_VSAP_EC
GO:0002465	0.0988	1	1	1	peripheral tolerance induction	BP	1	CD274	up_VSAP_EC
GO:0002652	0.0988	1	1	1	regulation of tolerance induction dependent upon immune response	BP	1	CD274	up_VSAP_EC
GO:0002654	0.0988	1	1	1	positive regulation of tolerance induction dependent upon immune	BP	1	CD274	up_VSAP_EC
GO:0002658	0.0988	1	1	1	regulation of peripheral tolerance induction	BP	1	CD274	up_VSAP_EC
GO:0002660	0.0988	1	1	1	positive regulation of peripheral tolerance	BP	1	CD274	up_VSAP_EC
GO:0002843	0.0988	1	1	1	regulation of tolerance induction to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0002845	0.0988	1	1	1	positive regulation of tolerance induction to	BP	1	CD274	up_VSAP_EC
GO:0006041	0.0988	1	1	1	glucosamine metabolic process	BP	1	GNPDA1	up_VSAP_EC
GO:0006043	0.0988	1	1	1	glucosamine catabolic process	BP	1	GNPDA1	up_VSAP_EC
GO:0006102	0.0988	1	1	1	isocitrate metabolic process	BP	1	IDH1	up_VSAP_EC
GO:0006148	0.0988	1	1	1	inosine catabolic process	BP	1	PNP	up_VSAP_EC
GO:0006526	0.0988	1	1	1	arginine biosynthetic process	BP	1	ASS1	up_VSAP_EC
GO:0006542	0.0988	1	1	1	glutamine biosynthetic process	BP	1	GLUL	up_VSAP_EC
GO:0006738	0.0988	1	1	1	nicotinamide riboside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0006982	0.0988	1	1	1	response to lipid hydroperoxide	BP	1	MGST1	up_VSAP_EC
GO:0007231	0.0988	1	1	1	osmosensory signaling pathway	BP	1	OSR1	up_VSAP_EC

GO:0007284	0.0988	1	1	1	spermatogonial cell division	BP	1	ZNF449	up_VSAP_EC
GO:0008614	0.0988	1	1	1	pyridoxine metabolic process	BP	1	PNPO	up_VSAP_EC
GO:0008615	0.0988	1	1	1	pyridoxine biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:0009110	0.0988	1	1	1	vitamin biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:0009682	0.0988	1	1	1	induced systemic resistance	BP	1	MYD88	up_VSAP_EC
GO:0015677	0.0988	1	1	1	copper ion import	BP	1	STEAP3	up_VSAP_EC
GO:0015811	0.0988	1	1	1	L-cystine transport	BP	1	CTNS	up_VSAP_EC
GO:0018166	0.0988	1	1	1	C-terminal protein-tyrosinylation	BP	1	TTL	up_VSAP_EC
GO:0018322	0.0988	1	1	1	protein tyrosinylation	BP	1	TTL	up_VSAP_EC
GO:0019402	0.0988	1	1	1	galactitol metabolic process	BP	1	GALK1	up_VSAP_EC
GO:0021796	0.0988	1	1	1	cerebral cortex regionalization	BP	1	EMX2	up_VSAP_EC
GO:0023016	0.0988	1	1	1	signal transduction by trans-phosphorylation	BP	1	OSR1	up_VSAP_EC
GO:0032747	0.0988	1	1	1	positive regulation of interleukin-23 production	BP	1	MYD88	up_VSAP_EC
GO:0034356	0.0988	1	1	1	NAD biosynthesis via nicotinamide riboside salvage pathway	BP	1	PNP	up_VSAP_EC
GO:0034395	0.0988	1	1	1	regulation of transcription from RNA polymerase II promoter in response to	BP	1	HMOX1	up_VSAP_EC
GO:0035801	0.0988	1	1	1	adrenal cortex development	BP	1	CITED2	up_VSAP_EC
GO:0035802	0.0988	1	1	1	adrenal cortex formation	BP	1	CITED2	up_VSAP_EC
GO:0036376	0.0988	1	1	1	sodium ion export across plasma membrane	BP	1	FXYD1	up_VSAP_EC
GO:0042078	0.0988	1	1	1	germ-line stem cell division	BP	1	ZBTB16	up_VSAP_EC
GO:0042364	0.0988	1	1	1	water-soluble vitamin biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:0042732	0.0988	1	1	1	D-xylose metabolic process	BP	1	DHDH	up_VSAP_EC
GO:0042819	0.0988	1	1	1	vitamin B6 biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:0042823	0.0988	1	1	1	pyridoxal phosphate biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:0042843	0.0988	1	1	1	D-xylose catabolic process	BP	1	DHDH	up_VSAP_EC
GO:0042904	0.0988	1	1	1	9-cis-retinoic acid biosynthetic process	BP	1	DHRS9	up_VSAP_EC
GO:0042905	0.0988	1	1	1	9-cis-retinoic acid metabolic process	BP	1	DHRS9	up_VSAP_EC
GO:0043251	0.0988	1	1	1	sodium-dependent organic anion transport	BP	1	SLC10A6	up_VSAP_EC
GO:0046495	0.0988	1	1	1	nicotinamide riboside metabolic process	BP	1	PNP	up_VSAP_EC
GO:0048133	0.0988	1	1	1	male germ-line stem cell asymmetric division	BP	1	ZBTB16	up_VSAP_EC
GO:0048250	0.0988	1	1	1	iron import into the mitochondrion	BP	1	SLC25A28	up_VSAP_EC
GO:0048743	0.0988	1	1	1	positive regulation of skeletal muscle fiber	BP	1	SHOX2	up_VSAP_EC
GO:0051852	0.0988	1	1	1	disruption by host of symbiont cells	BP	1	F2RL1	up_VSAP_EC
GO:0051873	0.0988	1	1	1	killing by host of symbiont cells	BP	1	F2RL1	up_VSAP_EC
GO:0051956	0.0988	1	1	1	negative regulation of amino acid transport	BP	1	OSR1	up_VSAP_EC
GO:0061615	0.0988	1	1	1	glycolytic process through fructose-6-phosphate	BP	1	GALK1	up_VSAP_EC
GO:0061620	0.0988	1	1	1	glycolytic process through glucose-6-phosphate	BP	1	GALK1	up_VSAP_EC
GO:0061622	0.0988	1	1	1	glycolytic process through glucose-1-phosphate	BP	1	GALK1	up_VSAP_EC
GO:0061623	0.0988	1	1	1	glycolytic process from galactose	BP	1	GALK1	up_VSAP_EC
GO:0070291	0.0988	1	1	1	N-acylethanolamine metabolic process	BP	1	NAPEPLD	up_VSAP_EC

GO:0070292	0.0988	1	1	1	N-acylphosphatidylethanola	BP	1	NAPEPLD	up_VSAP_EC
GO:0070637	0.0988	1	1	1	pyridine nucleoside metabolic process	BP	1	PNP	up_VSAP_EC
GO:0070638	0.0988	1	1	1	pyridine nucleoside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0070682	0.0988	1	1	1	proteasome regulatory particle assembly	BP	1	PSMD9	up_VSAP_EC
GO:0070942	0.0988	1	1	1	neutrophil mediated cytotoxicity	BP	1	F2RL1	up_VSAP_EC
GO:0070943	0.0988	1	1	1	neutrophil mediated killing of symbiont cell	BP	1	F2RL1	up_VSAP_EC
GO:0070944	0.0988	1	1	1	neutrophil mediated killing of bacterium	BP	1	F2RL1	up_VSAP_EC
GO:0070945	0.0988	1	1	1	neutrophil mediated killing of gram-negative	BP	1	F2RL1	up_VSAP_EC
GO:0070948	0.0988	1	1	1	regulation of neutrophil mediated cytotoxicity	BP	1	F2RL1	up_VSAP_EC
GO:0070949	0.0988	1	1	1	regulation of neutrophil mediated killing of	BP	1	F2RL1	up_VSAP_EC
GO:0070950	0.0988	1	1	1	regulation of neutrophil mediated killing of	BP	1	F2RL1	up_VSAP_EC
GO:0070951	0.0988	1	1	1	regulation of neutrophil mediated killing of gram-	BP	1	F2RL1	up_VSAP_EC
GO:0070960	0.0988	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_VSAP_EC
GO:0070962	0.0988	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_VSAP_EC
GO:0070963	0.0988	1	1	1	positive regulation of neutrophil mediated killing of gram-negative	BP	1	F2RL1	up_VSAP_EC
GO:0071449	0.0988	1	1	1	cellular response to lipid hydroperoxide	BP	1	MGST1	up_VSAP_EC
GO:0071499	0.0988	1	1	1	cellular response to laminar fluid shear stress	BP	1	ASS1	up_VSAP_EC
GO:0072071	0.0988	1	1	1	kidney interstitial fibroblast differentiation	BP	1	OSR1	up_VSAP_EC
GO:0072141	0.0988	1	1	1	renal interstitial fibroblast development	BP	1	OSR1	up_VSAP_EC
GO:0072165	0.0988	1	1	1	anterior mesonephric tubule development	BP	1	OSR1	up_VSAP_EC
GO:0072166	0.0988	1	1	1	posterior mesonephric tubule development	BP	1	OSR1	up_VSAP_EC
GO:0072167	0.0988	1	1	1	specification of mesonephric tubule	BP	1	OSR1	up_VSAP_EC
GO:0072168	0.0988	1	1	1	specification of anterior mesonephric tubule	BP	1	OSR1	up_VSAP_EC
GO:0072169	0.0988	1	1	1	specification of posterior mesonephric tubule	BP	1	OSR1	up_VSAP_EC
GO:0072184	0.0988	1	1	1	renal vesicle progenitor cell differentiation	BP	1	OSR1	up_VSAP_EC
GO:0072185	0.0988	1	1	1	metanephric cap development	BP	1	OSR1	up_VSAP_EC
GO:0072186	0.0988	1	1	1	metanephric cap morphogenesis	BP	1	OSR1	up_VSAP_EC
GO:0072194	0.0988	1	1	1	kidney smooth muscle tissue development	BP	1	OSR1	up_VSAP_EC
GO:0072208	0.0988	1	1	1	metanephric smooth muscle tissue	BP	1	OSR1	up_VSAP_EC
GO:0072258	0.0988	1	1	1	metanephric interstitial fibroblast differentiation	BP	1	OSR1	up_VSAP_EC
GO:0072259	0.0988	1	1	1	metanephric interstitial fibroblast development	BP	1	OSR1	up_VSAP_EC
GO:0072566	0.0988	1	1	1	chemokine (C-X-C motif) ligand 1 production	BP	1	MYD88	up_VSAP_EC
GO:0086013	0.0988	1	1	1	membrane repolarization during cardiac muscle cell action potential	BP	1	KCNE3	up_VSAP_EC
GO:0090094	0.0988	1	1	1	metanephric cap mesenchymal cell proliferation involved in	BP	1	OSR1	up_VSAP_EC
GO:0090107	0.0988	1	1	1	regulation of high-density lipoprotein particle	BP	1	LCAT	up_VSAP_EC
GO:0090198	0.0988	1	1	1	negative regulation of chemokine secretion	BP	1	F2RL1	up_VSAP_EC
GO:0097029	0.0988	1	1	1	mature conventional dendritic cell	BP	1	F2RL1	up_VSAP_EC
GO:0097039	0.0988	1	1	1	protein linear polyubiquitination	BP	1	RBCK1	up_VSAP_EC

GO:0097403	0.0988	1	1	1	cellular response to raffinose	BP	1	ZFP36L1	up_VSAP_EC
GO:0097712	0.0988	1	1	1	vesicle targeting, trans-Golgi to periciliary membrane compartment	BP	1	CEP19	up_VSAP_EC
GO:0098728	0.0988	1	1	1	germline stem cell asymmetric division	BP	1	ZBTB16	up_VSAP_EC
GO:0098915	0.0988	1	1	1	membrane repolarization during ventricular cardiac muscle cell action	BP	1	KCNE3	up_VSAP_EC
GO:0106135	0.0988	1	1	1	negative regulation of cardiac muscle cell	BP	1	KCNE3	up_VSAP_EC
GO:1900135	0.0988	1	1	1	positive regulation of renin secretion into blood	BP	1	F2RL1	up_VSAP_EC
GO:1901492	0.0988	1	1	1	positive regulation of lymphangiogenesis	BP	1	CCBE1	up_VSAP_EC
GO:1901545	0.0988	1	1	1	response to raffinose	BP	1	ZFP36L1	up_VSAP_EC
GO:1902302	0.0988	1	1	1	regulation of potassium ion export	BP	1	KCNE3	up_VSAP_EC
GO:1902303	0.0988	1	1	1	negative regulation of potassium ion export	BP	1	KCNE3	up_VSAP_EC
GO:1903259	0.0988	1	1	1	exon-exon junction complex disassembly	BP	1	PYM1	up_VSAP_EC
GO:1903276	0.0988	1	1	1	regulation of sodium ion export across plasma	BP	1	FXYD1	up_VSAP_EC
GO:1903278	0.0988	1	1	1	positive regulation of sodium ion export across	BP	1	FXYD1	up_VSAP_EC
GO:1903674	0.0988	1	1	1	regulation of cap-dependent translational	BP	1	NCK1	up_VSAP_EC
GO:1903676	0.0988	1	1	1	positive regulation of cap-dependent translational	BP	1	NCK1	up_VSAP_EC
GO:1903764	0.0988	1	1	1	regulation of potassium ion export across plasma	BP	1	KCNE3	up_VSAP_EC
GO:1903765	0.0988	1	1	1	negative regulation of potassium ion export across plasma membrane	BP	1	KCNE3	up_VSAP_EC
GO:1903946	0.0988	1	1	1	negative regulation of ventricular cardiac muscle cell action potential	BP	1	KCNE3	up_VSAP_EC
GO:1904580	0.0988	1	1	1	regulation of intracellular mRNA localization	BP	1	ZFP36L1	up_VSAP_EC
GO:1904582	0.0988	1	1	1	positive regulation of intracellular mRNA	BP	1	ZFP36L1	up_VSAP_EC
GO:1904674	0.0988	1	1	1	positive regulation of somatic stem cell	BP	1	LBH	up_VSAP_EC
GO:1904675	0.0988	1	1	1	regulation of somatic stem cell division	BP	1	LBH	up_VSAP_EC
GO:1904677	0.0988	1	1	1	positive regulation of somatic stem cell division	BP	1	LBH	up_VSAP_EC
GO:1905024	0.0988	1	1	1	regulation of membrane repolarization during ventricular cardiac muscle cell action potential	BP	1	KCNE3	up_VSAP_EC
GO:1905025	0.0988	1	1	1	negative regulation of membrane repolarization during ventricular cardiac muscle cell action	BP	1	KCNE3	up_VSAP_EC
GO:1905031	0.0988	1	1	1	regulation of membrane repolarization during cardiac muscle cell action	BP	1	KCNE3	up_VSAP_EC
GO:1905032	0.0988	1	1	1	negative regulation of membrane repolarization during cardiac muscle cell	BP	1	KCNE3	up_VSAP_EC
GO:1905404	0.0988	1	1	1	positive regulation of activated CD8-positive, alpha-beta T cell	BP	1	CD274	up_VSAP_EC
GO:1905407	0.0988	1	1	1	regulation of creatine transmembrane transporter activity	BP	1	OSR1	up_VSAP_EC
GO:1905408	0.0988	1	1	1	negative regulation of creatine transmembrane transporter activity	BP	1	OSR1	up_VSAP_EC
GO:2000035	0.0988	1	1	1	regulation of stem cell division	BP	1	LBH	up_VSAP_EC
GO:2000101	0.0988	1	1	1	regulation of mammary stem cell proliferation	BP	1	LBH	up_VSAP_EC
GO:2000103	0.0988	1	1	1	positive regulation of mammary stem cell	BP	1	LBH	up_VSAP_EC

GO:2000338	0.0988	1	1	1	regulation of chemokine (C-X-C motif) ligand 1	BP	1	MYD88	up_VSAP_EC
GO:2000346	0.0988	1	1	1	negative regulation of hepatocyte proliferation	BP	1	LIMS2	up_VSAP_EC
GO:2000543	0.0988	1	1	1	positive regulation of gastrulation	BP	1	OSR1	up_VSAP_EC
GO:2001186	0.0988	1	1	1	negative regulation of CD8-positive, alpha-beta T cell activation	BP	1	CD274	up_VSAP_EC
GO:0048874	0.0988	1	1	1	host-mediated regulation of intestinal microbiota	BP	1	NAPEPLD	up_VSAP_EC
GO:0051024	0.0988	1	1	1	positive regulation of immunoglobulin secretion	BP	1	STX4	up_VSAP_EC
GO:0070961	0.0988	1	1	1	positive regulation of neutrophil mediated	BP	1	F2RL1	up_VSAP_EC
GO:0003097	0.098885674	0.99619	1	4	renal water transport	BP	1	AQP1	up_ACOR_EC
GO:0010562	0.0989	0.935	25	312	positive regulation of phosphorus metabolic process	BP	1	ARHGEF2,VEGFA,NR1H4,JCAD,BCAR3,PTPN11,ILK,PPP1R12A,PTGS2,TNIK,YES1,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,SH3GLB1,CALM1,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0045937	0.0989	0.935	25	312	positive regulation of phosphate metabolic process	BP	1	ARHGEF2,VEGFA,NR1H4,JCAD,BCAR3,PTPN11,ILK,PPP1R12A,PTGS2,TNIK,YES1,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,SH3GLB1,CALM1,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0010927	0.0989	0.97	4	28	cellular component assembly involved in	BP	1	ACTN1,WDR1,SIX4,MYBPC2	down_VSAP_EC
GO:0048870	0.0989	0.977	3	451	cell motility	BP	1	CHL1,BAMBI,C3AR1	up_VPOR_VSMC
GO:0051674	0.0989	0.977	3	451	localization of cell	BP	1	CHL1,BAMBI,C3AR1	up_VPOR_VSMC
GO:0045668	0.0989	0.986	2	11	negative regulation of osteoblast differentiation	BP	1	TWIST2,GREM1	down_VCAV_EC
GO:0080134	0.0989	0.986	2	386	regulation of response to stress	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:2000027	0.0989	0.995	1	72	regulation of animal organ morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0072001	0.099	0.964	5	104	renal system development	BP	1	IRX3,DLL1,GREM1,OVOL1,GCNT4	up_AFEM_EC
GO:0007596	0.099	0.976	3	47	blood coagulation	BP	1	F5,F3,TFPI2	up_AFEM_EC
GO:0007389	0.099	0.984	2	137	pattern specification process	BP	1	TBX5,HOXA3	up_APUL_EC
GO:0070493	0.099	0.987	2	6	thrombin-activated receptor signaling	BP	0.969	IQGAP2,STMN1	up_VCAV_EC
GO:2001234	0.099	0.995	1	75	negative regulation of apoptotic signaling	BP	1	EYA1	up_AFEM_VSMC
GO:0016125	0.099	0.995	1	41	sterol metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0017015	0.099	0.995	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	BAMBI	up_VPOR_VSMC
GO:1903844	0.099	0.995	1	40	regulation of cellular response to transforming growth factor beta	BP	1	BAMBI	up_VPOR_VSMC
GO:0009206	0.099	0.995	1	39	purine ribonucleoside triphosphate biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0010817	0.0991	0.944	14	102	regulation of hormone levels	BP	1	LEP,TM7SF3,ERO1B,PRKCE,DKKL1,SCG5,PCSK6,CHD7,CCL5,RAB11B,EDN1,PFKL,PARK7,STC2	up_ACOR_VSMC
GO:1901576	0.0991	0.95	13	1877	organic substance biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,TNRC6B,NEDD4	down_ACOR_EC
GO:0007626	0.0991	0.955	8	53	locomotory behavior	BP	0.969	CHD7,HOXB8,TMOD1,NAV2,PREX2,SPTBN4,ALS2,ALDH1A3	up_VCAV_EC
GO:0033619	0.0991	0.971	4	19	membrane protein proteolysis	BP	1	PTPN3,DAG1,PSEN1,ERAP1	up_ACOR_VSMC
GO:0006936	0.0991	0.969	4	74	muscle contraction	BP	1	CHRM2,HTR1D,TBXA2R,DMPK	up_AFEM_EC
GO:0009913	0.0991	0.976	3	47	epidermal cell differentiation	BP	1	HOXA7,DLL1,FOSL2	up_AFEM_EC
GO:0002686	0.0991	0.978	3	12	negative regulation of leukocyte migration	BP	1	HOXA7,C5AR2,SLIT2	up_VSAP_EC
GO:0090230	0.0991	1	1	1	regulation of centromere complex assembly	BP	0.969	SENP6	up_VCAV_EC
GO:0090234	0.0991	1	1	1	regulation of kinetochore assembly	BP	0.969	SENP6	up_VCAV_EC

GO:0009566	0.0991	0.995	1	24	fertilization	BP	1	HOXA9	up_VFEM_EC
GO:0030048	0.0991	0.995	1	23	actin filament-based movement	BP	1	CAV1	up_VSAP_VSMC
GO:0048010	0.099100922	0.98456	2	20	vascular endothelial growth factor receptor	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0050832	0.09918758	0.99617	1	4	defense response to fungus	BP	1	RARRES2	up_ACOR_EC
GO:0016052	0.0992	0.962	6	34	carbohydrate catabolic process	BP	1	ENOSF1,PYGM,ALDOC,DDIT4,NEU3,GAA	up_ACOR_VSMC
GO:0042129	0.0992	0.97	4	35	regulation of T cell proliferation	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0008625	0.0992	0.97	4	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	ARHGEF2,SERPINE1,ATF3,MADD	down_VSAP_EC
GO:1990089	0.0992	0.987	2	6	response to nerve growth factor	BP	0.969	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:1990090	0.0992	0.987	2	6	cellular response to nerve growth factor stimulus	BP	0.969	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:0030334	0.0992	0.985	2	267	regulation of cell migration	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0009913	0.0992	0.995	1	47	epidermal cell differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0007166	0.0992	1	1	686	cell surface receptor signaling pathway	BP	1	GATA5	down_AFEM_VSMC
GO:0055065	0.0992	0.996	1	145	metal ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0022008	0.0993	0.944	14	406	neurogenesis	BP	1	IRX3,IRX5,HOXC10,LEP,DLL1,VXN,PLXNA4,NEFH,THRB,LGI4,CAMK2A,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0051099	0.0993	0.952	9	70	positive regulation of binding	BP	0.969	TMEM173,MEF2C,GATA3,RALB,BMP2,STMN1,MFNG,RAPGEF2,HMGB1	up_VCAV_EC
GO:1900182	0.0993	0.962	6	33	positive regulation of protein localization to	BP	1	LEP,PTPN22,PARP9,PSEN1,JUP,PARK7	up_ACOR_VSMC
GO:0032387	0.0993	0.971	4	20	negative regulation of intracellular transport	BP	1	FERMT1,OS9,INPP5K,PARK7	up_ACOR_VSMC
GO:0003219	0.0993	1	1	1	cardiac right ventricle formation	BP	1	SMARCD3	up_ACOR_VSMC
GO:0014722	0.0993	1	1	1	regulation of skeletal muscle contraction by calcium ion signaling	BP	1	DMPK	up_ACOR_VSMC
GO:0014852	0.0993	1	1	1	regulation of skeletal muscle contraction by neural stimulation via	BP	1	DMPK	up_ACOR_VSMC
GO:0014853	0.0993	1	1	1	regulation of excitatory postsynaptic membrane potential involved in skeletal muscle	BP	1	DMPK	up_ACOR_VSMC
GO:0051823	0.0993	1	1	1	regulation of synapse structural plasticity	BP	1	DMPK	up_ACOR_VSMC
GO:0010544	0.099362248	0.99616	1	4	negative regulation of platelet activation	BP	1	PRKCD	up_ACOR_EC
GO:0060429	0.0994	0.97	4	341	epithelium development	BP	1	ACVRL1,PDPN,HOXA7,SULF1	down_ACOR_EC
GO:0001890	0.0994	0.995	1	51	placenta development	BP	1	CITED2	down_VPOR_EC
GO:0034454	0.0994	0.997	1	2	microtubule anchoring at centrosome	BP	1	HOOK3	down_VSAP_EC
GO:0045637	0.0994	0.995	1	73	regulation of myeloid cell differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0022411	0.0995	0.946	12	130	cellular component disassembly	BP	1	ARHGEF2,PLK3,FSCN1,SMARCA4,WDR1,KIF5B,HIF1A,BNIP3,CDC37,HTT,CAPG,MID1	down_VSAP_EC
GO:0034504	0.0995	0.952	9	111	protein localization to nucleus	BP	1	ENSCAFG00000014978,SNUPN,TRIM8,GLI3,PARK7,ARL2BP,MAVS,SEC61B,GLIS2	down_VCAV_EC
GO:0033077	0.0995	0.971	4	22	T cell differentiation in thymus	BP	0.969	IL7R,GATA3,ITPKB,ZEB1	up_VCAV_EC
GO:0050858	0.0995	0.987	2	6	negative regulation of antigen receptor-mediated signaling	BP	1	ELF1,DUSP22	up_ACOR_VSMC
GO:0050860	0.0995	0.987	2	6	negative regulation of T cell receptor signaling	BP	1	ELF1,DUSP22	up_ACOR_VSMC
GO:0034754	0.0995	0.995	1	24	cellular hormone metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0060420	0.0996	0.971	4	18	regulation of heart growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:2000001	0.0996	0.978	3	13	regulation of DNA damage checkpoint	BP	1	WDR76,RNASEH2B,DDX39B	down_ACOR_VSMC
GO:0072358	0.0996	0.985	2	268	cardiovascular system development	BP	1	HOXA3,SLIT2	up_VPUL_VSMC

GO:1903510	0.0996	0.995	1	22	mucopolysaccharide metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0042632	0.0996	0.995	1	27	cholesterol homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0009855	0.0996	0.995	1	42	determination of bilateral symmetry	BP	1	NKX2-5	up_VPOR_VSMC
GO:1901655	0.099695033	0.98441	2	20	cellular response to ketone	BP	1	AQP1,PTGER4	up_ACOR_EC
GO:0030334	0.0997	0.931	32	267	regulation of cell migration	BP	1	HOXA7,TWIST2,WNT11,FAM107A,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,FUZ,PDGFD,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,SASH1,MYD88,ZNF580,STX4,ACVRL1,NCK1,HMOX1,TGFBR2,BAG4	up_VSAP_EC
GO:0050673	0.0997	0.946	12	135	epithelial cell proliferation	BP	1	VEGFA,SULF1,SPARC,JCAD,TGFBR1,ADAM17,MAGED1,CTNNB1,APOE,STRAP,NR4A1,SIX4	down_VSAP_EC
GO:0061351	0.0997	0.961	6	50	neural precursor cell proliferation	BP	1	ARHGEF2,HOOK3,ILK,HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0010592	0.0997	0.987	2	7	positive regulation of lamellipodium assembly	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:1903204	0.0997	0.986	2	9	negative regulation of oxidative stress-induced	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:0003012	0.0997	0.996	1	90	muscle system process	BP	1	ARG2	up_AORT_VSMC
GO:1903725	0.0997	0.995	1	30	regulation of phospholipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0090257	0.0997	0.995	1	52	regulation of muscle system process	BP	1	GATA5	up_VPUL_VSMC
GO:1903409	0.0997	0.995	1	24	reactive oxygen species biosynthetic process	BP	1	CAV1	up_VSAP_VSMC
GO:0050905	0.0998	0.966	5	26	neuromuscular process	BP	1	GLRB,POMK,APP,CLN8,GAA	up_ACOR_VSMC
GO:0010880	0.0998	0.987	2	7	regulation of release of sequestered calcium ion into cytosol by	BP	0.969	PDE4D,CHD7	up_VCAV_EC
GO:0014808	0.0998	0.987	2	7	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	0.969	PDE4D,CHD7	up_VCAV_EC
GO:1903514	0.0998	0.987	2	7	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	0.969	PDE4D,CHD7	up_VCAV_EC
GO:0010615	0.0998	1	1	1	positive regulation of cardiac muscle adaptation	BP	0.969	PPP3CA	up_VCAV_EC
GO:0014744	0.0998	1	1	1	positive regulation of muscle adaptation	BP	0.969	PPP3CA	up_VCAV_EC
GO:1903244	0.0998	1	1	1	positive regulation of cardiac muscle hypertrophy in response	BP	0.969	PPP3CA	up_VCAV_EC
GO:1905203	0.0998	1	1	1	regulation of connective tissue replacement	BP	0.969	PPP3CA	up_VCAV_EC
GO:1905205	0.0998	1	1	1	positive regulation of connective tissue	BP	0.969	PPP3CA	up_VCAV_EC
GO:0048563	0.099850546	0.99612	1	4	post-embryonic animal organ morphogenesis	BP	1	EFEMP1	up_ACOR_EC
GO:0009725	0.0999	0.935	24	188	response to hormone	BP	1	ACTN2,LEP,LBH,SKP2,PRKAA2,BMP4,MED14,LATS2,RERG,AR,FAM210B,ADCY6,CTSB,CREBRF,PTGDR,SESN3,PRKCE,AGRN,NR3C1,FAM107A,DDIT4,GNAQ,INPP5K,PARK7	up_ACOR_VSMC
GO:0046626	0.0999	0.977	3	18	regulation of insulin receptor signaling	BP	1	NR1H4,ENPP1,PTPN2	down_VSAP_EC
GO:0071470	0.0999	0.978	3	13	cellular response to osmotic stress	BP	0.969	LRRC8D,PTGS2,ARHGEF2	up_VCAV_EC
GO:0006211	0.0999	1	1	1	5-methylcytosine catabolic process	BP	0.969	TET2	up_VCAV_EC
GO:0019857	0.0999	1	1	1	5-methylcytosine metabolic process	BP	0.969	TET2	up_VCAV_EC
GO:0043588	0.0999	0.995	1	74	skin development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0002483	0.099918162	0.99611	1	4	antigen processing and presentation of endogenous peptide	BP	1	TAPBP	up_ACOR_EC
GO:0019885	0.099918162	0.99611	1	4	antigen processing and presentation of endogenous peptide	BP	1	TAPBP	up_ACOR_EC
GO:0051046	0.1	0.936	22	174	regulation of secretion	BP	1	EXPH5,TLR1,LEP,HTR2B,MBP,FBXL20,FERMT1,TM7SF3,CD274,ANKRD1,F2RL1,PTPN22,PRKCE,SCG5,CHD7,CCL5,EDN1,KCNC4,NOD2,SCAMP5,PREPL,PFKL	up_ACOR_VSMC

GO:0044271	0.1	0.952	11	1501	cellular nitrogen compound biosynthetic	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,TNRC6B,NEDD4	down_ACOR_EC
GO:0065008	0.1	0.959	7	1056	regulation of biological quality	BP	1	NR1H4,HTR7,HOXA3,PLCL1,PCSK1N,SLITRK5,NTRK2	up_APUL_EC
GO:0007431	0.1	0.971	4	19	salivary gland development	BP	1	FGF7,CLCN2,NTN4,NFIB	up_VSAP_EC
GO:0001944	0.1	0.976	3	263	vasculature development	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0006820	0.1	0.984	2	109	anion transport	BP	1	PDPN,ACSL3	down_ACOR_EC
GO:0015695	0.1	0.987	2	6	organic cation transport	BP	1	PSEN1,SLC25A20	up_ACOR_VSMC
GO:0034143	0.1	0.987	2	6	regulation of toll-like receptor 4 signaling	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0095500	0.1	0.987	2	6	acetylcholine receptor signaling pathway	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:1903831	0.1	0.987	2	6	signal transduction involved in cellular response to ammonium	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:1905144	0.1	0.987	2	6	response to acetylcholine	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:1905145	0.1	0.987	2	6	cellular response to acetylcholine	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:0071417	0.1	0.984	2	142	cellular response to organonitrogen	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0048729	0.1	0.984	2	209	tissue morphogenesis	BP	1	NKX2-5,ANKRD6	up_VPOR_VSMC
GO:0010559	0.1	0.987	2	6	regulation of glycoprotein biosynthetic process	BP	1	NECAB3,SOAT1	up_VSAP_EC
GO:1903018	0.1	0.987	2	6	regulation of glycoprotein metabolic process	BP	1	NECAB3,SOAT1	up_VSAP_EC
GO:0051279	0.1	0.995	1	19	regulation of release of sequestered calcium ion into cytosol	BP	1	LYN	down_ACOR_EC
GO:1903707	0.1	0.995	1	48	negative regulation of hemopoiesis	BP	1	GABPA	down_AFEM_EC
GO:0031584	0.1	0.997	1	2	activation of phospholipase D activity	BP	1	ARF4	down_VSAP_EC
GO:0035602	0.1	1	1	1	fibroblast growth factor receptor signaling pathway involved in negative regulation of	BP	1	FGFR2	up_ACOR_VSMC
GO:0035603	0.1	1	1	1	fibroblast growth factor receptor signaling pathway involved in	BP	1	FGFR2	up_ACOR_VSMC
GO:0035604	0.1	1	1	1	fibroblast growth factor receptor signaling pathway involved in positive regulation of cell	BP	1	FGFR2	up_ACOR_VSMC
GO:0003100	0.1	1	1	1	regulation of systemic arterial blood pressure by	BP	1	EDN1	up_ACOR_VSMC
GO:0060529	0.1	1	1	1	squamous basal epithelial stem cell differentiation involved in prostate gland acinus development	BP	1	FGFR2	up_ACOR_VSMC
GO:0003298	0.1	1	1	1	physiological muscle hypertrophy	BP	1	EDN1	up_ACOR_VSMC
GO:0003301	0.1	1	1	1	physiological cardiac muscle hypertrophy	BP	1	EDN1	up_ACOR_VSMC
GO:0031583	0.1	1	1	1	phospholipase D-activating G protein-coupled receptor signaling	BP	1	EDN1	up_ACOR_VSMC
GO:0035812	0.1	1	1	1	renal sodium excretion	BP	1	EDN1	up_ACOR_VSMC
GO:0035813	0.1	1	1	1	regulation of renal sodium excretion	BP	1	EDN1	up_ACOR_VSMC
GO:0035815	0.1	1	1	1	positive regulation of renal sodium excretion	BP	1	EDN1	up_ACOR_VSMC
GO:0042313	0.1	1	1	1	protein kinase C deactivation	BP	1	EDN1	up_ACOR_VSMC
GO:0043179	0.1	1	1	1	rhythmic excitation	BP	1	EDN1	up_ACOR_VSMC
GO:0051771	0.1	1	1	1	negative regulation of nitric-oxide synthase	BP	1	EDN1	up_ACOR_VSMC
GO:0060024	0.1	1	1	1	rhythmic synaptic transmission	BP	1	EDN1	up_ACOR_VSMC
GO:0060584	0.1	1	1	1	regulation of prostaglandin-	BP	1	EDN1	up_ACOR_VSMC

GO:0060585	0.1	1	1	1	positive regulation of prostaglandin-endoperoxide synthase	BP	1	EDN1	up_ACOR_VSMC
GO:0061049	0.1	1	1	1	cell growth involved in cardiac muscle cell	BP	1	EDN1	up_ACOR_VSMC
GO:0061050	0.1	1	1	1	regulation of cell growth involved in cardiac muscle cell development	BP	1	EDN1	up_ACOR_VSMC
GO:0061051	0.1	1	1	1	positive regulation of cell growth involved in cardiac muscle cell development	BP	1	EDN1	up_ACOR_VSMC
GO:0002695	0.1	0.995	1	44	negative regulation of leukocyte activation	BP	1	BPI	up_AORT_EC
GO:0023061	0.1	0.995	1	95	signal release	BP	1	WNT7A	up_AORT_VSMC
GO:0002677	0.1	1	1	1	negative regulation of chronic inflammatory	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0034146	0.1	1	1	1	toll-like receptor 5 signaling pathway	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0034147	0.1	1	1	1	regulation of toll-like receptor 5 signaling	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0034148	0.1	1	1	1	negative regulation of toll-like receptor 5 signaling	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0070429	0.1	1	1	1	negative regulation of nucleotide-binding oligomerization domain	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0072573	0.1	1	1	1	tolerance induction to lipopolysaccharide	BP	0.969	TNFAIP3	up_VCAV_EC
GO:2000348	0.1	1	1	1	regulation of CD40 signaling pathway	BP	0.969	TNFAIP3	up_VCAV_EC
GO:2000349	0.1	1	1	1	negative regulation of CD40 signaling pathway	BP	0.969	TNFAIP3	up_VCAV_EC
GO:0016485	0.1	0.995	1	73	protein processing	BP	1	C6	up_VCAV_VSMC
GO:0045910	0.1	0.995	1	14	negative regulation of DNA recombination	BP	1	CXHXorf57	up_VPOR_EC
GO:0072698	0.1	0.995	1	13	protein localization to microtubule cytoskeleton	BP	1	HOOK3	up_VPOR_EC
GO:1901890	0.1	0.995	1	13	positive regulation of cell junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0035051	0.1	0.995	1	41	cardiocyte differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:1901863	0.1	0.995	1	25	positive regulation of muscle tissue	BP	1	CYP26B1	up_VFEM_EC
GO:0035850	0.1	0.995	1	25	epithelial cell differentiation involved in	BP	1	SALL1	up_VSAP_VSMC
GO:0051694	0.100146294	0.99609	1	4	pointed-end actin filament capping	BP	1	TMOD1	up_ACOR_EC
GO:0030916	0.100303419	0.99608	1	4	otic vesicle formation	BP	1	SOX9	up_ACOR_EC
GO:1905941	0.100401623	0.99607	1	4	positive regulation of gonad development	BP	1	SOX9	up_ACOR_EC
GO:2000018	0.100401623	0.99607	1	4	regulation of male gonad development	BP	1	SOX9	up_ACOR_EC
GO:2000020	0.100401623	0.99607	1	4	positive regulation of male gonad development	BP	1	SOX9	up_ACOR_EC
GO:0032077	0.100407462	0.99607	1	4	positive regulation of deoxyribonuclease	BP	1	PRKCD	up_ACOR_EC
GO:0006521	0.100507091	0.99606	1	4	regulation of cellular amino acid metabolic	BP	1	NR1H4	up_ACOR_EC
GO:0009445	0.100861993	0.99604	1	4	putrescine metabolic process	BP	1	AZIN2	up_ACOR_EC
GO:0010628	0.101	0.923	59	527	positive regulation of gene expression	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,AXIN2,OSR2,INSIG2,PTGFR,PPARGC1B,HOXD3,CDH1,SLC6A4,FGF7,DLL1,OSR1,MAP3K5,TENT5C,KLF15,ZBTB16,RARG,CCBE1,PYM1,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,ZC3H10,EEF2,LARP6,MYD88,IKZF2,TFE3,NUP98,NPAS2,PRKAB1,RPUSD4,CDK9,PRMT2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,NCOA2,SMARCA2,EIF3D,ACVRL1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:0022008	0.101	0.932	26	406	neurogenesis	BP	1	LRP1,NAB2,NDN,SDC4,BMPR1A,LMO4,TRPV2,NUMBL,NAGLU,AKT2,CSPG4,SEMA3C,THY1,PEX5,TLX2,GLI3,NCDN,CDH2,GSDME,ENSCAFG00000017708,IRX5,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC

GO:0072359	0.101	0.933	24	368	circulatory system development	BP	1	NOTCH2,HSPB6,PDGFRB,DCN,ANGPT1,FBN1,BMPR1A,LOX,LMO4,RECK,ANPEP,SEMA3C,THY1,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,IFT57,CDH2,SPRED1,SHC1,GREM1,CLIC4	down_VCAV_EC
GO:0019941	0.101	0.936	21	258	modification-dependent protein catabolic process	BP	1	PRICKLE1,PLK3,SOCS5,HSP90B1,TRIB3,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,USP48,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,USP14,TNFAIP1	down_VSAP_EC
GO:0050896	0.101	0.948	16	2346	response to stimulus	BP	1	ACVRL1,LYN,IGF1R,PDPN,NRP2,HIVEP2,USP28,IPO7,ATRIP,SULF1,ELK3,HOXA1,WDR12,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0006820	0.101	0.942	15	109	anion transport	BP	1	LEP,SLC26A7,TCAF1,ABCA1,CLCN3,SLC17A5,LRRC8C,SCP2,SLCO1A2,PSEN1,CLN8,RAB11B,PLIN2,CFI,SLC25A12	up_ACOR_VSMC
GO:0007162	0.101	0.949	10	66	negative regulation of cell adhesion	BP	1	MBP,BMP4,PDE5A,CD274,PTPN22,SPINT2,RND1,DUSP22,FAM107A,PAG1	up_ACOR_VSMC
GO:0001952	0.101	0.961	6	34	regulation of cell-matrix adhesion	BP	1	HOXA7,FAM107A,ABL1,EMP2,PIK3R1,ACVRL1	up_VSAP_EC
GO:1990138	0.101	0.961	6	35	neuron projection extension	BP	1	SLIT2,ABL1,PLXNA4,DPYSL2,TTL,ULK1	up_VSAP_EC
GO:0034249	0.101	0.964	5	41	negative regulation of cellular amide metabolic	BP	1	SESN2,EIF4EBP1,CNOT7,APOE,EIF2S1	down_VSAP_EC
GO:0060401	0.101	0.964	5	42	cytosolic calcium ion transport	BP	1	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:1903531	0.101	0.964	5	41	negative regulation of secretion by cell	BP	1	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0045807	0.101	0.969	4	35	positive regulation of endocytosis	BP	1	LRP1,CLIP3,CYBA,GREM1	down_VCAV_EC
GO:0097006	0.101	0.971	4	19	regulation of plasma lipoprotein particle levels	BP	1	LIPC,LMF1,LCAT,SOAT1	up_VSAP_EC
GO:0006298	0.101	0.977	3	13	mismatch repair	BP	1	HMGB1,RPA1,PCNA	down_ACOR_VSMC
GO:0090184	0.101	0.977	3	14	positive regulation of kidney development	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0007045	0.101	0.976	3	23	cell-substrate adherens junction assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0048041	0.101	0.976	3	23	focal adhesion assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0051899	0.101	0.976	3	22	membrane depolarization	BP	1	DCN,PARK7,TPC3	down_VCAV_EC
GO:0002063	0.101	0.976	3	18	chondrocyte development	BP	1	SULF1,SERPINH1,CHSY1	down_VSAP_EC
GO:0006836	0.101	0.975	3	47	neurotransmitter transport	BP	1	KCNC4,CHRM2,CAMK2A	up_AFEM_EC
GO:0030509	0.101	0.975	3	47	BMP signaling pathway	BP	1	TMEM100,GREM1,GREM2	up_AFEM_EC
GO:0009893	0.101	0.98	3	995	positive regulation of metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0030888	0.101	0.977	3	13	regulation of B cell proliferation	BP	0.974	MEF2C,TLR4,PELI1	up_VCAV_EC
GO:0048048	0.101	0.977	3	13	embryonic eye morphogenesis	BP	0.971	PROX1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0046839	0.101	0.977	3	12	phospholipid dephosphorylation	BP	1	INPP5E,PLPP3,PLPP5	up_VSAP_EC
GO:0021846	0.101	0.985	2	11	cell proliferation in forebrain	BP	1	NUMBL,GLI3	down_VCAV_EC
GO:2001275	0.101	0.985	2	11	positive regulation of glucose import in response to insulin	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0048873	0.101	0.985	2	9	homeostasis of number of cells within a tissue	BP	1	PTPN11,EXOC5	down_VSAP_EC
GO:1905331	0.101	0.986	2	9	negative regulation of morphogenesis of an	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0043267	0.101	0.987	2	6	negative regulation of potassium ion transport	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:0072201	0.101	0.987	2	6	negative regulation of mesenchymal cell	BP	1	BMP4,CLSTN1	up_ACOR_VSMC
GO:0043009	0.101	0.984	2	227	chordate embryonic development	BP	1	HOXA9,HOXC6	up_AORT_EC
GO:0007548	0.101	0.983	2	68	sex differentiation	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0002683	0.101	0.984	2	126	negative regulation of immune system process	BP	1	HOXA9,HOXA7	up_VFEM_EC
GO:0017144	0.101	0.984	2	199	drug metabolic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0044283	0.101	0.984	2	201	small molecule biosynthetic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0001865	0.101	0.987	2	6	NK T cell differentiation	BP	1	ZBTB16,TGFBR2	up_VSAP_EC

GO:0030048	0.101	0.995	1	23	actin filament-based movement	BP	1	PDPN	down_ACOR_EC
GO:0043618	0.101	0.995	1	22	regulation of transcription from RNA polymerase II promoter in response to	BP	1	NEDD4	down_ACOR_EC
GO:0045921	0.101	0.995	1	24	positive regulation of exocytosis	BP	1	STX4	down_ACOR_EC
GO:0051225	0.101	0.995	1	49	spindle assembly	BP	1	GPSM2	down_AFEM_EC
GO:0036089	0.101	0.997	1	2	cleavage furrow formation	BP	1	SNX18	down_VCAV_EC
GO:0097176	0.101	0.997	1	2	epoxide metabolic process	BP	1	EPHX1	down_VCAV_EC
GO:1902548	0.101	0.997	1	2	negative regulation of cellular response to vascular endothelial	BP	1	DCN	down_VCAV_EC
GO:0016560	0.101	0.997	1	2	protein import into peroxisome matrix,	BP	1	PEX5	down_VCAV_EC
GO:0042439	0.101	0.997	1	2	ethanolamine-containing compound metabolic	BP	1	NAPEPLD	down_VCAV_EC
GO:1900747	0.101	0.997	1	2	negative regulation of vascular endothelial growth factor signaling	BP	1	DCN	down_VCAV_EC
GO:2000275	0.101	0.997	1	2	regulation of oxidative phosphorylation uncoupler activity	BP	1	PARK7	down_VCAV_EC
GO:0071962	0.101	0.997	1	2	mitotic sister chromatid cohesion, centromeric	BP	1	NAA10	down_VSAP_EC
GO:0060012	0.101	1	1	1	synaptic transmission, glycinergic	BP	1	GLRB	up_ACOR_VSMC
GO:0071873	0.101	1	1	1	response to norepinephrine	BP	1	APLP1	up_ACOR_VSMC
GO:0071874	0.101	1	1	1	cellular response to norepinephrine stimulus	BP	1	APLP1	up_ACOR_VSMC
GO:0097112	0.101	1	1	1	gamma-aminobutyric acid receptor clustering	BP	1	GLRB	up_ACOR_VSMC
GO:0038044	0.101	1	1	1	transforming growth factor-beta secretion	BP	1	FERMT1	up_ACOR_VSMC
GO:0051886	0.101	1	1	1	negative regulation of timing of anagen	BP	1	FERMT1	up_ACOR_VSMC
GO:1901860	0.101	1	1	1	positive regulation of mitochondrial DNA metabolic process	BP	1	PPARGC1A	up_ACOR_VSMC
GO:2001201	0.101	1	1	1	regulation of transforming growth factor-beta	BP	1	FERMT1	up_ACOR_VSMC
GO:2001203	0.101	1	1	1	positive regulation of transforming growth factor-beta secretion	BP	1	FERMT1	up_ACOR_VSMC
GO:0050727	0.101	0.995	1	74	regulation of inflammatory response	BP	1	TLR2	up_AFEM_VSMC
GO:0051146	0.101	0.995	1	76	striated muscle cell differentiation	BP	1	BEND2	up_AFEM_VSMC
GO:0046661	0.101	0.995	1	45	male sex differentiation	BP	1	HOXA9	up_AORT_EC
GO:0062013	0.101	0.995	1	27	positive regulation of small molecule metabolic	BP	1	NR1H4	up_APUL_EC
GO:0001707	0.101	0.995	1	25	mesoderm formation	BP	1	EYA1	up_VFEM_EC
GO:0051149	0.101	0.995	1	25	positive regulation of muscle cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0046620	0.101	0.995	1	30	regulation of organ growth	BP	1	TBX5	up_VPUL_EC
GO:0050728	0.101	0.995	1	31	negative regulation of inflammatory response	BP	1	NR1H4	up_VPUL_EC
GO:0090100	0.101	0.995	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	NEO1	up_VPUL_EC
GO:0050920	0.101	0.995	1	53	regulation of chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0051924	0.101	0.995	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0001658	0.101	0.995	1	24	branching involved in ureteric bud	BP	1	HOXA11	up_VSAP_VSMC
GO:2001238	0.101	0.995	1	23	positive regulation of extrinsic apoptotic	BP	1	CAV1	up_VSAP_VSMC
GO:0051048	0.101082623	0.97494	3	42	negative regulation of secretion	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:0021795	0.101087924	0.98407	2	20	cerebral cortex cell migration	BP	1	DIXDC1,NRP1	up_ACOR_EC

GO:0016032	0.101457178	0.96289	5	94	viral process	BP	1	ATG16L2,TRIM8,MAVS,LRRC15,CHMP4B	up_ACOR_EC
GO:0071214	0.101509072	0.96287	5	93	cellular response to abiotic stimulus	BP	1	SOX9,AQP1,PTGER4,FIGNL1,MFAP4	up_ACOR_EC
GO:0104004	0.101509072	0.96287	5	93	cellular response to environmental stimulus	BP	1	SOX9,AQP1,PTGER4,FIGNL1,MFAP4	up_ACOR_EC
GO:0060485	0.101556423	0.96285	5	93	mesenchyme development	BP	1	GATA4,SOX9,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0060219	0.1016224	0.99598	1	4	camera-type eye photoreceptor cell	BP	1	SOX9	up_ACOR_EC
GO:0032502	0.102	0.913	175	1661	developmental process	BP	1	EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,LGR6,PLCG2,LEP,LBH,AFF3,GATA5,GATA4,CD83,CDC7,ANGPT1,EPYC,HTR2B,RASSF2,FNDC5,MBP,ZRANB1,PRDX4,RECK,SHROOM3,FEZ1,MLLT3,ITM2C,FERMT1,BMP4,LNPK,TBX18,FGFR2,TP53BP1,GJA1,ELF1,ATRX,MED14,TRPS1,TLR3,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,SPINT1,GLRB,ISG15,ACSL6,ZNRF3,CD274,ZNF365,SASH1,LMO4,TMEM108,FGF18,FAM210B,ARHGEF26,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,EBF4,ZMYM2,ITPR1,PLAC8B,LIMS2,ANKRD1,PLEKHB2,F2RL1,CAMK2D,MARCH5,CTSB,BNIP3,EGLN1,CDKN1A,ENSCAFG00000006238,CLSTN1,LRRC8C,NRP1,PTPN22,GPM6A,CHD2,ULK2,DMPK,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,PTGDR,TBX20,BBX,TPT1,TBX5,CCDC3,MARF1,FZD3,AFF4,DKKL1,FRS2,CPAMD8,RND1,DAG1,POMK,APP,LAMA3,PSEN1,SEMA6D,TGFBR1,PCSK6,SYNJ2BP,CHD7,JUP,SPINK2,SIPA1L1,DDR2,CLN8,WWC2,FOSL2,PERP,PSKH1,RTKN2,SIAH1,SSH3,C10H2orf49,EDN1,NID1,HPGD,ARID5B,ASAP1,DMC1,PRELP,SERPINB5,JAM3,B2M,DISC1,AP2B1,TNFRSF11B,TACC1,GAA,ATXN10,FEZ2,SUN1,INPP5K,CNOT4,LHX9,WFS1,	up_ACOR_EC
GO:0042326	0.102	0.942	14	163	negative regulation of phosphorylation	BP	1	SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,DYNLL1,DNAJC10,PTPN2,APOE,LYN,STRAP,CBLC,ATF3,CDKN1A	down_VSAP_EC
GO:0051017	0.102	0.954	8	49	actin filament bundle assembly	BP	1	SYNPO2L,ARHGAP28,SYNPO2,NRP1,EVL,MYO1B,FAM107A,INPP5K	up_ACOR_VSMC
GO:0051480	0.102	0.954	8	50	regulation of cytosolic calcium ion concentration	BP	1	ADRA1B,PLCG2,HTR2B,ITPR1,F2RL1,PRKCE,CHD7,EDN1	up_ACOR_VSMC
GO:0006457	0.102	0.956	7	77	protein folding	BP	1	HSPB6,FKBP10,PDIA4,FKBP5,FKBP11,EMC6,CRTAP	down_VCAV_EC
GO:0006611	0.102	0.96	6	51	protein export from nucleus	BP	1	PTPN14,PTPN11,IWS1,SMG7,DDX39B,GSK3B	down_VSAP_EC
GO:0044706	0.102	0.965	5	27	multi-multicellular organism process	BP	1	RECK,CITED2,CTSB,DKKL1,HPGD	up_ACOR_VSMC
GO:0008544	0.102	0.968	4	75	epidermis development	BP	1	HOXA7,DLL1,OVOL1,FOSL2	up_AFEM_EC
GO:0045595	0.102	0.969	4	469	regulation of cell differentiation	BP	1	TBX5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0042136	0.102	0.97	4	21	neurotransmitter biosynthetic process	BP	0.976	CD34,TLR4,NOS3,NOS2	up_VCAV_EC
GO:0051129	0.102	0.968	4	221	negative regulation of cellular component	BP	1	ARHGEF2,SEMA3A,TWF1,RNF6	up_VPOR_EC
GO:0050793	0.102	0.97	4	731	regulation of developmental process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042307	0.102	0.976	3	23	positive regulation of protein import into	BP	1	ENSCAFG00000014978,GLI3,MAVS	down_VCAV_EC
GO:0046849	0.102	0.975	3	23	bone remodeling	BP	1	NOTCH2,NCDN,GREM1	down_VCAV_EC
GO:0061912	0.102	0.976	3	18	selective autophagy	BP	1	SESN2,CDC37,HTT	down_VSAP_EC
GO:0045071	0.102	0.977	3	12	negative regulation of viral genome replication	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0045598	0.102	0.975	3	47	regulation of fat cell differentiation	BP	1	CMKLR1,LEP,NAPEPLD	up_AFEM_EC
GO:0031146	0.102	0.977	3	12	SCF-dependent proteasomal ubiquitin-dependent protein	BP	1	FBXW4,FBXO4,FBXW5	up_VSAP_EC
GO:0048012	0.102	0.986	2	7	hepatocyte growth factor receptor signaling	BP	1	STMN1,RAC1	down_ACOR_VSMC
GO:0006110	0.102	0.985	2	9	regulation of glycolytic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0010002	0.102	0.985	2	9	cardioblast differentiation	BP	1	PRICKLE1,REST	down_VSAP_EC
GO:0030811	0.102	0.985	2	9	regulation of nucleotide catabolic process	BP	1	PGAM1,HIF1A	down_VSAP_EC

GO:0042987	0.102	0.985	2	10	amyloid precursor protein catabolic process	BP	1	APOE,LYN	down_VSAP_EC
GO:0043470	0.102	0.985	2	9	regulation of carbohydrate catabolic	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0003091	0.102	0.987	2	6	renal water homeostasis	BP	1	INPP5K,WFS1	up_ACOR_VSMC
GO:0006658	0.102	0.987	2	6	phosphatidylserine metabolic process	BP	1	SERINC3,SERINC1	up_ACOR_VSMC
GO:0006878	0.102	0.987	2	6	cellular copper ion homeostasis	BP	1	ATP7A,APP	up_ACOR_VSMC
GO:0071549	0.102	0.987	2	6	cellular response to dexamethasone stimulus	BP	1	NR3C1,DDIT4	up_ACOR_VSMC
GO:0098869	0.102	0.987	2	6	cellular oxidant detoxification	BP	1	SESN1,PARK7	up_ACOR_VSMC
GO:0021510	0.102	0.984	2	23	spinal cord development	BP	1	HOXC10,DLL1	up_AFEM_EC
GO:0021782	0.102	0.984	2	23	glial cell development	BP	1	DLL1,LGI4	up_AFEM_EC
GO:0034446	0.102	0.984	2	23	substrate adhesion-dependent cell spreading	BP	1	BVES,KANK1	up_AFEM_EC
GO:0046849	0.102	0.984	2	23	bone remodeling	BP	1	LEP,GREM1	up_AFEM_EC
GO:0045595	0.102	0.986	2	469	regulation of cell differentiation	BP	1	HOXA9,WNT7A	up_AORT_VSMC
GO:0035871	0.102	0.987	2	6	protein K11-linked deubiquitination	BP	0.978	TNFAIP3,USP37	up_VCAV_EC
GO:0031954	0.102	0.986	2	8	positive regulation of protein	BP	0.978	PDGFB,PDGFD	up_VCAV_EC
GO:0032530	0.102	0.987	2	6	regulation of microvillus organization	BP	0.976	PODXL,FSCN1	up_VCAV_EC
GO:0072574	0.102	0.987	2	6	hepatocyte proliferation	BP	1	LIMS2,SULF2	up_VSAP_EC
GO:0072575	0.102	0.987	2	6	epithelial cell proliferation involved in liver	BP	1	LIMS2,SULF2	up_VSAP_EC
GO:0072576	0.102	0.987	2	6	liver morphogenesis	BP	1	LIMS2,SULF2	up_VSAP_EC
GO:1900271	0.102	0.987	2	6	regulation of long-term synaptic potentiation	BP	1	FAM107A,ABL1	up_VSAP_EC
GO:0000271	0.102	0.995	1	22	polysaccharide biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0007565	0.102	0.995	1	23	female pregnancy	BP	1	ACSL4	down_ACOR_EC
GO:0051017	0.102	0.995	1	49	actin filament bundle assembly	BP	1	FSCN1	down_AFEM_EC
GO:0006477	0.102	0.997	1	2	protein sulfation	BP	1	HS3ST3B1	down_VCAV_EC
GO:0009051	0.102	0.997	1	2	pentose-phosphate shunt, oxidative branch	BP	1	PGLS	down_VCAV_EC
GO:0046368	0.102	0.997	1	2	GDP-L-fucose metabolic process	BP	1	FUT8	down_VCAV_EC
GO:0001649	0.102	0.995	1	54	osteoblast differentiation	BP	1	HDAC7	down_VPOR_EC
GO:0045055	0.102	0.995	1	52	regulated exocytosis	BP	1	RAB11B	down_VPOR_EC
GO:0019835	0.102	0.997	1	2	cytolysis	BP	1	MMD	down_VSAP_EC
GO:0060158	0.102	0.997	1	2	phospholipase C-activating dopamine receptor signaling	BP	1	GNAQ	down_VSAP_EC
GO:0014004	0.102	1	1	1	microglia differentiation	BP	1	APP	up_ACOR_VSMC
GO:0014005	0.102	1	1	1	microglia development	BP	1	APP	up_ACOR_VSMC
GO:0048669	0.102	1	1	1	collateral sprouting in absence of injury	BP	1	APP	up_ACOR_VSMC
GO:0061890	0.102	1	1	1	positive regulation of astrocyte activation	BP	1	APP	up_ACOR_VSMC
GO:0150003	0.102	1	1	1	regulation of spontaneous synaptic transmission	BP	1	APP	up_ACOR_VSMC
GO:1904475	0.102	1	1	1	regulation of Ras GTPase binding	BP	1	CCPG1	up_ACOR_VSMC
GO:1990390	0.102	1	1	1	protein K33-linked ubiquitination	BP	1	KLHL20	up_ACOR_VSMC
GO:2001106	0.102	1	1	1	regulation of Rho guanyl-nucleotide exchange factor activity	BP	1	CCPG1	up_ACOR_VSMC
GO:0016199	0.102	1	1	1	axon midline choice point recognition	BP	1	APP	up_ACOR_VSMC
GO:0038161	0.102	1	1	1	prolactin signaling pathway	BP	1	CREBRF	up_ACOR_VSMC

GO:0043402	0.102	1	1	1	glucocorticoid mediated signaling pathway	BP	1	CREBRF	up_ACOR_VSMC
GO:0098814	0.102	1	1	1	spontaneous synaptic transmission	BP	1	APP	up_ACOR_VSMC
GO:1900169	0.102	1	1	1	regulation of glucocorticoid mediated	BP	1	CREBRF	up_ACOR_VSMC
GO:1900170	0.102	1	1	1	negative regulation of glucocorticoid mediated signaling pathway	BP	1	CREBRF	up_ACOR_VSMC
GO:1902211	0.102	1	1	1	regulation of prolactin signaling pathway	BP	1	CREBRF	up_ACOR_VSMC
GO:1902213	0.102	1	1	1	positive regulation of prolactin signaling	BP	1	CREBRF	up_ACOR_VSMC
GO:0006887	0.102	0.995	1	99	exocytosis	BP	1	WNT7A	up_AORT_VSMC
GO:0071824	0.102	0.995	1	92	protein-DNA complex subunit organization	BP	1	ESR1	up_AORT_VSMC
GO:0009410	0.102	0.995	1	27	response to xenobiotic stimulus	BP	1	SLITRK5	up_APUL_EC
GO:0033138	0.102	0.995	1	28	positive regulation of peptidyl-serine	BP	1	NTRK2	up_APUL_EC
GO:0043435	0.102	1	1	1	response to corticotropin-releasing hormone	BP	0.976	NR4A1	up_VCAV_EC
GO:0071376	0.102	1	1	1	cellular response to corticotropin-releasing	BP	0.976	NR4A1	up_VCAV_EC
GO:0050727	0.102	0.995	1	74	regulation of inflammatory response	BP	1	C6	up_VCAV_VSMC
GO:0051196	0.102	0.995	1	13	regulation of coenzyme metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0009799	0.102	0.995	1	43	specification of symmetry	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048704	0.102	0.995	1	46	embryonic skeletal system morphogenesis	BP	1	HOXA3	up_VPOR_VSMC
GO:0009145	0.102	0.995	1	40	purine nucleoside triphosphate biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0008277	0.102	0.995	1	31	regulation of G protein-coupled receptor signaling	BP	1	RGS1	up_VPUL_EC
GO:0006641	0.102	0.995	1	25	triglyceride metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0008652	0.102	0.995	1	24	cellular amino acid biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0050806	0.102	0.995	1	25	positive regulation of synaptic transmission	BP	1	NETO1	up_VSAP_VSMC
GO:0051149	0.102	0.995	1	25	positive regulation of muscle cell differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:1901607	0.102	0.995	1	24	alpha-amino acid biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0032637	0.102	0.995	1	26	interleukin-8 production	BP	1	TLR2	up_VSAP_VSMC
GO:0032928	0.102027415	0.99594	1	4	regulation of superoxide anion generation	BP	1	PRKCD	up_ACOR_EC
GO:0010838	0.102152051	0.99593	1	4	positive regulation of keratinocyte proliferation	BP	1	CDH3	up_ACOR_EC
GO:0042493	0.102396081	0.95208	8	178	response to drug	BP	1	GATA4,SOX9,AQP1,AGRN,NOD2,PDE4A,GUCY1B1,PRKCD	up_ACOR_EC
GO:0046541	0.102398704	0.99591	1	4	saliva secretion	BP	1	AQP1	up_ACOR_EC
GO:0048207	0.102465629	0.99591	1	4	vesicle targeting, rough ER to cis-Golgi	BP	1	PREB	up_ACOR_EC
GO:0048208	0.102465629	0.99591	1	4	COPII vesicle coating	BP	1	PREB	up_ACOR_EC
GO:0044058	0.102580713	0.9959	1	4	regulation of digestive system process	BP	1	AQP1	up_ACOR_EC
GO:0072330	0.102584812	0.96757	4	68	monocarboxylic acid biosynthetic process	BP	1	NR1H4,THNSL2,PTGDS,ALDOC	up_ACOR_EC
GO:0016310	0.103	0.919	71	641	phosphorylation	BP	1	FZD1,CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,OSR1,MAP3K5,CDC42EP5,PDGFD,C1QTNF2,CNPPD1,COQ9,NDUFS1,ENSCAFG00000004260,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,GALK1,PIK3R1,MYC,PIK3IP1,RTN4RL1,SASH1,MYD88,NDUFS2,LRP4,PASK,STK16,FBXO7,LIMD1,TKFC,CDK9,FBLN1,ZFP36L2,RAF1,ZFYVE21,QARS,ACVRL1,FLOT1,PPP3CB,NCK1,NDUFV1,MAVS,ULK1,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC

GO:0048584	0.103	0.92	66	592	positive regulation of response to stimulus	BP	1	ADRA1B,VEGFD,TLR1,LGR6,PLCG2,LEP,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,SKP2,NACC2,COCH,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,TP53BP1,ELF1,TLR3,SH3RF2,PDE5A,CITED2,TP53INP1,CD274,SASH1,TMEM108,FGF18,CDKN2B,LIMS2,ANKRD1,F2RL1,ENPP4,BNIP3,C1S,CRLF3,CREBRF,NRP1,PTPN22,NPNT,UNC5B,C7,PRKCE,FRS2,PARP9,APP,PSEN1,CCL5,DUSP22,SIAH1,EDN1,NOD2,B2M,DISC1,SH3RF3,SERINC3,HERPUD1,MAP3K7,ENSCAFG00000029553,PARK7,IL18R1,RREB1,CRKL	up_ACOR_VSMC
GO:0050790	0.103	0.921	60	532	regulation of catalytic activity	BP	1	TNNT2,LEP,MAP3K8,HTR2B,RASSF2,USP6NL,MBP,RECK,BMP4,EVI5L,FGFR2,EIF4A2,SCARB2,SH3RF2,LATS2,PDE5A,PKP4,SASH1,LMO4,FGF18,CHN2,CDKN2B,CST3,F2RL1,DAPK1,CTSB,CDKN1A,NPNT,ATP7A,SMPD1,SH3RF1,CCNT1,MARF1,FRS2,PPP1R26,APP,PSEN1,SGSM2,SPINK2,CCL5,DDR2,PERP,DUSP22,EDN1,DYNC1I2,DUSP26,LRRC4,PRKAG3,DCUN1D4,SBF2,MAP3K7,INPP5K,SH3BP4,DYNC1I1,PARK7,GPATCH2,ZFYVE1,HMBOX1,BVES,LMF1	up_ACOR_VSMC
GO:0006793	0.103	0.922	56	948	phosphorus metabolic process	BP	1	GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,ADCY6,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,LCAT,EEF2K,H6PD,PLCL1,CSPG4,NT5C2,ENTPD3,THNSL2,PGLS,ATP5MC1,GFPT2,UQCR10,ASPN,PIGS,THY1,ADK,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,ARL2BP,AMPD2,MAVS,CDH2,GSDME,CAMK2D,FUT8,SPRED1,ACSS2,MAPRE3,CDKL2,DDR2,SHC1,FBH1,GREM1,NAPEPLD,ACAT1,BRSK1,CDK14	down_VCAV_EC
GO:0048598	0.103	0.932	26	207	embryonic morphogenesis	BP	1	AFF3,HTR2B,MBP,RECK,SHROOM3,BMP4,LNPK,FGFR2,GJA1,SEC24B,LATS2,CITED2,SPINT1,LMO4,ENSCAFG00000006238,SPINT2,TBX20,TBX5,FZD3,FRS2,DAG1,LAMA3,PSEN1,CHD7,C10H2orf49,EDN1	up_ACOR_VSMC
GO:0090407	0.103	0.936	19	177	organophosphate biosynthetic process	BP	0.978	NPR1,ADGRF5,PANK3,PDGFB,GK5,ADSS,GUCY1A1,SPTLC2,SAMD8,ITPKB,SH3GLB1,ELOVL7,ENSCAFG00000024323,GUCY1B1,PLCG2,NOS2,IMPA1,PIP5K1B,HIF1A	up_VCAV_EC
GO:0090596	0.103	0.946	11	84	sensory organ morphogenesis	BP	0.978	EPHB1,CHD7,GATA3,EDN1,PROX1,TSPAN12,JAG1,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0030100	0.103	0.948	10	70	regulation of endocytosis	BP	1	DNAJC6,PLCG2,ATXN2,F2RL1,LRPAP1,SYNJ2BP,GTF2A1L,B2M,SCAMP5,RAB5C	up_ACOR_VSMC
GO:0010959	0.103	0.955	7	79	regulation of metal ion transport	BP	1	PRNP,FXYD1,TRPV2,CACNB3,THY1,CYBA,PACSIN3	down_VCAV_EC
GO:1990823	0.103	0.959	6	39	response to leukemia inhibitory factor	BP	1	SLC25A5,B3GNT2,TFRC,NCL,CTH,MSC	down_ACOR_VSMC
GO:1990830	0.103	0.959	6	39	cellular response to leukemia inhibitory factor	BP	1	SLC25A5,B3GNT2,TFRC,NCL,CTH,MSC	down_ACOR_VSMC
GO:0050792	0.103	0.959	6	55	regulation of viral process	BP	1	P4HB,SMARCA4,CNOT7,APOE,REST,RAD23A	down_VSAP_EC
GO:0043269	0.103	0.958	6	135	regulation of ion transport	BP	1	KCNC4,KCND1,CAMK2A,FXYD1,DMPK,CLIC4	up_AFEM_EC
GO:0043624	0.103	0.96	6	39	cellular protein complex disassembly	BP	0.978	TMOD1,STMN1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0015031	0.103	0.964	5	510	protein transport	BP	1	LYN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:1901652	0.103	0.962	5	105	response to peptide	BP	1	LEP,CRY2,AVPR1A,CAMK2A,KANK1	up_AFEM_EC
GO:1901568	0.103	0.965	5	26	fatty acid derivative metabolic process	BP	1	PTGES,DAGLB,ABHD16A,HPGD,ENSCAFG00000023820	up_VSAP_EC
GO:0034097	0.103	0.975	3	238	response to cytokine	BP	1	NRP2,STX4,ASPN	down_ACOR_EC
GO:0035987	0.103	0.976	3	17	endodermal cell differentiation	BP	1	CTNNB1,INHBA,COL12A1	down_VSAP_EC
GO:0051893	0.103	0.975	3	20	regulation of focal adhesion assembly	BP	1	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0090109	0.103	0.975	3	20	regulation of cell-substrate junction	BP	1	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0050771	0.103	0.977	3	11	negative regulation of axonogenesis	BP	1	NRP1,ULK2,PSEN1	up_ACOR_VSMC
GO:0032418	0.103	0.976	3	17	lysosome localization	BP	0.978	KIT,SNAP23,FES	up_VCAV_EC
GO:0032613	0.103	0.977	3	14	interleukin-10 production	BP	0.978	CD34,TLR4,HMGB1	up_VCAV_EC
GO:0051646	0.103	0.977	3	12	mitochondrion localization	BP	0.978	NECTIN2,HIF1A,ATP2A1	up_VCAV_EC

GO:2000001	0.103	0.977	3	13	regulation of DNA damage checkpoint	BP	0.978	THOC1,ETAA1,CUL4A	up_VCAV_EC
GO:0030182	0.103	0.975	3	327	neuron differentiation	BP	1	FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0021952	0.103	0.977	3	13	central nervous system projection neuron	BP	1	SLIT2,PLXNA4,NFIB	up_VSAP_EC
GO:1901379	0.103	0.977	3	12	regulation of potassium ion transmembrane	BP	1	AMIGO1,KCNE3,KLHL24	up_VSAP_EC
GO:0050678	0.103	0.983	2	117	regulation of epithelial cell proliferation	BP	1	ACVRL1,SULF1	down_ACOR_EC
GO:0051222	0.103	0.983	2	103	positive regulation of protein transport	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0072172	0.103	0.986	2	7	mesonephric tubule formation	BP	1	GREM1,SIX4	down_ACOR_VSMC
GO:0050691	0.103	0.985	2	11	regulation of defense response to virus by host	BP	1	RNF216,MAVS	down_VCAV_EC
GO:0031343	0.103	0.985	2	10	positive regulation of cell killing	BP	1	FAM49B,PVR	down_VSAP_EC
GO:2001258	0.103	0.985	2	11	negative regulation of cation channel activity	BP	1	REM1,CALM1	down_VSAP_EC
GO:0048585	0.103	0.986	2	475	negative regulation of response to stimulus	BP	1	ARG2,ESR1	up_AORT_VSMC
GO:0051049	0.103	0.986	2	479	regulation of transport	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0050829	0.103	0.985	2	8	defense response to Gram-negative bacterium	BP	0.979	LYZ,TLR4	up_VCAV_EC
GO:0007276	0.103	0.983	2	130	gamete generation	BP	1	HOXA9,CYP26B1	up_VFEM_EC
GO:0009065	0.103	0.987	2	6	glutamine family amino acid catabolic process	BP	1	GOT1,ADHFE1	up_VSAP_EC
GO:0001776	0.103	0.995	1	23	leukocyte homeostasis	BP	1	LYN	down_ACOR_EC
GO:0008033	0.103	0.995	1	52	tRNA processing	BP	1	TSEN15	down_AFEM_EC
GO:0016579	0.103	0.995	1	49	protein deubiquitination	BP	1	USP33	down_AFEM_EC
GO:0009265	0.103	0.997	1	2	2'-deoxyribonucleotide biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0018171	0.103	0.997	1	2	peptidyl-cysteine oxidation	BP	1	PARK7	down_VCAV_EC
GO:0019249	0.103	0.997	1	2	lactate biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0032382	0.103	0.997	1	2	positive regulation of intracellular sterol	BP	1	SCP2	down_VCAV_EC
GO:0032385	0.103	0.997	1	2	positive regulation of intracellular cholesterol	BP	1	SCP2	down_VCAV_EC
GO:0046356	0.103	0.997	1	2	acetyl-CoA catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0060054	0.103	0.997	1	2	positive regulation of epithelial cell proliferation involved in wound healing	BP	1	B4GALT1	down_VCAV_EC
GO:0003343	0.103	0.997	1	2	septum transversum development	BP	1	ZFP36L1	down_VCAV_EC
GO:0070269	0.103	0.997	1	2	pyroptosis	BP	1	GSDME	down_VCAV_EC
GO:1901029	0.103	0.997	1	2	negative regulation of mitochondrial outer membrane permeabilization involved	BP	1	SLC35F6	down_VCAV_EC
GO:1902224	0.103	0.997	1	2	ketone body metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:1902339	0.103	0.997	1	2	positive regulation of apoptotic process involved in	BP	1	B4GALT1	down_VCAV_EC
GO:1902951	0.103	0.997	1	2	negative regulation of dendritic spine	BP	1	PRNP	down_VCAV_EC
GO:1904747	0.103	0.997	1	2	positive regulation of apoptotic process	BP	1	B4GALT1	down_VCAV_EC
GO:1905664	0.103	0.997	1	2	regulation of calcium ion import across plasma	BP	1	PRNP	down_VCAV_EC
GO:2000298	0.103	0.997	1	2	regulation of Rho-dependent protein serine/threonine kinase	BP	1	THY1	down_VCAV_EC
GO:2000823	0.103	0.997	1	2	regulation of androgen receptor activity	BP	1	PARK7	down_VCAV_EC
GO:2000825	0.103	0.997	1	2	positive regulation of androgen receptor	BP	1	PARK7	down_VCAV_EC
GO:0032379	0.103	0.997	1	2	positive regulation of intracellular lipid	BP	1	SCP2	down_VCAV_EC

GO:0042126	0.103	0.997	1	2	nitrate metabolic process	BP	1	SUOX	down_VCAV_EC
GO:0045764	0.103	0.997	1	2	positive regulation of cellular amino acid	BP	1	PARK7	down_VCAV_EC
GO:0046385	0.103	0.997	1	2	deoxyribose phosphate biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0046459	0.103	0.997	1	2	short-chain fatty acid metabolic process	BP	1	THNSL2	down_VCAV_EC
GO:0046950	0.103	0.997	1	2	cellular ketone body metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0048681	0.103	0.997	1	2	negative regulation of axon regeneration	BP	1	RGMA	down_VCAV_EC
GO:0051790	0.103	0.997	1	2	short-chain fatty acid biosynthetic process	BP	1	THNSL2	down_VCAV_EC
GO:0060994	0.103	0.997	1	2	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GLIS2	down_VCAV_EC
GO:0003342	0.103	0.997	1	2	proepicardium development	BP	1	ZFP36L1	down_VCAV_EC
GO:0086036	0.103	0.997	1	2	regulation of cardiac muscle cell membrane	BP	1	FXYD1	down_VCAV_EC
GO:0090155	0.103	0.997	1	2	negative regulation of sphingolipid biosynthetic	BP	1	ORMDL3	down_VCAV_EC
GO:0090156	0.103	0.997	1	2	cellular sphingolipid homeostasis	BP	1	ORMDL3	down_VCAV_EC
GO:1900060	0.103	0.997	1	2	negative regulation of ceramide biosynthetic	BP	1	ORMDL3	down_VCAV_EC
GO:1990442	0.103	0.997	1	2	intrinsic apoptotic signaling pathway in response to nitrosative	BP	1	PARK7	down_VCAV_EC
GO:0034157	0.103	1	1	1	positive regulation of toll-like receptor 7 signaling	BP	1	PTPN22	up_ACOR_VSMC
GO:0071613	0.103	1	1	1	granzyme B production	BP	1	PTPN22	up_ACOR_VSMC
GO:0071661	0.103	1	1	1	regulation of granzyme B production	BP	1	PTPN22	up_ACOR_VSMC
GO:0071663	0.103	1	1	1	positive regulation of granzyme B production	BP	1	PTPN22	up_ACOR_VSMC
GO:2000566	0.103	1	1	1	positive regulation of CD8-positive, alpha-beta T cell proliferation	BP	1	PTPN22	up_ACOR_VSMC
GO:2001187	0.103	1	1	1	positive regulation of CD8-positive, alpha-beta T cell activation	BP	1	PTPN22	up_ACOR_VSMC
GO:0034155	0.103	1	1	1	regulation of toll-like receptor 7 signaling	BP	1	PTPN22	up_ACOR_VSMC
GO:0035644	0.103	1	1	1	phosphoanandamide dephosphorylation	BP	1	PTPN22	up_ACOR_VSMC
GO:0046330	0.103	0.995	1	47	positive regulation of JNK cascade	BP	1	TAOK1	up_AORT_EC
GO:0007283	0.103	0.995	1	91	spermatogenesis	BP	1	HOXA9	up_AORT_VSMC
GO:0007043	0.103	0.995	1	28	cell-cell junction assembly	BP	1	NR1H4	up_APUL_EC
GO:0055092	0.103	0.995	1	28	sterol homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0006968	0.103	0.997	1	2	cellular defense response	BP	0.978	BCL10	up_VCAV_EC
GO:0002069	0.103	1	1	1	columnar/cuboidal epithelial cell maturation	BP	0.978	HIF1A	up_VCAV_EC
GO:0002248	0.103	1	1	1	connective tissue replacement involved in inflammatory response	BP	0.978	HIF1A	up_VCAV_EC
GO:0051541	0.103	1	1	1	elastin metabolic process	BP	0.978	HIF1A	up_VCAV_EC
GO:0060574	0.103	1	1	1	intestinal epithelial cell maturation	BP	0.978	HIF1A	up_VCAV_EC
GO:0061030	0.103	1	1	1	epithelial cell differentiation involved in mammary gland alveolus	BP	0.978	HIF1A	up_VCAV_EC
GO:2001253	0.103	1	1	1	regulation of histone H3-K36 trimethylation	BP	0.978	IWS1	up_VCAV_EC
GO:0045648	0.103	0.995	1	13	positive regulation of erythrocyte	BP	1	ACVR2A	up_VPOR_EC
GO:0070266	0.103	0.995	1	14	necroptotic process	BP	1	ARHGEF2	up_VPOR_EC
GO:0071675	0.103	0.995	1	13	regulation of mononuclear cell	BP	1	C3AR1	up_VPOR_EC
GO:0007605	0.103	0.995	1	27	sensory perception of sound	BP	1	SIX1	up_VFEM_EC

GO:0048332	0.103	0.995	1	26	mesoderm morphogenesis	BP	1	EYA1	up_VFEM_EC
GO:0009201	0.103	0.995	1	41	ribonucleoside triphosphate biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0071241	0.103	0.995	1	42	cellular response to inorganic substance	BP	1	FBP1	up_VFEM_VSMC
GO:2001022	0.103	0.995	1	42	positive regulation of response to DNA damage	BP	1	EYA1	up_VFEM_VSMC
GO:0055007	0.103	0.995	1	31	cardiac muscle cell differentiation	BP	1	TBX5	up_VPUL_EC
GO:1901654	0.103	0.995	1	31	response to ketone	BP	1	PTGER2	up_VPUL_EC
GO:0001707	0.103	0.995	1	25	mesoderm formation	BP	1	HOXA11	up_VSAP_VSMC
GO:0050818	0.103	0.995	1	24	regulation of coagulation	BP	1	CAV1	up_VSAP_VSMC
GO:0040017	0.103089993	0.95167	8	180	positive regulation of locomotion	BP	1	SOX9,AQP1,SEMA6D,FOXC2,LRRC15,CHMP4B,RARRES2,NRP1	up_ACOR_EC
GO:0097475	0.103334329	0.99584	1	4	motor neuron migration	BP	1	NRP1	up_ACOR_EC
GO:0071941	0.103352317	0.99583	1	4	nitrogen cycle metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0032287	0.10341734	0.99583	1	4	peripheral nervous system myelin	BP	1	SH3TC2	up_ACOR_EC
GO:2001135	0.103540947	0.99582	1	4	regulation of endocytic recycling	BP	1	ACTN2	up_ACOR_EC
GO:0048703	0.103593415	0.99581	1	4	embryonic viscerocranium morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:1902187	0.103620387	0.99581	1	4	negative regulation of viral release from host cell	BP	1	TRIM8	up_ACOR_EC
GO:2000480	0.103714145	0.9958	1	4	negative regulation of cAMP-dependent protein	BP	1	PKIB	up_ACOR_EC
GO:0030238	0.103745277	0.9958	1	4	male sex determination	BP	1	SOX9	up_ACOR_EC
GO:0015701	0.103889562	0.99579	1	4	bicarbonate transport	BP	1	CA4	up_ACOR_EC
GO:0060840	0.103969495	0.97392	3	42	artery development	BP	1	SMAD6,FOXC2,NRP1	up_ACOR_EC
GO:0010990	0.103989867	0.99578	1	4	regulation of SMAD protein complex assembly	BP	1	SMAD6	up_ACOR_EC
GO:0010991	0.103989867	0.99578	1	4	negative regulation of SMAD protein complex	BP	1	SMAD6	up_ACOR_EC
GO:0031401	0.104	0.924	42	358	positive regulation of protein modification process	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,SKP2,PRKAA2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,F2RL1,FAM129A,NRP1,PTPN22,NPNT,SMPD1,PRKCE,CCNT1,FRS2,PARP9,APP,PSEN1,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,SH3RF3,DCUN1D4,MAP3K7,WFS1,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0009887	0.104	0.933	21	314	animal organ morphogenesis	BP	1	NOTCH2,NAB2,FBN1,THBS3,BMPR1A,NAGLU,TBX15,HOXC4,CLSTN1,SEMA3C,ASPN,THY1,B4GALT1,GLI3,IFT57,CDH2,IRX5,RDH10,GREM1,FOXO3,THRB	down_VCAV_EC
GO:0031400	0.104	0.937	17	205	negative regulation of protein modification process	BP	1	SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,DNAJC10,NXN,PTPN2,SPOPL,APOE,LYN,STRAP,CBLC,ATF3,CDYL,CDKN1A,KDM3A	down_VSAP_EC
GO:0009101	0.104	0.939	15	113	glycoprotein biosynthetic process	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,ITM2C,B3GNT7,CCDC126,MAGT1,STT3B,FUT11,FUT8,POMK,PSEN1,EOGT,LMF1	up_ACOR_VSMC
GO:1901293	0.104	0.942	13	106	nucleoside phosphate biosynthetic process	BP	1	PRPSAP1,ACLY,RRM1,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0016331	0.104	0.948	10	66	morphogenesis of embryonic epithelium	BP	1	SHROOM3,BMP4,FGFR2,SEC24B,CITED2,SPINT1,LMO4,ENSCAFG00000006238,SPINT2,FZD3	up_ACOR_VSMC
GO:2000112	0.104	0.952	9	1119	regulation of cellular macromolecule biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0046777	0.104	0.95	9	86	protein autophosphorylation	BP	1	VEGFA,ENPP1,ERRFI1,TNIK,LYN,GSK3B,EIF2S1,PAK2,BTK	down_VSAP_EC
GO:0050890	0.104	0.95	9	67	cognition	BP	0.979	PLK2,PTCHD1,ATP8A1,RELN,MEF2C,CHD7,CREB1,HIF1A,DOP1B	up_VCAV_EC
GO:0034764	0.104	0.953	8	50	positive regulation of transmembrane transport	BP	1	ACTN2,PLCG2,TCAF1,AKAP6,PSEN1,FXYD1,AZIN2,PARK7	up_ACOR_VSMC
GO:0006469	0.104	0.955	7	78	negative regulation of protein kinase activity	BP	1	DCN,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1	down_VCAV_EC
GO:0009755	0.104	0.958	6	52	hormone-mediated signaling pathway	BP	1	PTPN11,PRCP,SMARCA4,UBA5,YWHAH,KDM3A	down_VSAP_EC

GO:0032675	0.104	0.959	6	34	regulation of interleukin-6 production	BP	1	TLR1,MBP,TLR3,F2RL1,PTPN22,NOD2	up_ACOR_VSMC
GO:0009410	0.104	0.964	5	27	response to xenobiotic stimulus	BP	1	NCEH1,SLITRK5,PRKCE,NR3C1,DDIT4	up_ACOR_VSMC
GO:0033866	0.104	0.969	4	22	nucleoside bisphosphate biosynthetic process	BP	1	ACLY,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0034030	0.104	0.969	4	22	ribonucleoside bisphosphate biosynthetic	BP	1	ACLY,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0034033	0.104	0.969	4	22	purine nucleoside bisphosphate biosynthetic	BP	1	ACLY,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0002821	0.104	0.968	4	30	positive regulation of adaptive immune	BP	1	SOCS5,FAM49B,PVR,TFRC	down_VSAP_EC
GO:1902882	0.104	0.968	4	29	regulation of response to oxidative stress	BP	1	P4HB,SESN2,HIF1A,CTNNB1	down_VSAP_EC
GO:0048259	0.104	0.968	4	24	regulation of receptor-mediated endocytosis	BP	0.979	SELE,BMP2K,HIST1H1A,PLCG2	up_VCAV_EC
GO:0048194	0.104	0.975	3	18	Golgi vesicle budding	BP	1	SEC24D,SEC23A,SEC13	down_VSAP_EC
GO:1901216	0.104	0.975	3	19	positive regulation of neuron death	BP	1	DDIT3,GSK3B,EIF2S1	down_VSAP_EC
GO:0007599	0.104	0.974	3	48	hemostasis	BP	1	F5,F3,TFPI2	up_AFEM_EC
GO:0072009	0.104	0.974	3	48	nephron epithelium development	BP	1	IRX3,DLL1,GREM1	up_AFEM_EC
GO:0045664	0.104	0.974	3	144	regulation of neuron differentiation	BP	1	ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0072358	0.104	0.974	3	268	cardiovascular system development	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0002067	0.104	0.977	3	12	glandular epithelial cell differentiation	BP	1	HNF4A,DLL1,RARG	up_VSAP_EC
GO:0035336	0.104	0.986	2	7	long-chain fatty-acyl-CoA metabolic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0003159	0.104	0.985	2	9	morphogenesis of an endothelium	BP	1	CTNNB1,STARD13	down_VSAP_EC
GO:0006541	0.104	0.985	2	9	glutamine metabolic process	BP	1	ASNS,NR1H4	down_VSAP_EC
GO:0010573	0.104	0.985	2	9	vascular endothelial growth factor production	BP	1	SULF1,HIF1A	down_VSAP_EC
GO:0010574	0.104	0.985	2	9	regulation of vascular endothelial growth factor	BP	1	SULF1,HIF1A	down_VSAP_EC
GO:0031114	0.104	0.985	2	9	regulation of microtubule depolymerization	BP	1	ARHGEF2,MID1	down_VSAP_EC
GO:0061154	0.104	0.985	2	9	endothelial tube morphogenesis	BP	1	CTNNB1,STARD13	down_VSAP_EC
GO:0071674	0.104	0.983	2	23	mononuclear cell migration	BP	1	CMKLR1,CCL5	up_AFEM_EC
GO:0009792	0.104	0.984	2	231	embryo development ending in birth or egg	BP	1	HOXA9,HOXC6	up_AORT_EC
GO:0034139	0.104	0.986	2	7	regulation of toll-like receptor 3 signaling	BP	0.979	TNFAIP3,PELI1	up_VCAV_EC
GO:1903428	0.104	0.985	2	8	positive regulation of reactive oxygen species biosynthetic process	BP	0.979	TLR4,RAB27A	up_VCAV_EC
GO:0048679	0.104	0.986	2	6	regulation of axon regeneration	BP	1	RTN4RL1,MAP2K2	up_VSAP_EC
GO:0010718	0.104	0.995	1	21	positive regulation of epithelial to mesenchymal	BP	1	PDPN	down_ACOR_EC
GO:0021536	0.104	0.995	1	21	diencephalon development	BP	1	NRP2	down_ACOR_EC
GO:0048483	0.104	0.995	1	19	autonomic nervous system development	BP	1	NRP2	down_ACOR_EC
GO:0060350	0.104	0.995	1	23	endochondral bone morphogenesis	BP	1	CSGALNACT1	down_ACOR_EC
GO:0086011	0.104	0.997	1	2	membrane repolarization during action potential	BP	1	CAV1	down_ACOR_VSMC
GO:0098903	0.104	0.997	1	2	regulation of membrane repolarization during action potential	BP	1	CAV1	down_ACOR_VSMC
GO:0061572	0.104	0.995	1	50	actin filament bundle organization	BP	1	FSCN1	down_AFEM_EC
GO:0007341	0.104	0.997	1	2	penetration of zona pellucida	BP	1	B4GALT1	down_VCAV_EC
GO:0009644	0.104	0.997	1	2	response to high light intensity	BP	1	AKT2	down_VCAV_EC
GO:0010915	0.104	0.997	1	2	regulation of very-low-density lipoprotein	BP	1	LRPAP1	down_VCAV_EC
GO:0010916	0.104	0.997	1	2	negative regulation of very-low-density lipoprotein particle	BP	1	LRPAP1	down_VCAV_EC

GO:0010985	0.104	0.997	1	2	negative regulation of lipoprotein particle	BP	1	LRPAP1	down_VCAV_EC
GO:0018307	0.104	0.997	1	2	enzyme active site formation	BP	1	PARK7	down_VCAV_EC
GO:0034104	0.104	0.997	1	2	negative regulation of tissue remodeling	BP	1	GREM1	down_VCAV_EC
GO:0036476	0.104	0.997	1	2	neuron death in response to hydrogen peroxide	BP	1	PARK7	down_VCAV_EC
GO:0036481	0.104	0.997	1	2	intrinsic apoptotic signaling pathway in response to hydrogen	BP	1	PARK7	down_VCAV_EC
GO:0045838	0.104	0.997	1	2	positive regulation of membrane potential	BP	1	AKT2	down_VCAV_EC
GO:0002861	0.104	0.997	1	2	regulation of inflammatory response to	BP	1	PARK7	down_VCAV_EC
GO:0051572	0.104	0.997	1	2	negative regulation of histone H3-K4	BP	1	PRMT6	down_VCAV_EC
GO:0098838	0.104	0.997	1	2	folate transmembrane transport	BP	1	FOLR2	down_VCAV_EC
GO:0110095	0.104	0.997	1	2	cellular detoxification of aldehyde	BP	1	PARK7	down_VCAV_EC
GO:0110096	0.104	0.997	1	2	cellular response to aldehyde	BP	1	PARK7	down_VCAV_EC
GO:1900154	0.104	0.997	1	2	regulation of bone trabecula formation	BP	1	GREM1	down_VCAV_EC
GO:1900155	0.104	0.997	1	2	negative regulation of bone trabecula formation	BP	1	GREM1	down_VCAV_EC
GO:1900157	0.104	0.997	1	2	regulation of bone mineralization involved in	BP	1	GREM1	down_VCAV_EC
GO:1900158	0.104	0.997	1	2	negative regulation of bone mineralization involved in bone	BP	1	GREM1	down_VCAV_EC
GO:1902956	0.104	0.997	1	2	regulation of mitochondrial electron transport, NADH to	BP	1	PARK7	down_VCAV_EC
GO:1903207	0.104	0.997	1	2	regulation of hydrogen peroxide-induced neuron	BP	1	PARK7	down_VCAV_EC
GO:1903208	0.104	0.997	1	2	negative regulation of hydrogen peroxide-	BP	1	PARK7	down_VCAV_EC
GO:1903862	0.104	0.997	1	2	positive regulation of oxidative phosphorylation	BP	1	PARK7	down_VCAV_EC
GO:1904447	0.104	0.997	1	2	folate import across plasma membrane	BP	1	FOLR2	down_VCAV_EC
GO:1905448	0.104	0.997	1	2	positive regulation of mitochondrial ATP synthesis coupled	BP	1	PARK7	down_VCAV_EC
GO:0006004	0.104	0.997	1	2	fucose metabolic process	BP	1	POFUT1	down_VCAV_EC
GO:0006404	0.104	0.997	1	2	RNA import into nucleus	BP	1	SNUPN	down_VCAV_EC
GO:0006620	0.104	0.997	1	2	posttranslational protein targeting to endoplasmic reticulum membrane	BP	1	SEC61B	down_VCAV_EC
GO:0042483	0.104	0.997	1	2	negative regulation of odontogenesis	BP	1	ASPN	down_VCAV_EC
GO:0045654	0.104	0.997	1	2	positive regulation of megakaryocyte	BP	1	RAB7B	down_VCAV_EC
GO:0046060	0.104	0.997	1	2	dATP metabolic process	BP	1	ADK	down_VCAV_EC
GO:0046689	0.104	0.997	1	2	response to mercury ion	BP	1	PARK7	down_VCAV_EC
GO:0051030	0.104	0.997	1	2	snRNA transport	BP	1	SNUPN	down_VCAV_EC
GO:0051044	0.104	0.997	1	2	positive regulation of membrane protein	BP	1	PACSIN3	down_VCAV_EC
GO:0060046	0.104	0.997	1	2	regulation of acrosome reaction	BP	1	B4GALT1	down_VCAV_EC
GO:0060056	0.104	0.997	1	2	mammary gland involution	BP	1	B4GALT1	down_VCAV_EC
GO:0061015	0.104	0.997	1	2	snRNA import into nucleus	BP	1	SNUPN	down_VCAV_EC
GO:0098706	0.104	0.997	1	2	ferric iron import across cell outer membrane	BP	1	ARHGAP1	down_VCAV_EC
GO:1900086	0.104	0.997	1	2	positive regulation of peptidyl-tyrosine	BP	1	GREM1	down_VCAV_EC
GO:1900426	0.104	0.997	1	2	positive regulation of defense response to	BP	1	CYBA	down_VCAV_EC
GO:1901072	0.104	0.997	1	2	glucosamine-containing compound catabolic	BP	1	CHID1	down_VCAV_EC

GO:1902430	0.104	0.997	1	2	negative regulation of amyloid-beta formation	BP	1	PRNP	down_VCAV_EC
GO:1902992	0.104	0.997	1	2	negative regulation of amyloid precursor protein catabolic process	BP	1	PRNP	down_VCAV_EC
GO:1904211	0.104	0.997	1	2	membrane protein proteolysis involved in retrograde protein	BP	1	HM13	down_VCAV_EC
GO:0001838	0.104	0.995	1	56	embryonic epithelial tube formation	BP	1	CITED2	down_VPOR_EC
GO:1901700	0.104	0.997	1	364	response to oxygen-containing compound	BP	1	JUP	down_VFEM_VSMC
GO:0045541	0.104	0.997	1	2	negative regulation of cholesterol biosynthetic	BP	1	APOE	down_VSAP_EC
GO:0090206	0.104	0.997	1	2	negative regulation of cholesterol metabolic	BP	1	APOE	down_VSAP_EC
GO:0106119	0.104	0.997	1	2	negative reguation of sterol biosynthetic	BP	1	APOE	down_VSAP_EC
GO:1901386	0.104	0.997	1	2	negative regulation of voltage-gated calcium	BP	1	REM1	down_VSAP_EC
GO:1901841	0.104	0.997	1	2	regulation of high voltage-gated calcium channel	BP	1	REM1	down_VSAP_EC
GO:1901842	0.104	0.997	1	2	negative regulation of high voltage-gated calcium channel activity	BP	1	REM1	down_VSAP_EC
GO:2001270	0.104	0.997	1	2	regulation of cysteine-type endopeptidase activity involved in	BP	1	PAK2	down_VSAP_EC
GO:0038018	0.104	1	1	1	Wnt receptor catabolic process	BP	1	ZNRF3	up_ACOR_VSMC
GO:0034130	0.104	1	1	1	toll-like receptor 1 signaling pathway	BP	1	TLR1	up_ACOR_VSMC
GO:0045410	0.104	1	1	1	positive regulation of interleukin-6 biosynthetic	BP	1	TLR1	up_ACOR_VSMC
GO:0021953	0.104	0.995	1	49	central nervous system neuron differentiation	BP	1	HOXC10	up_AORT_EC
GO:0055076	0.104	0.995	1	44	transition metal ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0048167	0.104	0.995	1	28	regulation of synaptic plasticity	BP	1	NTRK2	up_APUL_EC
GO:0050709	0.104	0.995	1	28	negative regulation of protein secretion	BP	1	NR1H4	up_APUL_EC
GO:0034421	0.104	1	1	1	post-translational protein acetylation	BP	0.979	ESCO1	up_VCAV_EC
GO:0051770	0.104	1	1	1	positive regulation of nitric-oxide synthase	BP	0.979	TLR4	up_VCAV_EC
GO:0070426	0.104	1	1	1	positive regulation of nucleotide-binding oligomerization domain	BP	0.979	TLR4	up_VCAV_EC
GO:0070430	0.104	1	1	1	positive regulation of nucleotide-binding oligomerization domain	BP	0.979	TLR4	up_VCAV_EC
GO:0035666	0.104	1	1	1	TRIF-dependent toll-like receptor signaling	BP	0.979	TLR4	up_VCAV_EC
GO:0038060	0.104	1	1	1	nitric oxide-cGMP-mediated signaling	BP	0.979	GUCY1B1	up_VCAV_EC
GO:0070434	0.104	1	1	1	positive regulation of nucleotide-binding oligomerization domain	BP	0.979	TLR4	up_VCAV_EC
GO:0030837	0.104	0.995	1	14	negative regulation of actin filament	BP	1	TWF1	up_VPOR_EC
GO:0061462	0.104	0.995	1	15	protein localization to lysosome	BP	1	GCC2	up_VPOR_EC
GO:0030010	0.104	0.995	1	41	establishment of cell polarity	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048771	0.104	0.995	1	43	tissue remodeling	BP	1	HOXA3	up_VPOR_VSMC
GO:0010466	0.104	0.995	1	32	negative regulation of peptidase activity	BP	1	PTGER2	up_VPUL_EC
GO:0010951	0.104	0.995	1	32	negative regulation of endopeptidase activity	BP	1	PTGER2	up_VPUL_EC
GO:0097305	0.104	0.995	1	31	response to alcohol	BP	1	PTGER2	up_VPUL_EC
GO:0007611	0.104	0.995	1	54	learning or memory	BP	1	LRRN4	up_VPUL_VSMC
GO:0001508	0.104	0.995	1	25	action potential	BP	1	CAV1	up_VSAP_VSMC
GO:0050729	0.104	0.995	1	25	positive regulation of inflammatory response	BP	1	TLR2	up_VSAP_VSMC

GO:0003170	0.104	0.995	1	25	heart valve development	BP	1	SHOX2	up_VSAP_VSMC
GO:0034349	0.104075229	0.99577	1	4	glial cell apoptotic process	BP	1	PRKCD	up_ACOR_EC
GO:0060729	0.104146276	0.99577	1	4	intestinal epithelial structure maintenance	BP	1	SOX9	up_ACOR_EC
GO:0044241	0.10427067	0.99576	1	4	lipid digestion	BP	1	AQP1	up_ACOR_EC
GO:0033623	0.104382122	0.99575	1	4	regulation of integrin activation	BP	1	PTGER4	up_ACOR_EC
GO:0060292	0.104620911	0.99573	1	4	long-term synaptic depression	BP	1	KCNB1	up_ACOR_EC
GO:0071073	0.104625319	0.99573	1	4	positive regulation of phospholipid biosynthetic	BP	1	NR1H4	up_ACOR_EC
GO:0051890	0.104661913	0.99572	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_ACOR_EC
GO:0032536	0.104751034	0.99572	1	4	regulation of cell projection size	BP	1	PLS1	up_ACOR_EC
GO:0098719	0.104861149	0.99571	1	4	sodium ion import across plasma membrane	BP	1	SLC9A9	up_ACOR_EC
GO:0034383	0.104869842	0.99571	1	4	low-density lipoprotein particle clearance	BP	1	NR1H4	up_ACOR_EC
GO:1901362	0.105	0.913	121	1293	organic cyclic compound biosynthetic process	BP	1	ELK3,PRPSAP1,SQLE,HMGB1,LSS,SREBF1,ACLY,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,HMGCR,HNRNPD,SREBF2,HINFP,NEDD4,RRM1,MED17,SLC29A1,MTDH,HEY1,SF1,SRRT,POLE,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,ENSCAFG00000018572,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,DHCR24,BRCA1,MVD,NOC2L,E2F8,ELOVL1,PPARD,POLH,YBX3,NCL,NUP62,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,FDFT1,RBM14,CYC1,POLR3F,HOXA10,ERF,TCERG1,ATP5F1A,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,NUDT1,HMGN1,CCT4,SIX4,CTPS1,MED16,ENSCAFG00000017103,ATP5F1D,POLR1C,NUDT3	down_ACOR_VSMC
GO:0051704	0.105	0.92	54	476	multi-organism process	BP	1	VEGFD,TLR1,PLCG2,LEP,USP6NL,TMEM255A,PRDX4,RECK,COCH,BMP4,MX1,ABCA1,ATRX,TLR3,PDE5A,CITED2,GLRB,ISG15,PTGIR,SASH1,PLAC8B,ANKRD1,F2RL1,CTSB,BNIP3,SLC17A5,PTPN22,GPM6A,ULK2,PRKCE,MARF1,AFF4,DKKL1,DAG1,PARP9,APP,CHD7,SPINK2,CCL5,CLN8,HPGD,NOD2,ATG16L2,DMC1,DDIT4,JAM3,NAALADL2,B2M,SERINC3,TNFRSF11B,INPP5K,HERPUD2,WDR48,WASL	up_ACOR_VSMC
GO:0009628	0.105	0.931	24	302	response to abiotic stimulus	BP	1	ARHGEF2,VEGFA,P4HB,PLOD2,PLK3,CASP3,HYOU1,PGK1,LRRC8A,BHLHE40,PTGS2,HIF1A,ADAM17,GNAQ,CRYAB,BNIP3,FAM162A,BACH1,HTT,REST,EIF2S1,RDH11,HIF1AN,CDKN1A	down_VSAP_EC
GO:0051052	0.105	0.936	18	145	regulation of DNA metabolic process	BP	0.979	PDGFB,GATA3,FIGNL1,UHRF2,HMBOX1,PRKD2,THOC1,ESCO1,TIMELESS,OTUD4,HMGB1,BLM,RAD17,USP37,CUL4A,ATRX,RBBP6,DCP2	up_VCAV_EC
GO:0098655	0.105	0.944	11	142	cation transmembrane transport	BP	1	PRNP,FXYD1,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SCARA5,CYBA,ARHGAP1	down_VCAV_EC
GO:0030900	0.105	0.946	10	101	forebrain development	BP	1	HOOK3,HIF1A,UBA6,UCHL5,CTNNB1,GSK3B,EXT1,DISC1,INHBA,NRP1	down_VSAP_EC
GO:0050863	0.105	0.949	9	69	regulation of T cell activation	BP	0.979	IL7R,GATA3,PELI1,ARG2,ITPKB,NCK1,BCL10,HMGB1,ZEB1	up_VCAV_EC
GO:0061025	0.105	0.949	9	69	membrane fusion	BP	0.979	TIE1,MX2,NECTIN2,SNAP23,CAV2,STX11,TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0010942	0.105	0.95	8	200	positive regulation of cell death	BP	1	F3,MLLT11,PLAGL2,CAMK2A,CYLD,DCUN1D3,AXIN2,FAP	up_AFEM_EC
GO:0016042	0.105	0.954	7	80	lipid catabolic process	BP	1	AKT2,ACAA1,PLCL1,PEX5,ENSCAFG00000017708,LONP2,ACAT1	down_VCAV_EC
GO:0001892	0.105	0.959	6	35	embryonic placenta development	BP	1	FGFR2,CITED2,SPINT1,EGLN1,ENSCAFG00000006238,SPINT2	up_ACOR_VSMC
GO:0007043	0.105	0.963	5	28	cell-cell junction assembly	BP	0.979	PRKCH,OCLN,TJP1,CTNNA1,FSCN1	up_VCAV_EC

GO:2001257	0.105	0.967	4	30	regulation of cation channel activity	BP	1	REM1,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0051146	0.105	0.966	4	76	striated muscle cell differentiation	BP	1	DLL1,GREM1,BVES,DMPK	up_AFEM_EC
GO:0021510	0.105	0.974	3	23	spinal cord development	BP	1	LMO4,GLI3,LOXL3	down_VCAV_EC
GO:0001837	0.105	0.974	3	48	epithelial to mesenchymal transition	BP	1	TMEM100,GREM1,AXIN2	up_AFEM_EC
GO:0002062	0.105	0.973	3	48	chondrocyte differentiation	BP	1	GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:0007019	0.105	0.976	3	13	microtubule depolymerization	BP	0.979	STMN1,TAOK1,ARHGEF2	up_VCAV_EC
GO:0034629	0.105	0.976	3	14	cellular protein-containing complex localization	BP	0.979	EXOC3L2,MZT1,NUP133	up_VCAV_EC
GO:0006040	0.105	0.976	3	12	amino sugar metabolic process	BP	1	RENBP,CHST7,GNPDA1	up_VSAP_EC
GO:1902305	0.105	0.976	3	12	regulation of sodium ion transmembrane transport	BP	1	OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0009262	0.105	0.985	2	7	deoxyribonucleotide metabolic process	BP	1	RRM1,NUDT1	down_ACOR_VSMC
GO:0006584	0.105	0.984	2	11	catecholamine metabolic process	BP	1	MAOA,PARK7	down_VCAV_EC
GO:0009712	0.105	0.984	2	11	catechol-containing compound metabolic	BP	1	MAOA,PARK7	down_VCAV_EC
GO:0070206	0.105	0.984	2	11	protein trimerization	BP	1	COL6A1,SCARA5	down_VCAV_EC
GO:0032781	0.105	0.984	2	10	positive regulation of ATPase activity	BP	1	DYNLL1,DNAJC10	down_VSAP_EC
GO:0045724	0.105	0.985	2	9	positive regulation of cilium assembly	BP	1	DYNLL1,HTT	down_VSAP_EC
GO:0045981	0.105	0.986	2	6	positive regulation of nucleotide metabolic	BP	1	PPARGC1A,PARK7	up_ACOR_VSMC
GO:0051444	0.105	0.986	2	6	negative regulation of ubiquitin-protein	BP	1	PSEN1,PARK7	up_ACOR_VSMC
GO:1900544	0.105	0.986	2	6	positive regulation of purine nucleotide	BP	1	PPARGC1A,PARK7	up_ACOR_VSMC
GO:1990000	0.105	0.986	2	6	amyloid fibril formation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0043928	0.105	0.985	2	8	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-	BP	0.979	CNOT6,CNOT7	up_VCAV_EC
GO:0090136	0.105	0.985	2	7	epithelial cell-cell adhesion	BP	0.979	KIT,CTNNA1	up_VCAV_EC
GO:0009719	0.105	0.984	2	395	response to endogenous stimulus	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0040007	0.105	0.984	2	276	growth	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0021795	0.105	0.995	1	20	cerebral cortex cell migration	BP	1	NRP2	down_ACOR_EC
GO:0022409	0.105	0.995	1	56	positive regulation of cell-cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0002262	0.105	0.995	1	54	myeloid cell homeostasis	BP	1	CITED2	down_VPOR_EC
GO:0006511	0.105	0.996	1	253	ubiquitin-dependent protein catabolic process	BP	1	USP12	down_VFEM_EC
GO:0038145	0.105	0.997	1	2	macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:0043456	0.105	0.997	1	2	regulation of pentose-phosphate shunt	BP	1	PGAM1	down_VSAP_EC
GO:0043471	0.105	0.997	1	2	regulation of cellular carbohydrate catabolic	BP	1	PGAM1	down_VSAP_EC
GO:1902226	0.105	0.997	1	2	regulation of macrophage colony-stimulating factor signaling pathway	BP	1	PTPN2	down_VSAP_EC
GO:1902227	0.105	0.997	1	2	negative regulation of macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:1903970	0.105	0.997	1	2	negative regulation of response to macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:1903973	0.105	0.997	1	2	negative regulation of cellular response to macrophage colony-	BP	1	PTPN2	down_VSAP_EC
GO:0019355	0.105	0.997	1	2	nicotinamide nucleotide biosynthetic process from aspartate	BP	1	NMNAT2	down_VSAP_EC
GO:0034627	0.105	0.997	1	2	'de novo' NAD biosynthetic process	BP	1	NMNAT2	down_VSAP_EC

GO:0034628	0.105	0.997	1	2	'de novo' NAD biosynthetic process from	BP	1	NMNAT2	down_VSAP_EC
GO:1904211	0.105	0.997	1	2	membrane protein proteolysis involved in retrograde protein	BP	1	HM13	down_VSAP_EC
GO:0043686	0.105	1	1	1	co-translational protein modification	BP	1	STT3B	up_ACOR_VSMC
GO:0007354	0.105	1	1	1	zygotic determination of anterior/posterior axis,	BP	1	PCSK6	up_ACOR_VSMC
GO:0032898	0.105	1	1	1	neurotrophin production	BP	1	PCSK6	up_ACOR_VSMC
GO:0032902	0.105	1	1	1	nerve growth factor production	BP	1	PCSK6	up_ACOR_VSMC
GO:0001763	0.105	0.995	1	78	morphogenesis of a branching structure	BP	1	EYA1	up_AFEM_VSMC
GO:0048705	0.105	0.995	1	95	skeletal system morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0010827	0.105	0.995	1	28	regulation of glucose transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0043271	0.105	0.995	1	28	negative regulation of ion transport	BP	1	HOXA3	up_APUL_EC
GO:0060675	0.105	0.995	1	29	ureteric bud morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0010750	0.105	1	1	1	positive regulation of nitric oxide mediated	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0052551	0.105	1	1	1	response to defense-related nitric oxide production by other organism involved in	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0052564	0.105	1	1	1	response to immune response of other organism involved in	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0052565	0.105	1	1	1	response to defense-related host nitric oxide	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0052572	0.105	1	1	1	response to host immune response	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0098923	0.105	1	1	1	retrograde trans-synaptic signaling by soluble gas	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0099163	0.105	1	1	1	synaptic signaling by nitric oxide	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0099543	0.105	1	1	1	trans-synaptic signaling by soluble gas	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0099548	0.105	1	1	1	trans-synaptic signaling by nitric oxide	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0099554	0.105	1	1	1	trans-synaptic signaling by soluble gas, modulating synaptic transmission	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0099555	0.105	1	1	1	trans-synaptic signaling by nitric oxide, modulating synaptic transmission	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0098924	0.105	1	1	1	retrograde trans-synaptic signaling by nitric oxide	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0098925	0.105	1	1	1	retrograde trans-synaptic signaling by nitric oxide, modulating synaptic	BP	0.979	GUCY1A1	up_VCAV_EC
GO:0048762	0.105	0.995	1	77	mesenchymal cell differentiation	BP	1	GATA5	up_VCAV_VSMC
GO:0060348	0.105	0.995	1	78	bone development	BP	1	LRRC17	up_VCAV_VSMC
GO:0030878	0.105	0.995	1	13	thyroid gland development	BP	1	HOXA3	up_VPOR_EC
GO:0007204	0.105	0.995	1	46	positive regulation of cytosolic calcium ion	BP	1	C3AR1	up_VPOR_VSMC
GO:0050905	0.105	0.995	1	26	neuromuscular process	BP	1	HOXC10	up_VFEM_EC
GO:0051963	0.105	0.995	1	26	regulation of synapse assembly	BP	1	SIX1	up_VFEM_EC
GO:0051147	0.105	0.995	1	44	regulation of muscle cell differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0035296	0.105	0.995	1	32	regulation of tube diameter	BP	1	HTR7	up_VPUL_EC
GO:0097746	0.105	0.995	1	32	regulation of blood vessel diameter	BP	1	HTR7	up_VPUL_EC
GO:0002685	0.105	0.995	1	55	regulation of leukocyte migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0035265	0.105	0.995	1	54	organ growth	BP	1	TBX5	up_VPUL_VSMC
GO:0010522	0.105	0.995	1	24	regulation of calcium ion transport into cytosol	BP	1	CAV1	up_VSAP_VSMC

GO:0032225	0.1050626	0.99569	1	4	regulation of synaptic transmission,	BP	1	CNTNAP4	up_ACOR_EC
GO:0021855	0.105067508	0.99569	1	4	hypothalamus cell migration	BP	1	NRP1	up_ACOR_EC
GO:0060340	0.105096846	0.99569	1	4	positive regulation of type I interferon-mediated signaling pathway	BP	1	MAVS	up_ACOR_EC
GO:0007351	0.105206957	0.99568	1	4	tripartite regional subdivision	BP	1	FZD5	up_ACOR_EC
GO:0008595	0.105206957	0.99568	1	4	anterior/posterior axis specification, embryo	BP	1	FZD5	up_ACOR_EC
GO:0090049	0.105237547	0.98296	2	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0140058	0.105346626	0.99567	1	4	neuron projection arborization	BP	1	NRP1	up_ACOR_EC
GO:0070857	0.10537398	0.99567	1	4	regulation of bile acid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:1904251	0.10537398	0.99567	1	4	regulation of bile acid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0030952	0.105388413	0.99566	1	4	establishment or maintenance of	BP	1	AQP1	up_ACOR_EC
GO:0003211	0.105475541	0.99566	1	4	cardiac ventricle formation	BP	1	TBX5	up_ACOR_EC
GO:0042636	0.105478634	0.99566	1	4	negative regulation of hair cycle	BP	1	CDH3	up_ACOR_EC
GO:0051799	0.105478634	0.99566	1	4	negative regulation of hair follicle development	BP	1	CDH3	up_ACOR_EC
GO:0003263	0.105543701	0.99565	1	4	cardioblast proliferation	BP	1	TBX5	up_ACOR_EC
GO:0009309	0.10555085	0.99565	1	4	amine biosynthetic process	BP	1	AZIN2	up_ACOR_EC
GO:0042401	0.10555085	0.99565	1	4	cellular biogenic amine biosynthetic process	BP	1	AZIN2	up_ACOR_EC
GO:0010464	0.105675401	0.98285	2	21	regulation of mesenchymal cell	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0097090	0.105712406	0.99564	1	4	presynaptic membrane organization	BP	1	LRP4	up_ACOR_EC
GO:0007617	0.105746768	0.99563	1	4	mating behavior	BP	1	MAPK8IP2	up_ACOR_EC
GO:1902946	0.105826983	0.99563	1	4	protein localization to early endosome	BP	1	NRP1	up_ACOR_EC
GO:0051173	0.106	0.915	83	874	positive regulation of nitrogen compound metabolic process	BP	0.981	PLK2,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,MEF2C,ATF3,CHD7,TIPARP,TLR4,NLRC5,GATA3,EDN1,RALB,APLNR,TCF4,FOXN2,ENSCAFG00000017103,NEDD9,IRF8,PELI1,PPP3CA,YES1,CASP8,MTOR,MAP3K3,BMP2,HHEX,CREM,SLK,CNOT6,PROX1,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,OTUD4,LDB2,JAG1,NSD1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,CNOT7,HMGB1,AHR,NOS2,PMAIP1,BLM,RIPK1,ITGA6,GPBP1,PDGFD,MTA2,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ATRX,NR4A1,JCAD,ZEB1,TET2,ARHGEF2,CDON,ZNF609	up_VCAV_EC
GO:0003006	0.106	0.933	20	180	developmental process involved in reproduction	BP	0.981	PCDH12,KIT,PDGFB,CHD7,TIPARP,EIF2B2,GATA3,PSME4,NECTIN2,MTOR,CDYL,MDFI,ARID4B,PTGS2,AFF4,HIF1A,KDM3A,ATRX,VASH1,FBXO5	up_VCAV_EC
GO:0010769	0.106	0.946	10	69	regulation of cell morphogenesis involved	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,FBLN1,PQBP1,TTL,MAP2K2	up_VSAP_EC
GO:1901360	0.106	0.958	8	2016	organic cyclic compound metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060828	0.106	0.953	7	82	regulation of canonical Wnt signaling pathway	BP	1	RECK,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0090304	0.106	0.96	7	1694	nucleic acid metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0019935	0.106	0.958	6	38	cyclic-nucleotide-mediated signaling	BP	0.979	CALCRL,PDE4D,APLNR,ABCA1,GUCY1B1,RAPGEF2	up_VCAV_EC
GO:0070663	0.106	0.962	5	50	regulation of leukocyte proliferation	BP	1	GPAM,PRNP,SDC4,GREM1,RAC2	down_VCAV_EC
GO:0006974	0.106	0.967	4	333	cellular response to DNA damage stimulus	BP	1	LYN,USP28,ATRIP,NEDD4	down_ACOR_EC
GO:0051254	0.106	0.967	4	431	positive regulation of RNA metabolic process	BP	1	HOXA11,HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:0001885	0.106	0.974	3	19	endothelial cell development	BP	1	MSN,CTNNB1,PLOD3	down_VSAP_EC

GO:0097006	0.106	0.974	3	19	regulation of plasma lipoprotein particle levels	BP	1	NR1H4,APOE,VLDLR	down_VSAP_EC
GO:0007267	0.106	0.974	3	332	cell-cell signaling	BP	1	TBX5,NR1H4,HTR7	up_VPUL_EC
GO:0000038	0.106	0.976	3	12	very long-chain fatty acid metabolic process	BP	1	ACAA1,PEX2,HACD4	up_VSAP_EC
GO:0045785	0.106	0.982	2	107	positive regulation of cell adhesion	BP	1	PDPN,STX4	down_ACOR_EC
GO:1901342	0.106	0.982	2	114	regulation of vasculature development	BP	1	ACVRL1,SULF1	down_ACOR_EC
GO:0045652	0.106	0.985	2	7	regulation of megakaryocyte	BP	1	PRMT1,HMGB2	down_ACOR_VSMC
GO:0031102	0.106	0.984	2	11	neuron projection regeneration	BP	1	THY1,RGMA	down_VCAV_EC
GO:0060135	0.106	0.984	2	10	maternal process involved in female pregnancy	BP	1	TMED2,PTGS2	down_VSAP_EC
GO:0030836	0.106	0.986	2	6	positive regulation of actin filament	BP	1	ACTN2,F2RL1	up_ACOR_VSMC
GO:0050996	0.106	0.986	2	6	positive regulation of lipid catabolic process	BP	1	PRKCE,ENSCAFG00000029553	up_ACOR_VSMC
GO:0007097	0.106	0.985	2	7	nuclear migration	BP	0.981	HOOK3,HHEX	up_VCAV_EC
GO:0051647	0.106	0.985	2	7	nucleus localization	BP	0.981	HOOK3,HHEX	up_VCAV_EC
GO:0120039	0.106	0.983	2	158	plasma membrane bounded cell projection	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0048665	0.106	0.986	2	6	neuron fate specification	BP	1	DLL1,HOXC10	up_VSAP_EC
GO:0060693	0.106	0.986	2	6	regulation of branching involved in salivary gland	BP	1	FGF7,NTN4	up_VSAP_EC
GO:0048010	0.106	0.995	1	20	vascular endothelial growth factor receptor	BP	1	SULF1	down_ACOR_EC
GO:0090303	0.106	0.995	1	18	positive regulation of wound healing	BP	1	PDPN	down_ACOR_EC
GO:0050793	0.106	1	1	731	regulation of developmental process	BP	1	GATA5	down_AFEM_VSMC
GO:0008406	0.106	0.995	1	57	gonad development	BP	1	CITED2	down_VPOR_EC
GO:0021915	0.106	0.995	1	58	neural tube development	BP	1	CITED2	down_VPOR_EC
GO:0045137	0.106	0.995	1	57	development of primary sexual characteristics	BP	1	CITED2	down_VPOR_EC
GO:0032025	0.106	0.997	1	2	response to cobalt ion	BP	1	BNIP3	down_VSAP_EC
GO:0071279	0.106	0.997	1	2	cellular response to cobalt ion	BP	1	BNIP3	down_VSAP_EC
GO:1990442	0.106	0.997	1	2	intrinsic apoptotic signaling pathway in response to nitrosative	BP	1	DDIT3	down_VSAP_EC
GO:0045764	0.106	0.997	1	2	positive regulation of cellular amino acid	BP	1	NR1H4	down_VSAP_EC
GO:0032498	0.106	1	1	1	detection of muramyl dipeptide	BP	1	NOD2	up_ACOR_VSMC
GO:0032499	0.106	1	1	1	detection of peptidoglycan	BP	1	NOD2	up_ACOR_VSMC
GO:1903532	0.106	0.995	1	78	positive regulation of secretion by cell	BP	1	TLR2	up_AFEM_VSMC
GO:0055001	0.106	0.995	1	47	muscle cell development	BP	1	SGCD	up_AORT_EC
GO:0010632	0.106	0.995	1	95	regulation of epithelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0045833	0.106	0.995	1	29	negative regulation of lipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0050954	0.106	0.995	1	30	sensory perception of mechanical stimulus	BP	1	HOXA1	up_APUL_EC
GO:0034109	0.106	0.995	1	14	homotypic cell-cell adhesion	BP	1	SLC7A11	up_VPOR_EC
GO:0055002	0.106	0.995	1	45	striated muscle cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0031214	0.106	0.995	1	45	biomineral tissue development	BP	1	HOXA3	up_VPOR_VSMC
GO:0007009	0.106	0.995	1	27	plasma membrane organization	BP	1	MTSS1	up_VFEM_EC
GO:0045739	0.106	0.995	1	26	positive regulation of DNA repair	BP	1	EYA1	up_VFEM_EC
GO:0006939	0.106	0.995	1	32	smooth muscle contraction	BP	1	HTR7	up_VPUL_EC
GO:0097530	0.106	0.995	1	33	granulocyte migration	BP	1	CCL24	up_VPUL_EC

GO:0045665	0.106	0.995	1	55	negative regulation of neuron differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0033002	0.106	0.995	1	55	muscle cell proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0010469	0.106	0.995	1	26	regulation of signaling receptor activity	BP	1	NETO1	up_VSAP_VSMC
GO:0002367	0.106	0.995	1	26	cytokine production involved in immune	BP	1	TLR2	up_VSAP_VSMC
GO:0048332	0.106	0.995	1	26	mesoderm morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:0007043	0.106	0.995	1	28	cell-cell junction assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0050905	0.106	0.995	1	26	neuromuscular process	BP	1	HOXC10	up_VSAP_VSMC
GO:0043981	0.106153259	0.9956	1	4	histone H4-K5 acetylation	BP	1	PHF20	up_ACOR_EC
GO:0043982	0.106153259	0.9956	1	4	histone H4-K8 acetylation	BP	1	PHF20	up_ACOR_EC
GO:0007214	0.106162457	0.9956	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	up_ACOR_EC
GO:0042219	0.106524984	0.99557	1	4	cellular modified amino acid catabolic process	BP	1	SARDH	up_ACOR_EC
GO:0032490	0.106623508	0.99556	1	4	detection of molecule of bacterial origin	BP	1	NOD2	up_ACOR_EC
GO:0051639	0.106705915	0.99555	1	4	actin filament network formation	BP	1	PLS1	up_ACOR_EC
GO:0006582	0.106745024	0.99555	1	4	melanin metabolic process	BP	1	CDH3	up_ACOR_EC
GO:0042438	0.106745024	0.99555	1	4	melanin biosynthetic process	BP	1	CDH3	up_ACOR_EC
GO:1904396	0.10682542	0.99554	1	4	regulation of neuromuscular junction	BP	1	LRP4	up_ACOR_EC
GO:0050808	0.106839983	0.96032	5	93	synapse organization	BP	1	CNTNAP4,PAK3,LRP4,LRRC4,NRP1	up_ACOR_EC
GO:0030035	0.106844341	0.99554	1	4	microspike assembly	BP	1	ACTN2	up_ACOR_EC
GO:0030182	0.107	0.924	35	327	neuron differentiation	BP	0.981	EPHB1,EDNRB,IFRD1,RELN,MEF2C,DLL4,RAPGEF1,GATA3,RAB11A,TCF4,NTN4,PPP3CA,BMP2,HMG20A,PREX2,GDPD5,PROX1,ENSCAFG00000010224,STMN1,PAK2,APOD,NCK1,FES,JAG1,MMD,RAPGEF2,CREB1,ZC4H2,SPTBN4,SKIL,HIF1A,ALS2,ZEB1,ARHGEF2,CDON	up_VCAV_EC
GO:0002684	0.107	0.927	29	239	positive regulation of immune system process	BP	1	VEGFD,TLR1,PLCG2,LEP,CD83,COCH,TP53BP1,ELF1,TLR3,ISG15,CD274,FAM210B,F2RL1,CDKN1A,C1S,CLSTN1,PTPN22,C7,PRKCE,PARP9,APP,PSEN1,CCL5,DUSP22,NOD2,B2M,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0030163	0.107	0.927	28	365	protein catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,TRIB3,MSN,SEL1L,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0008285	0.107	0.929	25	201	negative regulation of cell proliferation	BP	1	WNT11,HNF4A,CD274,AXIN2,LIMS2,PEX2,BTG1,DLL1,SAV1,ZBTB16,RARG,AMBRA1,MORC3,MFN2,PTGES,ZEB1,FBXO4,KDM2B,FBLN1,RAF1,NFIB,SMARCA2,ACVRL1,HMOX1,DPT	up_VSAP_EC
GO:0043408	0.107	0.93	23	211	regulation of MAPK cascade	BP	0.981	EPHB1,TEK,KIT,MAP3K11,TNIP1,PDGFB,ATF3,RAPGEF1,TLR4,EDN1,MAP3K3,BMP2,MADD,PAK2,PRKD2,TLR3,RAPGEF2,TAOK1,HMGB1,RIPK1,PDGFD,JCAD,CDON	up_VCAV_EC
GO:0051098	0.107	0.936	17	129	regulation of binding	BP	1	ARHGAP28,PLCL1,BMP4,XIRP1,CLSTN1,LRPAP1,SMARCD3,CCPG1,PARP9,APP,PSEN1,MITD1,AKTIP,B2M,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0045087	0.107	0.938	14	161	innate immune response	BP	1	ARHGEF2,NR1H4,FLNB,MYO1C,KIF5B,PTPN2,PVR,CNOT7,LYN,CDC37,GBP5,A2M,BTK,DEFB124	down_VSAP_EC
GO:0008202	0.107	0.953	7	80	steroid metabolic process	BP	1	LCAT,ACAA1,HSD3B7,SCP2,CYB5R3,CYP1B1,SOAT1	down_VCAV_EC
GO:2000147	0.107	0.952	7	169	positive regulation of cell motility	BP	1	CMKLR1,ANGPT4,TWIST2,LRRC15,LGR6,CCL5,ADAM17	up_AFEM_EC
GO:0070588	0.107	0.957	6	54	calcium ion transmembrane transport	BP	1	ERO1A,REM1,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0019217	0.107	0.962	5	27	regulation of fatty acid metabolic process	BP	1	INSIG2,ACACB,C1QTNF2,PDK2,LONP2	up_VSAP_EC
GO:0032635	0.107	0.967	4	37	interleukin-6 production	BP	1	BPI,CYBA,MAVS,RAB7B	down_VCAV_EC
GO:1904659	0.107	0.967	4	36	glucose transmembrane transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC

GO:0010466	0.107	0.967	4	32	negative regulation of peptidase activity	BP	1	PTGS2,CRYAB,PAK2,SPINK2	down_VSAP_EC
GO:0010951	0.107	0.967	4	32	negative regulation of endopeptidase activity	BP	1	PTGS2,CRYAB,PAK2,SPINK2	down_VSAP_EC
GO:0050728	0.107	0.967	4	31	negative regulation of inflammatory response	BP	1	NR1H4,SOCS5,PTPN2,APOE	down_VSAP_EC
GO:0051817	0.107	0.967	4	31	modification of morphology or physiology of other organism	BP	1	SMARCA4,APOE,REST,CALM1	down_VSAP_EC
GO:0097006	0.107	0.968	4	19	regulation of plasma lipoprotein particle levels	BP	1	LCAT,ABCA1,LRPAP1,LMF1	up_ACOR_VSMC
GO:0048518	0.107	0.975	4	1676	positive regulation of biological process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0055024	0.107	0.968	4	22	regulation of cardiac muscle tissue	BP	0.981	MEF2C,EDN1,BMP2,CREB1	up_VCAV_EC
GO:0007131	0.107	0.975	3	14	reciprocal meiotic recombination	BP	1	TRIP13,RAD51,MND1	down_ACOR_VSMC
GO:0035825	0.107	0.975	3	14	homologous recombination	BP	1	TRIP13,RAD51,MND1	down_ACOR_VSMC
GO:0001960	0.107	0.975	3	15	negative regulation of cytokine-mediated	BP	0.981	NLRC5,OTUD4,CNOT7	up_VCAV_EC
GO:0060761	0.107	0.975	3	15	negative regulation of response to cytokine	BP	0.981	NLRC5,OTUD4,CNOT7	up_VCAV_EC
GO:0001523	0.107	0.976	3	12	retinoid metabolic process	BP	1	DHRS4,RETSAT,DHRS9	up_VSAP_EC
GO:0019682	0.107	0.984	2	10	glyceraldehyde-3-phosphate metabolic	BP	1	TPI1,PGAM1	down_VSAP_EC
GO:0046676	0.107	0.984	2	9	negative regulation of insulin secretion	BP	1	PTPN11,REST	down_VSAP_EC
GO:0007512	0.107	0.986	2	6	adult heart development	BP	1	GJA1,CHD7	up_ACOR_VSMC
GO:0071467	0.107	0.986	2	6	cellular response to pH	BP	1	GJA1,RAB11B	up_ACOR_VSMC
GO:1905048	0.107	0.986	2	6	regulation of metallopeptidase activity	BP	1	MBP,RECK	up_ACOR_VSMC
GO:0043627	0.107	0.985	2	8	response to estrogen	BP	0.981	GATA3,ARID5A	up_VCAV_EC
GO:0007417	0.107	0.983	2	235	central nervous system development	BP	1	HOXC10,EMX2	up_VFEM_VSMC
GO:0048858	0.107	0.982	2	159	cell projection morphogenesis	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:2000145	0.107	0.983	2	279	regulation of cell motility	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0003417	0.107	0.986	2	6	growth plate cartilage development	BP	1	RARG,TGFBR2	up_VSAP_EC
GO:0032060	0.107	0.986	2	6	bleb assembly	BP	1	EMP2,EMP3	up_VSAP_EC
GO:0032332	0.107	0.986	2	6	positive regulation of chondrocyte	BP	1	HOXA11,ZBTB16	up_VSAP_EC
GO:0048278	0.107	0.994	1	25	vesicle docking	BP	1	STX4	down_ACOR_EC
GO:0015908	0.107	0.994	1	23	fatty acid transport	BP	1	ACSL3	down_ACOR_EC
GO:0033627	0.107	0.994	1	22	cell adhesion mediated by integrin	BP	1	LYN	down_ACOR_EC
GO:0007179	0.107	0.995	1	57	transforming growth factor beta receptor	BP	1	CITED2	down_VPOR_EC
GO:0034329	0.107	0.995	1	60	cell junction assembly	BP	1	HDAC7	down_VPOR_EC
GO:0043534	0.107	0.995	1	57	blood vessel endothelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0019941	0.107	0.996	1	258	modification-dependent protein catabolic process	BP	1	USP12	down_VFEM_EC
GO:0097154	0.107	0.997	1	2	GABAergic neuron differentiation	BP	1	INHBA	down_VSAP_EC
GO:0070662	0.107	0.997	1	2	mast cell proliferation	BP	1	LYN	down_VSAP_EC
GO:0070666	0.107	0.997	1	2	regulation of mast cell proliferation	BP	1	LYN	down_VSAP_EC
GO:0070668	0.107	0.997	1	2	positive regulation of mast cell proliferation	BP	1	LYN	down_VSAP_EC
GO:1903892	0.107	1	1	1	negative regulation of ATF6-mediated unfolded protein response	BP	1	WFS1	up_ACOR_VSMC
GO:0016191	0.107	1	1	1	synaptic vesicle uncoating	BP	1	DNAJC6	up_ACOR_VSMC
GO:0034343	0.107	1	1	1	type III interferon production	BP	1	TLR3	up_ACOR_VSMC
GO:0034344	0.107	1	1	1	regulation of type III interferon production	BP	1	TLR3	up_ACOR_VSMC

GO:0034346	0.107	1	1	1	positive regulation of type III interferon production	BP	1	TLR3	up_ACOR_VSMC
GO:0045356	0.107	1	1	1	positive regulation of interferon-alpha	BP	1	TLR3	up_ACOR_VSMC
GO:1901052	0.107	1	1	1	sarcosine metabolic process	BP	1	SARDH	up_ACOR_VSMC
GO:1901053	0.107	1	1	1	sarcosine catabolic process	BP	1	SARDH	up_ACOR_VSMC
GO:0002757	0.107	0.995	1	78	immune response-activating signal	BP	1	TLR2	up_AFEM_VSMC
GO:0051054	0.107	0.995	1	81	positive regulation of DNA metabolic process	BP	1	EYA1	up_AFEM_VSMC
GO:0098542	0.107	0.995	1	100	defense response to other organism	BP	1	ARG2	up_AORT_VSMC
GO:0001678	0.107	0.994	1	29	cellular glucose homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0002792	0.107	0.994	1	29	negative regulation of peptide secretion	BP	1	NR1H4	up_APUL_EC
GO:0071322	0.107	0.994	1	29	cellular response to carbohydrate stimulus	BP	1	NR1H4	up_APUL_EC
GO:1900076	0.107	0.994	1	29	regulation of cellular response to insulin	BP	1	NR1H4	up_APUL_EC
GO:0034343	0.107	1	1	1	type III interferon production	BP	0.981	TLR3	up_VCAV_EC
GO:0034344	0.107	1	1	1	regulation of type III interferon production	BP	0.981	TLR3	up_VCAV_EC
GO:0034346	0.107	1	1	1	positive regulation of type III interferon production	BP	0.981	TLR3	up_VCAV_EC
GO:0036506	0.107	1	1	1	maintenance of unfolded protein	BP	0.981	USP13	up_VCAV_EC
GO:0045356	0.107	1	1	1	positive regulation of interferon-alpha	BP	0.981	TLR3	up_VCAV_EC
GO:1904378	0.107	1	1	1	maintenance of unfolded protein involved in ERAD	BP	0.981	USP13	up_VCAV_EC
GO:0071622	0.107	0.995	1	13	regulation of granulocyte chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0090288	0.107	0.995	1	44	negative regulation of cellular response to growth factor stimulus	BP	1	BAMBI	up_VPOR_VSMC
GO:0021675	0.107	0.994	1	29	nerve development	BP	1	SIX1	up_VFEM_EC
GO:0061005	0.107	0.994	1	28	cell differentiation involved in kidney	BP	1	MTSS1	up_VFEM_EC
GO:0021543	0.107	0.995	1	49	pallium development	BP	1	EMX2	up_VFEM_VSMC
GO:0021953	0.107	0.994	1	49	central nervous system neuron differentiation	BP	1	HOXC10	up_VFEM_VSMC
GO:0045639	0.107	0.994	1	33	positive regulation of myeloid cell	BP	1	EVI2B	up_VPUL_EC
GO:0050796	0.107	0.994	1	33	regulation of insulin secretion	BP	1	NR1H4	up_VPUL_EC
GO:0030595	0.107	0.995	1	57	leukocyte chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0007009	0.107	0.994	1	27	plasma membrane organization	BP	1	CAV1	up_VSAP_VSMC
GO:0021761	0.107	0.994	1	27	limbic system development	BP	1	EMX2	up_VSAP_VSMC
GO:0031290	0.107028019	0.99552	1	4	retinal ganglion cell axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0035546	0.107093705	0.99552	1	4	interferon-beta secretion	BP	1	MAVS	up_ACOR_EC
GO:0035547	0.107093705	0.99552	1	4	regulation of interferon-beta secretion	BP	1	MAVS	up_ACOR_EC
GO:0035549	0.107093705	0.99552	1	4	positive regulation of interferon-beta secretion	BP	1	MAVS	up_ACOR_EC
GO:1902668	0.107096489	0.99552	1	4	negative regulation of axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0043268	0.107128169	0.99552	1	4	positive regulation of potassium ion transport	BP	1	ACTN2	up_ACOR_EC
GO:0021562	0.107196612	0.99551	1	4	vestibulocochlear nerve development	BP	1	NRP1	up_ACOR_EC
GO:0051124	0.10729616	0.9955	1	4	synaptic growth at neuromuscular junction	BP	1	LRP4	up_ACOR_EC
GO:0006959	0.107354264	0.98242	2	21	humoral immune response	BP	1	C7,RARRES2	up_ACOR_EC
GO:0016045	0.107696512	0.99547	1	4	detection of bacterium	BP	1	NOD2	up_ACOR_EC
GO:0098543	0.107696512	0.99547	1	4	detection of other organism	BP	1	NOD2	up_ACOR_EC

GO:0048841	0.107710795	0.99547	1	4	regulation of axon extension involved in	BP	1	NRP1	up_ACOR_EC
GO:0048731	0.108	0.91	131	1247	system development	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,PCDH19,HOXA9,SEZ6L,CDON,WNT11,HNF4A,CD274,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PPARGC1B,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,IL6R,IRX5,SLIT2,CRIP2,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,EPN2,HOXA6,OSR1,FUZ,WARS2,SAV1,KLF15,HPSE,PLXNA4,ANKRD54,CLDN1,ZBTB16,TOX,RARG,CCBE1,STAT6,HOXC4,RECK,PATZ1,PLPP3,GTF3C5,AMBRA1,F2RL1,DLX3,GLIS2,DDR2,MFN2,ZFP36L1,PIK3R1,TIAM1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,TBXA2R,SULF2,SHOX2,EEF2,RTN4RL1,SASH1,HOXC10,LOX,TFE3,LRP4,DPYSL2,GDPD5,DAGLB,CLCN2,E2F4,SMG9,MCPH1,KIF27,FBXO7,NTN4,CD83,NR2F6,KDM2B,ZFP36L2,HPGD,RAF1,PNP,NFIB,CYB5D2,CDNF,ZFAND5,ANPEP,PQBP1,TTL,PLEKHA5,QARS,ACVRL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,OGN,TRADD,PIR,LBH,LATS2	up_VSAP_EC
GO:0051239	0.108	0.917	61	859	regulation of multicellular organismal process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SIPA1L1,SULF1,CELF1,NR1H4,SERPINE1,SOCS5,SPARC,PRKACB,ERRFI1,JCAD,FAM49B,PGK1,PTPN11,DPYSL3,HOOK3,IFRD1,ILK,PRCP,TGFBR1,PTGS2,PIK3C2A,CHSY1,HOXB7,HIF1A,SLC45A3,THBS2,TNIK,ZPR1,PTPN2,EVI2B,PLCL1,MTDH,ADAM17,UST,MAGED1,CTNNB1,STARD13,TFRC,APOE,WWC3,LYN,STRAP,DDIT3,MMD,VLDLR,GBP5,REST,PRMT1,CALM1,RAB11FIP1,DISC1,LRRTM2,INHBA,BTK,SIX4,NRP1,YWHAH,KDM3A	down_VSAP_EC
GO:0032101	0.108	0.93	22	173	regulation of response to external stimulus	BP	1	NAPEPLD,C5AR2,SLC8B1,SLIT2,KLKB1,IL17RC,HPSE,PLXNA4,F2RL1,RTN4RL1,SASH1,MYD88,NLRX1,TKFC,RNF216,MAPKBP1,ZNF580,CYBA,STX4,PQBP1,MAVS,MAP2K2	up_VSAP_EC
GO:1903320	0.108	0.939	14	102	regulation of protein modification by small protein conjugation or	BP	1	SKP2,SH3RF2,ISG15,SASH1,PTPN22,PRKCE,PSEN1,NOD2,FAM107A,DCUN1D4,HERPUD1,WFS1,WDR48,PARK7	up_ACOR_VSMC
GO:0043588	0.108	0.943	11	74	skin development	BP	1	EXPH5,FERMT1,FGFR2,LATS2,SLITRK5,FZD3,PSEN1,JUP,FOSL2,WDR48,ZDHHC21	up_ACOR_VSMC
GO:0035264	0.108	0.948	9	56	multicellular organism growth	BP	1	FGFR2,ATRX,ATRN,PLAC8B,APP,CHD7,ARID5B,WDR48,STC2	up_ACOR_VSMC
GO:0032943	0.108	0.95	8	60	mononuclear cell proliferation	BP	0.984	IL7R,MEF2C,TLR4,PELI1,ARG2,ELF4,NCK1,HMGB1	up_VCAV_EC
GO:0046651	0.108	0.95	8	60	lymphocyte proliferation	BP	0.984	IL7R,MEF2C,TLR4,PELI1,ARG2,ELF4,NCK1,HMGB1	up_VCAV_EC
GO:1904018	0.108	0.952	7	69	positive regulation of vasculature development	BP	1	VEGFA,SERPINE1,JCAD,PIK3C2A,HIF1A,MTDH,NRP1	down_VSAP_EC
GO:0009799	0.108	0.953	7	43	specification of symmetry	BP	1	BMP4,GJA1,CITED2,TBX20,PSEN1,PCSK6,PSKH1	up_ACOR_VSMC
GO:0030218	0.108	0.957	6	42	erythrocyte differentiation	BP	0.981	HCLS1,ADGRF5,KIT,GATA3,HIF1A,TMOD3	up_VCAV_EC
GO:0014031	0.108	0.962	5	27	mesenchymal cell development	BP	1	HTR2B,BMP4,CITED2,NRP1,EDN1	up_ACOR_VSMC
GO:0014032	0.108	0.962	5	27	neural crest cell development	BP	1	HTR2B,BMP4,CITED2,NRP1,EDN1	up_ACOR_VSMC
GO:0031644	0.108	0.968	4	19	regulation of neurological system process	BP	1	WASF3,TMEM108,DMPK,APP	up_ACOR_VSMC
GO:0097435	0.108	0.965	4	230	supramolecular fiber organization	BP	1	MZT1,HOOK3,ARHGEF2,TWF1	up_VPOR_EC
GO:1901031	0.108	0.975	3	12	regulation of response to reactive oxygen species	BP	1	SESN3,SESN1,PARK7	up_ACOR_VSMC
GO:0021953	0.108	0.972	3	49	central nervous system neuron differentiation	BP	1	HOXC10,LEP,PLXNA4	up_AFEM_EC
GO:0045214	0.108	0.975	3	13	sarcomere organization	BP	0.981	MEF2C,EDN1,PROX1	up_VCAV_EC
GO:0045595	0.108	0.974	3	469	regulation of cell differentiation	BP	1	NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0051093	0.108	0.973	3	273	negative regulation of developmental process	BP	1	HOXA9,HOXA7,SIX1	up_VFEM_EC
GO:0009790	0.108	0.973	3	335	embryo development	BP	1	TBX5,HOXA3,FLRT3	up_VPUL_EC
GO:0031098	0.108	0.982	2	109	stress-activated protein kinase signaling cascade	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0046633	0.108	0.985	2	7	alpha-beta T cell proliferation	BP	1	ARG2,ELF4	down_ACOR_VSMC

GO:0043525	0.108	0.983	2	11	positive regulation of neuron apoptotic process	BP	1	PRNP,FOXO3	down_VCAV_EC
GO:0051932	0.108	0.984	2	9	synaptic transmission, GABAergic	BP	1	KIF5B,PLCL1	down_VSAP_EC
GO:0055094	0.108	0.984	2	9	response to lipoprotein particle	BP	1	SOCS5,APOE	down_VSAP_EC
GO:1903055	0.108	0.986	2	6	positive regulation of extracellular matrix	BP	1	DAG1,DDR2	up_ACOR_VSMC
GO:0045893	0.108	0.984	2	413	positive regulation of transcription, DNA-	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0051654	0.108	0.986	2	6	establishment of mitochondrion	BP	0.981	NECTIN2,HIF1A	up_VCAV_EC
GO:0032870	0.108	0.982	2	162	cellular response to hormone stimulus	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0090066	0.108	0.982	2	162	regulation of anatomical structure size	BP	1	CCL24,HTR7	up_VPUL_EC
GO:0072201	0.108	0.986	2	6	negative regulation of mesenchymal cell	BP	1	WNT11,NFIB	up_VSAP_EC
GO:1900017	0.108	0.986	2	6	positive regulation of cytokine production involved in inflammatory	BP	1	IL17RC,MYD88	up_VSAP_EC
GO:0007276	0.108	0.982	2	130	gamete generation	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0006865	0.108	0.994	1	23	amino acid transport	BP	1	PDPN	down_ACOR_EC
GO:0070836	0.108	0.997	1	2	caveola assembly	BP	1	CAV1	down_ACOR_VSMC
GO:1902850	0.108	0.994	1	52	microtubule cytoskeleton organization involved in	BP	1	GPSM2	down_AFEM_EC
GO:0010605	0.108	1	1	745	negative regulation of macromolecule metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0043112	0.108	0.994	1	57	receptor metabolic process	BP	1	RAB11B	down_VPOR_EC
GO:1903070	0.108	0.997	1	2	negative regulation of ER-associated ubiquitin-dependent protein	BP	1	USP14	down_VSAP_EC
GO:0033564	0.108	1	1	1	anterior/posterior axon guidance	BP	1	UNC5B	up_ACOR_VSMC
GO:0038190	0.108	1	1	1	VEGF-activated neuropilin signaling pathway	BP	1	NRP1	up_ACOR_VSMC
GO:0048842	0.108	1	1	1	positive regulation of axon extension involved in axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0051695	0.108	1	1	1	actin filament uncapping	BP	1	ACTN2	up_ACOR_VSMC
GO:0061441	0.108	1	1	1	renal artery morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0086097	0.108	1	1	1	phospholipase C-activating angiotensin-activated signaling	BP	1	ACTN2	up_ACOR_VSMC
GO:1902336	0.108	1	1	1	positive regulation of retinal ganglion cell axon	BP	1	NRP1	up_ACOR_VSMC
GO:1902378	0.108	1	1	1	VEGF-activated neuropilin signaling pathway involved in axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1902669	0.108	1	1	1	positive regulation of axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1905040	0.108	1	1	1	otic placode development	BP	1	NRP1	up_ACOR_VSMC
GO:2001137	0.108	1	1	1	positive regulation of endocytic recycling	BP	1	ACTN2	up_ACOR_VSMC
GO:0097191	0.108	0.995	1	79	extrinsic apoptotic signaling pathway	BP	1	EYA1	up_AFEM_VSMC
GO:0010817	0.108	0.995	1	102	regulation of hormone levels	BP	1	ESR1	up_AORT_VSMC
GO:0022407	0.108	0.995	1	96	regulation of cell-cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0048232	0.108	0.995	1	95	male gamete generation	BP	1	HOXA9	up_AORT_VSMC
GO:0048844	0.108	0.994	1	30	artery morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0072171	0.108	0.994	1	30	mesonephric tubule morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0003138	0.108	1	1	1	primary heart field specification	BP	0.981	MEF2C	up_VCAV_EC
GO:0003172	0.108	1	1	1	sinoatrial valve development	BP	0.981	MEF2C	up_VCAV_EC
GO:0007521	0.108	1	1	1	muscle cell fate determination	BP	0.981	MEF2C	up_VCAV_EC

GO:0003185	0.108	1	1	1	sinoatrial valve morphogenesis	BP	0.981	MEF2C	up_VCAV_EC
GO:0060025	0.108	1	1	1	regulation of synaptic activity	BP	0.981	MEF2C	up_VCAV_EC
GO:0071107	0.108	1	1	1	response to parathyroid hormone	BP	0.981	MEF2C	up_VCAV_EC
GO:0071374	0.108	1	1	1	cellular response to parathyroid hormone	BP	0.981	MEF2C	up_VCAV_EC
GO:1903367	0.108	1	1	1	positive regulation of fear response	BP	0.981	MEF2C	up_VCAV_EC
GO:2000987	0.108	1	1	1	positive regulation of behavioral fear response	BP	0.981	MEF2C	up_VCAV_EC
GO:0043434	0.108	0.995	1	80	response to peptide hormone	BP	1	CA2	up_VCAV_VSMC
GO:1902105	0.108	0.995	1	80	regulation of leukocyte differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0010677	0.108	0.994	1	14	negative regulation of cellular carbohydrate	BP	1	FBP1	up_VPOR_EC
GO:0034629	0.108	0.994	1	14	cellular protein-containing complex localization	BP	1	MZT1	up_VPOR_EC
GO:0044380	0.108	0.994	1	14	protein localization to cytoskeleton	BP	1	HOOK3	up_VPOR_EC
GO:0050994	0.108	0.994	1	14	regulation of lipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0060191	0.108	0.994	1	14	regulation of lipase activity	BP	1	ABHD5	up_VPOR_EC
GO:2000243	0.108	0.994	1	14	positive regulation of reproductive process	BP	1	SEMA3A	up_VPOR_EC
GO:0006836	0.108	0.994	1	47	neurotransmitter transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0045619	0.108	0.994	1	44	regulation of lymphocyte differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006720	0.108	0.994	1	25	isoprenoid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0006282	0.108	0.994	1	48	regulation of DNA repair	BP	1	EYA1	up_VFEM_VSMC
GO:0009913	0.108	0.994	1	47	epidermal cell differentiation	BP	1	SPINK5	up_VFEM_VSMC
GO:0055002	0.108	0.994	1	45	striated muscle cell development	BP	1	SHOX2	up_VFEM_VSMC
GO:0001959	0.108	0.994	1	33	regulation of cytokine-mediated signaling	BP	1	NR1H4	up_VPUL_EC
GO:0008543	0.108	0.994	1	27	fibroblast growth factor receptor signaling	BP	1	FGF5	up_VSAP_VSMC
GO:0033138	0.108	0.994	1	28	positive regulation of peptidyl-serine	BP	1	CAV1	up_VSAP_VSMC
GO:0021825	0.108130713	0.99543	1	4	substrate-dependent cerebral cortex tangential	BP	1	NRP1	up_ACOR_EC
GO:0006182	0.108145816	0.99543	1	4	cGMP biosynthetic process	BP	1	GUCY1B1	up_ACOR_EC
GO:0097104	0.108399532	0.99541	1	4	postsynaptic membrane assembly	BP	1	LRP4	up_ACOR_EC
GO:0099068	0.108399532	0.99541	1	4	postsynapse assembly	BP	1	LRP4	up_ACOR_EC
GO:2000311	0.108455235	0.9954	1	4	regulation of AMPA receptor activity	BP	1	MAPK8IP2	up_ACOR_EC
GO:0032233	0.108474978	0.98213	2	21	positive regulation of actin filament bundle	BP	1	SYNPO2,NRP1	up_ACOR_EC
GO:2000736	0.108550137	0.98211	2	21	regulation of stem cell differentiation	BP	1	SOX9,TBX5	up_ACOR_EC
GO:1902285	0.108744311	0.99538	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	NRP1	up_ACOR_EC
GO:0030199	0.108763649	0.98205	2	21	collagen fibril organization	BP	1	FMOD,FOXC2	up_ACOR_EC
GO:2000310	0.108795716	0.99537	1	4	regulation of NMDA receptor activity	BP	1	MAPK8IP2	up_ACOR_EC
GO:0050790	0.109	0.921	39	532	regulation of catalytic activity	BP	1	VEGFA,SOCS5,ERRFI1,NUAK1,PTPN11,TRIB3,PPP1R12A,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,ADAM17,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,APOE,LYN,FAM162A,CCNYL1,MMD,CBLC,GSK3B,VLDLR,SH3GLB1,TAX1BP3,HTT,REST,ABHD5,ARFGEF3,CALM1,PAK2,CDKN1A,SPINK2,ARF4,MADD	down_VSAP_EC
GO:0006928	0.109	0.933	18	557	movement of cell or subcellular component	BP	1	CMKLR1,ANGPT4,HOXA7,PLXNA4,TWIST2,HCK,GREM1,CAMK2A,LRRC15,RECK,TBXA2R,KIF1A,BVES,LGR6,CCL5,FAP,ADAM17,KANK1	up_AFEM_EC

GO:0051716	0.109	0.946	12	2001	cellular response to stimulus	BP	1	EYA1,MAP2K6,MME,AVPR1A,ENSCAFG00000018194,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3	up_VFEM_EC
GO:0010634	0.109	0.945	10	68	positive regulation of epithelial cell migration	BP	1	ENPP2,FGF7,ABL1,HDAC7,CCBE1,STAT5A,SASH1,ZNF580,HMOX1,TGFBR2	up_VSAP_EC
GO:0060485	0.109	0.946	9	93	mesenchyme development	BP	1	TGFBR1,HIF1A,ACTG2,ACTA2,CTNNB1,STRAP,GSK3B,SIX4,NRP1	down_VSAP_EC
GO:0007219	0.109	0.947	9	59	Notch signaling pathway	BP	1	HOXD3,GOT1,DLL1,EPN2,DTX2,ANXA4,GDPD5,TSPAN5,TGFBR2	up_VSAP_EC
GO:0070838	0.109	0.949	8	96	divalent metal ion transport	BP	1	PRNP,TRPV2,SLC39A6,CACNB3,THY1,TPC3,CYBA,PACSIN3	down_VCAV_EC
GO:0051272	0.109	0.951	7	170	positive regulation of cellular component	BP	1	CMKLR1,ANGPT4,TWIST2,LRRC15,LGR6,CCL5,ADAM17	up_AFEM_EC
GO:0008584	0.109	0.956	6	39	male gonad development	BP	1	SF1,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC
GO:0046546	0.109	0.956	6	39	development of primary male sexual	BP	1	SF1,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC
GO:0048660	0.109	0.957	6	35	regulation of smooth muscle cell proliferation	BP	1	BMP4,PTGIR,NDRG2,CDKN1A,CLSTN1,EDN1	up_ACOR_VSMC
GO:0006909	0.109	0.956	6	42	phagocytosis	BP	0.989	RAB27A,IRF8,ABCA1,ELMO1,HMGB1,PEAR1	up_VCAV_EC
GO:1902749	0.109	0.956	6	39	regulation of cell cycle G2/M phase transition	BP	0.989	RAB11A,TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0031623	0.109	0.961	5	31	receptor internalization	BP	1	NEDD4,CAV1,GREM1,TFRC,EZR	down_ACOR_VSMC
GO:0071772	0.109	0.96	5	50	response to BMP	BP	1	SMAD9,FBN1,CHRDL1,GREM1,RGMA	down_VCAV_EC
GO:0071773	0.109	0.96	5	50	cellular response to BMP stimulus	BP	1	SMAD9,FBN1,CHRDL1,GREM1,RGMA	down_VCAV_EC
GO:0015850	0.109	0.966	4	37	organic hydroxy compound transport	BP	1	LCAT,SCP2,PARK7,SOAT1	down_VCAV_EC
GO:0006638	0.109	0.966	4	30	neutral lipid metabolic process	BP	1	PTPN11,SEL1L,APOE,ABHD5	down_VSAP_EC
GO:0006639	0.109	0.966	4	30	acylglycerol metabolic process	BP	1	PTPN11,SEL1L,APOE,ABHD5	down_VSAP_EC
GO:0051651	0.109	0.966	4	31	maintenance of location in cell	BP	1	HSPA5,APOE,TLN1,KDELR2	down_VSAP_EC
GO:0006402	0.109	0.965	4	77	mRNA catabolic process	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:1901976	0.109	0.967	4	21	regulation of cell cycle checkpoint	BP	0.989	PROX1,THOC1,ETAA1,CUL4A	up_VCAV_EC
GO:0001775	0.109	0.973	3	219	cell activation	BP	1	LYN,PDPN,STX4	down_ACOR_EC
GO:1901880	0.109	0.974	3	19	negative regulation of protein depolymerization	BP	1	ARHGEF2,CAPG,MID1	down_VSAP_EC
GO:0043462	0.109	0.975	3	13	regulation of ATPase activity	BP	1	TNNT2,DYNC1I2,DYNC1I1	up_ACOR_VSMC
GO:0003333	0.109	0.975	3	12	amino acid transmembrane transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:1904951	0.109	0.982	2	108	positive regulation of establishment of protein localization	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0016075	0.109	0.985	2	7	rRNA catabolic process	BP	1	DIS3,EXOSC5	down_ACOR_VSMC
GO:0042407	0.109	0.985	2	7	cristae formation	BP	1	CHCHD3,SAMM50	down_ACOR_VSMC
GO:0061036	0.109	0.983	2	11	positive regulation of cartilage development	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:0001990	0.109	0.985	2	6	regulation of systemic arterial blood pressure by	BP	1	F2RL1,EDN1	up_ACOR_VSMC
GO:0060601	0.109	0.985	2	6	lateral sprouting from an epithelium	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:1902680	0.109	0.983	2	415	positive regulation of RNA biosynthetic process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:1903508	0.109	0.983	2	415	positive regulation of nucleic acid-templated	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0045737	0.109	0.984	2	8	positive regulation of cyclin-dependent protein serine/threonine kinase	BP	0.989	PDGFB,PROX1	up_VCAV_EC
GO:0034311	0.109	0.984	2	9	diol metabolic process	BP	0.989	SPTLC2,GCH1	up_VCAV_EC
GO:2000773	0.109	0.985	2	6	negative regulation of cellular senescence	BP	0.989	PLK2,MAP3K3	up_VCAV_EC
GO:0022008	0.109	0.983	2	406	neurogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0060020	0.109	0.985	2	6	Bergmann glial cell differentiation	BP	1	ABL1,PLPP3	up_VSAP_EC
GO:0060440	0.109	0.985	2	6	trachea formation	BP	1	MAP2K2,TGFBR2	up_VSAP_EC

GO:2000794	0.109	0.985	2	6	regulation of epithelial cell proliferation involved in lung morphogenesis	BP	1	FGF7,NFIB	up_VSAP_EC
GO:0019098	0.109	0.985	2	6	reproductive behavior	BP	1	THRB,CREBRF	up_VSAP_EC
GO:0035774	0.109	0.985	2	6	positive regulation of insulin secretion involved in cellular response to	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0043302	0.109	0.985	2	6	positive regulation of leukocyte degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0072666	0.109	0.994	1	21	establishment of protein localization to vacuole	BP	1	NEDD4	down_ACOR_EC
GO:0007045	0.109	0.994	1	23	cell-substrate adherens junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0009880	0.109	0.994	1	22	embryonic pattern specification	BP	1	NRP2	down_ACOR_EC
GO:0048041	0.109	0.994	1	23	focal adhesion assembly	BP	1	ACVRL1	down_ACOR_EC
GO:1903036	0.109	0.994	1	19	positive regulation of response to wounding	BP	1	PDPN	down_ACOR_EC
GO:0043632	0.109	0.996	1	262	modification-dependent macromolecule catabolic	BP	1	USP12	down_VFEM_EC
GO:0034384	0.109	0.997	1	2	high-density lipoprotein particle clearance	BP	1	APOE	down_VSAP_EC
GO:0035694	0.109	0.997	1	2	mitochondrial protein catabolic process	BP	1	BNIP3	down_VSAP_EC
GO:0008343	0.109	1	1	1	adult feeding behavior	BP	1	LEP	up_ACOR_VSMC
GO:0030300	0.109	1	1	1	regulation of intestinal cholesterol absorption	BP	1	LEP	up_ACOR_VSMC
GO:0032817	0.109	1	1	1	regulation of natural killer cell proliferation	BP	1	LEP	up_ACOR_VSMC
GO:0070060	0.109	1	1	1	'de novo' actin filament nucleation	BP	1	JMY	up_ACOR_VSMC
GO:0070093	0.109	1	1	1	negative regulation of glucagon secretion	BP	1	LEP	up_ACOR_VSMC
GO:1904478	0.109	1	1	1	regulation of intestinal absorption	BP	1	LEP	up_ACOR_VSMC
GO:1904729	0.109	1	1	1	regulation of intestinal lipid absorption	BP	1	LEP	up_ACOR_VSMC
GO:0050708	0.109	0.995	1	101	regulation of protein secretion	BP	1	ARG2	up_AORT_VSMC
GO:0050808	0.109	0.995	1	93	synapse organization	BP	1	WNT7A	up_AORT_VSMC
GO:0046620	0.109	0.994	1	30	regulation of organ growth	BP	1	TBX5	up_APUL_EC
GO:1903725	0.109	0.994	1	30	regulation of phospholipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0008202	0.109	0.995	1	80	steroid metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0030198	0.109	0.995	1	81	extracellular matrix organization	BP	1	TGFBI	up_VCAV_VSMC
GO:0008360	0.109	0.994	1	46	regulation of cell shape	BP	1	BAMBI	up_VPOR_VSMC
GO:0031338	0.109	0.994	1	28	regulation of vesicle fusion	BP	1	TRIM9	up_VFEM_EC
GO:0010976	0.109	0.994	1	47	positive regulation of neuron projection	BP	1	SHOX2	up_VFEM_VSMC
GO:0032412	0.109	0.994	1	46	regulation of ion transmembrane	BP	1	NETO1	up_VFEM_VSMC
GO:0001938	0.109	0.994	1	34	positive regulation of endothelial cell	BP	1	CCL24	up_VPUL_EC
GO:0044344	0.109	0.994	1	33	cellular response to fibroblast growth factor	BP	1	FLRT3	up_VPUL_EC
GO:0051261	0.109	0.994	1	33	protein depolymerization	BP	1	ARHGEF2	up_VPUL_EC
GO:0060411	0.109	0.994	1	33	cardiac septum morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0071774	0.109	0.994	1	33	response to fibroblast growth factor	BP	1	FLRT3	up_VPUL_EC
GO:0008406	0.109	0.994	1	57	gonad development	BP	1	SLIT2	up_VPUL_VSMC
GO:0043534	0.109	0.994	1	57	blood vessel endothelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0045137	0.109	0.994	1	57	development of primary sexual characteristics	BP	1	SLIT2	up_VPUL_VSMC
GO:0048754	0.109	0.994	1	57	branching morphogenesis of an epithelial tube	BP	1	SLIT2	up_VPUL_VSMC
GO:0032835	0.109279022	0.98192	2	21	glomerulus development	BP	1	AQP1,FOXC2	up_ACOR_EC

GO:0010771	0.109457112	0.98187	2	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	LRP4,NRP1	up_ACOR_EC
GO:0046474	0.109697728	0.97179	3	44	glycerophospholipid biosynthetic process	BP	1	NR1H4,PIGS,AGPAT2	up_ACOR_EC
GO:0051247	0.11	0.92	37	502	positive regulation of protein metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,MYH9,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,ILK,PPP1R12A,PTGS2,MSN,TNIK,YES1,ADAM17,MAGED1,CTNNB1,APOE,LYN,FAM162A,MMD,GSK3B,VLDLR,REST,CALM1,DISC1,RAD23A,PAK2,INHBA,TMTC3,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0045892	0.11	0.922	34	328	negative regulation of transcription, DNA-templated	BP	0.99	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,ELK3	up_VCAV_EC
GO:0044265	0.11	0.923	32	423	cellular macromolecule catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,TRIB3,MSN,SEL1L,USP12,DNAJC10,UBA6,ZPR1,UCHL5,SPOPL,SMG7,CNOT7,DNAJB9,SND1,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0009058	0.11	0.944	13	1910	biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,TNRC6B,NEDD4	down_ACOR_EC
GO:0060429	0.11	0.939	12	341	epithelium development	BP	1	IRX3,LBH,HOXA7,DLL1,THRB,TMEM100,GREM1,LUZP1,AXIN2,ADAM17,FOSL2,TNC	up_AFEM_EC
GO:0032103	0.11	0.944	10	69	positive regulation of response to external	BP	1	VEGFD,TLR3,SASH1,FGF18,F2RL1,NRP1,APP,CCL5,NOD2,PARK7	up_ACOR_VSMC
GO:0048736	0.11	0.944	10	66	appendage development	BP	1	AFF3,RECK,BMP4,LNPK,FGFR2,GJA1,ATRX,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0060173	0.11	0.944	10	66	limb development	BP	1	AFF3,RECK,BMP4,LNPK,FGFR2,GJA1,ATRX,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0061572	0.11	0.949	8	50	actin filament bundle organization	BP	1	SYNPO2L,ARHGAP28,SYNPO2,NRP1,EVL,MYO1B,FAM107A,INPP5K	up_ACOR_VSMC
GO:0006338	0.11	0.952	7	45	chromatin remodeling	BP	0.991	CHD7,GATA3,PSME4,BAZ1A,SMARCA4,TOP1,ATRX	up_VCAV_EC
GO:0090150	0.11	0.955	6	64	establishment of protein localization to membrane	BP	1	PRNP,AKT2,SSR2,SSR3,SEC61B,RAB31	down_VCAV_EC
GO:0032606	0.11	0.956	6	35	type I interferon production	BP	1	MYD88,NLRX1,RNF216,PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0072655	0.11	0.96	5	33	establishment of protein localization to	BP	1	SREBF1,TIMM44,TOMM34,SAMM50,PMPCA	down_ACOR_VSMC
GO:0044237	0.11	0.984	5	3491	cellular metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0003014	0.11	0.961	5	27	renal system process	BP	1	BMP4,F2RL1,EDN1,INPP5K,WFS1	up_ACOR_VSMC
GO:0035296	0.11	0.96	5	32	regulation of tube diameter	BP	0.991	EDNRB,DOCK4,EDN1,GUCY1A1,NOS2	up_VCAV_EC
GO:0097746	0.11	0.96	5	32	regulation of blood vessel diameter	BP	0.991	EDNRB,DOCK4,EDN1,GUCY1A1,NOS2	up_VCAV_EC
GO:0032677	0.11	0.966	4	22	regulation of interleukin-8 production	BP	0.99	PRKD2,TLR3,BCL10,RIPK1	up_VCAV_EC
GO:0070972	0.11	0.973	3	23	protein localization to endoplasmic reticulum	BP	1	SSR3,SEC61B,SEC61A1	down_VCAV_EC
GO:1902692	0.11	0.975	3	11	regulation of neuroblast proliferation	BP	1	SMARCD3,FZD3,DISC1	up_ACOR_VSMC
GO:0003407	0.11	0.974	3	15	neural retina development	BP	0.99	DLL4,TSPAN12,SMARCA4	up_VCAV_EC
GO:0070252	0.11	0.973	3	17	actin-mediated cell contraction	BP	0.99	PDE4D,STC1,KCNJ2	up_VCAV_EC
GO:0001556	0.11	0.984	2	7	oocyte maturation	BP	1	TRIP13,FBXO5	down_ACOR_VSMC
GO:1901522	0.11	0.983	2	9	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical	BP	1	SESN2,HIF1A	down_VSAP_EC
GO:0061437	0.11	0.983	2	10	renal system vasculature development	BP	1	ACTA2,NRP1	down_VSAP_EC
GO:0061440	0.11	0.983	2	10	kidney vasculature development	BP	1	ACTA2,NRP1	down_VSAP_EC
GO:0040015	0.11	0.985	2	6	negative regulation of multicellular organism	BP	1	PLAC8B,STC2	up_ACOR_VSMC
GO:0033209	0.11	0.982	2	24	tumor necrosis factor-mediated signaling	BP	1	CYLD,ADAM17	up_AFEM_EC

GO:0045844	0.11	0.982	2	24	positive regulation of striated muscle tissue	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0048636	0.11	0.982	2	24	positive regulation of muscle organ	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0061053	0.11	0.982	2	24	somite development	BP	1	DLL1,AXIN2	up_AFEM_EC
GO:0033630	0.11	0.984	2	7	positive regulation of cell adhesion mediated by	BP	0.99	PODXL,FERMT1	up_VCAV_EC
GO:1904018	0.11	0.981	2	69	positive regulation of vasculature development	BP	1	C3AR1,MTDH	up_VPOR_EC
GO:0003309	0.11	0.985	2	6	type B pancreatic cell differentiation	BP	1	HNF4A,DLL1	up_VSAP_EC
GO:0003323	0.11	0.985	2	6	type B pancreatic cell development	BP	1	HNF4A,DLL1	up_VSAP_EC
GO:0035883	0.11	0.985	2	6	enteroendocrine cell differentiation	BP	1	HNF4A,DLL1	up_VSAP_EC
GO:0046640	0.11	0.985	2	6	regulation of alpha-beta T cell proliferation	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0072176	0.11	0.985	2	6	nephric duct development	BP	1	WNT11,OSR1	up_VSAP_EC
GO:0097286	0.11	0.985	2	6	iron ion import	BP	1	SLC25A28,STEAP3	up_VSAP_EC
GO:0006875	0.11	0.981	2	129	cellular metal ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0002637	0.11	0.994	1	20	regulation of immunoglobulin	BP	1	STX4	down_ACOR_EC
GO:1902041	0.11	0.994	1	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	STX4	down_ACOR_EC
GO:0048701	0.11	0.994	1	25	embryonic cranial skeleton morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0070373	0.11	0.994	1	26	negative regulation of ERK1 and ERK2 cascade	BP	1	LYN	down_ACOR_EC
GO:0099175	0.11	0.994	1	21	regulation of postsynapse organization	BP	1	NRP2	down_ACOR_EC
GO:0051044	0.11	0.997	1	2	positive regulation of membrane protein	BP	1	APOE	down_VSAP_EC
GO:1900084	0.11	0.996	1	3	regulation of peptidyl-tyrosine	BP	1	VEGFA	down_VSAP_EC
GO:0010760	0.11	0.997	1	2	negative regulation of macrophage chemotaxis	BP	1	MMP28	down_VSAP_EC
GO:0019405	0.11	0.997	1	2	alditol catabolic process	BP	1	TPI1	down_VSAP_EC
GO:1905522	0.11	0.997	1	2	negative regulation of macrophage migration	BP	1	MMP28	down_VSAP_EC
GO:0050673	0.11	0.995	1	135	epithelial cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0071691	0.11	1	1	1	cardiac muscle thin filament assembly	BP	1	NEBL	up_ACOR_VSMC
GO:0032468	0.11	1	1	1	Golgi calcium ion homeostasis	BP	1	ATP2C1	up_ACOR_VSMC
GO:1902667	0.11	0.995	1	5	regulation of axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:0002764	0.11	0.994	1	80	immune response-regulating signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0015711	0.11	0.994	1	81	organic anion transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0045088	0.11	0.994	1	81	regulation of innate immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0050866	0.11	0.994	1	48	negative regulation of cell activation	BP	1	BPI	up_AORT_EC
GO:1903707	0.11	0.994	1	48	negative regulation of hemopoiesis	BP	1	HOXA9	up_AORT_EC
GO:0043900	0.11	0.995	1	104	regulation of multi-organism process	BP	1	ARG2	up_AORT_VSMC
GO:2000297	0.11	1	1	1	negative regulation of synapse maturation	BP	0.99	ARHGEF15	up_VCAV_EC
GO:0048638	0.11	0.994	1	82	regulation of developmental growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0051302	0.11	0.994	1	47	regulation of cell division	BP	1	FGF5	up_VPOR_VSMC
GO:0030509	0.11	0.994	1	47	BMP signaling pathway	BP	1	NKX2-5	up_VPOR_VSMC
GO:0042445	0.11	0.994	1	46	hormone metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0055001	0.11	0.994	1	47	muscle cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0030203	0.11	0.994	1	27	glycosaminoglycan metabolic process	BP	1	CHST7	up_VFEM_EC

GO:0120034	0.11	0.994	1	28	positive regulation of plasma membrane bounded cell projection	BP	1	CDC42EP5	up_VFEM_EC
GO:0061351	0.11	0.994	1	50	neural precursor cell proliferation	BP	1	EMX2	up_VFEM_VSMC
GO:2001237	0.11	0.994	1	33	negative regulation of extrinsic apoptotic	BP	1	ARHGEF2	up_VPUL_EC
GO:0061005	0.11	0.994	1	28	cell differentiation involved in kidney	BP	1	SALL1	up_VSAP_VSMC
GO:0051093	0.110375477	0.94069	11	273	negative regulation of developmental process	BP	1	CDH3,SOX9,DIXDC1,RGMA,SMAD6,ARHGDIB,FOXC2,TBX5,LRP4,NRP1,EFEMP1	up_ACOR_EC
GO:0072359	0.110387361	0.93602	14	368	circulatory system development	BP	1	GATA4,SOX9,AQP1,ENSCAFG00000004331,FZD5,PDLIM3,SMAD6,ACTN2,ESM1,DLX3,FOXC2,TBX5,C23H3orf58,NRP1	up_ACOR_EC
GO:0043901	0.110468977	0.97151	3	44	negative regulation of multi-organism process	BP	1	TRIM8,ARHGDIB,MAVS	up_ACOR_EC
GO:0044249	0.111	0.906	168	1851	cellular biosynthetic process	BP	1	ELK3,SCD,ACSL3,PRPSAP1,HMGB1,MCM6,SREBF1,ACLY,MCM4,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,RRM1,MED17,POLA1,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,POLA2,MPDU1,SRRT,GINS4,CTDNEP1,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,RAD51,XYLT1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,SMARCC1,PLK3,PCNA,DHX33,HOXA7,TONSL,ARG2,MCM10,UHRF1,CKS2,TKT,GMNN,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,ELOVL1,FARSA,PPARD,CDC6,POLH,YBX3,NCL,NUP62,MRPL37,DTL,VAC14,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,FDFT1,RBM14,CYC1,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,ATP5F1A,PUM3,CDC45,MAST2,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,GRWD1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,MRPL18,LIP	down_ACOR_VSMC
GO:0048518	0.111	0.919	47	1676	positive regulation of biological process	BP	1	HOXA9,CMKLR1,IRX3,LEP,LBH,PRR16,ANGPT4,DLL1,F3,GPAM,MLLT11,LMCD1,TWIST2,MAB21L1,THRB,TMEM100,PLAGL2,GREM1,NFE2L1,OVOL1,FAM53B,AVPR1A,TENT5C,CAMK2A,CLEC16A,CYLD,FXYD1,LRRC15,MYBL1,TBXA2R,EVI2B,DCUN1D3,BVES,LGR6,RAB7A,AXIN2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,FAP,ADAM17,AGPAT2,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0006897	0.111	0.93	20	158	endocytosis	BP	1	DNAJC6,PLCG2,LEP,CDC7,HTR2B,ABCA1,ATXN2,TMEM108,F2RL1,LRPAP1,APP,SYNJ2BP,PIK3C3,GTF2A1L,B2M,AP2B1,SCAMP5,TXNDC5,RAB5C,PIK3C2A	up_ACOR_VSMC
GO:0098609	0.111	0.937	13	181	cell-cell adhesion	BP	1	GPAM,KIRREL1,PRNP,SDC4,THY1,GLI3,ZFP36L1,CDH2,LOXL3,CD164,SHC1,RAC2,ZBTB16	down_VCAV_EC
GO:0050890	0.111	0.943	10	67	cognition	BP	1	FGF13,HRH1,LRRN4,GPR155,POMK,APP,PSEN1,CHD7,CLN8,FAM107A	up_ACOR_VSMC
GO:0010556	0.111	0.948	9	1137	regulation of macromolecule	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0051056	0.111	0.945	9	87	regulation of small GTPase mediated signal	BP	1	ARHGEF2,SIPA1L1,FARP1,APOE,PLEKHG2,ARFGEF3,NRP1,TNFAIP1,MADD	down_VSAP_EC
GO:0071214	0.111	0.945	9	93	cellular response to abiotic stimulus	BP	1	ARHGEF2,CASP3,PTGS2,CRYAB,BNIP3,REST,EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0104004	0.111	0.945	9	93	cellular response to environmental stimulus	BP	1	ARHGEF2,CASP3,PTGS2,CRYAB,BNIP3,REST,EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0032102	0.111	0.951	7	67	negative regulation of response to external	BP	1	NR1H4,SERPINE1,SOCS5,PTPN2,APOE,MMP28,NRP1	down_VSAP_EC
GO:0045580	0.111	0.956	6	35	regulation of T cell differentiation	BP	1	ABL1,ZBTB16,ZEB1,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0044774	0.111	0.96	5	30	mitotic DNA integrity checkpoint	BP	1	CDK1,CASP2,FANCI,TOPBP1,CLSPN	down_ACOR_VSMC
GO:0051048	0.111	0.959	5	42	negative regulation of secretion	BP	1	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:1904064	0.111	0.961	5	27	positive regulation of cation transmembrane	BP	1	ACTN2,PLCG2,AKAP6,FXYD1,PARK7	up_ACOR_VSMC
GO:0065008	0.111	0.963	5	1056	regulation of biological quality	BP	1	HOXA3,BAMBI,TRPC4,CYP26B1,C3AR1	up_VPOR_VSMC

GO:0042733	0.111	0.961	5	27	embryonic digit morphogenesis	BP	1	HOXA11,OSR2,OSR1,FBXW4,LRP4	up_VSAP_EC
GO:1903573	0.111	0.966	4	20	negative regulation of response to endoplasmic	BP	1	OS9,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0048814	0.111	0.973	3	19	regulation of dendrite morphogenesis	BP	1	SIPA1L1,TNIK,YWHAH	down_VSAP_EC
GO:1903391	0.111	0.973	3	21	regulation of adherens junction organization	BP	1	VEGFA,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0031341	0.111	0.974	3	13	regulation of cell killing	BP	1	LEP,F2RL1,B2M	up_ACOR_VSMC
GO:0010821	0.111	0.971	3	49	regulation of mitochondrion	BP	1	MLLT11,CLEC16A,PPARGC1A	up_AFEM_EC
GO:0001936	0.111	0.971	3	49	regulation of endothelial cell proliferation	BP	1	LEP,F3,ADAM17	up_AFEM_EC
GO:0046883	0.111	0.971	3	49	regulation of hormone secretion	BP	1	LEP,CRY2,CCL5	up_AFEM_EC
GO:0097009	0.111	0.974	3	13	energy homeostasis	BP	1	ACACB,DLL1,PASK	up_VSAP_EC
GO:0006644	0.111	0.981	2	118	phospholipid metabolic process	BP	1	LYN,ACSL3	down_ACOR_EC
GO:0060707	0.111	0.984	2	7	trophoblast giant cell differentiation	BP	1	E2F8,PLK4	down_ACOR_VSMC
GO:0019098	0.111	0.985	2	6	reproductive behavior	BP	1	CREBRF,APP	up_ACOR_VSMC
GO:0046716	0.111	0.985	2	6	muscle cell cellular homeostasis	BP	1	LAMP2,GAA	up_ACOR_VSMC
GO:1900271	0.111	0.985	2	6	regulation of long-term synaptic potentiation	BP	1	APP,FAM107A	up_ACOR_VSMC
GO:0017158	0.111	0.981	2	24	regulation of calcium ion-dependent exocytosis	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0048568	0.111	0.981	2	148	embryonic organ development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0043951	0.111	0.984	2	7	negative regulation of cAMP-mediated signaling	BP	0.993	PDE4D,APLNR	up_VCAV_EC
GO:0046578	0.111	0.981	2	77	regulation of Ras protein signal transduction	BP	1	ARHGEF2,FBP1	up_VPOR_EC
GO:0043009	0.111	0.982	2	227	chordate embryonic development	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0030335	0.111	0.981	2	165	positive regulation of cell migration	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0039532	0.111	0.985	2	6	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:1904923	0.111	0.985	2	6	regulation of autophagy of mitochondrion in response to mitochondrial	BP	1	MFN2,HTRA2	up_VSAP_EC
GO:0055090	0.111	0.985	2	6	acylglycerol homeostasis	BP	1	HNF4A,LIPC	up_VSAP_EC
GO:0070328	0.111	0.985	2	6	triglyceride homeostasis	BP	1	HNF4A,LIPC	up_VSAP_EC
GO:0016079	0.111	0.994	1	27	synaptic vesicle exocytosis	BP	1	STX4	down_ACOR_EC
GO:0043620	0.111	0.994	1	24	regulation of DNA-templated transcription in	BP	1	NEDD4	down_ACOR_EC
GO:0010033	0.111	1	1	772	response to organic substance	BP	1	GATA5	down_AFEM_VSMC
GO:0010033	0.111	1	1	772	response to organic substance	BP	1	MXRA5	down_AORT_VSMC
GO:0072175	0.111	0.994	1	60	epithelial tube formation	BP	1	CITED2	down_VPOR_EC
GO:1902261	0.111	1	1	1	positive regulation of delayed rectifier potassium channel	BP	1	AKAP6	up_ACOR_VSMC
GO:1903818	0.111	1	1	1	positive regulation of voltage-gated potassium	BP	1	AKAP6	up_ACOR_VSMC
GO:1903527	0.111	1	1	1	positive regulation of membrane tubulation	BP	1	ASAP1	up_ACOR_VSMC
GO:0003281	0.111	0.994	1	30	ventricular septum development	BP	1	TBX5	up_APUL_EC
GO:0055007	0.111	0.994	1	31	cardiac muscle cell differentiation	BP	1	TBX5	up_APUL_EC
GO:0055059	0.111	1	1	1	asymmetric neuroblast division	BP	0.996	ARHGEF2	up_VCAV_EC
GO:0051188	0.111	0.994	1	81	cofactor biosynthetic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0051495	0.111	0.994	1	82	positive regulation of cytoskeleton organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0008016	0.111	0.994	1	48	regulation of heart contraction	BP	1	NKX2-5	up_VPOR_VSMC

GO:0045621	0.111	0.994	1	28	positive regulation of lymphocyte	BP	1	TOX	up_VFEM_EC
GO:0045682	0.111	0.994	1	27	regulation of epidermis development	BP	1	HOXA7	up_VFEM_EC
GO:0010675	0.111	0.994	1	46	regulation of cellular carbohydrate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0002224	0.111	0.994	1	34	toll-like receptor signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0060415	0.111	0.994	1	27	muscle tissue morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0048640	0.11148631	0.98134	2	21	negative regulation of developmental growth	BP	1	TBX5,NRP1	up_ACOR_EC
GO:0043085	0.112	0.925	25	323	positive regulation of catalytic activity	BP	1	VEGFA,PTPN11,TRIB3,PPP1R12A,DYNLL1,DNAJC10,TNIK,ADAM17,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,LYN,FAM162A,MMD,GSK3B,VLDLR,SH3GLB1,TAX1BP3,REST,ABHD5,CALM1,PAK2,ARF4,MADD	down_VSAP_EC
GO:0043632	0.112	0.927	21	262	modification-dependent macromolecule catabolic process	BP	1	PRICKLE1,PLK3,SOCS5,HSP90B1,TRIB3,USP12,DNAJC10,UBA6,UCHL5,SPOPL,DNAJB9,USP48,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,USP14,TNFAIP1	down_VSAP_EC
GO:0070848	0.112	0.928	21	193	response to growth factor	BP	0.999	CXCL8,PDGFB,MEF2C,FERMT1,DLL4,RAPGEF1,GATA3,SMAD1,YES1,BMP2,HHEX,PRKD2,RAPGEF2,CTDSPL2,CREB1,RIPK1,SKIL,HIF1A,ENSCAFG00000002015,JCAD,ZEB1	up_VCAV_EC
GO:0080090	0.112	0.946	11	1734	regulation of primary metabolic process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0007178	0.112	0.942	10	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SULF1,HSPA5,SNX25,ILK,TGFBR1,NEO1,ADAM17,STRAP,INHBA,ENSCAFG00000018360	down_VSAP_EC
GO:0001101	0.112	0.943	10	65	response to acid chemical	BP	1	PRKAA2,ABCA1,CASTOR1,GLRB,ADCY6,UBR1,PTGDR,SESN3,PRKCE,SH3BP4	up_ACOR_VSMC
GO:1901605	0.112	0.943	10	67	alpha-amino acid metabolic process	BP	1	HNF4A,GOT1,GLUL,ADHFE1,ALDH6A1,ENSCAFG00000016140,AZIN2,ENSCAFG00000002977,ASS1,IDO2	up_VSAP_EC
GO:2000241	0.112	0.955	6	40	regulation of reproductive process	BP	1	FBXO5,CDK1,B4GALT1,CDC20,TTK,ASPM	down_ACOR_VSMC
GO:0048584	0.112	0.96	5	592	positive regulation of response to stimulus	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0090100	0.112	0.965	4	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SULF1,ILK,NEO1,INHBA	down_VSAP_EC
GO:0048538	0.112	0.966	4	20	thymus development	BP	1	CITED2,LMO4,PSEN1,CRKL	up_ACOR_VSMC
GO:0006304	0.112	0.966	4	22	DNA modification	BP	0.999	GATA3,OTUD4,MTA2,TET2	up_VCAV_EC
GO:0030512	0.112	0.972	3	24	negative regulation of transforming growth factor beta receptor	BP	1	VASN,FBN1,ASPN	down_VCAV_EC
GO:0032755	0.112	0.972	3	24	positive regulation of interleukin-6 production	BP	1	CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0061053	0.112	0.972	3	24	somite development	BP	1	BMPR1A,SEMA3C,LOXL3	down_VCAV_EC
GO:1903845	0.112	0.972	3	24	negative regulation of cellular response to transforming growth	BP	1	VASN,FBN1,ASPN	down_VCAV_EC
GO:0048747	0.112	0.972	3	20	muscle fiber development	BP	1	ACTN1,NEXN,HOMER1	down_VSAP_EC
GO:0030890	0.112	0.983	2	9	positive regulation of B cell proliferation	BP	1	TFRC,CDKN1A	down_VSAP_EC
GO:0010543	0.112	0.983	2	10	regulation of platelet activation	BP	1	APOE,LYN	down_VSAP_EC
GO:0007166	0.112	0.985	2	686	cell surface receptor signaling pathway	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0030851	0.112	0.983	2	8	granulocyte differentiation	BP	0.998	HCLS1,CUL4A	up_VCAV_EC
GO:0045663	0.112	0.984	2	7	positive regulation of myoblast differentiation	BP	0.998	MEF2C,CDON	up_VCAV_EC
GO:0072574	0.112	0.985	2	6	hepatocyte proliferation	BP	0.998	TNFAIP3,PROX1	up_VCAV_EC
GO:0072575	0.112	0.985	2	6	epithelial cell proliferation involved in liver	BP	0.998	TNFAIP3,PROX1	up_VCAV_EC
GO:0072576	0.112	0.985	2	6	liver morphogenesis	BP	0.998	TNFAIP3,PROX1	up_VCAV_EC
GO:0050865	0.112	0.981	2	135	regulation of cell activation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:1901699	0.112	0.981	2	164	cellular response to nitrogen compound	BP	1	NR1H4,ARHGEF2	up_VPUL_EC

GO:0006012	0.112	0.985	2	6	galactose metabolic process	BP	1	GALK2,GALK1	up_VSAP_EC
GO:0031579	0.112	0.985	2	6	membrane raft organization	BP	1	EMP2,FLOT1	up_VSAP_EC
GO:0042559	0.112	0.985	2	6	pteridine-containing compound biosynthetic	BP	1	ENSCAFG00000013986,PCBD1	up_VSAP_EC
GO:0008088	0.112	0.994	1	21	axo-dendritic transport	BP	1	SPG11	down_ACOR_EC
GO:0070227	0.112	0.994	1	25	lymphocyte apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0009653	0.112	1	1	773	anatomical structure morphogenesis	BP	1	GATA5	down_AFEM_VSMC
GO:0070887	0.112	1	1	775	cellular response to chemical stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0022027	0.112	0.997	1	2	interkinetic nuclear migration	BP	1	HOOK3	down_VSAP_EC
GO:0002576	0.112	0.997	1	2	platelet degranulation	BP	1	LYN	down_VSAP_EC
GO:0046166	0.112	0.997	1	2	glyceraldehyde-3-phosphate biosynthetic	BP	1	TPI1	down_VSAP_EC
GO:1905907	0.112	0.997	1	2	negative regulation of amyloid fibril formation	BP	1	CRYAB	down_VSAP_EC
GO:0007389	0.112	0.995	1	137	pattern specification process	BP	1	GATA5	down_VSAP_VSMC
GO:0002086	0.112	1	1	1	diaphragm contraction	BP	1	GAA	up_ACOR_VSMC
GO:0046069	0.112	1	1	1	cGMP catabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:0003011	0.112	1	1	1	involuntary skeletal muscle contraction	BP	1	GAA	up_ACOR_VSMC
GO:1905881	0.112	1	1	1	positive regulation of oogenesis	BP	1	PDE5A	up_ACOR_VSMC
GO:0043181	0.112	1	1	1	vacuolar sequestering	BP	1	GAA	up_ACOR_VSMC
GO:0060282	0.112	1	1	1	positive regulation of oocyte development	BP	1	PDE5A	up_ACOR_VSMC
GO:0044321	0.112	0.995	1	5	response to leptin	BP	1	LEP	up_AFEM_EC
GO:0031958	0.112	0.995	1	5	corticosteroid receptor signaling pathway	BP	1	CRY2	up_AFEM_EC
GO:0031998	0.112	0.995	1	5	regulation of fatty acid beta-oxidation	BP	1	ACACB	up_AFEM_EC
GO:0042921	0.112	0.995	1	5	glucocorticoid receptor signaling pathway	BP	1	CRY2	up_AFEM_EC
GO:0055091	0.112	0.995	1	5	phospholipid homeostasis	BP	1	GPAM	up_AFEM_EC
GO:1903011	0.112	0.995	1	5	negative regulation of bone development	BP	1	GREM1	up_AFEM_EC
GO:0030177	0.112	0.994	1	51	positive regulation of Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:0010796	0.112	0.997	1	2	regulation of multivesicular body size	BP	0.999	RAB11A	up_VCAV_EC
GO:0021879	0.112	0.994	1	15	forebrain neuron differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0045047	0.112	0.994	1	14	protein targeting to ER	BP	1	SRP54	up_VPOR_EC
GO:0072599	0.112	0.994	1	14	establishment of protein localization to endoplasmic reticulum	BP	1	SRP54	up_VPOR_EC
GO:0001764	0.112	0.994	1	45	neuron migration	BP	1	CHL1	up_VPOR_VSMC
GO:0006029	0.112	0.994	1	29	proteoglycan metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0009410	0.112	0.994	1	27	response to xenobiotic stimulus	BP	1	CYP26B1	up_VFEM_EC
GO:0055001	0.112	0.994	1	47	muscle cell development	BP	1	SHOX2	up_VFEM_VSMC
GO:0009749	0.112	0.994	1	34	response to glucose	BP	1	NR1H4	up_VPUL_EC
GO:0043244	0.112	0.994	1	34	regulation of protein complex disassembly	BP	1	ARHGEF2	up_VPUL_EC
GO:0007219	0.112	0.994	1	59	Notch signaling pathway	BP	1	GATA5	up_VPUL_VSMC
GO:0060560	0.112	0.994	1	58	developmental growth involved in	BP	1	SLIT2	up_VPUL_VSMC
GO:0008589	0.112	0.994	1	28	regulation of smoothened signaling pathway	BP	1	SHOX2	up_VSAP_VSMC
GO:0080135	0.112096769	0.94158	10	240	regulation of cellular response to stress	BP	1	EDEM2,FZD5,NOD2,RGMA,TNFRSF19,MAPK8IP2,FIGNL1,SH3RF3,CLU,PRKCD	up_ACOR_EC

GO:0010769	0.112205232	0.96339	4	69	regulation of cell morphogenesis involved	BP	1	BRSK1,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0045657	0.112736021	0.9947	1	5	positive regulation of monocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0002682	0.113	0.917	40	343	regulation of immune system process	BP	1	VEGFD,TMEM176B,TLR1,TMEM176A,PLCG2,LEP,CD83,RASSF2,COCH,BMP4,TP53BP1,ELF1,TLR3,PDE5A,ISG15,CD274,FAM210B,P4HTM,F2RL1,CDKN1A,C1S,CLSTN1,PTPN22,C7,PRKCE,PARP9,APP,PSEN1,CCL5,DUSP22,NOD2,JAM3,B2M,MAP3K7,CNOT4,WASL,PARK7,IL18R1,PAG1,TAPBPL	up_ACOR_VSMC
GO:1902679	0.113	0.919	34	329	negative regulation of RNA biosynthetic process	BP	0.999	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,ELK3	up_VCAV_EC
GO:1903507	0.113	0.919	34	329	negative regulation of nucleic acid-templated transcription	BP	0.999	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,ELK3	up_VCAV_EC
GO:0055086	0.113	0.924	25	237	nucleobase-containing small molecule metabolic process	BP	1	PRPSAP1,ACLY,HMGCR,NNT,RRM1,RAN,CDK1,PFAS,TK1,RNASEH2B,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,DCK,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,PGD,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0072511	0.113	0.946	8	97	divalent inorganic cation transport	BP	1	PRNP,TRPV2,SLC39A6,CACNB3,THY1,TPC3,CYBA,PACSIN3	down_VCAV_EC
GO:0034612	0.113	0.947	8	63	response to tumor necrosis factor	BP	0.999	CXCL8,GATA3,CASP8,GCH1,RIPK1,ENSCAFG00000002015,ARHGEF2,TJP2	up_VCAV_EC
GO:0098656	0.113	0.951	7	42	anion transmembrane transport	BP	1	SLC26A7,TCAF1,CLCN3,LRRC8C,PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:0015833	0.113	0.959	5	521	peptide transport	BP	1	LYN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0050680	0.113	0.958	5	44	negative regulation of epithelial cell proliferation	BP	1	SULF1,SPARC,MAGED1,APOE,STRAP	down_VSAP_EC
GO:0045445	0.113	0.959	5	27	myoblast differentiation	BP	1	CDON,BTG1,DLL1,MAP3K5,ZFP36L1	up_VSAP_EC
GO:0055017	0.113	0.966	4	19	cardiac muscle tissue growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0033627	0.113	0.965	4	22	cell adhesion mediated by integrin	BP	0.999	PODXL,FERMT1,SWAP70,ITGA6	up_VCAV_EC
GO:0046785	0.113	0.965	4	23	microtubule polymerization	BP	0.999	MZT1,STMN1,FES,FBXO5	up_VCAV_EC
GO:0008283	0.113	0.965	4	545	cell proliferation	BP	1	TBX5,HOXA3,CCL24,ARHGEF2	up_VPUL_EC
GO:0031952	0.113	0.973	3	15	regulation of protein autophosphorylation	BP	1	CAV1,GREM1,RAP2C	down_ACOR_VSMC
GO:1902893	0.113	0.972	3	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SMARCA4,HIF1A,KLF5	down_VSAP_EC
GO:0055065	0.113	0.97	3	145	metal ion homeostasis	BP	1	C3AR1,HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0002682	0.113	0.972	3	343	regulation of immune system process	BP	1	NR1H4,EVI2B,CCL24	up_VPUL_EC
GO:0016556	0.113	0.984	2	7	mRNA modification	BP	1	ENSCAFG00000019620,WTAP	down_ACOR_VSMC
GO:0060546	0.113	0.984	2	7	negative regulation of necroptotic process	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:0060547	0.113	0.984	2	7	negative regulation of necrotic cell death	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:0045058	0.113	0.982	2	12	T cell selection	BP	1	GLI3,LOXL3	down_VCAV_EC
GO:0048013	0.113	0.982	2	11	ephrin receptor signaling pathway	BP	1	SIPA1L1,PTPN11	down_VSAP_EC
GO:0097345	0.113	0.982	2	10	mitochondrial outer membrane	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:2000095	0.113	0.984	2	6	regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	MLLT3,ZNRF3	up_ACOR_VSMC
GO:0071071	0.113	0.983	2	8	regulation of phospholipid biosynthetic process	BP	0.999	ADGRF5,PDGFB	up_VCAV_EC
GO:0032835	0.113	0.994	1	21	glomerulus development	BP	1	SULF1	down_ACOR_EC
GO:0043550	0.113	0.994	1	21	regulation of lipid kinase activity	BP	1	LYN	down_ACOR_EC

GO:0030595	0.113	0.994	1	57	leukocyte chemotaxis	BP	1	HSD3B7	down_VPOR_EC
GO:0003085	0.113	0.997	1	2	negative regulation of systemic arterial blood	BP	1	PRCP	down_VSAP_EC
GO:0042701	0.113	0.997	1	2	progesterone secretion	BP	1	INHBA	down_VSAP_EC
GO:0045629	0.113	0.997	1	2	negative regulation of T-helper 2 cell	BP	1	SOCS5	down_VSAP_EC
GO:0030574	0.113	0.995	1	5	collagen catabolic process	BP	1	FAP	up_AFEM_EC
GO:0036158	0.113	0.995	1	5	outer dynein arm assembly	BP	1	DNAL1	up_AFEM_EC
GO:0007618	0.113	0.995	1	5	mating	BP	1	THRB	up_AFEM_EC
GO:0014009	0.113	0.995	1	5	glial cell proliferation	BP	1	LGI4	up_AFEM_EC
GO:0019430	0.113	0.995	1	5	removal of superoxide radicals	BP	1	SOD1	up_AFEM_EC
GO:0032695	0.113	0.995	1	5	negative regulation of interleukin-12 production	BP	1	CMKLR1	up_AFEM_EC
GO:0042269	0.113	0.995	1	5	regulation of natural killer cell mediated cytotoxicity	BP	1	LEP	up_AFEM_EC
GO:0002715	0.113	0.995	1	5	regulation of natural killer cell mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0046532	0.113	0.995	1	5	regulation of photoreceptor cell	BP	1	THRB	up_AFEM_EC
GO:0050862	0.113	0.995	1	5	positive regulation of T cell receptor signaling	BP	1	CYLD	up_AFEM_EC
GO:0003139	0.113	0.995	1	5	secondary heart field specification	BP	1	AXIN2	up_AFEM_EC
GO:0060346	0.113	0.995	1	5	bone trabecula formation	BP	1	GREM1	up_AFEM_EC
GO:0060644	0.113	0.995	1	5	mammary gland epithelial cell differentiation	BP	1	LBH	up_AFEM_EC
GO:0071450	0.113	0.995	1	5	cellular response to oxygen radical	BP	1	SOD1	up_AFEM_EC
GO:0071451	0.113	0.995	1	5	cellular response to superoxide	BP	1	SOD1	up_AFEM_EC
GO:1901186	0.113	0.995	1	5	positive regulation of ERBB signaling pathway	BP	1	ADAM17	up_AFEM_EC
GO:1901524	0.113	0.995	1	5	regulation of mitophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0030178	0.113	0.994	1	52	negative regulation of Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:0007406	0.113	1	1	1	negative regulation of neuroblast proliferation	BP	0.999	CTNNA1	up_VCAV_EC
GO:0035279	0.113	1	1	1	mRNA cleavage involved in gene silencing by	BP	0.999	MOV10	up_VCAV_EC
GO:0007168	0.113	1	1	1	receptor guanylyl cyclase signaling pathway	BP	0.999	NPR1	up_VCAV_EC
GO:0098795	0.113	1	1	1	mRNA cleavage involved in gene silencing	BP	0.999	MOV10	up_VCAV_EC
GO:1901490	0.113	0.997	1	2	regulation of lymphangiogenesis	BP	0.999	VASH1	up_VCAV_EC
GO:1901653	0.113	0.994	1	84	cellular response to peptide	BP	1	CA2	up_VCAV_VSMC
GO:0070098	0.113	0.994	1	14	chemokine-mediated signaling pathway	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0010463	0.113	0.994	1	28	mesenchymal cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0051153	0.113	0.994	1	28	regulation of striated muscle cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0035270	0.113	0.994	1	35	endocrine system development	BP	1	HOXA3	up_VPUL_EC
GO:0030833	0.113	0.994	1	59	regulation of actin filament polymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0006942	0.113	0.994	1	26	regulation of striated muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0050715	0.113	0.994	1	29	positive regulation of cytokine secretion	BP	1	TLR2	up_VSAP_VSMC
GO:1904064	0.113	0.994	1	27	positive regulation of cation transmembrane	BP	1	STIM1	up_VSAP_VSMC
GO:1901017	0.113102071	0.99466	1	5	negative regulation of potassium ion transmembrane	BP	1	ACTN2	up_ACOR_EC
GO:1901380	0.113102071	0.99466	1	5	negative regulation of potassium ion	BP	1	ACTN2	up_ACOR_EC

GO:0008283	0.114	0.911	61	545	cell proliferation	BP	1	EMX2,CDON,WNT11,HNF4A,CD274,AXIN2,C5AR2,OSR2,PTGFR,MAB21L1,LIMS2,IL6R,CRIP2,FGF7,ABL1,PEX2,BTG1,EMP2,DLL1,OSR1,PDGFD,NAA60,SAV1,HPSE,ZBTB16,RARG,STAT5A,STAT6,AMBRA1,F2RL1,MORC3,DDR2,MFN2,ZFP36L1,TIAM1,MYC,PTGES,ZEB1,FBXW4,SULF2,SHOX2,FBXO4,MYD88,DAGLB,E2F4,KDM2B,FBLN1,RAF1,PNP,TAF8,NFIB,ZNF580,STX4,SMARCA2,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,LBH,DPT	up_VSAP_EC
GO:0023052	0.114	0.917	45	1602	signaling	BP	1	CMKLR1,LEP,KCNC4,LBH,CRY2,GAS1,ANGPT4,CD40,DLL1,F3,PLXNA4,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,HTR1D,FAM53B,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,RECK,PTHLH,TBXA2R,BVES,LGR6,RAB7A,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,KANK1,TNC	up_AFEM_EC
GO:0006928	0.114	0.919	34	557	movement of cell or subcellular component	BP	1	PDGFRB,DCN,NDN,SDC4,GLIPR2,KANK2,BMPR1A,LMO4,RECK,RHOD,AKT2,DOCK10,SYDE1,HSD3B7,LAMA3,CSPG4,WIPF1,SEMA3C,THY1,PEX5,MYO1B,B4GALT1,GLI3,SASH1,IFT57,CDH2,FUT8,SPRED1,MGARP,TWIST2,DDR2,GREM1,RAC2,FOXO3	down_VCAV_EC
GO:0048589	0.114	0.925	23	188	developmental growth	BP	1	HOXA11,WNT11,ACACB,SLIT2,SLC6A4,FGF7,ABL1,DLL1,SAV1,PLXNA4,RARG,DDR2,ZFP36L1,FXN,GAS1,LRP4,DPYSL2,TAF8,TTL,HTRA2,ULK1,TGFBR2,LATS2	up_VSAP_EC
GO:0007005	0.114	0.935	13	175	mitochondrion organization	BP	1	SLC35F6,DCN,COA1,GABARAP,CHCHD10,POLDIP2,WDR45,PEX5,PARK7,CLEC16A,MPV17,MGARP,MTFR1L	down_VCAV_EC
GO:0060348	0.114	0.94	11	78	bone development	BP	1	HOXA11,PEX7,AXIN2,OSR2,INSIG2,RARG,SULF2,SHOX2,BGLAP,TGFBR2,CITED2	up_VSAP_EC
GO:0032868	0.114	0.949	7	66	response to insulin	BP	1	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,PTPN2	down_VSAP_EC
GO:0006479	0.114	0.95	7	45	protein methylation	BP	0.999	IWS1,GATA3,ARID4B,NSD1,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0008213	0.114	0.95	7	45	protein alkylation	BP	0.999	IWS1,GATA3,ARID4B,NSD1,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0051171	0.114	0.956	7	1697	regulation of nitrogen compound metabolic	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006915	0.114	0.958	5	550	apoptotic process	BP	1	LYN,IGF1R,PDPN,USP28,STX4	down_ACOR_EC
GO:0006661	0.114	0.965	4	23	phosphatidylinositol biosynthetic process	BP	0.999	PDGFB,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0007045	0.114	0.965	4	23	cell-substrate adherens junction assembly	BP	0.999	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0048041	0.114	0.965	4	23	focal adhesion assembly	BP	0.999	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0044238	0.114	1	3	3383	primary metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0008542	0.114	0.973	3	13	visual learning	BP	1	HRH1,LRRN4,APP	up_ACOR_VSMC
GO:0050817	0.114	0.97	3	50	coagulation	BP	1	F5,F3,TFPI2	up_AFEM_EC
GO:0051252	0.114	0.976	3	1051	regulation of RNA metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0065008	0.114	0.976	3	1056	regulation of biological quality	BP	1	HOXC10,WNT7A,ESR1	up_AORT_VSMC
GO:1990868	0.114	0.972	3	16	response to chemokine	BP	0.999	ACKR1,CXCL8,CXCR4	up_VCAV_EC
GO:1990869	0.114	0.972	3	16	cellular response to chemokine	BP	0.999	ACKR1,CXCL8,CXCR4	up_VCAV_EC
GO:0045944	0.114	0.971	3	287	positive regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0021517	0.114	0.982	2	12	ventral spinal cord development	BP	1	LMO4,GLI3	down_VCAV_EC
GO:0034103	0.114	0.982	2	12	regulation of tissue remodeling	BP	1	B4GALT1,GREM1	down_VCAV_EC
GO:0035239	0.114	0.981	2	299	tube morphogenesis	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0051281	0.114	0.982	2	10	positive regulation of release of sequestered calcium ion into cytosol	BP	1	HTT,CALM1	down_VSAP_EC
GO:2000727	0.114	0.984	2	7	positive regulation of cardiac muscle cell	BP	0.999	MEF2C,EDN1	up_VCAV_EC
GO:0032232	0.114	0.983	2	7	negative regulation of actin filament bundle	BP	0.999	ARHGAP28,STMN1	up_VCAV_EC

GO:0032620	0.114	0.983	2	8	interleukin-17 production	BP	0.999	TLR4,ARG2	up_VCAV_EC
GO:0051497	0.114	0.983	2	7	negative regulation of stress fiber assembly	BP	0.999	ARHGAP28,STMN1	up_VCAV_EC
GO:0060546	0.114	0.983	2	7	negative regulation of necroptotic process	BP	0.999	PELI1,ARHGEF2	up_VCAV_EC
GO:0060547	0.114	0.983	2	7	negative regulation of necrotic cell death	BP	0.999	PELI1,ARHGEF2	up_VCAV_EC
GO:0009792	0.114	0.981	2	231	embryo development ending in birth or egg	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0034637	0.114	0.994	1	25	cellular carbohydrate biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0140029	0.114	0.994	1	28	exocytic process	BP	1	STX4	down_ACOR_EC
GO:0021872	0.114	0.994	1	19	forebrain generation of neurons	BP	1	NRP2	down_ACOR_EC
GO:0032799	0.114	0.997	1	2	low-density lipoprotein receptor particle	BP	1	APOE	down_VSAP_EC
GO:0038091	0.114	0.997	1	2	positive regulation of cell proliferation by VEGF-activated platelet derived growth factor receptor	BP	1	VEGFA	down_VSAP_EC
GO:0045650	0.114	0.997	1	2	negative regulation of macrophage	BP	1	PTPN2	down_VSAP_EC
GO:0019433	0.114	0.997	1	2	triglyceride catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0038086	0.114	0.997	1	2	VEGF-activated platelet-derived growth factor receptor signaling	BP	1	VEGFA	down_VSAP_EC
GO:0046598	0.114	0.997	1	2	positive regulation of viral entry into host cell	BP	1	P4HB	down_VSAP_EC
GO:0048148	0.114	0.997	1	2	behavioral response to cocaine	BP	1	HOMER1	down_VSAP_EC
GO:0051006	0.114	0.997	1	2	positive regulation of lipoprotein lipase activity	BP	1	ABHD5	down_VSAP_EC
GO:0061043	0.114	0.997	1	2	regulation of vascular wound healing	BP	1	SERPINE1	down_VSAP_EC
GO:0061365	0.114	0.997	1	2	positive regulation of triglyceride lipase activity	BP	1	ABHD5	down_VSAP_EC
GO:0002093	0.114	1	1	1	auditory receptor cell morphogenesis	BP	1	SEC24B	up_ACOR_VSMC
GO:0060088	0.114	1	1	1	auditory receptor cell stereocilium organization	BP	1	SEC24B	up_ACOR_VSMC
GO:0021747	0.114	1	1	1	cochlear nucleus development	BP	1	SEC24B	up_ACOR_VSMC
GO:0010225	0.114	0.995	1	5	response to UV-C	BP	1	DCUN1D3	up_AFEM_EC
GO:0007213	0.114	0.995	1	5	G protein-coupled acetylcholine receptor	BP	1	CHRM2	up_AFEM_EC
GO:0009713	0.114	0.995	1	5	catechol-containing compound biosynthetic	BP	1	MOXD1	up_AFEM_EC
GO:0010661	0.114	0.995	1	5	positive regulation of muscle cell apoptotic	BP	1	CAMK2A	up_AFEM_EC
GO:0014823	0.114	0.995	1	5	response to activity	BP	1	PPARGC1A	up_AFEM_EC
GO:0019062	0.114	0.995	1	5	virion attachment to host cell	BP	1	LRRC15	up_AFEM_EC
GO:0032460	0.114	0.995	1	5	negative regulation of protein oligomerization	BP	1	CRYAB	up_AFEM_EC
GO:0032463	0.114	0.995	1	5	negative regulation of protein	BP	1	CRYAB	up_AFEM_EC
GO:0035929	0.114	0.995	1	5	steroid hormone secretion	BP	1	CRY2	up_AFEM_EC
GO:0040034	0.114	0.995	1	5	regulation of development,	BP	1	DLL1	up_AFEM_EC
GO:0042423	0.114	0.995	1	5	catecholamine biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0044406	0.114	0.995	1	5	adhesion of symbiont to host	BP	1	LRRC15	up_AFEM_EC
GO:0044650	0.114	0.995	1	5	adhesion of symbiont to host cell	BP	1	LRRC15	up_AFEM_EC
GO:0045603	0.114	0.995	1	5	positive regulation of endothelial cell	BP	1	TMEM100	up_AFEM_EC
GO:0048168	0.114	0.995	1	5	regulation of neuronal synaptic plasticity	BP	1	CAMK2A	up_AFEM_EC
GO:0055026	0.114	0.995	1	5	negative regulation of cardiac muscle tissue	BP	1	DLL1	up_AFEM_EC
GO:0070886	0.114	0.995	1	5	positive regulation of calcineurin-NFAT signaling	BP	1	LMCD1	up_AFEM_EC

GO:0106058	0.114	0.995	1	5	positive regulation of calcineurin-mediated	BP	1	LMCD1	up_AFEM_EC
GO:1903077	0.114	0.995	1	5	negative regulation of protein localization to	BP	1	LRRC15	up_AFEM_EC
GO:1903580	0.114	0.995	1	5	positive regulation of ATP metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:1904376	0.114	0.995	1	5	negative regulation of protein localization to cell	BP	1	LRRC15	up_AFEM_EC
GO:1905906	0.114	0.995	1	5	regulation of amyloid fibril formation	BP	1	CRYAB	up_AFEM_EC
GO:0051047	0.114	0.994	1	84	positive regulation of secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0002791	0.114	0.994	1	104	regulation of peptide secretion	BP	1	ARG2	up_AORT_VSMC
GO:1904888	0.114	0.994	1	31	cranial skeletal system development	BP	1	HOXA1	up_APUL_EC
GO:0021503	0.114	1	1	1	neural fold bending	BP	0.999	LUZP1	up_VCAV_EC
GO:0045341	0.114	1	1	1	MHC class I biosynthetic process	BP	0.999	NLRC5	up_VCAV_EC
GO:0045343	0.114	1	1	1	regulation of MHC class I biosynthetic process	BP	0.999	NLRC5	up_VCAV_EC
GO:0045345	0.114	1	1	1	positive regulation of MHC class I biosynthetic	BP	0.999	NLRC5	up_VCAV_EC
GO:0051926	0.114	0.994	1	14	negative regulation of calcium ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0001837	0.114	0.994	1	48	epithelial to mesenchymal transition	BP	1	BAMBI	up_VPOR_VSMC
GO:0007411	0.114	0.994	1	45	axon guidance	BP	1	CHL1	up_VPOR_VSMC
GO:0097485	0.114	0.994	1	45	neuron projection guidance	BP	1	CHL1	up_VPOR_VSMC
GO:0097529	0.114	0.994	1	52	myeloid leukocyte migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0050954	0.114	0.994	1	30	sensory perception of mechanical stimulus	BP	1	SIX1	up_VFEM_EC
GO:0007030	0.114	0.994	1	49	Golgi organization	BP	1	ATP8B4	up_VFEM_VSMC
GO:0022898	0.114	0.994	1	48	regulation of transmembrane	BP	1	NETO1	up_VFEM_VSMC
GO:0048839	0.114	0.994	1	50	inner ear development	BP	1	EYA1	up_VFEM_VSMC
GO:0062014	0.114	0.994	1	35	negative regulation of small molecule metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0019217	0.114	0.994	1	27	regulation of fatty acid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0034763	0.114	0.994	1	27	negative regulation of transmembrane transport	BP	1	CAV1	up_VSAP_VSMC
GO:0045445	0.114	0.994	1	27	myoblast differentiation	BP	1	PITX1	up_VSAP_VSMC
GO:0051153	0.114	0.994	1	28	regulation of striated muscle cell differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0032642	0.114940404	0.98035	2	22	regulation of chemokine production	BP	1	NR1H4,MAVS	up_ACOR_EC
GO:0048869	0.115	0.905	118	1119	cellular developmental process	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,NAPEPLD,TWIST2,HOXA9,CDON,WNT11,HNF4A,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,ENPP2,RADIL,PPARGC1B,GJB5,IRX5,SLIT2,ZHX3,HOXD3,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,OSR1,MAP3K5,CDC42EP5,ADAMTSL4,WARS2,SAV1,KLF15,ANXA4,PLXNA4,ARL4A,RILPL2,ANKRD54,CDC42EP2,ZBTB16,TOX,ALDH6A1,RARG,STAT6,PATZ1,PLPP3,GTF3C5,F2RL1,DLX3,GLIS2,MORC3,DDR2,ZFP36L1,PIK3R1,TIAM1,GAS1,BATF2,MYC,IRX3,ZEB1,SULF2,SHOX2,EEF2,RTN4RL1,HOXC10,POLDIP2,MYD88,TFE3,LRP4,DPYSL2,GDPD5,ZADH2,DAGLB,HPS4,FRMD6,CLCN2,E2F4,FBXO7,NTN4,LIMD1,CDK9,CD83,NR2F6,FBLN1,ZFP36L2,PLEKHB2,YPEL3,RAF1,PNP,TAF8,NFIB,CYB5D2,CDNF,PRELP,ANPEP,PQBP1,TTL,ACVRL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,MAP2K2,TGFBR2,CITED2,OGN,PIR,LBH,KEAP1,SOAT1,LATS2	up_VSAP_EC
GO:0044283	0.115	0.923	25	201	small molecule biosynthetic process	BP	1	ACSM3,LIPC,INSIG2,ACACB,GOT1,GLUL,ENSCAFG00000013986,COQ9,HSD17B8,PPIP5K1,PDK2,GALK1,ENTPD3,PTGES,HACD4,ENSCAFG00000016140,PCBD1,PC,DHRS9,MVK,PNPO,PNP,CYB5R3,ASS1,DDIT4	up_VSAP_EC

GO:0002682	0.115	0.936	12	343	regulation of immune system process	BP	1	HOXA9,CMKLR1,LEP,HOXA7,CD40,DLL1,BPI,GPAM,CYLD,EVI2B,CCL5,ADAM17	up_AFEM_EC
GO:0072330	0.115	0.941	10	68	monocarboxylic acid biosynthetic process	BP	1	ACSM3,LIPC,INSIG2,ACACB,HSD17B8,GALK1,PTGES,HACD4,DHRS9,DDIT4	up_VSAP_EC
GO:0045184	0.115	0.958	5	532	establishment of protein localization	BP	1	LYN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0016233	0.115	0.964	4	22	telomere capping	BP	1	HNRNPD,AURKB,NEK2,TINF2	down_ACOR_VSMC
GO:0008645	0.115	0.963	4	37	hexose transmembrane transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC
GO:0015749	0.115	0.963	4	37	monosaccharide transmembrane transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC
GO:0034219	0.115	0.963	4	37	carbohydrate transmembrane transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC
GO:0055088	0.115	0.963	4	37	lipid homeostasis	BP	1	GPAM,LCAT,ORMDL3,SOAT1	down_VCAV_EC
GO:0035821	0.115	0.963	4	32	modification of morphology or physiology	BP	1	SMARCA4,APOE,REST,CALM1	down_VSAP_EC
GO:0009888	0.115	0.964	4	545	tissue development	BP	1	TBX5,HOXA3,NR1H4,FLRT3	up_VPUL_EC
GO:0046634	0.115	0.971	3	24	regulation of alpha-beta T cell activation	BP	1	GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0006505	0.115	0.973	3	13	GPI anchor metabolic process	BP	1	PIGN,PIGS,PIGG	up_ACOR_VSMC
GO:0006506	0.115	0.973	3	13	GPI anchor biosynthetic process	BP	1	PIGN,PIGS,PIGG	up_ACOR_VSMC
GO:0097755	0.115	0.973	3	12	positive regulation of blood vessel diameter	BP	1	F2RL1,PTGDR,DOCK5	up_ACOR_VSMC
GO:0043491	0.115	0.97	3	50	protein kinase B signaling	BP	1	LEP,F3,TMEM100	up_AFEM_EC
GO:0060042	0.115	0.972	3	14	retina morphogenesis in camera-type eye	BP	0.999	PROX1,TSPAN12,CDON	up_VCAV_EC
GO:0035066	0.115	0.983	2	7	positive regulation of histone acetylation	BP	1	BRCA1,TADA2A	down_ACOR_VSMC
GO:0022603	0.115	0.981	2	301	regulation of anatomical structure morphogenesis	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0097320	0.115	0.984	2	6	plasma membrane tubulation	BP	1	ASAP1,WASL	up_ACOR_VSMC
GO:0000076	0.115	0.983	2	7	DNA replication checkpoint	BP	0.999	RAD17,TOPBP1	up_VCAV_EC
GO:0032990	0.115	0.98	2	167	cell part morphogenesis	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:2000147	0.115	0.98	2	169	positive regulation of cell motility	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0043086	0.115	0.98	2	170	negative regulation of catalytic activity	BP	1	PTGER2,FLRT3	up_VPUL_EC
GO:0048706	0.115	0.994	1	59	embryonic skeletal system development	BP	1	TBX15	down_VPOR_EC
GO:0001844	0.115	0.996	1	2	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	BP	1	SH3GLB1	down_VSAP_EC
GO:0031034	0.115	0.997	1	2	myosin filament assembly	BP	1	MYBPC2	down_VSAP_EC
GO:0042271	0.115	0.997	1	2	susceptibility to natural killer cell mediated	BP	1	PVR	down_VSAP_EC
GO:0051204	0.115	0.996	1	2	protein insertion into mitochondrial membrane	BP	1	SH3GLB1	down_VSAP_EC
GO:0060370	0.115	0.997	1	2	susceptibility to T cell mediated cytotoxicity	BP	1	PVR	down_VSAP_EC
GO:0060426	0.115	0.996	1	2	lung vasculature development	BP	1	ERRFI1	down_VSAP_EC
GO:0071688	0.115	0.997	1	2	striated muscle myosin thick filament assembly	BP	1	MYBPC2	down_VSAP_EC
GO:1900739	0.115	0.996	1	2	regulation of protein insertion into mitochondrial membrane involved in apoptotic	BP	1	SH3GLB1	down_VSAP_EC
GO:1900740	0.115	0.996	1	2	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic	BP	1	SH3GLB1	down_VSAP_EC
GO:0006528	0.115	0.997	1	2	asparagine metabolic process	BP	1	ASNS	down_VSAP_EC
GO:0072615	0.115	0.997	1	2	interleukin-17 secretion	BP	1	NR1H4	down_VSAP_EC
GO:0009304	0.115	1	1	1	tRNA transcription	BP	1	GTF3C1	up_ACOR_VSMC
GO:0002316	0.115	1	1	1	follicular B cell differentiation	BP	1	PLCG2	up_ACOR_VSMC

GO:0042791	0.115	1	1	1	5S class rRNA transcription by RNA	BP	1	GTF3C1	up_ACOR_VSMC
GO:0001919	0.115	0.994	1	5	regulation of receptor recycling	BP	1	BVES	up_AFEM_EC
GO:0010759	0.115	0.994	1	5	positive regulation of macrophage chemotaxis	BP	1	CMKLR1	up_AFEM_EC
GO:0010765	0.115	0.994	1	5	positive regulation of sodium ion transport	BP	1	FXYD1	up_AFEM_EC
GO:0061004	0.115	0.995	1	5	pattern specification involved in kidney	BP	1	IRX3	up_AFEM_EC
GO:0071850	0.115	0.995	1	5	mitotic cell cycle arrest	BP	1	FAP	up_AFEM_EC
GO:0072048	0.115	0.995	1	5	renal system pattern specification	BP	1	IRX3	up_AFEM_EC
GO:0051091	0.115	0.994	1	87	positive regulation of DNA-binding transcription factor activity	BP	1	TLR2	up_AFEM_VSMC
GO:0051051	0.115	0.994	1	112	negative regulation of transport	BP	1	ARG2	up_AORT_VSMC
GO:0090100	0.115	0.994	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	NPNT	up_APUL_EC
GO:0014721	0.115	1	1	1	twitch skeletal muscle contraction	BP	0.999	ATP2A1	up_VCAV_EC
GO:0014724	0.115	1	1	1	regulation of twitch skeletal muscle	BP	0.999	ATP2A1	up_VCAV_EC
GO:0045989	0.115	1	1	1	positive regulation of striated muscle	BP	0.999	ATP2A1	up_VCAV_EC
GO:0003010	0.115	1	1	1	voluntary skeletal muscle contraction	BP	0.999	ATP2A1	up_VCAV_EC
GO:0031443	0.115	1	1	1	fast-twitch skeletal muscle fiber contraction	BP	0.999	ATP2A1	up_VCAV_EC
GO:0031446	0.115	1	1	1	regulation of fast-twitch skeletal muscle fiber	BP	0.999	ATP2A1	up_VCAV_EC
GO:0031448	0.115	1	1	1	positive regulation of fast-twitch skeletal muscle	BP	0.999	ATP2A1	up_VCAV_EC
GO:0051659	0.115	1	1	1	maintenance of mitochondrion location	BP	0.999	ATP2A1	up_VCAV_EC
GO:0002697	0.115	0.994	1	85	regulation of immune effector process	BP	1	C6	up_VCAV_VSMC
GO:0006111	0.115	0.994	1	15	regulation of gluconeogenesis	BP	1	FBP1	up_VPOR_EC
GO:0030808	0.115	0.994	1	15	regulation of nucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0032495	0.115	0.994	1	15	response to muramyl dipeptide	BP	1	ARHGEF2	up_VPOR_EC
GO:0045022	0.115	0.994	1	15	early endosome to late endosome transport	BP	1	HOOK3	up_VPOR_EC
GO:0045912	0.115	0.994	1	15	negative regulation of carbohydrate metabolic	BP	1	FBP1	up_VPOR_EC
GO:1900371	0.115	0.994	1	15	regulation of purine nucleotide biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0007519	0.115	0.994	1	49	skeletal muscle tissue development	BP	1	CYP26B1	up_VPOR_VSMC
GO:1903707	0.115	0.994	1	48	negative regulation of hemopoiesis	BP	1	HOXA9	up_VFEM_VSMC
GO:0009746	0.115	0.994	1	35	response to hexose	BP	1	NR1H4	up_VPUL_EC
GO:0034284	0.115	0.994	1	35	response to monosaccharide	BP	1	NR1H4	up_VPUL_EC
GO:0035107	0.115	0.994	1	60	appendage morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0035108	0.115	0.994	1	60	limb morphogenesis	BP	1	TBX5	up_VPUL_VSMC
GO:0072073	0.115	0.994	1	60	kidney epithelium development	BP	1	SLIT2	up_VPUL_VSMC
GO:0061097	0.115	0.994	1	27	regulation of protein tyrosine kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:1901606	0.115815161	0.98011	2	22	alpha-amino acid catabolic process	BP	1	THNSL2,SARDH	up_ACOR_EC
GO:0006833	0.115973283	0.99438	1	5	water transport	BP	1	AQP1	up_ACOR_EC

GO:0006796	0.116	0.911	55	938	phosphate-containing compound metabolic process	BP	1	GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,ADCY6,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,LCAT,EEF2K,H6PD,PLCL1,CSPG4,NT5C2,ENTPD3,THNSL2,PGLS,ATP5MC1,GFPT2,UQCR10,ASPN,PIGS,THY1,ADK,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,ARL2BP,AMPD2,MAVS,CDH2,GSDME,CAMK2D,SPRED1,ACSS2,MAPRE3,CDKL2,DDR2,SHC1,FBH1,GREM1,NAPEPLD,ACAT1,BRSK1,CDK14	down_VCAV_EC
GO:0007417	0.116	0.93	16	235	central nervous system development	BP	1	SMAD9,LRP1,NDN,BMPR1A,LMO4,NUMBL,NAGLU,ENSCAFG00000018277,HAPLN3,PEX5,VCAN,GLI3,CDH2,LOXL3,FOXO3,ZBTB16	down_VCAV_EC
GO:0051716	0.116	0.939	14	2001	cellular response to stimulus	BP	1	ACVRL1,LYN,IGF1R,PDPN,NRP2,HIVEP2,USP28,IPO7,ATRIP,SULF1,WDR12,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0032787	0.116	0.937	11	144	monocarboxylic acid metabolic process	BP	1	GPAM,AKT2,ACAA1,ME3,THNSL2,PEX5,PARK7,ACSS2,RDH10,LONP2,ACAT1	down_VCAV_EC
GO:0010876	0.116	0.942	9	92	lipid localization	BP	1	ENPP1,PTPN11,OSBPL9,PTPN2,APOE,OSBPL6,ABHD5,INHBA,ESYT3	down_VSAP_EC
GO:0072659	0.116	0.948	7	82	protein localization to plasma membrane	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,CDH2,RAB31	down_VCAV_EC
GO:0009746	0.116	0.953	6	35	response to hexose	BP	1	PRKAA2,LPL,SLC2A5,PRKCE,RAB11B,PFKL	up_ACOR_VSMC
GO:0034284	0.116	0.953	6	35	response to monosaccharide	BP	1	PRKAA2,LPL,SLC2A5,PRKCE,RAB11B,PFKL	up_ACOR_VSMC
GO:0014020	0.116	0.957	5	41	primary neural tube formation	BP	1	PRICKLE1,PRKACB,TMED2,HIF1A,SDC4	down_VSAP_EC
GO:0071704	0.116	0.983	5	3535	organic substance metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0043550	0.116	0.964	4	21	regulation of lipid kinase activity	BP	1	TEK,PPP2R5A,PDGFB,SH3GLB1	up_VCAV_EC
GO:0051050	0.116	0.97	3	235	positive regulation of transport	BP	1	ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0016070	0.116	0.979	3	1479	RNA metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0021517	0.116	0.973	3	12	ventral spinal cord development	BP	1	LMO4,TBX20,CLN8	up_ACOR_VSMC
GO:0070663	0.116	0.969	3	50	regulation of leukocyte proliferation	BP	1	LEP,GPAM,GREM1	up_AFEM_EC
GO:0071772	0.116	0.969	3	50	response to BMP	BP	1	TMEM100,GREM1,GREM2	up_AFEM_EC
GO:0071773	0.116	0.969	3	50	cellular response to BMP stimulus	BP	1	TMEM100,GREM1,GREM2	up_AFEM_EC
GO:0045022	0.116	0.972	3	15	early endosome to late endosome transport	BP	1	HOOK3,DNAJC13,LMTK2	up_VCAV_EC
GO:0048732	0.116	0.98	2	116	gland development	BP	1	HOXA3,SULF1	down_ACOR_EC
GO:0007157	0.116	0.981	2	12	heterophilic cell-cell adhesion via plasma membrane cell adhesion	BP	1	CDH2,CD164	down_VCAV_EC
GO:0050896	0.116	1	2	2346	response to stimulus	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:1904424	0.116	0.984	2	6	regulation of GTP binding	BP	1	ARHGAP28,CCPG1	up_ACOR_VSMC
GO:0051254	0.116	0.982	2	431	positive regulation of RNA metabolic process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0033032	0.116	0.983	2	7	regulation of myeloid cell apoptotic process	BP	1	MEF2C,ITPKB	up_VCAV_EC
GO:0002820	0.116	0.983	2	7	negative regulation of adaptive immune	BP	1	IL7R,THOC1	up_VCAV_EC
GO:0002823	0.116	0.983	2	7	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	IL7R,THOC1	up_VCAV_EC
GO:0050884	0.116	0.982	2	8	neuromuscular process controlling posture	BP	1	TMEM150C,GCH1	up_VCAV_EC
GO:0051693	0.116	0.982	2	8	actin filament capping	BP	1	TMOD1,TMOD3	up_VCAV_EC
GO:0090279	0.116	0.982	2	8	regulation of calcium ion import	BP	1	PDGFB,STC1	up_VCAV_EC
GO:0044089	0.116	0.98	2	170	positive regulation of cellular component	BP	1	CCL24,FLRT3	up_VPUL_EC
GO:0051272	0.116	0.98	2	170	positive regulation of cellular component	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0010522	0.116	0.993	1	24	regulation of calcium ion transport into cytosol	BP	1	LYN	down_ACOR_EC

GO:0015893	0.116	0.993	1	26	drug transport	BP	1	PDPN	down_ACOR_EC
GO:0022029	0.116	0.993	1	23	telencephalon cell migration	BP	1	NRP2	down_ACOR_EC
GO:0030512	0.116	0.993	1	24	negative regulation of transforming growth factor beta receptor	BP	1	ASPN	down_ACOR_EC
GO:0071333	0.116	0.993	1	25	cellular response to glucose stimulus	BP	1	STX4	down_ACOR_EC
GO:1903845	0.116	0.993	1	24	negative regulation of cellular response to transforming growth	BP	1	ASPN	down_ACOR_EC
GO:0010988	0.116	0.996	1	2	regulation of low-density lipoprotein particle	BP	1	NR1H4	down_VSAP_EC
GO:0002513	0.116	0.996	1	2	tolerance induction to self antigen	BP	1	LYN	down_VSAP_EC
GO:2001020	0.116	0.994	1	88	regulation of response to DNA damage stimulus	BP	1	EYA1	up_AFEM_VSMC
GO:0035296	0.116	0.993	1	32	regulation of tube diameter	BP	1	HTR7	up_APUL_EC
GO:0045446	0.116	0.993	1	32	endothelial cell differentiation	BP	1	ARHGEF26	up_APUL_EC
GO:0050728	0.116	0.993	1	31	negative regulation of inflammatory response	BP	1	NR1H4	up_APUL_EC
GO:0097746	0.116	0.993	1	32	regulation of blood vessel diameter	BP	1	HTR7	up_APUL_EC
GO:0001525	0.116	0.994	1	173	angiogenesis	BP	1	HOXA3	up_APUL_VSMC
GO:0002009	0.116	0.994	1	177	morphogenesis of an epithelium	BP	1	TBX5	up_APUL_VSMC
GO:0003231	0.116	0.994	1	48	cardiac ventricle development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003279	0.116	0.993	1	48	cardiac septum development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0009913	0.116	0.993	1	47	epidermal cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006733	0.116	0.993	1	45	oxidoreduction coenzyme metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0009142	0.116	0.994	1	46	nucleoside triphosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0006941	0.116	0.993	1	36	striated muscle contraction	BP	1	MYBPC2	up_VPUL_EC
GO:0002687	0.116	0.993	1	36	positive regulation of leukocyte migration	BP	1	CCL24	up_VPUL_EC
GO:0006814	0.116	0.993	1	28	sodium ion transport	BP	1	NETO1	up_VSAP_VSMC
GO:0010463	0.116	0.993	1	28	mesenchymal cell proliferation	BP	1	SHOX2	up_VSAP_VSMC
GO:0048863	0.116816749	0.96132	4	70	stem cell differentiation	BP	1	SOX9,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0042327	0.117	0.917	34	289	positive regulation of phosphorylation	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,IL6R,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,DDR2,TRAF7,SASH1,MYD88,LRP4,CDK9,RAF1,ACVRL1,FLOT1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0007420	0.117	0.925	21	169	brain development	BP	1	EMX2,PCDH19,SEZ6L,CDON,SLIT2,SLC6A4,ABL1,DLL1,PLXNA4,CTNS,RTN4RL1,DPYSL2,GDPD5,SMG9,MCPH1,KIF27,KDM2B,NFIB,QARS,HTRA2,TGFBR2	up_VSAP_EC
GO:0051051	0.117	0.939	10	112	negative regulation of transport	BP	1	NR1H4,ENPP1,PTPN11,REM1,CRYAB,REST,CALM1,RAB11FIP1,LRRTM2,RHBDF2	down_VSAP_EC
GO:0021915	0.117	0.942	9	58	neural tube development	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3,PSEN1	up_ACOR_VSMC
GO:0030326	0.117	0.945	8	51	embryonic limb morphogenesis	BP	1	AFF3,RECK,BMP4,LNPK,GJA1,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0035113	0.117	0.945	8	51	embryonic appendage morphogenesis	BP	1	AFF3,RECK,BMP4,LNPK,GJA1,TBX5,PSEN1,CHD7	up_ACOR_VSMC
GO:0010810	0.117	0.945	8	60	regulation of cell-substrate adhesion	BP	1	TEK,FERMT1,NEDD9,SLK,ANGPT2,APOD,JAG1,ENSCAFG00000002015	up_VCAV_EC
GO:0051179	0.117	0.955	7	1747	localization	BP	1	CHL1,HOXA3,NKX2-5,LHFPL4,BAMBI,TRPC4,C3AR1	up_VPOR_VSMC
GO:0071702	0.117	0.953	6	687	organic substance transport	BP	1	LYN,PDPN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0046916	0.117	0.952	6	35	cellular transition metal ion homeostasis	BP	1	FXN,MYC,SCARA5,FTL,HMOX1,NCOA4	up_VSAP_EC
GO:1904888	0.117	0.957	5	31	cranial skeletal system development	BP	1	EIF4A3,INSIG1,MMP14,TBX15,SIX4	down_ACOR_VSMC
GO:0001503	0.117	0.955	5	109	ossification	BP	1	XYLT1,TWIST2,GREM1,PTHLH,AXIN2	up_AFEM_EC

GO:0050770	0.117	0.962	4	39	regulation of axonogenesis	BP	1	TRPV2,THY1,UST,BRSK1	down_VCAV_EC
GO:0098739	0.117	0.964	4	20	import across plasma membrane	BP	1	SLC2A5,PSEN1,CLN8,SLC8A1	up_ACOR_VSMC
GO:0018108	0.117	0.961	4	79	peptidyl-tyrosine phosphorylation	BP	1	LEP,HCK,GREM1,ADAM17	up_AFEM_EC
GO:0071347	0.117	0.963	4	25	cellular response to interleukin-1	BP	1	CXCL8,MAPK13,OTUD4,HIF1A	up_VCAV_EC
GO:0051443	0.117	0.971	3	15	positive regulation of ubiquitin-protein	BP	1	UBE2S,CDC20,DCUN1D5	down_ACOR_VSMC
GO:1901799	0.117	0.97	3	24	negative regulation of proteasomal protein catabolic process	BP	1	PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:1901019	0.117	0.97	3	20	regulation of calcium ion transmembrane transporter activity	BP	1	REM1,HTT,CALM1	down_VSAP_EC
GO:0001935	0.117	0.969	3	50	endothelial cell proliferation	BP	1	LEP,F3,ADAM17	up_AFEM_EC
GO:0010562	0.117	0.97	3	312	positive regulation of phosphorus metabolic	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0045937	0.117	0.97	3	312	positive regulation of phosphate metabolic	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0017145	0.117	0.972	3	13	stem cell division	BP	1	ZBTB16,ZFP36L2,LBH	up_VSAP_EC
GO:0099024	0.117	0.972	3	13	plasma membrane invagination	BP	1	F2RL1,XKR8,ARHGAP12	up_VSAP_EC
GO:0016242	0.117	0.972	3	13	negative regulation of macroautophagy	BP	1	POLDIP2,HTRA2,HMOX1	up_VSAP_EC
GO:0000076	0.117	0.983	2	7	DNA replication checkpoint	BP	1	TOPBP1,CLSPN	down_ACOR_VSMC
GO:0051093	0.117	0.98	2	273	negative regulation of developmental process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0002833	0.117	0.981	2	12	positive regulation of response to biotic	BP	1	SASH1,CYBA	down_VCAV_EC
GO:2001273	0.117	0.981	2	12	regulation of glucose import in response to	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0048532	0.117	0.982	2	9	anatomical structure arrangement	BP	1	HSPA5,NRP1	down_VSAP_EC
GO:0060384	0.117	0.982	2	9	innervation	BP	1	SULF1,NRP1	down_VSAP_EC
GO:0071696	0.117	0.984	2	6	ectodermal placode development	BP	1	NRP1,FRS2	up_ACOR_VSMC
GO:0097327	0.117	0.98	2	25	response to antineoplastic agent	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0019725	0.117	0.98	2	245	cellular homeostasis	BP	1	ENSCAFG00000005494,TAOK1	up_AORT_EC
GO:0003222	0.117	0.984	2	6	ventricular trabecula myocardium	BP	1	CHD7,DLL4	up_VCAV_EC
GO:0046885	0.117	0.983	2	7	regulation of hormone biosynthetic process	BP	1	BMP2,HIF1A	up_VCAV_EC
GO:0060872	0.117	0.984	2	6	semicircular canal development	BP	1	CHD7,ZEB1	up_VCAV_EC
GO:2000515	0.117	0.982	2	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	ARG2,HMGB1	up_VCAV_EC
GO:0071560	0.117	0.979	2	72	cellular response to transforming growth	BP	1	ENSCAFG00000002015,ASPN	up_VPOR_EC
GO:0090092	0.117	0.979	2	72	regulation of transmembrane receptor protein serine/threonine	BP	1	ASPN,ACVR2A	up_VPOR_EC
GO:0034763	0.117	0.993	1	27	negative regulation of transmembrane transport	BP	1	NEDD4	down_ACOR_EC
GO:0044706	0.117	0.993	1	27	multi-multicellular organism process	BP	1	ACSL4	down_ACOR_EC
GO:0046889	0.117	0.993	1	24	positive regulation of lipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0002246	0.117	0.996	1	2	wound healing involved in inflammatory response	BP	1	HIF1A	down_VSAP_EC
GO:0002431	0.117	0.996	1	2	Fc receptor mediated stimulatory signaling	BP	1	LYN	down_VSAP_EC
GO:1903377	0.117	0.996	1	2	negative regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0090594	0.117	0.996	1	2	inflammatory response to wounding	BP	1	HIF1A	down_VSAP_EC
GO:0035120	0.117	1	1	1	post-embryonic appendage	BP	1	ATRX	up_ACOR_VSMC
GO:0035127	0.117	1	1	1	post-embryonic limb morphogenesis	BP	1	ATRX	up_ACOR_VSMC

GO:0035128	0.117	1	1	1	post-embryonic forelimb morphogenesis	BP	1	ATRX	up_ACOR_VSMC
GO:0097393	0.117	1	1	1	telomeric repeat-containing RNA	BP	1	ATRX	up_ACOR_VSMC
GO:0097394	0.117	1	1	1	telomeric repeat-containing RNA transcription by RNA	BP	1	ATRX	up_ACOR_VSMC
GO:1901580	0.117	1	1	1	regulation of telomeric RNA transcription from RNA pol II promoter	BP	1	ATRX	up_ACOR_VSMC
GO:1901581	0.117	1	1	1	negative regulation of telomeric RNA transcription from RNA	BP	1	ATRX	up_ACOR_VSMC
GO:1901582	0.117	1	1	1	positive regulation of telomeric RNA transcription from RNA	BP	1	ATRX	up_ACOR_VSMC
GO:0002237	0.117	0.994	1	85	response to molecule of bacterial origin	BP	1	TLR2	up_AFEM_VSMC
GO:0030001	0.117	0.994	1	172	metal ion transport	BP	1	HOXA3	up_APUL_VSMC
GO:0051665	0.117	0.996	1	2	membrane raft localization	BP	1	MALL	up_VCAV_EC
GO:1990456	0.117	1	1	1	mitochondrion-endoplasmic reticulum	BP	1	PDZD8	up_VCAV_EC
GO:0010335	0.117	1	1	1	response to non-ionic osmotic stress	BP	1	PTGS2	up_VCAV_EC
GO:0031394	0.117	1	1	1	positive regulation of prostaglandin biosynthetic process	BP	1	PTGS2	up_VCAV_EC
GO:0046642	0.117	0.996	1	2	negative regulation of alpha-beta T cell	BP	1	ARG2	up_VCAV_EC
GO:0061302	0.117	0.996	1	2	smooth muscle cell-matrix adhesion	BP	1	APOD	up_VCAV_EC
GO:0071471	0.117	1	1	1	cellular response to non-ionic osmotic stress	BP	1	PTGS2	up_VCAV_EC
GO:1905397	0.117	0.996	1	2	activated CD8-positive, alpha-beta T cell	BP	1	ARG2	up_VCAV_EC
GO:1905402	0.117	0.996	1	2	regulation of activated CD8-positive, alpha-beta T cell apoptotic process	BP	1	ARG2	up_VCAV_EC
GO:2000097	0.117	0.996	1	2	regulation of smooth muscle cell-matrix	BP	1	APOD	up_VCAV_EC
GO:2000098	0.117	0.996	1	2	negative regulation of smooth muscle cell-matrix	BP	1	APOD	up_VCAV_EC
GO:2000562	0.117	0.996	1	2	negative regulation of CD4-positive, alpha-beta T cell proliferation	BP	1	ARG2	up_VCAV_EC
GO:0006623	0.117	0.993	1	16	protein targeting to vacuole	BP	1	GCC2	up_VPOR_EC
GO:0051193	0.117	0.993	1	15	regulation of cofactor metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0050920	0.117	0.993	1	53	regulation of chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0071772	0.117	0.993	1	50	response to BMP	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071773	0.117	0.993	1	50	cellular response to BMP stimulus	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003206	0.117	0.993	1	51	cardiac chamber morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0009127	0.117	0.993	1	47	purine nucleoside monophosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0009168	0.117	0.993	1	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0035150	0.117	0.993	1	36	regulation of tube size	BP	1	HTR7	up_VPUL_EC
GO:0050880	0.117	0.993	1	36	regulation of blood vessel size	BP	1	HTR7	up_VPUL_EC
GO:0090276	0.117	0.993	1	36	regulation of peptide hormone secretion	BP	1	NR1H4	up_VPUL_EC
GO:1904659	0.117	0.993	1	36	glucose transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:1990138	0.117	0.993	1	35	neuron projection extension	BP	1	FLRT3	up_VPUL_EC
GO:0045927	0.117	0.993	1	61	positive regulation of growth	BP	1	TBX5	up_VPUL_VSMC
GO:0042632	0.117	0.993	1	27	cholesterol homeostasis	BP	1	CAV1	up_VSAP_VSMC

GO:0043549	0.117163161	0.9384	10	244	regulation of kinase activity	BP	1	PKIB,ENSCAFG00000004331,FZD5,DUSP26,PAK3,LRRC15,LRRC4,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0019730	0.11723761	0.99426	1	5	antimicrobial humoral response	BP	1	RARRES2	up_ACOR_EC
GO:0032677	0.117538304	0.97964	2	22	regulation of interleukin-8 production	BP	1	NOD2,MAVS	up_ACOR_EC
GO:0032649	0.117573674	0.97957	2	23	regulation of interferon-gamma production	BP	1	NR1H4,FZD5	up_ACOR_EC
GO:0055002	0.117590811	0.96882	3	45	striated muscle cell development	BP	1	MYOZ2,TMOD1,ACTN2	up_ACOR_EC
GO:0034220	0.117877423	0.94303	8	188	ion transmembrane transport	BP	1	CLIC3,AQP1,KCNB1,ACTN2,SLC25A42,MAPK8IP2,SLC9A9,PM20D1	up_ACOR_EC
GO:0035239	0.118	0.915	35	299	tube morphogenesis	BP	1	HOXA11,FZD1,HOXA7,WNT11,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,FUZ,WARS2,HPSE,RARG,CCBE1,ZFP36L1,IRX3,ZEB1,TBXA2R,SHOX2,SASH1,LOX,KDM2B,HPGD,NFIB,ANPEP,ACVRL1,HMOX1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0010941	0.118	0.927	17	524	regulation of cell death	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,AXIN2,PPARGC1A,CCL5,FAP	up_AFEM_EC
GO:0072001	0.118	0.939	10	104	renal system development	BP	1	SULF1,ENSCAFG00000032470,ILK,HOXB7,ACTA2,MAGED1,CTNNB1,MYO1E,SIX4,NRP1	down_VSAP_EC
GO:0048545	0.118	0.939	10	68	response to steroid hormone	BP	1	LBH,SKP2,BMP4,MED14,AR,CREBRF,NR3C1,FAM107A,DDIT4,PARK7	up_ACOR_VSMC
GO:0055074	0.118	0.941	9	95	calcium ion homeostasis	BP	1	ERO1A,ATP2B1,TMTC2,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:1901653	0.118	0.947	7	84	cellular response to peptide	BP	1	LRP1,PRNP,ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0050870	0.118	0.952	6	42	positive regulation of T cell activation	BP	1	IL7R,GATA3,ITPKB,NCK1,BCL10,HMGB1	up_VCAV_EC
GO:0002761	0.118	0.952	6	36	regulation of myeloid leukocyte differentiation	BP	1	HOXA7,PPARGC1B,ZFP36L1,PIK3R1,MYC,TFE3	up_VSAP_EC
GO:0030038	0.118	0.957	5	31	contractile actin filament bundle assembly	BP	1	ARHGEF15,ARHGAP28,MTOR,STMN1,TNFAIP1	up_VCAV_EC
GO:0030183	0.118	0.957	5	30	B cell differentiation	BP	1	KIT,HHEX,MFNG,PLCG2,ATP11C	up_VCAV_EC
GO:0043149	0.118	0.957	5	31	stress fiber assembly	BP	1	ARHGEF15,ARHGAP28,MTOR,STMN1,TNFAIP1	up_VCAV_EC
GO:0032879	0.118	0.958	5	767	regulation of localization	BP	1	TBX5,HOXA3,NR1H4,CCL24,ARHGEF2	up_VPUL_EC
GO:0051492	0.118	0.957	5	28	regulation of stress fiber assembly	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,BAG4	up_VSAP_EC
GO:0010033	0.118	0.964	4	772	response to organic substance	BP	1	FGF5,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0001708	0.118	0.963	4	20	cell fate specification	BP	1	HOXA11,CDON,DLL1,HOXC10	up_VSAP_EC
GO:0060612	0.118	0.971	3	14	adipose tissue development	BP	1	CDK4,PPARD,AMER1	down_ACOR_VSMC
GO:0001658	0.118	0.97	3	24	branching involved in ureteric bud	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0001759	0.118	0.972	3	13	organ induction	BP	1	GATA5,BMP4,FRS2	up_ACOR_VSMC
GO:0033687	0.118	0.972	3	13	osteoblast proliferation	BP	1	OSR2,ABL1,HPSE	up_VSAP_EC
GO:0045944	0.118	0.969	3	287	positive regulation of transcription by RNA polymerase II	BP	1	HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:0090231	0.118	0.983	2	7	regulation of spindle checkpoint	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:0090266	0.118	0.983	2	7	regulation of mitotic cell cycle spindle assembly	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:1903504	0.118	0.983	2	7	regulation of mitotic spindle checkpoint	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:0072678	0.118	0.981	2	10	T cell migration	BP	1	MSN,ADAM17	down_VSAP_EC
GO:0050918	0.118	0.981	2	10	positive chemotaxis	BP	1	VEGFA,NRP1	down_VSAP_EC
GO:2000406	0.118	0.983	2	6	positive regulation of T cell migration	BP	1	APP,CCL5	up_ACOR_VSMC
GO:0006635	0.118	0.979	2	25	fatty acid beta-oxidation	BP	1	LEP,ACACB	up_AFEM_EC
GO:0033143	0.118	0.979	2	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	LBH,CRY2	up_AFEM_EC
GO:0098693	0.118	0.979	2	25	regulation of synaptic vesicle cycle	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:1903312	0.118	0.979	2	25	negative regulation of mRNA metabolic process	BP	1	TENT5C,AXIN2	up_AFEM_EC

GO:0021801	0.118	0.983	2	6	cerebral cortex radial glia guided migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0022030	0.118	0.983	2	6	telencephalon glial cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0045687	0.118	0.982	2	7	positive regulation of glial cell differentiation	BP	1	MTOR,BMP2	up_VCAV_EC
GO:0032101	0.118	0.979	2	173	regulation of response to external stimulus	BP	1	NR1H4,CCL24	up_VPUL_EC
GO:0051270	0.118	0.98	2	296	regulation of cellular component movement	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0045944	0.118	0.995	1	287	positive regulation of transcription by RNA polymerase II	BP	1	MOSPD1	down_VFEM_EC
GO:0045893	0.118	0.996	1	413	positive regulation of transcription, DNA-	BP	1	GATA5	down_VFEM_VSMC
GO:0060816	0.118	0.996	1	2	random inactivation of X chromosome	BP	1	CDYL	down_VSAP_EC
GO:1903297	0.118	0.996	1	2	regulation of hypoxia-induced intrinsic apoptotic signaling	BP	1	HYOU1	down_VSAP_EC
GO:1903298	0.118	0.996	1	2	negative regulation of hypoxia-induced intrinsic apoptotic signaling	BP	1	HYOU1	down_VSAP_EC
GO:1902714	0.118	0.996	1	2	negative regulation of interferon-gamma	BP	1	NR1H4	down_VSAP_EC
GO:0010466	0.118	0.993	1	32	negative regulation of peptidase activity	BP	1	PCSK1N	up_APUL_EC
GO:0010951	0.118	0.993	1	32	negative regulation of endopeptidase activity	BP	1	PCSK1N	up_APUL_EC
GO:0030534	0.118	0.993	1	33	adult behavior	BP	1	SLITRK5	up_APUL_EC
GO:0010511	0.118	0.996	1	2	regulation of phosphatidylinositol	BP	1	PDGFB	up_VCAV_EC
GO:0033634	0.118	1	1	1	positive regulation of cell-cell adhesion mediated by	BP	1	PODXL	up_VCAV_EC
GO:0035711	0.118	0.996	1	2	T-helper 1 cell activation	BP	1	HMGB1	up_VCAV_EC
GO:1900125	0.118	0.996	1	2	regulation of hyaluronan biosynthetic process	BP	1	PDGFB	up_VCAV_EC
GO:0050804	0.118	0.994	1	87	modulation of chemical synaptic transmission	BP	1	CA2	up_VCAV_VSMC
GO:0099177	0.118	0.994	1	87	regulation of trans-synaptic signaling	BP	1	CA2	up_VCAV_VSMC
GO:0007224	0.118	0.993	1	50	smoothened signaling pathway	BP	1	SHOX2	up_VFEM_VSMC
GO:0008286	0.118	0.993	1	36	insulin receptor signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0031109	0.118	0.993	1	36	microtubule polymerization or	BP	1	ARHGEF2	up_VPUL_EC
GO:0002761	0.118	0.993	1	36	regulation of myeloid leukocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0030041	0.118	0.993	1	62	actin filament polymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0060491	0.118	0.993	1	62	regulation of cell projection assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0120032	0.118	0.993	1	62	regulation of plasma membrane bounded cell	BP	1	SLIT2	up_VPUL_VSMC
GO:1901888	0.118	0.993	1	29	regulation of cell junction assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0007189	0.118176069	0.97946	2	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	PTH1R,PTGIR	up_ACOR_EC
GO:0046661	0.118220936	0.96858	3	45	male sex differentiation	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:2000060	0.118491551	0.96847	3	45	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	PIAS1,CLU,RNF114	up_ACOR_EC
GO:0065003	0.119	0.908	57	616	protein-containing complex assembly	BP	1	TEK,HCLS1,GBP5,SELP,CDA,MX2,BAIAP2L1,VWF,TLR4,SMAD1,IRF8,SNAP91,TMOD1,NASP,MTOR,ACPP,SNAP23,LRRC8C,LNX2,SCAF11,CNOT6,ABCA1,NCKAP1,MZT1,RIOK3,IQGAP2,STMN1,SNX2,CENPC,NCK1,KCNJ2,FES,HIST1H1A,EHD4,BCL10,SENP6,PAN3,PRPF39,CNOT7,GCH1,ASF1A,HMGB1,PMAIP1,ARPC5L,BLM,RIPK1,LSM14A,MCU,ZW10,ATRX,ALDH1A3,HP1BP3,P2RX2,TNFAIP1,TMOD3,FSCN1,FBXO5	up_VCAV_EC
GO:0042127	0.119	0.929	15	452	regulation of cell proliferation	BP	1	LEP,LBH,CD40,DLL1,F3,GPAM,MAB21L1,HCK,GREM1,OVOL1,AXIN2,FAP,ADAM17,FOSL2,TNC	up_AFEM_EC

GO:0006402	0.119	0.938	10	77	mRNA catabolic process	BP	1	RNPS1,EIF4A3,EDC3,HNRNPD,THRAP3,EDC4,SMG9,FASTKD3,ENSCAFG00000015189,EXOSC5	down_ACOR_VSMC
GO:0008150	0.119	1	10	5646	biological_process	BP	1	HOXC6,SLITRK5,CYP1A1,LIMK1,GATA5,CA2,LRRC17,C6,TGFBI,ENSCAFG00000028814	up_VCAV_VSMC
GO:0019219	0.119	0.944	9	1151	regulation of nucleobase-containing compound metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0045017	0.119	0.944	8	52	glycerolipid biosynthetic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,PIGN,PIGS,PIGG,CRLS1	up_ACOR_VSMC
GO:0010634	0.119	0.947	7	68	positive regulation of epithelial cell migration	BP	1	VEGFA,SPARC,JCAD,PIK3C2A,HIF1A,ADAM17,NRP1	down_VSAP_EC
GO:0048523	0.119	0.956	6	1399	negative regulation of cellular process	BP	1	CHL1,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0110110	0.119	0.956	5	34	positive regulation of animal organ	BP	1	HOXB7,TNFAIP3,CD34,GATA3,BMP2	up_VCAV_EC
GO:0051250	0.119	0.961	4	38	negative regulation of lymphocyte activation	BP	1	PRNP,SDC4,GLI3,LOXL3	down_VCAV_EC
GO:0046903	0.119	0.969	3	255	secretion	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0034754	0.119	0.969	3	24	cellular hormone metabolic process	BP	1	CYP1B1,RETSAT,RDH10	down_VCAV_EC
GO:0030177	0.119	0.968	3	51	positive regulation of Wnt signaling pathway	BP	1	FAM53B,LGR6,KANK1	up_AFEM_EC
GO:0006351	0.119	0.974	3	1069	transcription, DNA-templated	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0002832	0.119	0.971	3	15	negative regulation of response to biotic	BP	1	TNFAIP3,ARG2,RIOK3	up_VCAV_EC
GO:0070528	0.119	0.971	3	13	protein kinase C signaling	BP	1	SEZ6L,WNT11,FLOT1	up_VSAP_EC
GO:0034762	0.119	0.979	2	122	regulation of transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0019985	0.119	0.982	2	7	translesion synthesis	BP	1	PCNA,DTL	down_ACOR_VSMC
GO:0043604	0.119	0.98	2	288	amide biosynthetic process	BP	1	DARS,EIF3M	down_AFEM_EC
GO:0030195	0.119	0.981	2	10	negative regulation of blood coagulation	BP	1	SERPINE1,APOE	down_VSAP_EC
GO:1900047	0.119	0.981	2	10	negative regulation of hemostasis	BP	1	SERPINE1,APOE	down_VSAP_EC
GO:0048278	0.119	0.979	2	25	vesicle docking	BP	1	CAMK2A,BVES	up_AFEM_EC
GO:0048701	0.119	0.979	2	25	embryonic cranial skeleton morphogenesis	BP	1	TBX15,IRX5	up_AFEM_EC
GO:0072676	0.119	0.979	2	25	lymphocyte migration	BP	1	CCL5,ADAM17	up_AFEM_EC
GO:0006760	0.119	0.982	2	8	folic acid-containing compound metabolic	BP	1	PIPOX,GCH1	up_VCAV_EC
GO:0045664	0.119	0.979	2	144	regulation of neuron differentiation	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0001525	0.119	0.979	2	173	angiogenesis	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:0014031	0.119	0.993	1	27	mesenchymal cell development	BP	1	NRP2	down_ACOR_EC
GO:0014032	0.119	0.993	1	27	neural crest cell development	BP	1	NRP2	down_ACOR_EC
GO:0021885	0.119	0.993	1	24	forebrain cell migration	BP	1	NRP2	down_ACOR_EC
GO:0034446	0.119	0.993	1	23	substrate adhesion-dependent cell spreading	BP	1	PDPN	down_ACOR_EC
GO:0045682	0.119	0.993	1	27	regulation of epidermis development	BP	1	HOXA7	down_ACOR_EC
GO:0044242	0.119	0.993	1	57	cellular lipid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0045766	0.119	0.993	1	63	positive regulation of angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:1902680	0.119	0.996	1	415	positive regulation of RNA biosynthetic process	BP	1	GATA5	down_VFEM_VSMC
GO:1903508	0.119	0.996	1	415	positive regulation of nucleic acid-templated	BP	1	GATA5	down_VFEM_VSMC
GO:0006437	0.119	0.996	1	2	tyrosyl-tRNA aminoacylation	BP	1	YARS	down_VSAP_EC
GO:0006617	0.119	0.996	1	2	SRP-dependent cotranslational protein targeting to membrane,	BP	1	SRP54	down_VSAP_EC
GO:0009191	0.119	0.996	1	2	ribonucleoside diphosphate catabolic	BP	1	ENTPD4	down_VSAP_EC
GO:0009756	0.119	0.996	1	2	carbohydrate mediated signaling	BP	1	SMARCA4	down_VSAP_EC

GO:0009757	0.119	0.996	1	2	hexose mediated signaling	BP	1	SMARCA4	down_VSAP_EC
GO:0010182	0.119	0.996	1	2	sugar mediated signaling pathway	BP	1	SMARCA4	down_VSAP_EC
GO:0010255	0.119	0.996	1	2	glucose mediated signaling pathway	BP	1	SMARCA4	down_VSAP_EC
GO:0036123	0.119	0.996	1	2	histone H3-K9 dimethylation	BP	1	KDM3A	down_VSAP_EC
GO:0090209	0.119	0.996	1	2	negative regulation of triglyceride metabolic	BP	1	APOE	down_VSAP_EC
GO:1902659	0.119	0.996	1	2	regulation of glucose mediated signaling	BP	1	SMARCA4	down_VSAP_EC
GO:1902661	0.119	0.996	1	2	positive regulation of glucose mediated	BP	1	SMARCA4	down_VSAP_EC
GO:0006972	0.119	0.996	1	2	hyperosmotic response	BP	1	ARHGEF2	down_VSAP_EC
GO:0071474	0.119	0.996	1	2	cellular hyperosmotic response	BP	1	ARHGEF2	down_VSAP_EC
GO:0000086	0.119	0.993	1	52	G2/M transition of mitotic cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0006820	0.119	0.994	1	109	anion transport	BP	1	SLC20A2	up_AORT_VSMC
GO:0044057	0.119	0.994	1	110	regulation of system process	BP	1	WNT7A	up_AORT_VSMC
GO:0060411	0.119	0.993	1	33	cardiac septum morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0072078	0.119	0.993	1	33	nephron tubule morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0055080	0.119	0.994	1	176	cation homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0031547	0.119	1	1	1	brain-derived neurotrophic factor	BP	1	RAPGEF2	up_VCAV_EC
GO:0036065	0.119	0.996	1	2	fucosylation	BP	1	MFNG	up_VCAV_EC
GO:0036066	0.119	0.996	1	2	protein O-linked fucosylation	BP	1	MFNG	up_VCAV_EC
GO:0061073	0.119	1	1	1	ciliary body morphogenesis	BP	1	JAG1	up_VCAV_EC
GO:0061444	0.119	1	1	1	endocardial cushion cell development	BP	1	JAG1	up_VCAV_EC
GO:0071321	0.119	1	1	1	cellular response to cGMP	BP	1	RAPGEF2	up_VCAV_EC
GO:0061443	0.119	1	1	1	endocardial cushion cell differentiation	BP	1	JAG1	up_VCAV_EC
GO:0070305	0.119	1	1	1	response to cGMP	BP	1	RAPGEF2	up_VCAV_EC
GO:0000460	0.119	0.993	1	15	maturation of 5.8S rRNA	BP	1	RRP15	up_VPOR_EC
GO:0006826	0.119	0.993	1	15	iron ion transport	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0046330	0.119	0.993	1	47	positive regulation of JNK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030326	0.119	0.993	1	51	embryonic limb morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0035113	0.119	0.993	1	51	embryonic appendage morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006022	0.119	0.993	1	29	aminoglycan metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0007519	0.119	0.993	1	49	skeletal muscle tissue development	BP	1	SHOX2	up_VFEM_VSMC
GO:0007416	0.119	0.993	1	36	synapse assembly	BP	1	FLRT3	up_VPUL_EC
GO:0010770	0.119	0.993	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0048167	0.119	0.993	1	28	regulation of synaptic plasticity	BP	1	NETO1	up_VSAP_VSMC
GO:0060675	0.119	0.993	1	29	ureteric bud morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:0071447	0.119015212	0.99408	1	5	cellular response to hydroperoxide	BP	1	PRKCD	up_ACOR_EC
GO:0072007	0.119485884	0.99403	1	5	mesangial cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0072143	0.119485884	0.99403	1	5	mesangial cell development	BP	1	FOXC2	up_ACOR_EC
GO:1904238	0.119485884	0.99403	1	5	pericyte cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0060976	0.119533228	0.97909	2	22	coronary vasculature development	BP	1	SMAD6,NRP1	up_ACOR_EC

GO:0019883	0.119560879	0.99402	1	5	antigen processing and presentation of endogenous antigen	BP	1	TAPBP	up_ACOR_EC
GO:0010759	0.119626673	0.99401	1	5	positive regulation of macrophage chemotaxis	BP	1	RARRES2	up_ACOR_EC
GO:0016043	0.12	0.901	130	1973	cellular component organization	BP	1	ARHGEF2,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,NR1H4,FMNL3,PLK3,C1QTNF6,SERPINE1,ACTN1,ETV6,SPARC,VASP,SGK1,ERO1A,ENPP1,P4HA1,SEC24D,TPM4,AKAP2,PTPN11,EXOC5,CORO1C,FSCN1,FLNB,SEC23A,MZT1,DPYSL3,LRRC8A,HOOK3,IFRD1,ENSCAFG00000007260,FBLIM1,ILK,PPP1R12A,SMARCA4,ANKRA2,SESN2,SRP54,WDR1,MYO1C,MSN,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TUBB,IWS1,TNIK,NAA10,UBA6,ZPR1,MORF4L2,TMSB10,NEO1,SMG7,USO1,ESM1,PRPF3,DDX39B,ADAM17,BRD2,UST,CNOT7,CDH11,ACTR3,PALLD,CTNNB1,KPNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,PLOD3,IGFBP7,KLF5,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,FAM162A,PLEKHG2,TLN1,CLCN3,PLS3,GSK3B,VLDLR,NEXN,CDC37,DAAM1,GBP5,CCSER2,SH3GLB1,MYO1E,SDC4,HTT,REST,ENSCAFG00000017326,ZMYND8,EIF2S1,PRMT1,P3H4,EXT1,DISC1,PAK2,CLTC,LRRTM2,CAPG,INHBA,SIX4,CDKN1A,RSL24D1,SLC25A46,NRP1,ARF4,YWHAH,COL12A1,ENSCAFG00000030508,BLZF1,TNFAIP1,SEC13,KDM3A,MYBPC2,MID1	down_VSAP_EC
GO:0019219	0.12	0.902	107	1151	regulation of nucleobase-containing compound metabolic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,MTOR,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,ESCO1,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,NOS2,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0023014	0.12	0.923	20	248	signal transduction by protein phosphorylation	BP	1	VEGFA,JCAD,PTPN11,TRIB3,ILK,TNIK,PTPN2,MAGED1,CTNNB1,APOE,LYN,CBLC,ATF3,MAPK10,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0051640	0.12	0.924	19	174	organelle localization	BP	1	KIT,RAB11A,KIF3C,RAB27A,EXOC6,NECTIN2,HOOK3,SNAP23,HHEX,CAV2,PDZD8,CENPC,EXOC5,FES,STX11,ZW10,HIF1A,SHROOM2,ATP2A1	up_VCAV_EC
GO:0016053	0.12	0.935	11	97	organic acid biosynthetic process	BP	1	PDGFB,EDN1,PTGS1,PROX1,ELOVL7,ENSCAFG00000024323,PTGS2,GCH1,HIF1A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0046394	0.12	0.935	11	97	carboxylic acid biosynthetic process	BP	1	PDGFB,EDN1,PTGS1,PROX1,ELOVL7,ENSCAFG00000024323,PTGS2,GCH1,HIF1A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0033673	0.12	0.942	8	84	negative regulation of kinase activity	BP	1	SOCS5,ERRFI1,TRIB3,PTPN2,APOE,LYN,CBLC,CDKN1A	down_VSAP_EC
GO:0015931	0.12	0.943	8	59	nucleobase-containing compound transport	BP	1	IWS1,SLC35A3,QKI,HHEX,THOC1,SMG7,NUP133,RIPK1	up_VCAV_EC
GO:0051017	0.12	0.946	7	49	actin filament bundle assembly	BP	1	FSCN1,LIMA1,NF2,STMN1,RAC1,PDXP,EZR	down_ACOR_VSMC
GO:0007568	0.12	0.947	7	50	aging	BP	1	PLK2,PDE4D,ARG2,MAP3K3,APOD,SMC5,VASH1	up_VCAV_EC
GO:0046330	0.12	0.947	7	47	positive regulation of JNK cascade	BP	1	MAP3K11,TLR4,EDN1,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0045665	0.12	0.95	6	55	negative regulation of neuron differentiation	BP	1	DPYSL3,IFRD1,APOE,REST,NRP1,YWHAH	down_VSAP_EC
GO:0071356	0.12	0.95	6	57	cellular response to tumor necrosis factor	BP	1	ARHGEF2,NR1H4,ILK,PTPN2,ADAM17,ENSCAFG00000002015	down_VSAP_EC
GO:0044260	0.12	0.965	6	2593	cellular macromolecule metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC

GO:0002181	0.12	0.951	6	35	cytoplasmic translation	BP	1	RPL15,EIF3G,EIF3K,EIF3L,EIF3D,NCK1	up_VSAP_EC
GO:0006637	0.12	0.956	5	32	acyl-CoA metabolic process	BP	1	ACLY,MVD,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0035383	0.12	0.956	5	32	thioester metabolic process	BP	1	ACLY,MVD,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0009991	0.12	0.954	5	110	response to extracellular stimulus	BP	1	LEP,CLEC16A,POSTN,ACACB,PPARGC1A	up_AFEM_EC
GO:0048639	0.12	0.96	4	39	positive regulation of developmental growth	BP	1	GPAM,BMPR1A,TRPV2,PEX5	down_VCAV_EC
GO:1903672	0.12	0.963	4	20	positive regulation of sprouting angiogenesis	BP	1	ABL1,HDAC7,DLL1,HMOX1	up_VSAP_EC
GO:0061035	0.12	0.969	3	24	regulation of cartilage development	BP	1	GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:0048483	0.12	0.969	3	19	autonomic nervous system development	BP	1	CTNNB1,PDS5B,NRP1	down_VSAP_EC
GO:0060389	0.12	0.969	3	21	pathway-restricted SMAD protein phosphorylation	BP	1	SNX25,STRAP,INHBA	down_VSAP_EC
GO:0042130	0.12	0.971	3	13	negative regulation of T cell proliferation	BP	1	BMP4,PDE5A,CD274	up_ACOR_VSMC
GO:0045843	0.12	0.971	3	13	negative regulation of striated muscle tissue	BP	1	BMP4,TBX5,FRS2	up_ACOR_VSMC
GO:0032774	0.12	0.974	3	1073	RNA biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0097659	0.12	0.974	3	1072	nucleic acid-templated transcription	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0071470	0.12	0.971	3	13	cellular response to osmotic stress	BP	1	OSR1,ZFP36L1,SLC12A6	up_VSAP_EC
GO:0030497	0.12	0.981	2	8	fatty acid elongation	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:1901978	0.12	0.982	2	7	positive regulation of cell cycle checkpoint	BP	1	NDC80,GEN1	down_ACOR_VSMC
GO:0006518	0.12	0.98	2	290	peptide metabolic process	BP	1	DARS,EIF3M	down_AFEM_EC
GO:0006625	0.12	0.98	2	12	protein targeting to peroxisome	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0015919	0.12	0.98	2	12	peroxisomal membrane transport	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0043574	0.12	0.98	2	12	peroxisomal transport	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0072662	0.12	0.98	2	12	protein localization to peroxisome	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0072663	0.12	0.98	2	12	establishment of protein localization to peroxisome	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0009595	0.12	0.983	2	6	detection of biotic stimulus	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0035239	0.12	0.98	2	299	tube morphogenesis	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:0009617	0.12	0.979	2	133	response to bacterium	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0030203	0.12	0.993	1	27	glycosaminoglycan metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0034333	0.12	0.993	1	25	adherens junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0048167	0.12	0.993	1	28	regulation of synaptic plasticity	BP	1	STX4	down_ACOR_EC
GO:0071326	0.12	0.993	1	26	cellular response to monosaccharide stimulus	BP	1	STX4	down_ACOR_EC
GO:0071331	0.12	0.993	1	26	cellular response to hexose stimulus	BP	1	STX4	down_ACOR_EC
GO:0016477	0.12	0.996	1	426	cell migration	BP	1	JUP	down_VFEM_VSMC
GO:0061072	0.12	0.996	1	2	iris morphogenesis	BP	1	HIF1A	down_VSAP_EC
GO:0061582	0.12	0.996	1	2	intestinal epithelial cell migration	BP	1	PTPN11	down_VSAP_EC
GO:0090149	0.12	0.996	1	2	mitochondrial membrane fission	BP	1	SLC25A46	down_VSAP_EC
GO:0051249	0.12	0.993	1	107	regulation of lymphocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0007612	0.12	0.993	1	33	learning	BP	1	NTRK2	up_APUL_EC
GO:0040008	0.12	0.994	1	179	regulation of growth	BP	1	TBX5	up_APUL_VSMC
GO:0061061	0.12	0.994	1	179	muscle structure development	BP	1	TBX5	up_APUL_VSMC
GO:0031282	0.12	1	1	1	regulation of guanylate cyclase activity	BP	1	NOS2	up_VCAV_EC
GO:0031284	0.12	1	1	1	positive regulation of guanylate cyclase activity	BP	1	NOS2	up_VCAV_EC

GO:0043129	0.12	1	1	1	surfactant homeostasis	BP	1	ADGRF5	up_VCAV_EC
GO:0045026	0.12	1	1	1	plasma membrane fusion	BP	1	TIE1	up_VCAV_EC
GO:0019230	0.12	0.996	1	2	proprioception	BP	1	TMEM150C	up_VCAV_EC
GO:0051349	0.12	1	1	1	positive regulation of lyase activity	BP	1	NOS2	up_VCAV_EC
GO:1903778	0.12	0.996	1	2	protein localization to vacuolar membrane	BP	1	SH3GLB1	up_VCAV_EC
GO:1900024	0.12	0.993	1	16	regulation of substrate adhesion-dependent cell	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0060538	0.12	0.993	1	51	skeletal muscle organ development	BP	1	CYP26B1	up_VPOR_VSMC
GO:1905330	0.12	0.993	1	48	regulation of morphogenesis of an	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030308	0.12	0.993	1	49	negative regulation of cell growth	BP	1	FBP1	up_VFEM_VSMC
GO:0008645	0.12	0.993	1	37	hexose transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0015749	0.12	0.993	1	37	monosaccharide transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0030282	0.12	0.993	1	37	bone mineralization	BP	1	HOXA3	up_VPUL_EC
GO:0030838	0.12	0.993	1	37	positive regulation of actin filament	BP	1	CCL24	up_VPUL_EC
GO:0034219	0.12	0.993	1	37	carbohydrate transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0055088	0.12	0.993	1	37	lipid homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0006638	0.12	0.993	1	30	neutral lipid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0006639	0.12	0.993	1	30	acylglycerol metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0060688	0.12	0.993	1	29	regulation of morphogenesis of a	BP	1	SHOX2	up_VSAP_VSMC
GO:0001886	0.12034297	0.99394	1	5	endothelial cell morphogenesis	BP	1	ARHGEF26	up_ACOR_EC
GO:0048513	0.120534346	0.91632	30	906	animal organ development	BP	1	CPAMD8,CDH3,NR1H4,TMOD1,GATA4,SOX9,PTH1R,NDRG2,AQP1,FZD5,SEMA6D,DIXDC1,PDLIM3,LHX9,SMAD6,ACTN2,DLX3,TNFRSF19,PTGER4,DCLK2,ADAMTSL2,FOXC2,TBX5,LRP4,CLSTN1,C23H3orf58,RARRES2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0046688	0.120595227	0.99391	1	5	response to copper ion	BP	1	AQP1	up_ACOR_EC
GO:0014706	0.121	0.928	15	112	striated muscle tissue development	BP	1	TNNT2,ACTN2,BMP4,FGFR2,GJA1,CITED2,NEBL,ANKRD1,EGLN1,TBX20,TBX5,FRS2,CHD7,EDN1,BVES	up_ACOR_VSMC
GO:0046578	0.121	0.942	8	77	regulation of Ras protein signal transduction	BP	1	ARHGEF2,FARP1,APOE,PLEKHG2,ARFGEF3,NRP1,TNFAIP1,MADD	down_VSAP_EC
GO:0048659	0.121	0.951	6	36	smooth muscle cell proliferation	BP	1	BMP4,PTGIR,NDRG2,CDKN1A,CLSTN1,EDN1	up_ACOR_VSMC
GO:0002831	0.121	0.95	6	42	regulation of response to biotic stimulus	BP	1	TNFAIP3,TMEM173,ARG2,NECTIN2,RIOK3,HMGB1	up_VCAV_EC
GO:0043901	0.121	0.95	6	44	negative regulation of multi-organism process	BP	1	TNFAIP3,IRF8,ARG2,RIOK3,PROX1,ARHGDIB	up_VCAV_EC
GO:0043434	0.121	0.959	4	80	response to peptide hormone	BP	1	LEP,CRY2,CAMK2A,KANK1	up_AFEM_EC
GO:0006084	0.121	0.97	3	15	acetyl-CoA metabolic process	BP	1	ACLY,MVD,PDHA1	down_ACOR_VSMC
GO:0010522	0.121	0.969	3	24	regulation of calcium ion transport into cytosol	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0034333	0.121	0.968	3	25	adherens junction assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0006835	0.121	0.97	3	13	dicarboxylic acid transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:1905209	0.121	0.971	3	13	positive regulation of cardiocyte differentiation	BP	1	BMP4,TBX5,EDN1	up_ACOR_VSMC
GO:0043330	0.121	0.97	3	16	response to exogenous dsRNA	BP	1	TMEM173,RALB,TLR3	up_VCAV_EC
GO:0006488	0.121	0.981	2	8	dolichol-linked oligosaccharide	BP	1	MPDU1,NUS1	down_ACOR_VSMC
GO:0051782	0.121	0.982	2	7	negative regulation of cell division	BP	1	E2F8,ASPM	down_ACOR_VSMC
GO:0014910	0.121	0.98	2	13	regulation of smooth muscle cell migration	BP	1	PDGFRB,BMPR1A	down_VCAV_EC
GO:0071384	0.121	0.98	2	12	cellular response to corticosteroid stimulus	BP	1	NR3C1,ZFP36L1	down_VCAV_EC

GO:0071385	0.121	0.98	2	12	cellular response to glucocorticoid stimulus	BP	1	NR3C1,ZFP36L1	down_VCAV_EC
GO:0033003	0.121	0.981	2	8	regulation of mast cell activation	BP	1	NECTIN2,FES	up_VCAV_EC
GO:0019725	0.121	0.979	2	245	cellular homeostasis	BP	1	TRPC4,C3AR1	up_VPOR_VSMC
GO:0050806	0.121	0.993	1	25	positive regulation of synaptic transmission	BP	1	STX4	down_ACOR_EC
GO:0050905	0.121	0.993	1	26	neuromuscular process	BP	1	HOXA1	down_ACOR_EC
GO:0014068	0.121	0.993	1	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	NEDD4	down_ACOR_EC
GO:0070167	0.121	0.993	1	29	regulation of biomineral tissue development	BP	1	ASPN	down_ACOR_EC
GO:0009892	0.121	1	1	835	negative regulation of metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0033500	0.121	0.993	1	64	carbohydrate homeostasis	BP	1	RAB11B	down_VPOR_EC
GO:0042593	0.121	0.993	1	64	glucose homeostasis	BP	1	RAB11B	down_VPOR_EC
GO:0046879	0.121	0.993	1	63	hormone secretion	BP	1	RAB11B	down_VPOR_EC
GO:0051650	0.121	0.993	1	65	establishment of vesicle localization	BP	1	RAB11B	down_VPOR_EC
GO:0002176	0.121	0.995	1	3	male germ cell proliferation	BP	1	SPINK2	down_VSAP_EC
GO:0036093	0.121	0.995	1	3	germ cell proliferation	BP	1	SPINK2	down_VSAP_EC
GO:0061771	0.121	0.996	1	2	response to caloric restriction	BP	1	APOE	down_VSAP_EC
GO:0098926	0.121	0.996	1	2	postsynaptic signal transduction	BP	1	KPNA1	down_VSAP_EC
GO:0099527	0.121	0.996	1	2	postsynapse to nucleus signaling pathway	BP	1	KPNA1	down_VSAP_EC
GO:1904714	0.121	0.996	1	2	regulation of chaperone-mediated autophagy	BP	1	PLK3	down_VSAP_EC
GO:0098696	0.121	1	1	1	regulation of neurotransmitter receptor localization to postsynaptic	BP	1	DAG1	up_ACOR_VSMC
GO:0098942	0.121	1	1	1	retrograde trans-synaptic signaling by trans-synaptic protein complex	BP	1	DAG1	up_ACOR_VSMC
GO:0099545	0.121	1	1	1	trans-synaptic signaling by trans-synaptic complex	BP	1	DAG1	up_ACOR_VSMC
GO:0099633	0.121	1	1	1	protein localization to postsynaptic specialization membrane	BP	1	DAG1	up_ACOR_VSMC
GO:0099645	0.121	1	1	1	neurotransmitter receptor localization to postsynaptic	BP	1	DAG1	up_ACOR_VSMC
GO:0110011	0.121	1	1	1	regulation of basement membrane organization	BP	1	DAG1	up_ACOR_VSMC
GO:1904259	0.121	1	1	1	regulation of basement membrane assembly involved in embryonic	BP	1	DAG1	up_ACOR_VSMC
GO:1904261	0.121	1	1	1	positive regulation of basement membrane assembly involved in	BP	1	DAG1	up_ACOR_VSMC
GO:2001197	0.121	1	1	1	basement membrane assembly involved in embryonic body	BP	1	DAG1	up_ACOR_VSMC
GO:0021682	0.121	1	1	1	nerve maturation	BP	1	DAG1	up_ACOR_VSMC
GO:0006302	0.121	0.993	1	97	double-strand break repair	BP	1	EYA1	up_AFEM_VSMC
GO:0031349	0.121	0.993	1	90	positive regulation of defense response	BP	1	TLR2	up_AFEM_VSMC
GO:0001822	0.121	0.993	1	98	kidney development	BP	1	ARG2	up_AORT_VSMC
GO:0010975	0.121	0.993	1	103	regulation of neuron projection development	BP	1	WNT7A	up_AORT_VSMC
GO:0042060	0.121	0.993	1	103	wound healing	BP	1	WNT7A	up_AORT_VSMC
GO:0042110	0.121	0.993	1	109	T cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0036493	0.121	0.996	1	2	positive regulation of translation in response to endoplasmic reticulum	BP	1	NCK1	up_VCAV_EC

GO:0010569	0.121	0.993	1	17	regulation of double-strand break repair via homologous	BP	1	CXHXorf57	up_VPOR_EC
GO:0140013	0.121	0.993	1	50	meiotic nuclear division	BP	1	CYP26B1	up_VPOR_VSMC
GO:0090257	0.121	0.993	1	52	regulation of muscle system process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060759	0.121	0.993	1	37	regulation of response to cytokine stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0055092	0.121	0.993	1	28	sterol homeostasis	BP	1	CAV1	up_VSAP_VSMC
GO:2001244	0.121	0.993	1	27	positive regulation of intrinsic apoptotic	BP	1	CAV1	up_VSAP_VSMC
GO:0046597	0.121554789	0.99381	1	5	negative regulation of viral entry into host cell	BP	1	TRIM8	up_ACOR_EC
GO:0051260	0.121859841	0.95283	5	100	protein homooligomerization	BP	1	KCTD12,KCNB1,ACTN2,CLU,CHMP4B	up_ACOR_EC
GO:0031348	0.121911509	0.96714	3	46	negative regulation of defense response	BP	1	NR1H4,FNDC4,PTGER4	up_ACOR_EC
GO:0009887	0.122	0.912	37	314	animal organ morphogenesis	BP	1	TNNT2,SMAD6,GATA5,GATA4,HTR2B,MLLT3,BMP4,FGFR2,GJA1,SEC24B,CITED2,ZNRF3,FGF18,LIMS2,ANKRD1,EGLN1,CLSTN1,NRP1,NPNT,SMARCD3,TBX20,TBX5,FZD3,FRS2,DAG1,PSEN1,TGFBR1,CHD7,PERP,EDN1,ARID5B,SERPINB5,TNFRSF11B,GAA,LHX9,WDR48,CRKL	up_ACOR_VSMC
GO:0030029	0.122	0.915	29	239	actin filament-based process	BP	1	SYNPO2L,TNNT2,PDLIM3,EPB41L4A,ARHGAP28,ACTN2,KCNE3,SYNPO2,XIRP1,WASF3,NEBL,F2RL1,JMY,NRP1,EVL,PRKCE,MYO1B,TTC17,RND1,JUP,SIPA1L1,SSH3,EDN1,FAM107A,JAM3,INPP5K,WASL,ATP2C1,MYOZ2	up_ACOR_VSMC
GO:0090066	0.122	0.928	14	162	regulation of anatomical structure size	BP	1	LRRC8A,IFRD1,WDR1,MSN,HTR7,ACTA2,ACTR3,APOE,PLOD3,TWF1,PLEKHG2,CLCN3,CAPG,NRP1	down_VSAP_EC
GO:0002791	0.122	0.929	14	104	regulation of peptide secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,PASK,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0048562	0.122	0.932	12	102	embryonic organ morphogenesis	BP	1	HOXB7,MEF2C,CHD7,GATA3,EDN1,HOXB8,PROX1,MDFI,HOXB5,HIF1A,ALDH1A3,ZEB1	up_VCAV_EC
GO:0045088	0.122	0.941	8	81	regulation of innate immune response	BP	1	NR1H4,PTPN2,PVR,CNOT7,LYN,CDC37,GBP5,A2M	down_VSAP_EC
GO:0002440	0.122	0.942	8	51	production of molecular mediator of immune	BP	1	TP53BP1,TLR3,F2RL1,PTPN22,NOD2,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0048729	0.122	0.941	8	209	tissue morphogenesis	BP	1	IRX3,DLL1,TMEM100,GREM1,LUZP1,ADAM17,GCNT4,TNC	up_AFEM_EC
GO:0071236	0.122	0.95	6	39	cellular response to antibiotic	BP	1	TNFAIP3,PDGFB,MEF2C,MAPK13,TIMELESS,RIPK1	up_VCAV_EC
GO:0070585	0.122	0.955	5	34	protein localization to mitochondrion	BP	1	SREBF1,TIMM44,TOMM34,SAMM50,PMPCA	down_ACOR_VSMC
GO:0045807	0.122	0.954	5	35	positive regulation of endocytosis	BP	1	SELE,RAB27A,PPP3CA,HIST1H1A,PLCG2	up_VCAV_EC
GO:0045639	0.122	0.96	4	33	positive regulation of myeloid cell	BP	1	HIF1A,EVI2B,PRMT1,INHBA	down_VSAP_EC
GO:0060711	0.122	0.962	4	21	labyrinthine layer development	BP	1	FGFR2,SPINT1,EGLN1,SPINT2	up_ACOR_VSMC
GO:0051179	0.122	0.97	4	1747	localization	BP	1	SLC20A2,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0048468	0.122	0.961	4	553	cell development	BP	1	MYBPC2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1904591	0.122	0.968	3	25	positive regulation of protein import	BP	1	ENSCAFG00000014978,GLI3,MAVS	down_VCAV_EC
GO:2000177	0.122	0.968	3	26	regulation of neural precursor cell	BP	1	GLI3,CDH2,FOXO3	down_VCAV_EC
GO:0046324	0.122	0.969	3	20	regulation of glucose import	BP	1	NR1H4,ENPP1,PTPN11	down_VSAP_EC
GO:0030219	0.122	0.969	3	16	megakaryocyte differentiation	BP	1	KIT,FLI1,MEF2C	up_VCAV_EC
GO:0051345	0.122	0.967	3	151	positive regulation of hydrolase activity	BP	1	ENSCAFG00000002015,ABHD5,ENSCAFG00000032731	up_VPOR_EC
GO:0098662	0.122	0.978	2	131	inorganic cation transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0031954	0.122	0.981	2	8	positive regulation of protein	BP	1	GREM1,RAP2C	down_ACOR_VSMC
GO:2000105	0.122	0.981	2	7	positive regulation of DNA-dependent DNA	BP	1	E2F8,CDK2	down_ACOR_VSMC
GO:0035115	0.122	0.98	2	12	embryonic forelimb morphogenesis	BP	1	RECK,RDH10	down_VCAV_EC
GO:0050856	0.122	0.98	2	12	regulation of T cell receptor signaling	BP	1	PRNP,THY1	down_VCAV_EC

GO:0071825	0.122	0.98	2	12	protein-lipid complex subunit organization	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0071827	0.122	0.98	2	12	plasma lipoprotein particle organization	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0006458	0.122	0.98	2	10	'de novo' protein folding	BP	1	ERO1A,SH3GLB1	down_VSAP_EC
GO:0048485	0.122	0.981	2	9	sympathetic nervous system development	BP	1	CTNNB1,NRP1	down_VSAP_EC
GO:0018208	0.122	0.982	2	7	peptidyl-proline modification	BP	1	EGLN1,P4HA1	up_ACOR_VSMC
GO:0034205	0.122	0.982	2	7	amyloid-beta formation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0097106	0.122	0.982	2	6	postsynaptic density organization	BP	1	TMEM108,LRRC4	up_ACOR_VSMC
GO:0099084	0.122	0.982	2	6	postsynaptic specialization	BP	1	TMEM108,LRRC4	up_ACOR_VSMC
GO:0071559	0.122	0.978	2	75	response to transforming growth factor beta	BP	1	ENSCAFG00000002015,ASPN	up_VPOR_EC
GO:0055080	0.122	0.978	2	176	cation homeostasis	BP	1	HOXA3,NEO1	up_VPUL_EC
GO:0007016	0.122	0.995	1	3	cytoskeletal anchoring at plasma membrane	BP	1	TLN2	down_VCAV_EC
GO:0033169	0.122	0.995	1	3	histone H3-K9 demethylation	BP	1	HR	down_VCAV_EC
GO:2001205	0.122	0.995	1	3	negative regulation of osteoclast development	BP	1	FBN1	down_VCAV_EC
GO:0009914	0.122	0.993	1	64	hormone transport	BP	1	RAB11B	down_VPOR_EC
GO:0016331	0.122	0.993	1	66	morphogenesis of embryonic epithelium	BP	1	CITED2	down_VPOR_EC
GO:0035148	0.122	0.993	1	66	tube formation	BP	1	CITED2	down_VPOR_EC
GO:0009967	0.122	0.996	1	435	positive regulation of signal transduction	BP	1	GATA5	down_VFEM_VSMC
GO:1903365	0.122	0.996	1	2	regulation of fear response	BP	1	APOE	down_VSAP_EC
GO:1904781	0.122	0.996	1	2	positive regulation of protein localization to	BP	1	GSK3B	down_VSAP_EC
GO:2000586	0.122	0.996	1	2	regulation of platelet-derived growth factor receptor-beta signaling	BP	1	PTPN2	down_VSAP_EC
GO:2000587	0.122	0.996	1	2	negative regulation of platelet-derived growth factor receptor-beta	BP	1	PTPN2	down_VSAP_EC
GO:2000822	0.122	0.996	1	2	regulation of behavioral fear response	BP	1	APOE	down_VSAP_EC
GO:0032274	0.122	0.996	1	2	gonadotropin secretion	BP	1	INHBA	down_VSAP_EC
GO:0070858	0.122	0.996	1	2	negative regulation of bile acid biosynthetic process	BP	1	NR1H4	down_VSAP_EC
GO:1904252	0.122	0.996	1	2	negative regulation of bile acid metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0007283	0.122	0.993	1	91	spermatogenesis	BP	1	HOXA9	up_AFEM_VSMC
GO:0006520	0.122	0.993	1	114	cellular amino acid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0050678	0.122	0.993	1	117	regulation of epithelial cell proliferation	BP	1	WNT7A	up_AORT_VSMC
GO:0001959	0.122	0.993	1	33	regulation of cytokine-mediated signaling	BP	1	NR1H4	up_APUL_EC
GO:0042471	0.122	0.993	1	34	ear morphogenesis	BP	1	HOXA1	up_APUL_EC
GO:0050796	0.122	0.993	1	33	regulation of insulin secretion	BP	1	NR1H4	up_APUL_EC
GO:0048589	0.122	0.994	1	188	developmental growth	BP	1	TBX5	up_APUL_VSMC
GO:0098771	0.122	0.994	1	180	inorganic ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0002316	0.122	1	1	1	follicular B cell differentiation	BP	1	PLCG2	up_VCAV_EC
GO:0007290	0.122	1	1	1	spermatid nucleus elongation	BP	1	KDM3A	up_VCAV_EC
GO:0046293	0.122	1	1	1	formaldehyde biosynthetic process	BP	1	KDM3A	up_VCAV_EC
GO:0003012	0.122	0.993	1	90	muscle system process	BP	1	GATA5	up_VCAV_VSMC
GO:0031396	0.122	0.993	1	90	regulation of protein ubiquitination	BP	1	LIMK1	up_VCAV_VSMC
GO:0030595	0.122	0.993	1	57	leukocyte chemotaxis	BP	1	C3AR1	up_VPOR_VSMC

GO:0051924	0.122	0.993	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_VPOR_VSMC
GO:1902106	0.122	0.993	1	31	negative regulation of leukocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0030324	0.122	0.993	1	64	lung development	BP	1	TBX5	up_VPUL_VSMC
GO:0048738	0.122	0.993	1	64	cardiac muscle tissue development	BP	1	TBX5	up_VPUL_VSMC
GO:0015718	0.122	0.993	1	30	monocarboxylic acid transport	BP	1	SLC16A12	up_VSAP_VSMC
GO:0042133	0.122	0.993	1	30	neurotransmitter metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0043271	0.122	0.993	1	28	negative regulation of ion transport	BP	1	CAV1	up_VSAP_VSMC
GO:0010642	0.122103426	0.99376	1	5	negative regulation of platelet-derived growth factor receptor signaling	BP	1	PTGIR	up_ACOR_EC
GO:0072132	0.122124	0.9783	2	23	mesenchyme morphogenesis	BP	1	SOX9,FOXC2	up_ACOR_EC
GO:0090330	0.122192644	0.99375	1	5	regulation of platelet aggregation	BP	1	PRKCD	up_ACOR_EC
GO:0051224	0.12228981	0.96696	3	47	negative regulation of protein transport	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:1904950	0.12228981	0.96696	3	47	negative regulation of establishment of protein localization	BP	1	NR1H4,KCNB1,PTGER4	up_ACOR_EC
GO:0046532	0.122359744	0.99373	1	5	regulation of photoreceptor cell	BP	1	SOX9	up_ACOR_EC
GO:0007530	0.122656214	0.9937	1	5	sex determination	BP	1	SOX9	up_ACOR_EC
GO:0034162	0.122676484	0.9937	1	5	toll-like receptor 9 signaling pathway	BP	1	NR1H4	up_ACOR_EC
GO:0032488	0.122806495	0.99368	1	5	Cdc42 protein signal transduction	BP	1	NRP1	up_ACOR_EC
GO:0032489	0.122806495	0.99368	1	5	regulation of Cdc42 protein signal	BP	1	NRP1	up_ACOR_EC
GO:0009966	0.123	0.916	26	868	regulation of signal transduction	BP	1	CMKLR1,LEP,LBH,CRY2,GAS1,DLL1,F3,MLLT11,LMCD1,TMEM100,PLAGL2,GREM1,FAM53B,GREM2,CLEC16A,CYLD,POSTN,LRRC15,RECK,LGR6,RAB7A,AXIN2,CCL5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0006091	0.123	0.923	18	139	generation of precursor metabolites and energy	BP	1	DLST,C1QTNF2,COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,PHKA2,FXN,GALK1,NDUFS2,PASK,MTFR1L,IDH1,IDH3A,ENSCAFG00000006639,NDUFV1,GNPDA1,DDIT4	up_VSAP_EC
GO:0043065	0.123	0.926	15	188	positive regulation of apoptotic process	BP	1	CASP3,PTPN2,MAGED1,CTNNB1,LYN,BNIP3,DDIT3,FAM162A,ATF3,SH3GLB1,HTT,REST,PAK2,INHBA,SPINK2	down_VSAP_EC
GO:0034645	0.123	0.938	11	1546	cellular macromolecule biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,NEDD4	down_ACOR_EC
GO:2001242	0.123	0.941	8	62	regulation of intrinsic apoptotic signaling	BP	1	FIGNL1,NCK1,PTGS2,PMAIP1,SKIL,HIF1A,IVNS1ABP,ARHGEF2	up_VCAV_EC
GO:0006814	0.123	0.955	5	28	sodium ion transport	BP	1	FGF13,PTPN3,DMPK,FXYD1,SLC8A1	up_ACOR_VSMC
GO:0043200	0.123	0.955	5	26	response to amino acid	BP	1	CASTOR1,GLRB,UBR1,SESN3,SH3BP4	up_ACOR_VSMC
GO:0032092	0.123	0.959	4	38	positive regulation of protein binding	BP	1	LRP1,PLCL1,PARK7,MAPRE3	down_VCAV_EC
GO:0035296	0.123	0.96	4	32	regulation of tube diameter	BP	1	HTR7,ACTA2,APOE,PLOD3	down_VSAP_EC
GO:0097746	0.123	0.96	4	32	regulation of blood vessel diameter	BP	1	HTR7,ACTA2,APOE,PLOD3	down_VSAP_EC
GO:1902106	0.123	0.96	4	31	negative regulation of leukocyte differentiation	BP	1	SOCS5,PTPN2,CTNNB1,LYN	down_VSAP_EC
GO:0030850	0.123	0.961	4	20	prostate gland development	BP	1	BMP4,FGFR2,FRS2,SERPINB5	up_ACOR_VSMC
GO:0030500	0.123	0.96	4	25	regulation of bone mineralization	BP	1	MEF2C,BMP2,BMP2K,HIF1A	up_VCAV_EC
GO:0031399	0.123	0.961	4	559	regulation of protein modification process	BP	1	CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0035295	0.123	0.968	3	356	tube development	BP	1	TBX5,HOXA3,CCL24	up_VPUL_EC
GO:0042254	0.123	0.978	2	128	ribosome biogenesis	BP	1	RPSA,WDR12	down_ACOR_EC
GO:0002683	0.123	0.978	2	126	negative regulation of immune system process	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0071709	0.123	0.981	2	8	membrane assembly	BP	1	CAV1,EMP2	down_ACOR_VSMC
GO:0043921	0.123	0.98	2	10	modulation by host of viral transcription	BP	1	SMARCA4,REST	down_VSAP_EC

GO:0052312	0.123	0.98	2	10	modulation of transcription in other organism involved in	BP	1	SMARCA4,REST	down_VSAP_EC
GO:0052472	0.123	0.98	2	10	modulation by host of symbiont transcription	BP	1	SMARCA4,REST	down_VSAP_EC
GO:0021680	0.123	0.98	2	10	cerebellar Purkinje cell layer development	BP	1	HSPA5,AARS	down_VSAP_EC
GO:0007252	0.123	0.982	2	6	I-kappaB phosphorylation	BP	1	TLR3,MAP3K7	up_ACOR_VSMC
GO:0033262	0.123	0.982	2	6	regulation of nuclear cell cycle DNA replication	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0051895	0.123	0.981	2	7	negative regulation of focal adhesion assembly	BP	1	DUSP22,FAM107A	up_ACOR_VSMC
GO:1903392	0.123	0.981	2	7	negative regulation of adherens junction	BP	1	DUSP22,FAM107A	up_ACOR_VSMC
GO:0021954	0.123	0.978	2	26	central nervous system neuron development	BP	1	LEP,PLXNA4	up_AFEM_EC
GO:0007588	0.123	0.981	2	7	excretion	BP	1	STC1,EDN1	up_VCAV_EC
GO:0040012	0.123	0.979	2	303	regulation of locomotion	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0140056	0.123	0.993	1	28	organelle localization by membrane tethering	BP	1	STX4	down_ACOR_EC
GO:0060491	0.123	0.993	1	62	regulation of cell projection assembly	BP	1	FSCN1	down_AFEM_EC
GO:0120032	0.123	0.993	1	62	regulation of plasma membrane bounded cell	BP	1	FSCN1	down_AFEM_EC
GO:0034329	0.123	0.993	1	60	cell junction assembly	BP	1	FSCN1	down_AFEM_EC
GO:0090521	0.123	0.995	1	3	glomerular visceral epithelial cell migration	BP	1	KANK2	down_VCAV_EC
GO:0003205	0.123	0.993	1	67	cardiac chamber development	BP	1	CITED2	down_VPOR_EC
GO:0030278	0.123	0.993	1	66	regulation of ossification	BP	1	HDAC7	down_VPOR_EC
GO:0044093	0.123	0.996	1	437	positive regulation of molecular function	BP	1	JUP	down_VFEM_VSMC
GO:0051254	0.123	0.996	1	431	positive regulation of RNA metabolic process	BP	1	GATA5	down_VFEM_VSMC
GO:0030043	0.123	0.996	1	2	actin filament fragmentation	BP	1	WDR1	down_VSAP_EC
GO:0048715	0.123	0.996	1	2	negative regulation of oligodendrocyte	BP	1	CTNNB1	down_VSAP_EC
GO:0097114	0.123	0.996	1	2	NMDA glutamate receptor clustering	BP	1	APOE	down_VSAP_EC
GO:0035771	0.123	0.996	1	2	interleukin-4-mediated signaling pathway	BP	1	PTPN2	down_VSAP_EC
GO:0060211	0.123	0.996	1	2	regulation of nuclear-transcribed mRNA poly(A)	BP	1	CNOT7	down_VSAP_EC
GO:0060213	0.123	0.996	1	2	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	BP	1	CNOT7	down_VSAP_EC
GO:0098779	0.123	0.996	1	2	positive regulation of mitophagy in response to mitochondrial	BP	1	CDC37	down_VSAP_EC
GO:1901526	0.123	0.996	1	2	positive regulation of mitophagy	BP	1	CDC37	down_VSAP_EC
GO:1901628	0.123	0.996	1	2	positive regulation of postsynaptic membrane organization	BP	1	APOE	down_VSAP_EC
GO:1901629	0.123	0.996	1	2	regulation of presynaptic membrane organization	BP	1	APOE	down_VSAP_EC
GO:0003007	0.123	0.993	1	94	heart morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0030855	0.123	0.994	1	183	epithelial cell differentiation	BP	1	HOXB5	up_APUL_VSMC
GO:0006553	0.123	0.996	1	2	lysine metabolic process	BP	1	PIPOX	up_VCAV_EC
GO:2000617	0.123	0.996	1	2	positive regulation of histone H3-K9 acetylation	BP	1	GATA3	up_VCAV_EC
GO:1903984	0.123	0.996	1	2	positive regulation of TRAIL-activated apoptotic signaling pathway	BP	1	ATF3	up_VCAV_EC
GO:1990034	0.123	1	1	1	calcium ion export across plasma membrane	BP	1	ATP2B1	up_VCAV_EC
GO:0051348	0.123	0.993	1	90	negative regulation of transferase activity	BP	1	LIMK1	up_VCAV_VSMC
GO:0002685	0.123	0.993	1	55	regulation of leukocyte migration	BP	1	C3AR1	up_VPOR_VSMC

GO:0060048	0.123	0.993	1	30	cardiac muscle contraction	BP	1	MAP2K6	up_VFEM_EC
GO:0006109	0.123	0.993	1	51	regulation of carbohydrate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0032409	0.123	0.993	1	52	regulation of transporter activity	BP	1	NETO1	up_VFEM_VSMC
GO:0032092	0.123	0.993	1	38	positive regulation of protein binding	BP	1	HOXA3	up_VPUL_EC
GO:0030323	0.123	0.993	1	65	respiratory tube development	BP	1	TBX5	up_VPUL_VSMC
GO:0032075	0.123261385	0.99364	1	5	positive regulation of nuclease activity	BP	1	PRKCD	up_ACOR_EC
GO:0090153	0.123289738	0.99363	1	5	regulation of sphingolipid biosynthetic process	BP	1	PRKCD	up_ACOR_EC
GO:1905038	0.123289738	0.99363	1	5	regulation of membrane lipid metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:2000303	0.123289738	0.99363	1	5	regulation of ceramide biosynthetic process	BP	1	PRKCD	up_ACOR_EC
GO:0019359	0.123476964	0.97792	2	23	nicotinamide nucleotide biosynthetic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0019363	0.123476964	0.97792	2	23	pyridine nucleotide biosynthetic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0021670	0.123640603	0.99359	1	5	lateral ventricle development	BP	1	AQP1	up_ACOR_EC
GO:0065007	0.124	0.896	223	3499	biological regulation	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,CELF1,ASNS,MYH9,SLC39A7,NR1H4,FMNL3,PLK3,ENSCAFG00000013214,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,SPARC,MEIS2,SGK1,ERO1A,PRKACB,PTPN14,ENPP1,ERRFI1,ITGA2,JCAD,SNX25,CBX5,CASP3,FAM49B,ENSCAFG00000003477,HYOU1,PGK1,AKAP2,WSB1,BCAR3,NUAK1,PTPN11,EXOC5,ATP2B1,FSCN1,AARS,DPYSL3,LRRC8A,HOOK3,TRIB3,PGAM1,IFRD1,FARP1,TMED2,PUM3,PM20D2,FBLIM1,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,REM1,WDR1,MYO1C,TMTC2,PIK3C2A,CHSY1,MSN,UACA,HOXB7,KIF5B,LMAN1,HIF1A,HTR7,CX3CL1,ENSCAFG00000000562,DYNLL1,SLC45A3,TUBB,IWS1,THBS2,DNAJC10,YIPF5,ACTG2,TNIK,NAA10,NXN,RGS2,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,EIF2B1,EVI2B,PVR,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,ESM1,DDX39B,ADAM17,AGRN,ACTA2,BRD2,EIF4EBP1,SKAP2,UST,PDIA4,CNOT7,CDH11,ACTR3,ADGRE5,MAGED1,GNAQ,CTNNB1,KPNB1,ANLN,CRYAB,STARD13,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,PTP4A1,WWC3,PDE1A,PLOD3,ZC3H15,IGFBP7,KLF5,UBA5,MMP28,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,FAM162A,	down_VSAP_EC
GO:0051130	0.124	0.915	26	342	positive regulation of cellular component organization	BP	1	VEGFA,SERPINE1,FSCN1,DPYSL3,WDR1,MSN,LMAN1,HIF1A,DYNLL1,ACTR3,CTNNB1,ANLN,ENSCAFG00000002015,APOE,LYN,BNIP3,FAM162A,GSK3B,VLDLR,CDC37,GBP5,SH3GLB1,SDC4,HTT,LRRTM2,NRP1	down_VSAP_EC
GO:0080135	0.124	0.915	26	240	regulation of cellular response to stress	BP	1	EPHB1,PLK2,MAP3K11,CD34,TLR4,EDN1,FIGNL1,ARG2,MAP3K3,BMP2,THOC1,TLR3,NCK1,TIMELESS,PTGS2,ETAA1,TAOK1,GCH1,HMGB1,PMAIP1,RIPK1,SKIL,CUL4A,HIF1A,VASH1,ARHGEF2	up_VCAV_EC
GO:0006811	0.124	0.915	25	330	ion transport	BP	1	SLC39A7,ERO1A,SLC7A5,ENPP1,ATP2B1,LRRC8A,SLC38A1,REM1,WDR1,KIF5B,NDUFA4L2,SLC20A1,CTNNB1,TFRC,APOE,LYN,DDIT3,CLCN3,SLC7A11,NKAIN1,SLC20A2,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0065007	0.124	0.939	17	3499	biological regulation	BP	1	NR1H4,TBX5,MAPK10,BPI,HTR7,HOXA3,PLCL1,TUBB4A,PCSK1N,ARHGEF26,LZTS1,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,PDE1A	up_APUL_EC
GO:0009611	0.124	0.932	11	122	response to wounding	BP	1	SERPINE1,DPYSL3,IFRD1,PRCP,HIF1A,ADAM17,APOE,LYN,SLC7A11,ITGB3,SDC4	down_VSAP_EC
GO:0048871	0.124	0.932	11	120	multicellular organismal homeostasis	BP	1	PTPN11,EXOC5,PRCP,PTGS2,PLCL1,CTNNB1,TFRC,STRAP,DDIT3,KDM3A,HOMER1	down_VSAP_EC
GO:0048863	0.124	0.938	9	70	stem cell differentiation	BP	1	EDNRB,KIT,MEF2C,EDN1,SOX18,HHEX,JAG1,HIF1A,KDM3A	up_VCAV_EC
GO:0005996	0.124	0.94	8	85	monosaccharide metabolic process	BP	1	ENPP1,TPI1,PGAM1,SESN2,SLC45A3,PTPN2,ATF3,GALE	down_VSAP_EC
GO:0043434	0.124	0.94	8	80	response to peptide hormone	BP	1	NR1H4,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,PTPN2,NR4A1	down_VSAP_EC
GO:0071375	0.124	0.944	7	68	cellular response to peptide hormone stimulus	BP	1	NR1H4,ENPP1,PTPN11,TRIB3,MYO1C,PTPN2,NR4A1	down_VSAP_EC

GO:0019722	0.124	0.944	7	45	calcium-mediated signaling	BP	1	HTR2B,C28H10orf71,ITPR1,DMPK,RCAN2,EDN1,NCALD	up_ACOR_VSMC
GO:0048869	0.124	0.947	7	1119	cellular developmental process	BP	1	TBX5,MAPK10,ARHGEF26,SLITRK5,WIF1,NPNT,NTRK2	up_APUL_EC
GO:0012501	0.124	0.953	5	561	programmed cell death	BP	1	LYN,IGF1R,PDPN,USP28,STX4	down_ACOR_EC
GO:0050790	0.124	0.953	5	532	regulation of catalytic activity	BP	1	LYN,IGF1R,PRKAR2A,MYO1D,ASPN	down_ACOR_EC
GO:0060840	0.124	0.953	5	42	artery development	BP	1	PRICKLE1,LTBP1,ADAMTS6,APOE,NRP1	down_VSAP_EC
GO:0045621	0.124	0.954	5	28	positive regulation of lymphocyte	BP	1	ZBTB16,TOX,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0001938	0.124	0.959	4	34	positive regulation of endothelial cell	BP	1	VEGFA,JCAD,TGFBR1,ADAM17	down_VSAP_EC
GO:0050796	0.124	0.959	4	33	regulation of insulin secretion	BP	1	NR1H4,PTPN11,HIF1A,REST	down_VSAP_EC
GO:0048278	0.124	0.96	4	25	vesicle docking	BP	1	EXOC6,CAV2,EXOC5,STX11	up_VCAV_EC
GO:0048538	0.124	0.961	4	20	thymus development	BP	1	ABL1,RAF1,MAP2K2,CITED2	up_VSAP_EC
GO:0061614	0.124	0.968	3	20	pri-miRNA transcription by RNA polymerase II	BP	1	SMARCA4,HIF1A,KLF5	down_VSAP_EC
GO:0030178	0.124	0.966	3	52	negative regulation of Wnt signaling pathway	BP	1	GREM1,CYLD,AXIN2	up_AFEM_EC
GO:0048583	0.124	0.973	3	1095	regulation of response to stimulus	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0031401	0.124	0.967	3	358	positive regulation of protein modification	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:1903706	0.124	0.977	2	119	regulation of hemopoiesis	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0046164	0.124	0.979	2	11	alcohol catabolic process	BP	1	TPI1,APOE	down_VSAP_EC
GO:0050778	0.124	0.977	2	141	positive regulation of immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0003014	0.124	0.992	1	27	renal system process	BP	1	SULF1	down_ACOR_EC
GO:0051239	0.124	1	1	859	regulation of multicellular organismal process	BP	1	GATA5	down_AFEM_VSMC
GO:1904350	0.124	0.995	1	3	regulation of protein catabolic process in the	BP	1	LRP1	down_VCAV_EC
GO:1905165	0.124	0.995	1	3	regulation of lysosomal protein catabolic process	BP	1	LRP1	down_VCAV_EC
GO:0006421	0.124	0.996	1	2	asparaginyl-tRNA aminoacylation	BP	1	NARS	down_VSAP_EC
GO:0018242	0.124	0.996	1	2	protein O-linked glycosylation via serine	BP	1	GALNT1	down_VSAP_EC
GO:0035356	0.124	0.996	1	2	cellular triglyceride homeostasis	BP	1	NR1H4	down_VSAP_EC
GO:1904177	0.124	0.996	1	2	regulation of adipose tissue development	BP	1	NR1H4	down_VSAP_EC
GO:1904179	0.124	0.996	1	2	positive regulation of adipose tissue	BP	1	NR1H4	down_VSAP_EC
GO:0002253	0.124	0.993	1	92	activation of immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0032874	0.124	0.993	1	57	positive regulation of stress-activated MAPK	BP	1	TAOK1	up_AORT_EC
GO:0009749	0.124	0.993	1	34	response to glucose	BP	1	NR1H4	up_APUL_EC
GO:0035120	0.124	1	1	1	post-embryonic appendage	BP	1	ATRX	up_VCAV_EC
GO:0035127	0.124	1	1	1	post-embryonic limb morphogenesis	BP	1	ATRX	up_VCAV_EC
GO:0035128	0.124	1	1	1	post-embryonic forelimb morphogenesis	BP	1	ATRX	up_VCAV_EC
GO:0097393	0.124	1	1	1	telomeric repeat-containing RNA	BP	1	ATRX	up_VCAV_EC
GO:0097394	0.124	1	1	1	telomeric repeat-containing RNA transcription by RNA	BP	1	ATRX	up_VCAV_EC
GO:1901580	0.124	1	1	1	regulation of telomeric RNA transcription from RNA pol II promoter	BP	1	ATRX	up_VCAV_EC
GO:1901581	0.124	1	1	1	negative regulation of telomeric RNA transcription from RNA	BP	1	ATRX	up_VCAV_EC
GO:1901582	0.124	1	1	1	positive regulation of telomeric RNA transcription from RNA	BP	1	ATRX	up_VCAV_EC
GO:0050808	0.124	0.993	1	93	synapse organization	BP	1	SLITRK5	up_VCAV_VSMC

GO:0001755	0.124	0.993	1	16	neural crest cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:1990868	0.124	0.993	1	16	response to chemokine	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:1990869	0.124	0.993	1	16	cellular response to chemokine	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0006352	0.124	0.993	1	56	DNA-templated transcription, initiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0043523	0.124	0.993	1	52	regulation of neuron apoptotic process	BP	1	CHL1	up_VPOR_VSMC
GO:0003206	0.124	0.993	1	51	cardiac chamber morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060538	0.124	0.993	1	51	skeletal muscle organ development	BP	1	SHOX2	up_VFEM_VSMC
GO:0048469	0.124	0.992	1	31	cell maturation	BP	1	IRX5	up_VSAP_VSMC
GO:0072171	0.124	0.992	1	30	mesonephric tubule morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:1901222	0.124	0.992	1	32	regulation of NIK/NF-kappaB signaling	BP	1	TLR2	up_VSAP_VSMC
GO:0032602	0.124085983	0.97775	2	23	chemokine production	BP	1	NR1H4,MAVS	up_ACOR_EC
GO:1901626	0.124351988	0.99352	1	5	regulation of postsynaptic membrane organization	BP	1	LRP4	up_ACOR_EC
GO:1905939	0.124565006	0.9935	1	5	regulation of gonad development	BP	1	SOX9	up_ACOR_EC
GO:0048268	0.124616363	0.99349	1	5	clathrin coat assembly	BP	1	CALY	up_ACOR_EC
GO:0032460	0.124721477	0.99348	1	5	negative regulation of protein oligomerization	BP	1	CLU	up_ACOR_EC
GO:0032463	0.124721477	0.99348	1	5	negative regulation of protein	BP	1	CLU	up_ACOR_EC
GO:2001138	0.124750557	0.99348	1	5	regulation of phospholipid transport	BP	1	PRKCD	up_ACOR_EC
GO:2001140	0.124750557	0.99348	1	5	positive regulation of phospholipid transport	BP	1	PRKCD	up_ACOR_EC
GO:0007213	0.124941055	0.99346	1	5	G protein-coupled acetylcholine receptor	BP	1	AGRN	up_ACOR_EC
GO:0002252	0.125	0.919	21	166	immune effector process	BP	1	PLCG2,LEP,TP53BP1,MX1,TLR3,ISG15,F2RL1,BNIP3,C1S,PTPN22,C7,PRKCE,PARP9,APP,PSEN1,DUSP22,DDIT4,B2M,SERINC3,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0006897	0.125	0.922	17	158	endocytosis	BP	1	SELE,CXCL8,CALCRL,RAB27A,IRF8,PIK3C2A,PPP3CA,BMP2K,RALBP1,ABCA1,ELMO1,SNX2,HIST1H1A,PLCG2,HMGB1,DNAJC13,PEAR1	up_VCAV_EC
GO:0006650	0.125	0.932	11	78	glycerophospholipid metabolic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,PIGN,PIGS,PIGG,CRLS1,SERINC3,SERINC1,INPP5K	up_ACOR_VSMC
GO:0007548	0.125	0.935	10	68	sex differentiation	BP	1	GATA4,PRDX4,ATRX,CITED2,CHD7,SPINK2,ARID5B,DMC1,LHX9,WDR48	up_ACOR_VSMC
GO:0048519	0.125	0.942	9	1554	negative regulation of biological process	BP	1	NR1H4,TBX5,BPI,HOXA3,PLCL1,TUBB4A,PCSK1N,LZTS1,NTRK2	up_APUL_EC
GO:0043583	0.125	0.94	8	59	ear development	BP	1	CHD7,GATA3,EDN1,BMP2,PROX1,JAG1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0000045	0.125	0.944	7	46	autophagosome assembly	BP	1	FEZ1,TP53INP1,GABARAPL1,PSEN1,PIK3C3,ATG16L2,FEZ2	up_ACOR_VSMC
GO:0080090	0.125	0.95	7	1734	regulation of primary metabolic process	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0002706	0.125	0.949	6	35	regulation of lymphocyte mediated immunity	BP	1	LEP,TP53BP1,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0090276	0.125	0.949	6	36	regulation of peptide hormone secretion	BP	1	LEP,TM7SF3,PRKCE,CHD7,CCL5,PFKL	up_ACOR_VSMC
GO:0090276	0.125	0.949	6	36	regulation of peptide hormone secretion	BP	1	HNF4A,SLC8B1,PASK,KCNB1,STX4,PPP3CB	up_VSAP_EC
GO:0007586	0.125	0.961	4	20	digestion	BP	1	LEP,SLC26A7,HRH2,NOD2	up_ACOR_VSMC
GO:0007613	0.125	0.96	4	20	memory	BP	1	FGF13,HRH1,LRRN4,PSEN1	up_ACOR_VSMC
GO:0022600	0.125	0.961	4	20	digestive system process	BP	1	LEP,SLC26A7,HRH2,NOD2	up_ACOR_VSMC
GO:0030193	0.125	0.967	3	21	regulation of blood coagulation	BP	1	SERPINE1,APOE,LYN	down_VSAP_EC
GO:1900046	0.125	0.967	3	21	regulation of hemostasis	BP	1	SERPINE1,APOE,LYN	down_VSAP_EC
GO:0097178	0.125	0.969	3	14	ruffle assembly	BP	1	ARHGEF26,EVL,INPP5K	up_ACOR_VSMC
GO:0007589	0.125	0.968	3	16	body fluid secretion	BP	1	EDN1,CREB1,HIF1A	up_VCAV_EC
GO:0034340	0.125	0.969	3	15	response to type I interferon	BP	1	NLRC5,CNOT7,LSM14A	up_VCAV_EC

GO:0022414	0.125	0.966	3	294	reproductive process	BP	1	HOXA9,AVPR1A,CYP26B1	up_VFEM_EC
GO:0016050	0.125	0.977	2	119	vesicle organization	BP	1	SPG11,STX4	down_ACOR_EC
GO:0030033	0.125	0.981	2	7	microvillus assembly	BP	1	FSCN1,EZR	down_ACOR_VSMC
GO:0009887	0.125	0.978	2	314	animal organ morphogenesis	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0046627	0.125	0.979	2	10	negative regulation of insulin receptor signaling	BP	1	ENPP1,PTPN2	down_VSAP_EC
GO:0050793	0.125	0.982	2	731	regulation of developmental process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0086002	0.125	0.981	2	7	cardiac muscle cell action potential involved in	BP	1	KCNE3,JUP	up_ACOR_VSMC
GO:0010507	0.125	0.977	2	26	negative regulation of autophagy	BP	1	LEP,CLEC16A	up_AFEM_EC
GO:0032637	0.125	0.977	2	26	interleukin-8 production	BP	1	LEP,BPI	up_AFEM_EC
GO:0009605	0.125	0.98	2	538	response to external stimulus	BP	1	ARG2,ESR1	up_AORT_VSMC
GO:0061082	0.125	0.98	2	8	myeloid leukocyte cytokine production	BP	1	KIT,TLR4	up_VCAV_EC
GO:0034086	0.125	0.981	2	7	maintenance of sister chromatid cohesion	BP	1	SMC5,ATRX	up_VCAV_EC
GO:0034088	0.125	0.981	2	7	maintenance of mitotic sister chromatid cohesion	BP	1	SMC5,ATRX	up_VCAV_EC
GO:0072012	0.125	0.98	2	9	glomerulus vasculature development	BP	1	PDGFB,GPR4	up_VCAV_EC
GO:0009314	0.125	0.977	2	143	response to radiation	BP	1	EYA1,MME	up_VFEM_EC
GO:0008284	0.125	0.978	2	238	positive regulation of cell proliferation	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0010633	0.125	0.992	1	28	negative regulation of epithelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:2001242	0.125	0.993	1	62	regulation of intrinsic apoptotic signaling	BP	1	IVNS1ABP	down_AFEM_EC
GO:0009966	0.125	1	1	868	regulation of signal transduction	BP	1	GATA5	down_AFEM_VSMC
GO:0071295	0.125	0.994	1	3	cellular response to vitamin	BP	1	KANK2	down_VCAV_EC
GO:0007548	0.125	0.993	1	68	sex differentiation	BP	1	CITED2	down_VPOR_EC
GO:0001818	0.125	0.993	1	65	negative regulation of cytokine production	BP	1	HDAC7	down_VPOR_EC
GO:0008582	0.125	0.996	1	2	regulation of synaptic growth at neuromuscular	BP	1	SIX4	down_VSAP_EC
GO:0010891	0.125	0.996	1	2	negative regulation of sequestering of	BP	1	ABHD5	down_VSAP_EC
GO:0021502	0.125	0.996	1	2	neural fold elevation formation	BP	1	HIF1A	down_VSAP_EC
GO:0030910	0.125	0.996	1	2	olfactory placode formation	BP	1	SIX4	down_VSAP_EC
GO:0061055	0.125	0.996	1	2	myotome development	BP	1	SIX4	down_VSAP_EC
GO:0071698	0.125	0.996	1	2	olfactory placode development	BP	1	SIX4	down_VSAP_EC
GO:0071699	0.125	0.996	1	2	olfactory placode morphogenesis	BP	1	SIX4	down_VSAP_EC
GO:0097411	0.125	0.996	1	2	hypoxia-inducible factor-1alpha signaling pathway	BP	1	HIF1A	down_VSAP_EC
GO:0098528	0.125	0.996	1	2	skeletal muscle fiber differentiation	BP	1	SIX4	down_VSAP_EC
GO:1903651	0.125	0.996	1	2	positive regulation of cytoplasmic transport	BP	1	MSN	down_VSAP_EC
GO:2000643	0.125	0.996	1	2	positive regulation of early endosome to late endosome transport	BP	1	MSN	down_VSAP_EC
GO:0046292	0.125	0.996	1	2	formaldehyde metabolic process	BP	1	KDM3A	down_VSAP_EC
GO:0060070	0.125	0.993	1	105	canonical Wnt signaling pathway	BP	1	WNT7A	up_AORT_VSMC
GO:0033033	0.125	0.996	1	2	negative regulation of myeloid cell apoptotic	BP	1	ITPKB	up_VCAV_EC
GO:0036258	0.125	0.996	1	2	multivesicular body assembly	BP	1	RAB11A	up_VCAV_EC
GO:0002253	0.125	0.993	1	92	activation of immune response	BP	1	C6	up_VCAV_VSMC
GO:0003007	0.125	0.993	1	94	heart morphogenesis	BP	1	GATA5	up_VCAV_VSMC

GO:0060485	0.125	0.993	1	93	mesenchyme development	BP	1	GATA5	up_VCAV_VSMC
GO:0097300	0.125	0.992	1	17	programmed necrotic cell death	BP	1	ARHGEF2	up_VPOR_EC
GO:0009156	0.125	0.992	1	50	ribonucleoside monophosphate	BP	1	FBP1	up_VFEM_VSMC
GO:0042742	0.125	0.992	1	39	defense response to bacterium	BP	1	NR1H4	up_VPUL_EC
GO:1902904	0.125	0.992	1	38	negative regulation of supramolecular fiber	BP	1	ARHGEF2	up_VPUL_EC
GO:1901654	0.125	0.992	1	31	response to ketone	BP	1	CAV1	up_VSAP_VSMC
GO:0071600	0.125066084	0.99344	1	5	otic vesicle morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0006531	0.125087915	0.99344	1	5	aspartate metabolic process	BP	1	NMNAT2	up_ACOR_EC
GO:0009651	0.125253851	0.99342	1	5	response to salt stress	BP	1	AQP1	up_ACOR_EC
GO:0032402	0.125411862	0.9934	1	5	melanosome transport	BP	1	CDH3	up_ACOR_EC
GO:0051904	0.125411862	0.9934	1	5	pigment granule transport	BP	1	CDH3	up_ACOR_EC
GO:0035023	0.125803919	0.96562	3	46	regulation of Rho protein signal transduction	BP	1	ARHGDIB,NRP1,ARHGEF26	up_ACOR_EC
GO:0009893	0.126	0.9	69	995	positive regulation of metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,MYH9,NR1H4,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,TMED2,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,MSN,HIF1A,SLC45A3,ACTG2,TNIK,ZPR1,PTPN2,YES1,PEG3,MTDH,DDX39B,ADAM17,ACTA2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,APOE,KLF5,LYN,BNIP3,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,SH3GLB1,HTT,REST,ABHD5,CALM1,DISC1,RAD23A,PAK2,INHBA,NR4A1,CDKN1A,TMTC3,NRP1,SH3RF3,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0044283	0.126	0.919	20	201	small molecule biosynthetic process	BP	1	PDGFB,ATF3,EDN1,PTGS1,FAM3C,SPTLC2,BMP2,ITPKB,PROX1,ENSCAFG00000010596,ELOVL7,ENSCAFG00000024323,PTGS2,PLCG2,GCH1,IMPA1,HIF1A,KDM3A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0048568	0.126	0.931	11	148	embryonic organ development	BP	1	FBN1,BMPR1A,NAGLU,TBX15,HOXC4,TEAD1,GLI3,ZFP36L1,IFT57,IRX5,RDH10	down_VCAV_EC
GO:0045444	0.126	0.934	10	84	fat cell differentiation	BP	1	ADGRF5,PPARG,GATA3,LRRC8C,BMP2,JAG1,PTGS2,CREB1,ITGA6,NR4A1	up_VCAV_EC
GO:0061564	0.126	0.936	9	119	axon development	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,GLI3,UST,RGMA,BRSK1	down_VCAV_EC
GO:0007281	0.126	0.94	8	60	germ cell development	BP	1	KIT,PSME4,NECTIN2,MTOR,CDYL,AFF4,KDM3A,FBXO5	up_VCAV_EC
GO:0070661	0.126	0.939	8	63	leukocyte proliferation	BP	1	IL7R,MEF2C,TLR4,PELI1,ARG2,ELF4,NCK1,HMGB1	up_VCAV_EC
GO:0006816	0.126	0.942	7	84	calcium ion transport	BP	1	PRNP,TRPV2,CACNB3,THY1,TPC3,CYBA,PACSIN3	down_VCAV_EC
GO:1901605	0.126	0.946	6	67	alpha-amino acid metabolic process	BP	1	THNSL2,PARK7,ENSCAFG00000002977,CRTAP,GLS2,ACAT1	down_VCAV_EC
GO:0007165	0.126	0.953	6	1496	signal transduction	BP	1	DKK2,LNPEP,ERC1,TAOK1,CTNNAL1,GPR155	up_AORT_EC
GO:0050954	0.126	0.953	5	30	sensory perception of mechanical stimulus	BP	1	KIT,CHD7,NAV2,SPTBN4,P2RX2	up_VCAV_EC
GO:0043488	0.126	0.953	5	28	regulation of mRNA stability	BP	1	AXIN2,TENT5C,ZFP36L1,SAMD4B,ZFP36L2	up_VSAP_EC
GO:0050709	0.126	0.953	5	28	negative regulation of protein secretion	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1	up_VSAP_EC
GO:0031532	0.126	0.958	4	31	actin cytoskeleton reorganization	BP	1	SIPA1L1,MYH9,TNIK,NRP1	down_VSAP_EC
GO:0006942	0.126	0.959	4	26	regulation of striated muscle contraction	BP	1	PDE4D,STC1,KCNJ2,ATP2A1	up_VCAV_EC
GO:0044237	0.126	1	3	3491	cellular metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0021695	0.126	0.967	3	20	cerebellar cortex development	BP	1	HSPA5,PTPN11,AARS	down_VSAP_EC
GO:0015696	0.126	0.968	3	14	ammonium transport	BP	1	PSEN1,SLC25A20,PARK7	up_ACOR_VSMC
GO:0030182	0.126	0.966	3	327	neuron differentiation	BP	1	MAPK10,SLITRK5,NTRK2	up_APUL_EC
GO:0001909	0.126	0.968	3	18	leukocyte mediated cytotoxicity	BP	1	IL7R,RAB27A,NECTIN2	up_VCAV_EC
GO:0042509	0.126	0.968	3	17	regulation of tyrosine phosphorylation of STAT	BP	1	HCLS1,KIT,CNOT7	up_VCAV_EC

GO:0000003	0.126	0.966	3	295	reproduction	BP	1	HOXA9,AVPR1A,CYP26B1	up_VFEM_EC
GO:0032873	0.126	0.969	3	13	negative regulation of stress-activated MAPK	BP	1	F2RL1,MYC,QARS	up_VSAP_EC
GO:0070303	0.126	0.969	3	13	negative regulation of stress-activated protein kinase signaling cascade	BP	1	F2RL1,MYC,QARS	up_VSAP_EC
GO:0009306	0.126	0.977	2	127	protein secretion	BP	1	LYN,STX4	down_ACOR_EC
GO:2001044	0.126	0.98	2	8	regulation of integrin-mediated signaling	BP	1	EMP2,PHACTR4	down_ACOR_VSMC
GO:0000038	0.126	0.978	2	12	very long-chain fatty acid metabolic process	BP	1	ACAA1,PEX5	down_VCAV_EC
GO:0006040	0.126	0.979	2	12	amino sugar metabolic process	BP	1	CHID1,GFPT2	down_VCAV_EC
GO:0010469	0.126	0.977	2	26	regulation of signaling receptor activity	BP	1	GREM2,ADAM17	up_AFEM_EC
GO:0032088	0.126	0.977	2	26	negative regulation of NF-kappaB transcription	BP	1	CMKLR1,CYLD	up_AFEM_EC
GO:0032368	0.126	0.977	2	26	regulation of lipid transport	BP	1	LEP,CRY2	up_AFEM_EC
GO:0002320	0.126	0.98	2	7	lymphoid progenitor cell differentiation	BP	1	KIT,GATA3	up_VCAV_EC
GO:0002360	0.126	0.982	2	6	T cell lineage commitment	BP	1	IL6,MTOR	up_VCAV_EC
GO:0043369	0.126	0.982	2	6	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BP	1	IL6,MTOR	up_VCAV_EC
GO:0007169	0.126	0.977	2	178	transmembrane receptor protein tyrosine kinase	BP	1	NR1H4,FLRT3	up_VPUL_EC
GO:0002009	0.126	0.977	2	177	morphogenesis of an epithelium	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0006022	0.126	0.992	1	29	aminoglycan metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:1900086	0.126	0.996	1	2	positive regulation of peptidyl-tyrosine	BP	1	GREM1	down_ACOR_VSMC
GO:0050679	0.126	0.992	1	62	positive regulation of epithelial cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0051173	0.126	1	1	874	positive regulation of nitrogen compound	BP	1	GATA5	down_AFEM_VSMC
GO:0010634	0.126	0.992	1	68	positive regulation of epithelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0090150	0.126	0.992	1	64	establishment of protein localization to membrane	BP	1	RAB11B	down_VPOR_EC
GO:0051603	0.126	0.994	1	305	proteolysis involved in cellular protein catabolic	BP	1	USP12	down_VFEM_EC
GO:0042127	0.126	0.996	1	452	regulation of cell proliferation	BP	1	JUP	down_VFEM_VSMC
GO:0035166	0.126	0.996	1	2	post-embryonic hemopoiesis	BP	1	MYO1E	down_VSAP_EC
GO:0048875	0.126	0.996	1	2	chemical homeostasis within a tissue	BP	1	HOMER1	down_VSAP_EC
GO:0001822	0.126	0.993	1	98	kidney development	BP	1	EYA1	up_AFEM_VSMC
GO:0048232	0.126	0.993	1	95	male gamete generation	BP	1	HOXA9	up_AFEM_VSMC
GO:0070304	0.126	0.992	1	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	TAOK1	up_AORT_EC
GO:0030900	0.126	0.993	1	101	forebrain development	BP	1	WNT7A	up_AORT_VSMC
GO:0061333	0.126	0.992	1	35	renal tubule morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0062014	0.126	0.992	1	35	negative regulation of small molecule metabolic	BP	1	NR1H4	up_APUL_EC
GO:1905371	0.126	0.996	1	2	ceramide phosphoethanolamine	BP	1	SAMD8	up_VCAV_EC
GO:1905373	0.126	0.996	1	2	ceramide phosphoethanolamine	BP	1	SAMD8	up_VCAV_EC
GO:0044110	0.126	0.996	1	2	growth involved in symbiotic interaction	BP	1	IRF8	up_VCAV_EC
GO:0044116	0.126	0.996	1	2	growth of symbiont involved in interaction	BP	1	IRF8	up_VCAV_EC
GO:0044117	0.126	0.996	1	2	growth of symbiont in host	BP	1	IRF8	up_VCAV_EC
GO:0044126	0.126	0.996	1	2	regulation of growth of symbiont in host	BP	1	IRF8	up_VCAV_EC
GO:0044130	0.126	0.996	1	2	negative regulation of growth of symbiont in	BP	1	IRF8	up_VCAV_EC

GO:0044144	0.126	0.996	1	2	modulation of growth of symbiont involved in interaction with host	BP	1	IRF8	up_VCAV_EC
GO:0044146	0.126	0.996	1	2	negative regulation of growth of symbiont involved in interaction	BP	1	IRF8	up_VCAV_EC
GO:0050769	0.126	0.993	1	95	positive regulation of neurogenesis	BP	1	LIMK1	up_VCAV_VSMC
GO:0043270	0.126	0.992	1	56	positive regulation of ion transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:0060047	0.126	0.992	1	57	heart contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071229	0.126	0.992	1	51	cellular response to acid chemical	BP	1	CYP26B1	up_VPOR_VSMC
GO:0010717	0.126	0.992	1	32	regulation of epithelial to mesenchymal transition	BP	1	TIAM1	up_VFEM_EC
GO:2001237	0.126	0.992	1	33	negative regulation of extrinsic apoptotic	BP	1	EYA1	up_VFEM_EC
GO:0046434	0.126	0.992	1	52	organophosphate catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046425	0.126	0.992	1	39	regulation of JAK-STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:0048736	0.126	0.992	1	66	appendage development	BP	1	TBX5	up_VPUL_VSMC
GO:0050768	0.126	0.992	1	66	negative regulation of neurogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0060173	0.126	0.992	1	66	limb development	BP	1	TBX5	up_VPUL_VSMC
GO:0031397	0.126	0.992	1	30	negative regulation of protein ubiquitination	BP	1	CAV1	up_VSAP_VSMC
GO:0034767	0.126	0.992	1	31	positive regulation of ion transmembrane transport	BP	1	STIM1	up_VSAP_VSMC
GO:0048341	0.126467323	0.99329	1	5	paraxial mesoderm formation	BP	1	FOXC2	up_ACOR_EC
GO:0007608	0.126470291	0.99329	1	5	sensory perception of smell	BP	1	PDE4A	up_ACOR_EC
GO:0008064	0.126661472	0.95681	4	72	regulation of actin polymerization or	BP	1	TMOD1,ACTN2,PAK3,PRKCD	up_ACOR_EC
GO:0030832	0.126661472	0.95681	4	72	regulation of actin filament length	BP	1	TMOD1,ACTN2,PAK3,PRKCD	up_ACOR_EC
GO:0048869	0.126711801	0.90909	36	1119	cellular developmental process	BP	1	SH3TC2,MYOZ2,CDH3,TMOD1,GATA4,BRSK1,TRPS1,SOX9,RHOU,PTH1R,FZD5,CCDC3,DIXDC1,RGMA,SMAD6,ACTN2,PAK3,DLX3,PTGER4,PIAS1,DCLK2,MAPK8IP2,FOXC2,FIGNL1,TBX5,LRP4,CLSTN1,PRELP,RBM38,TP53INP2,NRP1,ARHGEF26,PRKCD,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:0032071	0.126721456	0.99326	1	5	regulation of endodeoxyribonuclease	BP	1	PRKCD	up_ACOR_EC
GO:0002689	0.126835439	0.99325	1	5	negative regulation of leukocyte chemotaxis	BP	1	MMP28	up_ACOR_EC
GO:0030509	0.126850167	0.96518	3	47	BMP signaling pathway	BP	1	RGMA,SMAD6,LRP4	up_ACOR_EC
GO:0055065	0.127	0.923	16	145	metal ion homeostasis	BP	1	CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0007276	0.127	0.924	15	130	gamete generation	BP	1	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,ARID4B,HIST1H1A,AFF4,KDM3A,ATRX,SPATA6,FBXO5	up_VCAV_EC
GO:0009267	0.127	0.936	9	60	cellular response to starvation	BP	1	PRKAA2,GABARAPL1,CDKN1A,SESN3,PIK3C3,LAMP2,SESN1,BMT2,ZFYVE1	up_ACOR_VSMC
GO:0051924	0.127	0.939	8	53	regulation of calcium ion transport	BP	1	PLCG2,SARAF,CACNB3,PRKCE,CHD7,INPP5K,WFS1,STC2	up_ACOR_VSMC
GO:0007165	0.127	0.944	8	1496	signal transduction	BP	1	NR1H4,RGS1,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043112	0.127	0.946	6	57	receptor metabolic process	BP	1	VEGFA,SNX25,HIF1A,TFRC,APOE,LRRTM2	down_VSAP_EC
GO:1903039	0.127	0.947	6	43	positive regulation of leukocyte cell-cell	BP	1	IL7R,GATA3,ITPKB,NCK1,BCL10,HMGB1	up_VCAV_EC
GO:0022406	0.127	0.952	5	35	membrane docking	BP	1	EXOC6,CAV2,PDZD8,EXOC5,STX11	up_VCAV_EC
GO:0042391	0.127	0.957	4	81	regulation of membrane potential	BP	1	MLLT11,FXYD1,BVES,DMPK	up_AFEM_EC
GO:0021510	0.127	0.959	4	23	spinal cord development	BP	1	RELN,DLL4,HOXB8,GDPD5	up_VCAV_EC
GO:0032233	0.127	0.959	4	21	positive regulation of actin filament bundle	BP	1	WNT11,ARHGEF5,ABL1,BAG4	up_VSAP_EC
GO:0048856	0.127	0.976	3	1533	anatomical structure development	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC

GO:0031167	0.127	0.98	2	8	rRNA methylation	BP	1	FBL,EMG1	down_ACOR_VSMC
GO:0003148	0.127	0.978	2	13	outflow tract septum morphogenesis	BP	1	BMPR1A,SEMA3C	down_VCAV_EC
GO:0048519	0.127	0.989	2	1554	negative regulation of biological process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0006929	0.127	0.979	2	10	substrate-dependent cell migration	BP	1	ITGA2,NRP1	down_VSAP_EC
GO:0048143	0.127	0.981	2	6	astrocyte activation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0030097	0.127	0.977	2	244	hemopoiesis	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0061061	0.127	0.977	2	179	muscle structure development	BP	1	TBX5,MYBPC2	up_VPUL_EC
GO:0098771	0.127	0.977	2	180	inorganic ion homeostasis	BP	1	HOXA3,NEO1	up_VPUL_EC
GO:0072332	0.127	0.992	1	29	intrinsic apoptotic signaling pathway by p53	BP	1	USP28	down_ACOR_EC
GO:0098876	0.127	0.992	1	29	vesicle-mediated transport to the plasma	BP	1	ACSL3	down_ACOR_EC
GO:0016054	0.127	0.992	1	61	organic acid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0046395	0.127	0.992	1	61	carboxylic acid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0048870	0.127	0.996	1	451	cell motility	BP	1	JUP	down_VFEM_VSMC
GO:0051674	0.127	0.996	1	451	localization of cell	BP	1	JUP	down_VFEM_VSMC
GO:0030214	0.127	0.996	1	2	hyaluronan catabolic process	BP	1	CEMIP2	down_VSAP_EC
GO:0030997	0.127	0.996	1	2	regulation of centriole-centriole cohesion	BP	1	CTNNB1	down_VSAP_EC
GO:0051918	0.127	0.996	1	2	negative regulation of fibrinolysis	BP	1	SERPINE1	down_VSAP_EC
GO:1904798	0.127	0.996	1	2	positive regulation of core promoter binding	BP	1	CTNNB1	down_VSAP_EC
GO:0098722	0.127	0.996	1	2	asymmetric stem cell division	BP	1	ARHGEF2	down_VSAP_EC
GO:0008406	0.127	0.992	1	57	gonad development	BP	1	HOXA9	up_AORT_EC
GO:0045137	0.127	0.992	1	57	development of primary sexual characteristics	BP	1	HOXA9	up_AORT_EC
GO:0051301	0.127	0.993	1	117	cell division	BP	1	WNT7A	up_AORT_VSMC
GO:0072001	0.127	0.993	1	104	renal system development	BP	1	ARG2	up_AORT_VSMC
GO:0002224	0.127	0.992	1	34	toll-like receptor signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0009746	0.127	0.992	1	35	response to hexose	BP	1	NR1H4	up_APUL_EC
GO:0034284	0.127	0.992	1	35	response to monosaccharide	BP	1	NR1H4	up_APUL_EC
GO:0071076	0.127	1	1	1	RNA 3' uridylation	BP	1	TUT7	up_VCAV_EC
GO:1990573	0.127	0.996	1	2	potassium ion import across plasma membrane	BP	1	KCNJ3	up_VCAV_EC
GO:0046133	0.127	0.996	1	2	pyrimidine ribonucleoside catabolic process	BP	1	CDA	up_VCAV_EC
GO:0046135	0.127	0.996	1	2	pyrimidine nucleoside catabolic process	BP	1	CDA	up_VCAV_EC
GO:0030501	0.127	0.992	1	16	positive regulation of bone mineralization	BP	1	ACVR2A	up_VPOR_EC
GO:0055081	0.127	0.992	1	17	anion homeostasis	BP	1	HOXA3	up_VPOR_EC
GO:0016202	0.127	0.992	1	39	regulation of striated muscle tissue	BP	1	TBX5	up_VPUL_EC
GO:0043624	0.127	0.992	1	39	cellular protein complex disassembly	BP	1	ARHGEF2	up_VPUL_EC
GO:0032102	0.127	0.992	1	67	negative regulation of response to external	BP	1	SLIT2	up_VPUL_VSMC
GO:0050890	0.127	0.992	1	67	cognition	BP	1	LRRN4	up_VPUL_VSMC
GO:0097119	0.127026939	0.99323	1	5	postsynaptic density protein 95 clustering	BP	1	LRRC4	up_ACOR_EC
GO:0022898	0.127221	0.96501	3	48	regulation of transmembrane	BP	1	ACTN2,MAPK8IP2,PM20D1	up_ACOR_EC
GO:0071340	0.127236498	0.99321	1	5	skeletal muscle acetylcholine-gated	BP	1	LRP4	up_ACOR_EC
GO:0072070	0.127250141	0.9932	1	5	loop of Henle development	BP	1	AQP1	up_ACOR_EC

GO:0032271	0.127259804	0.95652	4	73	regulation of protein polymerization	BP	1	TMOD1,PAK3,PRKCD,TUBB4A	up_ACOR_EC
GO:0008283	0.127340674	0.91849	19	545	cell proliferation	BP	1	CDH3,SOX9,PTH1R,NDRG2,AQP1,FZD5,DIXDC1,PTGIR,LHX9,SMAD6,ESM1,PIAS1,FOXC2,FIGNL1,TBX5,CLSTN1,C23H3orf58,PRKCD,PYGO2	up_ACOR_EC
GO:0043455	0.127360736	0.99319	1	5	regulation of secondary metabolic process	BP	1	CDH3	up_ACOR_EC
GO:0009064	0.127366941	0.9768	2	23	glutamine family amino acid metabolic process	BP	1	NR1H4,NIT2	up_ACOR_EC
GO:0097366	0.127367617	0.99319	1	5	response to bronchodilator	BP	1	GUCY1B1	up_ACOR_EC
GO:0022029	0.127723479	0.9767	2	23	telencephalon cell migration	BP	1	DIXDC1,NRP1	up_ACOR_EC
GO:1903077	0.127811263	0.99314	1	5	negative regulation of protein localization to	BP	1	LRRC15	up_ACOR_EC
GO:1904376	0.127811263	0.99314	1	5	negative regulation of protein localization to cell	BP	1	LRRC15	up_ACOR_EC
GO:1902337	0.127880053	0.99314	1	5	regulation of apoptotic process involved in	BP	1	FOXC2	up_ACOR_EC
GO:1904748	0.127880053	0.99314	1	5	regulation of apoptotic process involved in	BP	1	FOXC2	up_ACOR_EC
GO:0061042	0.127892347	0.99313	1	5	vascular wound healing	BP	1	FOXC2	up_ACOR_EC
GO:0006901	0.127925395	0.99313	1	5	vesicle coating	BP	1	PREB	up_ACOR_EC
GO:0009896	0.127944271	0.94464	6	127	positive regulation of catabolic process	BP	1	EDEM2,PIAS1,CLU,TP53INP2,RNF114,PRKCD	up_ACOR_EC
GO:0033235	0.127960164	0.99313	1	5	positive regulation of protein sumoylation	BP	1	PIAS1	up_ACOR_EC
GO:0010639	0.127980707	0.94461	6	128	negative regulation of organelle organization	BP	1	TMOD1,ARHGAP6,ARHGAP28,CHMP4B,PRKCD,TUBB4A	up_ACOR_EC
GO:0050789	0.128	0.902	86	3295	regulation of biological process	BP	1	HOXA9,CMKLR1,MT2A,IRX3,IRX5,HOXC10,HOXA10,LEP,KCNC4,LBH,PRR16,CRY2,ENSCAFG00000009113,RAB20,GAS1,ANGPT4,HOXA7,CD40,DLL1,CRYAB,KCND1,F3,PLXNA4,BPI,GPAM,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,TWIST2,MAB21L1,THRB,LGI4,MYO1D,MFAP4,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,HTR1D,NFE2L1,OVOL1,FAM53B,AVPR1A,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,FXYD1,LRRC15,FAM13A,MYBL1,RECK,NR3C1,PTHLH,TBXA2R,EVI2B,DCUN1D3,REEP2,EAF1,BVES,LGR6,RAB7A,AXIN2,YEATS2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,CLIC4,AGPAT2,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0045934	0.128	0.905	41	407	negative regulation of nucleobase-containing compound metabolic process	BP	1	EDNRB,HCLS1,CDA,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,PPP3CA,TENT2,BMP2,HMG20A,HHEX,CREM,PROX1,UHRF2,MDFI,HMBOX1,THOC1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,BLM,RAD17,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0042127	0.128	0.908	33	452	regulation of cell proliferation	BP	1	VEGFA,SULF1,SPARC,PTPN14,JCAD,ILK,TGFBR1,PTGS2,HIF1A,PTPN2,ESM1,ADAM17,SKAP2,CNOT7,MAGED1,CTNNB1,TFRC,APOE,LYN,STRAP,PDS5B,TAX1BP3,SDC4,REST,ENSCAFG00000017326,PRMT1,DISC1,INHBA,NR4A1,BTK,SIX4,CDKN1A,MARCKSL1	down_VSAP_EC
GO:0120039	0.128	0.924	14	158	plasma membrane bounded cell projection morphogenesis	BP	1	SIPA1L1,SGK1,PTPN11,IFRD1,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0034248	0.128	0.93	11	125	regulation of cellular amide metabolic process	BP	1	NR1H4,PLK3,AARS,PGAM1,PUM3,SESN2,EIF4EBP1,CNOT7,APOE,EIF5,EIF2S1	down_VSAP_EC
GO:0060255	0.128	0.936	11	1782	regulation of macromolecule metabolic	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0050793	0.128	0.936	9	731	regulation of developmental process	BP	1	C3AR1,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,MTDH,RNF6	up_VPOR_EC
GO:0055076	0.128	0.942	7	44	transition metal ion homeostasis	BP	1	FXN,SLC25A28,MYC,SCARA5,FTL,HMOX1,NCOA4	up_VSAP_EC
GO:0061326	0.128	0.946	6	41	renal tubule development	BP	1	HOXB7,MEF2C,GATA3,MTSS1,BMP2,JAG1	up_VCAV_EC
GO:0072080	0.128	0.946	6	41	nephron tubule development	BP	1	HOXB7,MEF2C,GATA3,MTSS1,BMP2,JAG1	up_VCAV_EC
GO:0010001	0.128	0.95	5	54	glial cell differentiation	BP	1	LRP1,NAB2,AKT2,GLI3,CDH2	down_VCAV_EC

GO:0070167	0.128	0.952	5	29	regulation of biomineral tissue development	BP	1	BMP4,GJA1,ISG15,DDR2,SLC8A1	up_ACOR_VSMC
GO:0031532	0.128	0.952	5	31	actin cytoskeleton reorganization	BP	1	TEK,KIT,BAIAP2L1,FES,ARHGDIB	up_VCAV_EC
GO:0001942	0.128	0.952	5	28	hair follicle development	BP	1	FGF7,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0022404	0.128	0.952	5	28	molting cycle process	BP	1	FGF7,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0022405	0.128	0.952	5	28	hair cycle process	BP	1	FGF7,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0001776	0.128	0.958	4	23	leukocyte homeostasis	BP	1	HMGB1,CORO1A,BAP1,PIK3CD	down_ACOR_VSMC
GO:0007399	0.128	0.958	4	564	nervous system development	BP	1	HOXA3,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043550	0.128	0.959	4	21	regulation of lipid kinase activity	BP	1	AMBRA1,RBL2,PIK3R1,PIK3IP1	up_VSAP_EC
GO:0030857	0.128	0.967	3	15	negative regulation of epithelial cell	BP	1	CAV1,EZH2,HOXA7	down_ACOR_VSMC
GO:0034645	0.128	0.975	3	1546	cellular macromolecule biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0070830	0.128	0.968	3	14	bicellular tight junction assembly	BP	1	PRKCH,OCLN,TJP1	up_VCAV_EC
GO:0120192	0.128	0.968	3	14	tight junction assembly	BP	1	PRKCH,OCLN,TJP1	up_VCAV_EC
GO:0048513	0.128	0.97	3	906	animal organ development	BP	1	SLITRK5,GATA5,LRRC17	up_VCAV_VSMC
GO:0040011	0.128	0.967	3	505	locomotion	BP	1	CHL1,BAMBI,C3AR1	up_VPOR_VSMC
GO:2000514	0.128	0.968	3	13	regulation of CD4-positive, alpha-beta T cell	BP	1	CD274,CD83,TGFBR2	up_VSAP_EC
GO:0050673	0.128	0.976	2	135	epithelial cell proliferation	BP	1	ACVRL1,SULF1	down_ACOR_EC
GO:0097150	0.128	0.978	2	13	neuronal stem cell population maintenance	BP	1	CDH2,FOXO3	down_VCAV_EC
GO:1902930	0.128	0.978	2	10	regulation of alcohol biosynthetic process	BP	1	APOE,REST	down_VSAP_EC
GO:0032801	0.128	0.979	2	10	receptor catabolic process	BP	1	SNX25,APOE	down_VSAP_EC
GO:0043555	0.128	0.979	2	10	regulation of translation in response to stress	BP	1	SESN2,EIF2S1	down_VSAP_EC
GO:0051797	0.128	0.978	2	10	regulation of hair follicle development	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0071548	0.128	0.98	2	7	response to dexamethasone	BP	1	NR3C1,DDIT4	up_ACOR_VSMC
GO:1904646	0.128	0.981	2	6	cellular response to amyloid-beta	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:1901699	0.128	0.976	2	164	cellular response to nitrogen compound	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0035886	0.128	0.98	2	8	vascular smooth muscle cell differentiation	BP	1	KIT,PDGFB	up_VCAV_EC
GO:0040017	0.128	0.977	2	180	positive regulation of locomotion	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0060688	0.128	0.992	1	29	regulation of morphogenesis of a	BP	1	SULF1	down_ACOR_EC
GO:0051648	0.128	0.992	1	69	vesicle localization	BP	1	RAB11B	down_VPOR_EC
GO:0070647	0.128	0.994	1	311	protein modification by small protein conjugation	BP	1	USP12	down_VFEM_EC
GO:0010647	0.128	0.996	1	460	positive regulation of cell communication	BP	1	GATA5	down_VFEM_VSMC
GO:0007021	0.128	0.994	1	3	tubulin complex assembly	BP	1	CRYAB	down_VSAP_EC
GO:0046886	0.128	0.996	1	2	positive regulation of hormone biosynthetic	BP	1	HIF1A	down_VSAP_EC
GO:0048671	0.128	0.996	1	2	negative regulation of collateral sprouting	BP	1	IFRD1	down_VSAP_EC
GO:0051643	0.128	0.996	1	2	endoplasmic reticulum localization	BP	1	ESYT3	down_VSAP_EC
GO:1903265	0.128	0.996	1	2	positive regulation of tumor necrosis factor-mediated signaling	BP	1	ADAM17	down_VSAP_EC
GO:2000671	0.128	0.996	1	2	regulation of motor neuron apoptotic process	BP	1	ZPR1	down_VSAP_EC
GO:2000672	0.128	0.996	1	2	negative regulation of motor neuron apoptotic	BP	1	ZPR1	down_VSAP_EC
GO:0097048	0.128	0.996	1	2	dendritic cell apoptotic process	BP	1	LYN	down_VSAP_EC
GO:2000668	0.128	0.996	1	2	regulation of dendritic cell apoptotic process	BP	1	LYN	down_VSAP_EC

GO:2000670	0.128	0.996	1	2	positive regulation of dendritic cell apoptotic	BP	1	LYN	down_VSAP_EC
GO:0051186	0.128	0.993	1	159	cofactor metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC
GO:0043010	0.128	0.992	1	96	camera-type eye development	BP	1	IRX5	up_AFEM_VSMC
GO:1901991	0.128	0.992	1	56	negative regulation of mitotic cell cycle phase	BP	1	TAOK1	up_AORT_EC
GO:0021987	0.128	0.992	1	37	cerebral cortex development	BP	1	NTRK2	up_APUL_EC
GO:0007507	0.128	0.993	1	194	heart development	BP	1	TBX5	up_APUL_VSMC
GO:0046580	0.128	0.992	1	18	negative regulation of Ras protein signal	BP	1	FBP1	up_VPOR_EC
GO:0003015	0.128	0.992	1	58	heart process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035296	0.128	0.992	1	32	regulation of tube diameter	BP	1	AVPR1A	up_VFEM_EC
GO:0097746	0.128	0.992	1	32	regulation of blood vessel diameter	BP	1	AVPR1A	up_VFEM_EC
GO:0001649	0.128	0.992	1	54	osteoblast differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0034404	0.128	0.992	1	50	nucleobase-containing small molecule	BP	1	FBP1	up_VFEM_VSMC
GO:0009124	0.128	0.992	1	51	nucleoside monophosphate	BP	1	FBP1	up_VFEM_VSMC
GO:0003205	0.128	0.992	1	67	cardiac chamber development	BP	1	TBX5	up_VPUL_VSMC
GO:0048644	0.128	0.992	1	31	muscle organ morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0006939	0.128	0.992	1	32	smooth muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0055026	0.128180565	0.9931	1	5	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0060670	0.128215659	0.9931	1	5	branching involved in labyrinthine layer	BP	1	FZD5	up_ACOR_EC
GO:0043217	0.128375951	0.99308	1	5	myelin maintenance	BP	1	SH3TC2	up_ACOR_EC
GO:0030072	0.128646825	0.96445	3	48	peptide hormone secretion	BP	1	NR1H4,AQP1,KCNB1	up_ACOR_EC
GO:0072643	0.128681571	0.99305	1	5	interferon-gamma secretion	BP	1	NR1H4	up_ACOR_EC
GO:0055001	0.128731449	0.96444	3	47	muscle cell development	BP	1	MYOZ2,TMOD1,ACTN2	up_ACOR_EC
GO:0019216	0.128948358	0.94921	5	101	regulation of lipid metabolic process	BP	1	NR1H4,ENSCAFG00000004331,CCDC3,RARRES2,PRKCD	up_ACOR_EC
GO:0060736	0.128956302	0.99302	1	5	prostate gland growth	BP	1	SOX9	up_ACOR_EC
GO:0051240	0.129	0.906	36	489	positive regulation of multicellular organismal process	BP	1	ARHGEF2,VEGFA,SULF1,CELF1,NR1H4,SERPINE1,SOCS5,SPARC,JCAD,FAM49B,DPYSL3,ILK,PTGS2,PIK3C2A,HOXB7,HIF1A,EVI2B,MTDH,ADAM17,MAGED1,CTNNB1,TFRC,APOE,LYN,DDIT3,MMD,VLDLR,GBP5,REST,PRMT1,DISC1,LRRTM2,INHBA,SIX4,NRP1,KDM3A	down_VSAP_EC
GO:0032446	0.129	0.909	30	255	protein modification by small protein conjugation	BP	1	PCGF5,SKP2,SH3RF2,ISG15,SASH1,KLHL20,MARCH5,PTPN22,OS9,UBE2H,SH3RF1,RNF24,PRKCE,RNF19A,PSEN1,SHPRH,RNF141,NOD2,FAM107A,SH3RF3,DCUN1D4,RNF181,HERPUD1,CNOT4,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,PARK7	up_ACOR_VSMC
GO:0016049	0.129	0.921	16	124	cell growth	BP	1	WNT11,HNF4A,FAM107A,SLIT2,ABL1,PLXNA4,RARG,DPYSL2,WISP2,KDM2B,IGFBP6,TTL,SMARCA2,ACVRL1,ULK1,TGFBR2	up_VSAP_EC
GO:0016049	0.129	0.929	11	124	cell growth	BP	1	ENPP1,IFRD1,SMARCA4,SESN2,ESM1,ADAM17,CTNNB1,IGFBP7,INHBA,CDKN1A,NRP1	down_VSAP_EC
GO:0072175	0.129	0.935	9	60	epithelial tube formation	BP	1	SHROOM3,BMP4,FGFR2,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0061572	0.129	0.942	7	50	actin filament bundle organization	BP	1	FSCN1,LIMA1,NF2,STMN1,RAC1,PDXP,EZR	down_ACOR_VSMC
GO:0030282	0.129	0.946	6	37	bone mineralization	BP	1	BMP4,FGFR2,GJA1,ISG15,DDR2,SLC8A1	up_ACOR_VSMC
GO:0007605	0.129	0.952	5	27	sensory perception of sound	BP	1	MBP,COCH,USP53,CHD7,WFS1	up_ACOR_VSMC
GO:0072332	0.129	0.952	5	29	intrinsic apoptotic signaling pathway by p53	BP	1	CDKN1A,JMY,PERP,DDIT4,ZMAT3	up_ACOR_VSMC
GO:0060350	0.129	0.958	4	23	endochondral bone morphogenesis	BP	1	NAB2,MMP14,POC1A,SERPINH1	down_ACOR_VSMC
GO:0031323	0.129	0.967	4	1788	regulation of cellular metabolic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC

GO:1903201	0.129	0.966	3	20	regulation of oxidative stress-induced cell death	BP	1	P4HB,HIF1A,CTNNB1	down_VSAP_EC
GO:0030970	0.129	0.967	3	14	retrograde protein transport, ER to cytosol	BP	1	OS9,HERPUD1,FAF2	up_ACOR_VSMC
GO:1903513	0.129	0.967	3	14	endoplasmic reticulum to cytosol transport	BP	1	OS9,HERPUD1,FAF2	up_ACOR_VSMC
GO:0010604	0.129	0.969	3	919	positive regulation of macromolecule metabolic	BP	1	TLR2,EYA1,HOXA9	up_AFEM_VSMC
GO:0006950	0.129	0.971	3	1102	response to stress	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0014910	0.129	0.968	3	13	regulation of smooth muscle cell migration	BP	1	DOCK4,PDGFB,MEF2C	up_VCAV_EC
GO:0070884	0.129	0.967	3	16	regulation of calcineurin-NFAT signaling cascade	BP	1	HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0106056	0.129	0.967	3	16	regulation of calcineurin-mediated signaling	BP	1	HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0030878	0.129	0.968	3	13	thyroid gland development	BP	1	HOXD3,RAF1,MAP2K2	up_VSAP_EC
GO:0038084	0.129	0.977	2	13	vascular endothelial growth factor signaling	BP	1	PDGFRB,DCN	down_VCAV_EC
GO:0044275	0.129	0.978	2	10	cellular carbohydrate catabolic process	BP	1	TPI1,PGAM1	down_VSAP_EC
GO:0032459	0.129	0.978	2	12	regulation of protein oligomerization	BP	1	CRYAB,APOE	down_VSAP_EC
GO:0007218	0.129	0.98	2	7	neuropeptide signaling pathway	BP	1	GLRB,SCG5	up_ACOR_VSMC
GO:0001817	0.129	0.976	2	182	regulation of cytokine production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0007610	0.129	0.976	2	146	behavior	BP	1	NETO1,GATM	up_VSAP_VSMC
GO:1900157	0.129	0.996	1	2	regulation of bone mineralization involved in	BP	1	GREM1	down_ACOR_VSMC
GO:1900158	0.129	0.996	1	2	negative regulation of bone mineralization involved in bone	BP	1	GREM1	down_ACOR_VSMC
GO:1901096	0.129	0.994	1	3	regulation of autophagosome	BP	1	CLEC16A	down_VCAV_EC
GO:0060600	0.129	0.994	1	3	dichotomous subdivision of an epithelial terminal	BP	1	SEMA3C	down_VCAV_EC
GO:0060666	0.129	0.994	1	3	dichotomous subdivision of terminal units involved in salivary gland	BP	1	SEMA3C	down_VCAV_EC
GO:0023056	0.129	0.996	1	462	positive regulation of signaling	BP	1	GATA5	down_VFEM_VSMC
GO:0001835	0.129	0.996	1	2	blastocyst hatching	BP	1	RBBP8	down_VSAP_EC
GO:0006705	0.129	0.996	1	2	mineralocorticoid biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0010792	0.129	0.996	1	2	DNA double-strand break processing involved in repair via single-strand	BP	1	RBBP8	down_VSAP_EC
GO:0014045	0.129	0.996	1	2	establishment of endothelial blood-brain	BP	1	CTNNB1	down_VSAP_EC
GO:0022009	0.129	0.996	1	2	central nervous system vasculogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0031944	0.129	0.996	1	2	negative regulation of glucocorticoid metabolic	BP	1	REST	down_VSAP_EC
GO:0031947	0.129	0.996	1	2	negative regulation of glucocorticoid biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0032342	0.129	0.996	1	2	aldosterone biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0032345	0.129	0.996	1	2	negative regulation of aldosterone metabolic	BP	1	REST	down_VSAP_EC
GO:0032347	0.129	0.996	1	2	regulation of aldosterone biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0032348	0.129	0.996	1	2	negative regulation of aldosterone biosynthetic	BP	1	REST	down_VSAP_EC
GO:0045002	0.129	0.996	1	2	double-strand break repair via single-strand	BP	1	RBBP8	down_VSAP_EC
GO:0045837	0.129	0.994	1	3	negative regulation of membrane potential	BP	1	BNIP3	down_VSAP_EC
GO:0048096	0.129	0.996	1	2	chromatin-mediated maintenance of	BP	1	CTNNB1	down_VSAP_EC
GO:0060066	0.129	0.996	1	2	oviduct development	BP	1	CTNNB1	down_VSAP_EC
GO:0060856	0.129	0.996	1	2	establishment of blood-brain barrier	BP	1	CTNNB1	down_VSAP_EC
GO:0071684	0.129	0.996	1	2	organism emergence from protective structure	BP	1	RBBP8	down_VSAP_EC

GO:0090032	0.129	0.996	1	2	negative regulation of steroid hormone	BP	1	REST	down_VSAP_EC
GO:1901963	0.129	0.996	1	2	regulation of cell proliferation involved in outflow tract	BP	1	CTNNB1	down_VSAP_EC
GO:2000065	0.129	0.996	1	2	negative regulation of cortisol biosynthetic	BP	1	REST	down_VSAP_EC
GO:0035188	0.129	0.996	1	2	hatching	BP	1	RBBP8	down_VSAP_EC
GO:2000739	0.129	0.996	1	2	regulation of mesenchymal stem cell	BP	1	REST	down_VSAP_EC
GO:0010811	0.129	0.992	1	36	positive regulation of cell-substrate adhesion	BP	1	NPNT	up_APUL_EC
GO:0031109	0.129	0.992	1	36	microtubule polymerization or	BP	1	TUBB4A	up_APUL_EC
GO:0035270	0.129	0.992	1	35	endocrine system development	BP	1	HOXA3	up_APUL_EC
GO:0045778	0.129	0.992	1	35	positive regulation of ossification	BP	1	NPNT	up_APUL_EC
GO:0072088	0.129	0.992	1	36	nephron epithelium morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0071650	0.129	0.996	1	2	negative regulation of chemokine (C-C motif)	BP	1	ARG2	up_VCAV_EC
GO:2001270	0.129	0.996	1	2	regulation of cysteine-type endopeptidase activity involved in	BP	1	PAK2	up_VCAV_EC
GO:0006471	0.129	0.992	1	17	protein ADP-ribosylation	BP	1	PUM3	up_VPOR_EC
GO:0001954	0.129	0.992	1	17	positive regulation of cell-matrix adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0034644	0.129	0.992	1	32	cellular response to UV	BP	1	MME	up_VFEM_EC
GO:0048639	0.129	0.992	1	39	positive regulation of developmental growth	BP	1	TBX5	up_VPUL_EC
GO:1904892	0.129	0.992	1	40	regulation of STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:0007548	0.129	0.992	1	68	sex differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0048545	0.129	0.992	1	68	response to steroid hormone	BP	1	SLIT2	up_VPUL_VSMC
GO:0031623	0.129	0.992	1	31	receptor internalization	BP	1	CAV1	up_VSAP_VSMC
GO:0060048	0.129	0.992	1	30	cardiac muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0019062	0.129061746	0.993	1	5	virion attachment to host cell	BP	1	LRRC15	up_ACOR_EC
GO:0044406	0.129061746	0.993	1	5	adhesion of symbiont to host	BP	1	LRRC15	up_ACOR_EC
GO:0044650	0.129061746	0.993	1	5	adhesion of symbiont to host cell	BP	1	LRRC15	up_ACOR_EC
GO:0051248	0.129098478	0.92657	12	316	negative regulation of protein metabolic process	BP	1	PKIB,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,CST3,LRRC15,LRRC4,AZIN2,PRKCD,DBNDD2	up_ACOR_EC
GO:0120035	0.129206499	0.93973	7	160	regulation of plasma membrane bounded cell projection organization	BP	1	BRSK1,RGMA,PLS1,PAK3,LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0002691	0.129391842	0.99297	1	5	regulation of cellular extravasation	BP	1	PTGER4	up_ACOR_EC
GO:0032411	0.129499435	0.97612	2	24	positive regulation of transporter activity	BP	1	ACTN2,PRKCD	up_ACOR_EC
GO:0032270	0.129524433	0.919	17	479	positive regulation of cellular protein metabolic process	BP	1	SOX9,ENSCAFG00000004331,EDEM2,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0006699	0.129538253	0.99295	1	5	bile acid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:0007289	0.129692945	0.99293	1	5	spermatid nucleus differentiation	BP	1	PYGO2	up_ACOR_EC
GO:0003207	0.129702889	0.99293	1	5	cardiac chamber formation	BP	1	TBX5	up_ACOR_EC
GO:0014029	0.129744081	0.99293	1	5	neural crest formation	BP	1	SOX9	up_ACOR_EC
GO:0007413	0.129844302	0.99292	1	5	axonal fasciculation	BP	1	NRP1	up_ACOR_EC
GO:0106030	0.129844302	0.99292	1	5	neuron projection fasciculation	BP	1	NRP1	up_ACOR_EC
GO:0061035	0.129882582	0.97601	2	24	regulation of cartilage development	BP	1	SOX9,EFEMP1	up_ACOR_EC
GO:0003264	0.129943497	0.99291	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_ACOR_EC

GO:0003266	0.129943497	0.99291	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_ACOR_EC
GO:0032989	0.13	0.906	35	292	cellular component morphogenesis	BP	1	ACTN2,CDC7,EPYC,ZRANB1,SHROOM3,FEZ1,FGFR2,SEC24B,WASF3,LATS2,ZNF365,TMEM108,ARHGEF26,NEBL,ZMYM2,NRP1,GPM6A,ULK2,UNC5B,SPINT2,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,EDN1,FEZ2,WASL,DOCK5,BVES,RREB1,CRKL,MYOZ2	up_ACOR_VSMC
GO:0051050	0.13	0.92	16	235	positive regulation of transport	BP	1	LRP1,PRNP,SDC4,FXYD1,TRPV2,CLIP3,ENSCAFG00000014978,AKT2,SCP2,THY1,GLI3,PARK7,CYBA,MAVS,CDH2,GREM1	down_VCAV_EC
GO:0009059	0.13	0.934	11	1563	macromolecule biosynthetic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,NEDD4	down_ACOR_EC
GO:0072503	0.13	0.933	9	97	cellular divalent inorganic cation homeostasis	BP	1	SLC39A7,ERO1A,ATP2B1,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0002685	0.13	0.941	7	55	regulation of leukocyte migration	BP	1	SELP,CXCL8,STK10,MMP28,SWAP70,APOD,HMGB1	up_VCAV_EC
GO:0009127	0.13	0.95	5	47	purine nucleoside monophosphate biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0009168	0.13	0.95	5	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0032206	0.13	0.958	4	23	positive regulation of telomere maintenance	BP	1	HNRNPD,AURKB,NEK2,CCT4	down_ACOR_VSMC
GO:0045597	0.13	0.964	3	253	positive regulation of cell differentiation	BP	1	ACVRL1,LYN,PDPN	down_ACOR_EC
GO:0034340	0.13	0.967	3	15	response to type I interferon	BP	1	IRAK1,SLC29A1,CACTIN	down_ACOR_VSMC
GO:0070227	0.13	0.965	3	25	lymphocyte apoptotic process	BP	1	GPAM,GLI3,TSC22D3	down_VCAV_EC
GO:0071704	0.13	1	3	3535	organic substance metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0007215	0.13	0.968	3	13	glutamate receptor signaling pathway	BP	1	DAPK1,APP,GNAQ	up_ACOR_VSMC
GO:0032495	0.13	0.966	3	15	response to muramyl dipeptide	BP	1	TNFAIP3,JAG1,ARHGEF2	up_VCAV_EC
GO:0071310	0.13	0.967	3	634	cellular response to organic substance	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0016101	0.13	0.967	3	13	diterpenoid metabolic process	BP	1	DHRS4,RETSAT,DHRS9	up_VSAP_EC
GO:0007409	0.13	0.976	2	109	axonogenesis	BP	1	SPG11,NRP2	down_ACOR_EC
GO:0001783	0.13	0.979	2	8	B cell apoptotic process	BP	1	AURKB,NOC2L	down_ACOR_VSMC
GO:1901020	0.13	0.979	2	8	negative regulation of calcium ion transmembrane	BP	1	GSTO1,REM1	down_ACOR_VSMC
GO:1903170	0.13	0.979	2	8	negative regulation of calcium ion	BP	1	GSTO1,REM1	down_ACOR_VSMC
GO:0070925	0.13	0.977	2	293	organelle assembly	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0045581	0.13	0.977	2	13	negative regulation of T cell differentiation	BP	1	GLI3,LOXL3	down_VCAV_EC
GO:1900078	0.13	0.977	2	13	positive regulation of cellular response to	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0048806	0.13	0.978	2	10	genitalia development	BP	1	PTPN11,CTNNB1	down_VSAP_EC
GO:0050877	0.13	0.976	2	164	nervous system process	BP	1	NTRK2,HOXA1	up_APUL_EC
GO:0048745	0.13	0.979	2	8	smooth muscle tissue development	BP	1	TIPARP,PROX1	up_VCAV_EC
GO:2000178	0.13	0.98	2	7	negative regulation of neural precursor cell	BP	1	RAPGEF1,CTNNA1	up_VCAV_EC
GO:0031347	0.13	0.976	2	144	regulation of defense response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0071322	0.13	0.992	1	29	cellular response to carbohydrate stimulus	BP	1	STX4	down_ACOR_EC
GO:0070646	0.13	0.992	1	63	protein modification by small protein removal	BP	1	USP33	down_AFEM_EC
GO:0048863	0.13	0.992	1	70	stem cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:1904018	0.13	0.992	1	69	positive regulation of vasculature development	BP	1	HDAC7	down_VPOR_EC
GO:2000116	0.13	0.992	1	67	regulation of cysteine-type endopeptidase	BP	1	CST3	down_VPOR_EC
GO:0061419	0.13	0.995	1	2	positive regulation of transcription from RNA polymerase II promoter in response to hypoxia	BP	1	HIF1A	down_VSAP_EC

GO:0009150	0.13	0.993	1	161	purine ribonucleotide metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0000077	0.13	0.992	1	60	DNA damage checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0051962	0.13	0.992	1	112	positive regulation of nervous system	BP	1	WNT7A	up_AORT_VSMC
GO:0035150	0.13	0.992	1	36	regulation of tube size	BP	1	HTR7	up_APUL_EC
GO:0050880	0.13	0.992	1	36	regulation of blood vessel size	BP	1	HTR7	up_APUL_EC
GO:0090276	0.13	0.992	1	36	regulation of peptide hormone secretion	BP	1	NR1H4	up_APUL_EC
GO:0110053	0.13	0.992	1	98	regulation of actin filament organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0048247	0.13	0.992	1	16	lymphocyte chemotaxis	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0098927	0.13	0.992	1	17	vesicle-mediated transport between endosomal compartments	BP	1	HOOK3	up_VPOR_EC
GO:0033002	0.13	0.992	1	55	muscle cell proliferation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0048706	0.13	0.992	1	59	embryonic skeletal system development	BP	1	HOXA3	up_VPOR_VSMC
GO:0009743	0.13	0.992	1	40	response to carbohydrate	BP	1	NR1H4	up_VPUL_EC
GO:0010565	0.13	0.992	1	40	regulation of cellular ketone metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0016571	0.13	0.992	1	39	histone methylation	BP	1	NR1H4	up_VPUL_EC
GO:0048634	0.13	0.992	1	40	regulation of muscle organ development	BP	1	TBX5	up_VPUL_EC
GO:0032103	0.13	0.992	1	69	positive regulation of response to external	BP	1	SLIT2	up_VPUL_VSMC
GO:0038061	0.13	0.992	1	34	NIK/NF-kappaB signaling	BP	1	TLR2	up_VSAP_VSMC
GO:0001658	0.130045881	0.97596	2	24	branching involved in ureteric bud	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0046477	0.130100768	0.99289	1	5	glycosylceramide catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0045859	0.130195266	0.93266	9	219	regulation of protein kinase activity	BP	1	PKIB,FZD5,DUSP26,PAK3,LRRC15,LRRC4,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0007618	0.130239556	0.99287	1	5	mating	BP	1	MAPK8IP2	up_ACOR_EC
GO:0006591	0.130275604	0.99287	1	5	ornithine metabolic process	BP	1	AZIN2	up_ACOR_EC
GO:0002830	0.13051974	0.99284	1	5	positive regulation of type 2 immune response	BP	1	NOD2	up_ACOR_EC
GO:0030517	0.130536101	0.99284	1	5	negative regulation of axon extension	BP	1	NRP1	up_ACOR_EC
GO:0001944	0.131	0.907	31	263	vasculature development	BP	1	HOXA7,WNT11,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,WARS2,HPSE,CCBE1,RECK,PLPP3,DLX3,ZFP36L1,TBXA2R,SASH1,LOX,HPGD,ZFAND5,ANPEP,ACVRL1,PPP3CB,HMOX1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0098657	0.131	0.916	19	181	import into cell	BP	1	SELE,CXCL8,CALCRL,RAB27A,SLC39A8,IRF8,PIK3C2A,PPP3CA,BMP2K,RALBP1,ABCA1,KCNJ3,ELMO1,SNX2,HIST1H1A,PLCG2,HMGB1,DNAJC13,PEAR1	up_VCAV_EC
GO:0030155	0.131	0.921	15	180	regulation of cell adhesion	BP	1	VEGFA,SERPINE1,SOCS5,FAM49B,NUAK1,PTPN11,PPP1R12A,PTPN2,ENSCAFG00000002015,TFRC,LYN,GSK3B,SDC4,LMO7,NRP1	down_VSAP_EC
GO:0071900	0.131	0.921	15	131	regulation of protein serine/threonine kinase activity	BP	1	KIT,TNFAIP3,MAP3K11,PDGFB,TLR4,EDN1,RALB,BMP2,HHEX,PROX1,MADD,RAPGEF2,BLM,RIPK1,PDGFD	up_VCAV_EC
GO:0032504	0.131	0.924	13	152	multicellular organism reproduction	BP	1	CELF1,ETV6,PTPN11,TMED2,PTGS2,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0048609	0.131	0.924	13	152	multicellular organismal reproductive process	BP	1	CELF1,ETV6,PTPN11,TMED2,PTGS2,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0019318	0.131	0.933	9	75	hexose metabolic process	BP	1	ATF3,FAM3C,PGM2,ENSCAFG00000010596,GALE,CHST1,ENSCAFG00000024323,APOD,PMAIP1	up_VCAV_EC
GO:0045444	0.131	0.936	8	84	fat cell differentiation	BP	1	ERO1A,ENPP1,TRIB3,PTGS2,KLF5,BNIP3,DDIT3,NR4A1	down_VSAP_EC
GO:0001818	0.131	0.937	8	65	negative regulation of cytokine production	BP	1	TNFAIP3,CD34,TLR4,GATA3,HOMER3,ARG2,APOD,HMGB1	up_VCAV_EC
GO:0046890	0.131	0.94	7	51	regulation of lipid biosynthetic process	BP	1	ACSL3,SREBF1,SF1,CTDNEP1,INSIG1,CDK4,BRCA1	down_ACOR_VSMC

GO:0048754	0.131	0.944	6	57	branching morphogenesis of an epithelial tube	BP	1	ILK,HOXB7,MAGED1,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0032412	0.131	0.949	5	46	regulation of ion transmembrane	BP	1	REM1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0090288	0.131	0.949	5	44	negative regulation of cellular response to growth factor stimulus	BP	1	SULF1,HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:0001892	0.131	0.95	5	35	embryonic placenta development	BP	1	PCDH12,PDGFB,MDFI,HIF1A,VASH1	up_VCAV_EC
GO:0033047	0.131	0.95	5	33	regulation of mitotic sister chromatid segregation	BP	1	SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0009064	0.131	0.957	4	23	glutamine family amino acid metabolic process	BP	1	PFAS,ARG2,AADAT,CTPS1	down_ACOR_VSMC
GO:0033559	0.131	0.957	4	21	unsaturated fatty acid metabolic process	BP	1	CYP2J2,EDN1,HPGD,ELOVL7	up_ACOR_VSMC
GO:0035556	0.131	0.959	4	845	intracellular signal transduction	BP	1	ERC1,TAOK1,CTNNAL1,GPR155	up_AORT_EC
GO:0046634	0.131	0.957	4	24	regulation of alpha-beta T cell activation	BP	1	GATA3,ARG2,ITPKB,HMGB1	up_VCAV_EC
GO:0032637	0.131	0.965	3	26	interleukin-8 production	BP	1	PARK7,BPI,MAVS	down_VCAV_EC
GO:0060740	0.131	0.967	3	13	prostate gland epithelium morphogenesis	BP	1	BMP4,FGFR2,FRS2	up_ACOR_VSMC
GO:0044267	0.131	0.988	2	1583	cellular protein metabolic process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0090278	0.131	0.978	2	10	negative regulation of peptide hormone	BP	1	PTPN11,REST	down_VSAP_EC
GO:0003181	0.131	0.979	2	7	atrioventricular valve morphogenesis	BP	1	SMAD6,TBX5	up_ACOR_VSMC
GO:1900120	0.131	0.979	2	7	regulation of receptor binding	BP	1	PLCL1,B2M	up_ACOR_VSMC
GO:0001662	0.131	0.979	2	7	behavioral fear response	BP	1	MEF2C,ALS2	up_VCAV_EC
GO:0002209	0.131	0.979	2	7	behavioral defense response	BP	1	MEF2C,ALS2	up_VCAV_EC
GO:0042596	0.131	0.979	2	7	fear response	BP	1	MEF2C,ALS2	up_VCAV_EC
GO:0048643	0.131	0.979	2	7	positive regulation of skeletal muscle tissue	BP	1	MEF2C,CDON	up_VCAV_EC
GO:0043066	0.131	0.976	2	253	negative regulation of apoptotic process	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0006814	0.131	0.992	1	28	sodium ion transport	BP	1	NEDD4	down_ACOR_EC
GO:0021761	0.131	0.992	1	27	limbic system development	BP	1	NRP2	down_ACOR_EC
GO:0030324	0.131	0.992	1	64	lung development	BP	1	SRSF6	down_AFEM_EC
GO:0048513	0.131	1	1	906	animal organ development	BP	1	GATA5	down_AFEM_VSMC
GO:0061525	0.131	0.994	1	3	hindgut development	BP	1	GLI3	down_VCAV_EC
GO:0010560	0.131	0.994	1	3	positive regulation of glycoprotein biosynthetic	BP	1	SOAT1	down_VCAV_EC
GO:1903020	0.131	0.994	1	3	positive regulation of glycoprotein metabolic	BP	1	SOAT1	down_VCAV_EC
GO:0045595	0.131	0.995	1	469	regulation of cell differentiation	BP	1	GATA5	down_VFEM_VSMC
GO:0031620	0.131	0.995	1	2	regulation of fever generation	BP	1	PTGS2	down_VSAP_EC
GO:0031622	0.131	0.995	1	2	positive regulation of fever generation	BP	1	PTGS2	down_VSAP_EC
GO:0035617	0.131	0.995	1	2	stress granule disassembly	BP	1	KIF5B	down_VSAP_EC
GO:1905289	0.131	0.995	1	2	regulation of CAMKK-AMPK signaling cascade	BP	1	HTT	down_VSAP_EC
GO:0060155	0.131	1	1	1	platelet dense granule organization	BP	1	ABCA1	up_ACOR_VSMC
GO:0002360	0.131	0.992	1	6	T cell lineage commitment	BP	1	CYLD	up_AFEM_EC
GO:0043369	0.131	0.992	1	6	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BP	1	CYLD	up_AFEM_EC
GO:0048846	0.131	0.992	1	6	axon extension involved in axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:1902284	0.131	0.992	1	6	neuron projection extension involved in neuron projection	BP	1	PLXNA4	up_AFEM_EC
GO:2000114	0.131	0.993	1	6	regulation of establishment of cell	BP	1	KANK1	up_AFEM_EC

GO:0046328	0.131	0.992	1	61	regulation of JNK cascade	BP	1	TAOK1	up_AORT_EC
GO:0008286	0.131	0.992	1	36	insulin receptor signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0006072	0.131	0.995	1	2	glycerol-3-phosphate metabolic process	BP	1	GK5	up_VCAV_EC
GO:0007144	0.131	0.995	1	2	female meiosis I	BP	1	FBXO5	up_VCAV_EC
GO:0097350	0.131	0.995	1	2	neutrophil clearance	BP	1	HMGB1	up_VCAV_EC
GO:0043062	0.131	0.992	1	99	extracellular structure organization	BP	1	TGFBI	up_VCAV_VSMC
GO:1903522	0.131	0.992	1	58	regulation of blood circulation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010769	0.131	0.992	1	69	regulation of cell morphogenesis involved	BP	1	SLIT2	up_VPUL_VSMC
GO:0042307	0.131012556	0.97574	2	23	positive regulation of protein import into	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0072525	0.131306315	0.97559	2	24	pyridine-containing compound biosynthetic	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:2000810	0.131372104	0.99274	1	5	regulation of bicellular tight junction assembly	BP	1	FZD5	up_ACOR_EC
GO:0019221	0.131436846	0.94791	5	102	cytokine-mediated signaling pathway	BP	1	NR1H4,CCDC3,MAVS,LRRC15,LRRC4	up_ACOR_EC
GO:0032755	0.131687879	0.97547	2	24	positive regulation of interleukin-6 production	BP	1	NOD2,MAVS	up_ACOR_EC
GO:0061551	0.131819956	0.99269	1	5	trigeminal ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0098581	0.131864027	0.99269	1	5	detection of external biotic stimulus	BP	1	NOD2	up_ACOR_EC
GO:0048666	0.132	0.917	17	258	neuron development	BP	1	NDN,SDC4,TRPV2,NUMBL,NAGLU,SEMA3C,THY1,TLX2,GLI3,NCDN,ENSCAFG00000017708,IRX5,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0048858	0.132	0.921	14	159	cell projection morphogenesis	BP	1	SIPA1L1,SGK1,PTPN11,IFRD1,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0034330	0.132	0.928	11	80	cell junction organization	BP	1	WNT11,FAM107A,LIMS2,CDH1,ABL1,HDAC7,CLDN1,F2RL1,AJM1,ACVRL1,FLOT1	up_VSAP_EC
GO:0051604	0.132	0.932	9	102	protein maturation	BP	1	SERPINH1,MYH9,SERPINE1,ERO1A,PRKACB,ENSCAFG00000005575,PGK1,NAA10,A2M	down_VSAP_EC
GO:0016358	0.132	0.936	8	58	dendrite development	BP	1	EPHB1,RELN,MEF2C,PPP3CA,PREX2,ENSCAFG00000010224,PAK2,RAPGEF2	up_VCAV_EC
GO:0046488	0.132	0.94	7	44	phosphatidylinositol metabolic process	BP	1	PIP5K1B,PLCG2,HTR2B,PIGN,PIGS,PIGG,INPP5K	up_ACOR_VSMC
GO:0050803	0.132	0.943	6	55	regulation of synapse structure or activity	BP	1	TUBB,APOE,DISC1,LRRTM2,SIX4,ARF4	down_VSAP_EC
GO:0050807	0.132	0.943	6	55	regulation of synapse organization	BP	1	TUBB,APOE,DISC1,LRRTM2,SIX4,ARF4	down_VSAP_EC
GO:0045598	0.132	0.944	6	47	regulation of fat cell differentiation	BP	1	PPARG,GATA3,BMP2,JAG1,PTGS2,CREB1	up_VCAV_EC
GO:0009566	0.132	0.957	4	24	fertilization	BP	1	AAAS,B4GALT1,HOXA9,CCT4	down_ACOR_VSMC
GO:1905952	0.132	0.955	4	33	regulation of lipid localization	BP	1	PTPN11,PTPN2,APOE,ABHD5	down_VSAP_EC
GO:0021795	0.132	0.965	3	20	cerebral cortex cell migration	BP	1	CTNNB1,DISC1,NRP1	down_VSAP_EC
GO:0009059	0.132	0.974	3	1563	macromolecule biosynthetic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0050702	0.132	0.967	3	13	interleukin-1 beta secretion	BP	1	ABCA1,F2RL1,NOD2	up_ACOR_VSMC
GO:0048662	0.132	0.965	3	18	negative regulation of smooth muscle cell	BP	1	TNFAIP3,MEF2C,APOD	up_VCAV_EC
GO:0046638	0.132	0.976	2	13	positive regulation of alpha-beta T cell	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:0060443	0.132	0.976	2	13	mammary gland morphogenesis	BP	1	B4GALT1,GLI3	down_VCAV_EC
GO:0050850	0.132	0.977	2	11	positive regulation of calcium-mediated	BP	1	HTT,CALM1	down_VSAP_EC
GO:0016197	0.132	0.975	2	78	endosomal transport	BP	1	GCC2,TMEM87B	up_VPOR_EC
GO:0043087	0.132	0.975	2	83	regulation of GTPase activity	BP	1	ENSCAFG00000002015,ENSCAFG00000032731	up_VPOR_EC
GO:0000904	0.132	0.975	2	181	cell morphogenesis involved in differentiation	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0006921	0.132	0.979	2	7	cellular component disassembly involved in execution phase of	BP	1	DFFB,DEDD2	up_VSAP_EC
GO:0030262	0.132	0.979	2	7	apoptotic nuclear changes	BP	1	DFFB,DEDD2	up_VSAP_EC

GO:0090036	0.132	0.979	2	7	regulation of protein kinase C signaling	BP	1	SEZ6L,WNT11	up_VSAP_EC
GO:0042255	0.132	0.991	1	29	ribosome assembly	BP	1	RPSA	down_ACOR_EC
GO:0035904	0.132	0.991	1	25	aorta development	BP	1	ACVRL1	down_ACOR_EC
GO:0031915	0.132	0.995	1	2	positive regulation of synaptic plasticity	BP	1	CDC20	down_ACOR_VSMC
GO:0031325	0.132	1	1	914	positive regulation of cellular metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0010359	0.132	0.994	1	3	regulation of anion channel activity	BP	1	PRNP	down_VCAV_EC
GO:0032105	0.132	0.994	1	3	negative regulation of response to extracellular	BP	1	KANK2	down_VCAV_EC
GO:0032108	0.132	0.994	1	3	negative regulation of response to nutrient	BP	1	KANK2	down_VCAV_EC
GO:0008356	0.132	0.994	1	3	asymmetric cell division	BP	1	ZBTB16	down_VCAV_EC
GO:0030002	0.132	0.994	1	3	cellular anion homeostasis	BP	1	ENSCAFG00000018277	down_VCAV_EC
GO:0030320	0.132	0.994	1	3	cellular monovalent inorganic anion	BP	1	ENSCAFG00000018277	down_VCAV_EC
GO:0034499	0.132	0.994	1	3	late endosome to Golgi transport	BP	1	RAB7B	down_VCAV_EC
GO:1904526	0.132	0.994	1	3	regulation of microtubule binding	BP	1	MAPRE3	down_VCAV_EC
GO:0002573	0.132	0.992	1	71	myeloid leukocyte differentiation	BP	1	CITED2	down_VPOR_EC
GO:0001867	0.132	0.995	1	2	complement activation, lectin pathway	BP	1	A2M	down_VSAP_EC
GO:0010870	0.132	0.995	1	2	positive regulation of receptor biosynthetic	BP	1	HIF1A	down_VSAP_EC
GO:0048102	0.132	0.994	1	3	autophagic cell death	BP	1	SH3GLB1	down_VSAP_EC
GO:0060123	0.132	0.995	1	2	regulation of growth hormone secretion	BP	1	PTPN11	down_VSAP_EC
GO:0061316	0.132	0.995	1	2	canonical Wnt signaling pathway involved in heart	BP	1	CTNNB1	down_VSAP_EC
GO:1902725	0.132	0.995	1	2	negative regulation of satellite cell	BP	1	SIX4	down_VSAP_EC
GO:0010884	0.132	0.992	1	6	positive regulation of lipid storage	BP	1	ACACB	up_AFEM_EC
GO:0031641	0.132	0.992	1	6	regulation of myelination	BP	1	LGI4	up_AFEM_EC
GO:2000273	0.132	0.992	1	6	positive regulation of signaling receptor activity	BP	1	ADAM17	up_AFEM_EC
GO:0031570	0.132	0.991	1	61	DNA integrity checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0060047	0.132	0.992	1	57	heart contraction	BP	1	SGCD	up_AORT_EC
GO:0072028	0.132	0.991	1	37	nephron morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0017182	0.132	0.995	1	2	peptidyl-diphthamide metabolic process	BP	1	DPH5	up_VCAV_EC
GO:0017183	0.132	0.995	1	2	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	BP	1	DPH5	up_VCAV_EC
GO:0061009	0.132	0.995	1	2	common bile duct development	BP	1	HHEX	up_VCAV_EC
GO:0097476	0.132	1	1	1	spinal cord motor neuron migration	BP	1	RELN	up_VCAV_EC
GO:0097477	0.132	1	1	1	lateral motor column neuron migration	BP	1	RELN	up_VCAV_EC
GO:0150066	0.132	1	1	1	negative regulation of deacetylase activity	BP	1	KDM5A	up_VCAV_EC
GO:1900451	0.132	1	1	1	positive regulation of glutamate receptor	BP	1	RELN	up_VCAV_EC
GO:1901726	0.132	1	1	1	negative regulation of histone deacetylase	BP	1	KDM5A	up_VCAV_EC
GO:1902076	0.132	1	1	1	regulation of lateral motor column neuron	BP	1	RELN	up_VCAV_EC
GO:1902078	0.132	1	1	1	positive regulation of lateral motor column	BP	1	RELN	up_VCAV_EC
GO:1905483	0.132	1	1	1	regulation of motor neuron migration	BP	1	RELN	up_VCAV_EC
GO:1905485	0.132	1	1	1	positive regulation of motor neuron migration	BP	1	RELN	up_VCAV_EC
GO:2000969	0.132	1	1	1	positive regulation of AMPA receptor activity	BP	1	RELN	up_VCAV_EC

GO:0031064	0.132	1	1	1	negative regulation of histone deacetylation	BP	1	KDM5A	up_VCAV_EC
GO:0038026	0.132	1	1	1	reelin-mediated signaling pathway	BP	1	RELN	up_VCAV_EC
GO:0045054	0.132	0.995	1	2	constitutive secretory pathway	BP	1	RAB27A	up_VCAV_EC
GO:0031663	0.132	0.992	1	17	lipopolysaccharide-mediated signaling	BP	1	MTDH	up_VPOR_EC
GO:0110111	0.132	0.992	1	17	negative regulation of animal organ	BP	1	ASPN	up_VPOR_EC
GO:0007626	0.132	0.992	1	53	locomotory behavior	BP	1	CHL1	up_VPOR_VSMC
GO:0010001	0.132	0.992	1	54	glial cell differentiation	BP	1	TRPC4	up_VPOR_VSMC
GO:1903046	0.132	0.992	1	55	meiotic cell cycle process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0014902	0.132	0.991	1	34	myotube differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0006470	0.132	0.992	1	54	protein dephosphorylation	BP	1	EYA1	up_VFEM_VSMC
GO:0033135	0.132	0.991	1	40	regulation of peptidyl-serine phosphorylation	BP	1	PTGER2	up_VPUL_EC
GO:1903531	0.132	0.991	1	41	negative regulation of secretion by cell	BP	1	NR1H4	up_VPUL_EC
GO:0051099	0.132	0.992	1	70	positive regulation of binding	BP	1	HOXA3	up_VPUL_VSMC
GO:0051216	0.132	0.992	1	70	cartilage development	BP	1	HOXA3	up_VPUL_VSMC
GO:0090263	0.132	0.991	1	33	positive regulation of canonical Wnt signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0072641	0.132027121	0.99267	1	5	type I interferon secretion	BP	1	MAVS	up_ACOR_EC
GO:0072642	0.132027121	0.99267	1	5	interferon-alpha secretion	BP	1	MAVS	up_ACOR_EC
GO:1902739	0.132027121	0.99267	1	5	regulation of interferon-alpha secretion	BP	1	MAVS	up_ACOR_EC
GO:1902741	0.132027121	0.99267	1	5	positive regulation of interferon-alpha secretion	BP	1	MAVS	up_ACOR_EC
GO:0031344	0.132382424	0.93787	7	161	regulation of cell projection organization	BP	1	BRSK1,RGMA,PLS1,PAK3,LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0072033	0.132530896	0.99261	1	5	renal vesicle formation	BP	1	SOX9	up_ACOR_EC
GO:0071679	0.132533042	0.99261	1	5	commissural neuron axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0061549	0.132912955	0.99257	1	5	sympathetic ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0040007	0.133	0.904	33	276	growth	BP	1	LGR6,LEP,DCBLD2,BMP4,CRIM1,FGFR2,GJA1,ATRX,LATS2,RERG,TMEM108,ATRN,PLAC8B,CDKN1A,CRLF3,ENSCAFG00000006238,NRP1,ULK2,TBX20,TBX5,APP,CHD7,DDR2,WWC2,EDN1,ARID5B,FAM107A,IGFBP7,WFS1,WDR48,NAIF1,SH3BP4,STC2	up_ACOR_VSMC
GO:1902532	0.133	0.909	25	204	negative regulation of intracellular signal transduction	BP	1	RASSF2,PRKAA2,BMP4,CASTOR1,NDRG2,ITPR1,F2RL1,UBR1,PTPN22,SMPD1,APLP1,SESN3,DAG1,SYNJ2BP,WWC2,SESN1,DUSP26,LRRC4,DDIT4,HERPUD1,INPP5K,BMT2,WFS1,SH3BP4,PARK7	up_ACOR_VSMC
GO:0002684	0.133	0.914	19	239	positive regulation of immune system process	BP	1	VEGFA,NR1H4,SERPINE1,SOCS5,FAM49B,HIF1A,PTPN2,EIF2B1,EVI2B,PVR,ADAM17,SKAP2,TFRC,LYN,GBP5,PRMT1,A2M,INHBA,CDKN1A	down_VSAP_EC
GO:0060341	0.133	0.916	17	255	regulation of cellular localization	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,SCP2,TRIM8,THY1,GLI3,PARK7,ZFP36L1,CYBA,MAVS,CDH2,GLIS2,ARHGAP1,RAC2	down_VCAV_EC
GO:0031323	0.133	0.933	11	1788	regulation of cellular metabolic process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0007254	0.133	0.932	9	67	JNK cascade	BP	1	EPHB1,MAP3K11,SH2D3C,TLR4,EDN1,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0007610	0.133	0.942	6	146	behavior	BP	1	LEP,THRB,LGI4,HTR1D,AVPR1A,GCNT4	up_AFEM_EC
GO:0097237	0.133	0.943	6	42	cellular response to toxic substance	BP	1	TNFAIP3,PDGFB,MAPK13,TIMELESS,GCH1,RIPK1	up_VCAV_EC
GO:0042742	0.133	0.955	4	39	defense response to bacterium	BP	1	BPI,CYBA,MAVS,SHC1	down_VCAV_EC
GO:0045638	0.133	0.955	4	33	negative regulation of myeloid cell	BP	1	PTPN2,CTNNB1,LYN,PRMT1	down_VSAP_EC
GO:0046889	0.133	0.956	4	24	positive regulation of lipid biosynthetic process	BP	1	ADGRF5,MTOR,PTGS2,CREB1	up_VCAV_EC
GO:0035272	0.133	0.957	4	21	exocrine system development	BP	1	FGF7,CLCN2,NTN4,NFIB	up_VSAP_EC

GO:0007338	0.133	0.965	3	16	single fertilization	BP	1	B4GALT1,HOXA9,CCT4	down_ACOR_VSMC
GO:0008088	0.133	0.964	3	21	axo-dendritic transport	BP	1	HIF1A,TRAK1,AP3S1	down_VSAP_EC
GO:1902108	0.133	0.966	3	14	regulation of mitochondrial membrane permeability involved in	BP	1	RHOT1,BNIP3,NAIF1	up_ACOR_VSMC
GO:2000112	0.133	0.97	3	1119	regulation of cellular macromolecule biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0055085	0.133	0.963	3	284	transmembrane transport	BP	1	NETO1,STIM1,CAV1	up_VSAP_VSMC
GO:0060548	0.133	0.976	2	294	negative regulation of cell death	BP	1	IVNS1ABP,SRSF6	down_AFEM_EC
GO:0003382	0.133	0.977	2	11	epithelial cell morphogenesis	BP	1	FLNB,PLOD3	down_VSAP_EC
GO:0060291	0.133	0.977	2	11	long-term synaptic potentiation	BP	1	APOE,LRRTM2	down_VSAP_EC
GO:0046633	0.133	0.979	2	7	alpha-beta T cell proliferation	BP	1	CD274,PTPN22	up_ACOR_VSMC
GO:0061307	0.133	0.979	2	7	cardiac neural crest cell differentiation involved in heart development	BP	1	BMP4,CITED2	up_ACOR_VSMC
GO:0061308	0.133	0.979	2	7	cardiac neural crest cell development involved in heart development	BP	1	BMP4,CITED2	up_ACOR_VSMC
GO:0033028	0.133	0.978	2	8	myeloid cell apoptotic process	BP	1	MEF2C,ITPKB	up_VCAV_EC
GO:0019953	0.133	0.975	2	152	sexual reproduction	BP	1	HOXA9,CYP26B1	up_VFEM_EC
GO:0045597	0.133	0.975	2	253	positive regulation of cell differentiation	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0017156	0.133	0.991	1	32	calcium ion regulated exocytosis	BP	1	STX4	down_ACOR_EC
GO:0018364	0.133	0.995	1	2	peptidyl-glutamine methylation	BP	1	FBL	down_ACOR_VSMC
GO:0030323	0.133	0.991	1	65	respiratory tube development	BP	1	SRSF6	down_AFEM_EC
GO:0010604	0.133	1	1	919	positive regulation of macromolecule metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0030449	0.133	0.994	1	3	regulation of complement activation	BP	1	A2M	down_VCAV_EC
GO:2000257	0.133	0.994	1	3	regulation of protein activation cascade	BP	1	A2M	down_VCAV_EC
GO:0010594	0.133	0.992	1	71	regulation of endothelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0051049	0.133	0.995	1	479	regulation of transport	BP	1	JUP	down_VFEM_VSMC
GO:0002154	0.133	0.995	1	2	thyroid hormone mediated signaling	BP	1	PRCP	down_VSAP_EC
GO:0030091	0.133	0.994	1	3	protein repair	BP	1	MSRB3	down_VSAP_EC
GO:0003226	0.133	1	1	1	right ventricular compact myocardium	BP	1	CHD7	up_ACOR_VSMC
GO:0021553	0.133	1	1	1	olfactory nerve development	BP	1	CHD7	up_ACOR_VSMC
GO:0021604	0.133	0.992	1	6	cranial nerve structural organization	BP	1	PLXNA4	up_AFEM_EC
GO:0021612	0.133	0.992	1	6	facial nerve structural organization	BP	1	PLXNA4	up_AFEM_EC
GO:0032042	0.133	0.992	1	6	mitochondrial DNA metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0033273	0.133	0.992	1	6	response to vitamin	BP	1	POSTN	up_AFEM_EC
GO:0033689	0.133	0.992	1	6	negative regulation of osteoblast proliferation	BP	1	GREM1	up_AFEM_EC
GO:0042403	0.133	0.992	1	6	thyroid hormone metabolic process	BP	1	GCNT4	up_AFEM_EC
GO:0050892	0.133	0.992	1	6	intestinal absorption	BP	1	LEP	up_AFEM_EC
GO:0072348	0.133	0.992	1	6	sulfur compound transport	BP	1	SLC6A6	up_AFEM_EC
GO:0051222	0.133	0.992	1	103	positive regulation of protein transport	BP	1	TLR2	up_AFEM_VSMC
GO:0072001	0.133	0.992	1	104	renal system development	BP	1	EYA1	up_AFEM_VSMC
GO:0007093	0.133	0.991	1	59	mitotic cell cycle checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0007409	0.133	0.992	1	109	axonogenesis	BP	1	WNT7A	up_AORT_VSMC

GO:1903706	0.133	0.992	1	119	regulation of hemopoiesis	BP	1	HOXA9	up_AORT_VSMC
GO:0055088	0.133	0.991	1	37	lipid homeostasis	BP	1	NR1H4	up_APUL_EC
GO:1904659	0.133	0.991	1	36	glucose transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0000050	0.133	0.995	1	2	urea cycle	BP	1	ARG2	up_VCAV_EC
GO:0070673	0.133	0.995	1	2	response to interleukin-18	BP	1	PDGFB	up_VCAV_EC
GO:0010760	0.133	0.995	1	2	negative regulation of macrophage chemotaxis	BP	1	MMP28	up_VCAV_EC
GO:0032696	0.133	0.995	1	2	negative regulation of interleukin-13 production	BP	1	ARG2	up_VCAV_EC
GO:1905522	0.133	0.995	1	2	negative regulation of macrophage migration	BP	1	MMP28	up_VCAV_EC
GO:0030900	0.133	0.992	1	101	forebrain development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0015849	0.133	0.991	1	56	organic acid transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:0046942	0.133	0.991	1	56	carboxylic acid transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:1901861	0.133	0.991	1	41	regulation of muscle tissue development	BP	1	TBX5	up_VPUL_EC
GO:0048863	0.133	0.992	1	70	stem cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0044344	0.133	0.991	1	33	cellular response to fibroblast growth factor	BP	1	FGF5	up_VSAP_VSMC
GO:0071774	0.133	0.991	1	33	response to fibroblast growth factor	BP	1	FGF5	up_VSAP_VSMC
GO:1902667	0.133095754	0.99255	1	5	regulation of axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0046068	0.13339738	0.99251	1	5	cGMP metabolic process	BP	1	GUCY1B1	up_ACOR_EC
GO:2000574	0.133405147	0.99221	1	6	regulation of microtubule motor activity	BP	1	DYNC1I1	up_ACOR_EC
GO:0030512	0.133660214	0.97489	2	24	negative regulation of transforming growth factor beta receptor	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:1903845	0.133660214	0.97489	2	24	negative regulation of cellular response to transforming growth	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:0071704	0.134	0.884	309	3535	organic substance metabolic process	BP	1	FADS2,ELK3,SCD,ACSL3,PRPSAP1,SQLE,FADS1,HMGB1,MCM6,RNPS1,LSS,SREBF1,ACLY,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,ENSCAFG00000016095,PPRC1,USP4,SF3B2,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,THOP1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,HOXA3,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,CTDNEP1,RAD54L,POLE,DDX23,NAB2,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,NF2,PFAS,EDC4,AURKB,NONO,MMP14,HNRNPL,TK1,CDKN2C,TOPBP1,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,RNF152,DIS3,TKT,GMNN,DHCR24,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,EIF5	down_ACOR_VSMC
GO:0000902	0.134	0.906	29	266	cell morphogenesis	BP	1	EPHB1,TEK,IL7R,KIT,IFRD1,RELN,MEF2C,STC1,GATA3,RAB11A,ARAP3,NEDD9,PPP3CA,PREX2,PDZD8,PROX1,ENSCAFG00000010224,STMN1,FLNB,SNX2,FES,RAPGEF2,CREB1,FMNL3,SPTBN4,ALS2,ENSCAFG00000002015,ARHGEF2,ZMYM2	up_VCAV_EC
GO:0030155	0.134	0.911	22	180	regulation of cell adhesion	BP	1	HOXA7,FAM107A,CD274,CDH1,ABL1,EMP2,DLL1,ZBTB16,PIK3R1,TFE3,ECM2,CD83,FBLN1,PNP,STX4,ACVRL1,ASS1,FLOT1,NCK1,TGFBR2,CITED2,BAG4	up_VSAP_EC

GO:0051093	0.134	0.914	18	273	negative regulation of developmental process	BP	1	DCN,VASN,FBN1,BMPR1A,ASPN,THY1,TLX2,GLI3,ZFP36L1,LOXL3,SPRED1,TSC22D3,TWIST2,PRKCSH,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0048872	0.134	0.938	7	85	homeostasis of number of cells	BP	1	GPAM,ZFP36L1,CDH2,TSC22D3,NAPEPLD,FOXO3,ANKRD54	down_VCAV_EC
GO:0002695	0.134	0.948	5	44	negative regulation of leukocyte activation	BP	1	SOCS5,PTPN2,LYN,SDC4,BTK	down_VSAP_EC
GO:0045598	0.134	0.948	5	47	regulation of fat cell differentiation	BP	1	ENPP1,TRIB3,PTGS2,KLF5,DDIT3	down_VSAP_EC
GO:0051224	0.134	0.947	5	47	negative regulation of protein transport	BP	1	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:1904950	0.134	0.947	5	47	negative regulation of establishment of protein localization	BP	1	NR1H4,PTPN11,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0009968	0.134	0.954	4	392	negative regulation of signal transduction	BP	1	LYN,IGF1R,SULF1,ASPN	down_ACOR_EC
GO:0031110	0.134	0.956	4	24	regulation of microtubule polymerization or depolymerization	BP	1	STMN1,FES,TAOK1,ARHGEF2	up_VCAV_EC
GO:0055008	0.134	0.956	4	24	cardiac muscle tissue morphogenesis	BP	1	CHD7,DLL4,BMP2,PROX1	up_VCAV_EC
GO:0048701	0.134	0.963	3	25	embryonic cranial skeleton morphogenesis	BP	1	TBX15,IRX5,RDH10	down_VCAV_EC
GO:2001238	0.134	0.964	3	23	positive regulation of extrinsic apoptotic	BP	1	ATF3,PAK2,INHBA	down_VSAP_EC
GO:0007632	0.134	0.965	3	14	visual behavior	BP	1	HRH1,LRRN4,APP	up_ACOR_VSMC
GO:0071277	0.134	0.965	3	15	cellular response to calcium ion	BP	1	MEF2C,TJP1,ITPKB	up_VCAV_EC
GO:0002694	0.134	0.974	2	126	regulation of leukocyte activation	BP	1	LYN,STX4	down_ACOR_EC
GO:0016242	0.134	0.976	2	13	negative regulation of macroautophagy	BP	1	POLDIP2,CLEC16A	down_VCAV_EC
GO:0007173	0.134	0.975	2	27	epidermal growth factor receptor signaling	BP	1	RAB7A,ADAM17	up_AFEM_EC
GO:0019217	0.134	0.975	2	27	regulation of fatty acid metabolic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0030510	0.134	0.975	2	27	regulation of BMP signaling pathway	BP	1	GREM1,GREM2	up_AFEM_EC
GO:0007420	0.134	0.975	2	169	brain development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0002228	0.134	0.977	2	9	natural killer cell mediated immunity	BP	1	RAB27A,NECTIN2	up_VCAV_EC
GO:0042267	0.134	0.977	2	9	natural killer cell mediated cytotoxicity	BP	1	RAB27A,NECTIN2	up_VCAV_EC
GO:0048638	0.134	0.974	2	82	regulation of developmental growth	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0051056	0.134	0.974	2	87	regulation of small GTPase mediated signal	BP	1	ARHGEF2,FBP1	up_VPOR_EC
GO:2000178	0.134	0.979	2	7	negative regulation of neural precursor cell	BP	1	LIMS2,KDM2B	up_VSAP_EC
GO:0055065	0.134	0.975	2	145	metal ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0002688	0.134	0.991	1	34	regulation of leukocyte chemotaxis	BP	1	LYN	down_ACOR_EC
GO:2000106	0.134	0.991	1	29	regulation of leukocyte apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0048864	0.134	0.991	1	29	stem cell development	BP	1	NRP2	down_ACOR_EC
GO:0042262	0.134	0.995	1	2	DNA protection	BP	1	NUDT1	down_ACOR_VSMC
GO:0010917	0.134	0.995	1	2	negative regulation of mitochondrial membrane potential	BP	1	PRELID1	down_ACOR_VSMC
GO:0006508	0.134	0.995	1	483	proteolysis	BP	1	CST3	down_AORT_EC
GO:0001542	0.134	0.994	1	3	ovulation from ovarian follicle	BP	1	FOXO3	down_VCAV_EC
GO:0036480	0.134	0.994	1	3	neuron intrinsic apoptotic signaling pathway in response to oxidative	BP	1	PARK7	down_VCAV_EC
GO:1903376	0.134	0.994	1	3	regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:0006643	0.134	0.991	1	68	membrane lipid metabolic process	BP	1	GBGT1	down_VPOR_EC
GO:0090092	0.134	0.991	1	72	regulation of transmembrane receptor protein serine/threonine	BP	1	CITED2	down_VPOR_EC

GO:2000027	0.134	0.991	1	72	regulation of animal organ morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0044257	0.134	0.994	1	327	cellular protein catabolic process	BP	1	USP12	down_VFEM_EC
GO:0019371	0.134	0.995	1	2	cyclooxygenase pathway	BP	1	PTGS2	down_VSAP_EC
GO:0009259	0.134	0.992	1	166	ribonucleotide metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0000303	0.134	0.992	1	6	response to superoxide	BP	1	SOD1	up_AFEM_EC
GO:0000423	0.134	0.992	1	6	mitophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0042755	0.134	0.992	1	6	eating behavior	BP	1	LEP	up_AFEM_EC
GO:0003128	0.134	0.992	1	6	heart field specification	BP	1	AXIN2	up_AFEM_EC
GO:0000305	0.134	0.992	1	6	response to oxygen radical	BP	1	SOD1	up_AFEM_EC
GO:0010960	0.134	0.992	1	6	magnesium ion homeostasis	BP	1	CNNM4	up_AFEM_EC
GO:0001990	0.134	0.992	1	6	regulation of systemic arterial blood pressure by	BP	1	AVPR1A	up_AFEM_EC
GO:0060379	0.134	0.992	1	6	cardiac muscle cell myoblast differentiation	BP	1	GREM1	up_AFEM_EC
GO:0070601	0.134	0.992	1	6	centromeric sister chromatid cohesion	BP	1	AXIN2	up_AFEM_EC
GO:0085029	0.134	0.992	1	6	extracellular matrix assembly	BP	1	MFAP4	up_AFEM_EC
GO:0090051	0.134	0.992	1	6	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	TBXA2R	up_AFEM_EC
GO:0097186	0.134	0.992	1	6	amelogenesis	BP	1	CNNM4	up_AFEM_EC
GO:1904263	0.134	0.992	1	6	positive regulation of TORC1 signaling	BP	1	CLEC16A	up_AFEM_EC
GO:1905048	0.134	0.992	1	6	regulation of metallopeptidase activity	BP	1	RECK	up_AFEM_EC
GO:1905564	0.134	0.992	1	6	positive regulation of vascular endothelial cell	BP	1	ADAM17	up_AFEM_EC
GO:0007517	0.134	0.992	1	100	muscle organ development	BP	1	BEND2	up_AFEM_VSMC
GO:0050708	0.134	0.992	1	101	regulation of protein secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0003015	0.134	0.991	1	58	heart process	BP	1	SGCD	up_AORT_EC
GO:0007369	0.134	0.991	1	63	gastrulation	BP	1	DUSP2	up_AORT_EC
GO:0010631	0.134	0.992	1	118	epithelial cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0090132	0.134	0.992	1	118	epithelium migration	BP	1	WNT7A	up_AORT_VSMC
GO:0001570	0.134	0.991	1	37	vasculogenesis	BP	1	NTRK2	up_APUL_EC
GO:0016571	0.134	0.991	1	39	histone methylation	BP	1	NR1H4	up_APUL_EC
GO:0035093	0.134	1	1	1	spermatogenesis, exchange of chromosomal	BP	1	PSME4	up_VCAV_EC
GO:2000325	0.134	0.995	1	2	regulation of nuclear receptor transcription	BP	1	CNOT6	up_VCAV_EC
GO:2000327	0.134	0.995	1	2	positive regulation of nuclear receptor transcription coactivator	BP	1	CNOT6	up_VCAV_EC
GO:0035092	0.134	1	1	1	sperm chromatin condensation	BP	1	PSME4	up_VCAV_EC
GO:0060430	0.134	0.995	1	2	lung saccule development	BP	1	CREB1	up_VCAV_EC
GO:0060838	0.134	0.995	1	2	lymphatic endothelial cell fate commitment	BP	1	PROX1	up_VCAV_EC
GO:0007435	0.134	0.991	1	18	salivary gland morphogenesis	BP	1	SEMA3A	up_VPOR_EC
GO:0021872	0.134	0.991	1	19	forebrain generation of neurons	BP	1	SEMA3A	up_VPOR_EC
GO:0032272	0.134	0.991	1	18	negative regulation of protein polymerization	BP	1	TWF1	up_VPOR_EC
GO:0015849	0.134	0.991	1	56	organic acid transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0046942	0.134	0.991	1	56	carboxylic acid transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0006694	0.134	0.991	1	42	steroid biosynthetic process	BP	1	NR1H4	up_VPUL_EC

GO:0035051	0.134	0.991	1	41	cardiocyte differentiation	BP	1	TBX5	up_VPUL_EC
GO:0045834	0.134	0.991	1	41	positive regulation of lipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0010594	0.134	0.991	1	71	regulation of endothelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0007612	0.134	0.991	1	33	learning	BP	1	NETO1	up_VSAP_VSMC
GO:0001959	0.134	0.991	1	33	regulation of cytokine-mediated signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0051606	0.134	0.991	1	33	detection of stimulus	BP	1	TLR2	up_VSAP_VSMC
GO:0035296	0.134	0.991	1	32	regulation of tube diameter	BP	1	CAV1	up_VSAP_VSMC
GO:0097746	0.134	0.991	1	32	regulation of blood vessel diameter	BP	1	CAV1	up_VSAP_VSMC
GO:0061077	0.13451561	0.97457	2	25	chaperone-mediated protein folding	BP	1	CLU,FKBP11	up_ACOR_EC
GO:0048008	0.134842261	0.97453	2	24	platelet-derived growth factor receptor signaling	BP	1	PTGIR,NRP1	up_ACOR_EC
GO:0048870	0.135	0.896	51	451	cell motility	BP	1	FGF13,VEGFD,LGR6,HTR2B,TCAF1,ZRANB1,RECK,FERMT1,BMP4,GJA1,HRH1,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,GPM6A,EVL,SPINT2,TBX20,TBX5,PRKCE,FZD3,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,ARID5B,FAM107A,JAM3,DISC1,SUN1,WASL,DOCK5,ENSCAFG00000029553,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0051674	0.135	0.896	51	451	localization of cell	BP	1	FGF13,VEGFD,LGR6,HTR2B,TCAF1,ZRANB1,RECK,FERMT1,BMP4,GJA1,HRH1,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,GPM6A,EVL,SPINT2,TBX20,TBX5,PRKCE,FZD3,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,ARID5B,FAM107A,JAM3,DISC1,SUN1,WASL,DOCK5,ENSCAFG00000029553,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0032879	0.135	0.898	45	767	regulation of localization	BP	1	GPAM,PDGFRB,SLC35F6,LRP1,DCN,PRNP,SDC4,GLIPR2,BMPR1A,LMO4,RECK,FXYD1,TRPV2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,DOCK10,SYDE1,SCP2,LAMA3,CACNB3,TRIM8,SEMA3C,LRPAP1,THY1,B4GALT1,GLI3,PARK7,ZFP36L1,SASH1,CYBA,MAVS,CDH2,SPRED1,GLIS2,TWIST2,ARHGAP1,DDR2,GREM1,EVI5L,RAC2,CLIC4,FOXO3,PACSIN3	down_VCAV_EC
GO:0007417	0.135	0.907	26	235	central nervous system development	BP	1	EPHB1,PTCHD1,RELN,CHD7,DLL4,TLR4,EIF2B2,HOXB8,B3GNT5,MTOR,NAV2,HOOK3,BMP2,HHEX,GDPD5,PROX1,ENSCAFG00000010224,APOD,RAPGEF2,CREB1,SPTBN4,HIF1A,ATRX,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:0006935	0.135	0.915	18	143	chemotaxis	BP	1	ACKR3,ARHGEF5,C5AR2,ACKR2,ENPP2,SLC8B1,SLIT2,IL17RC,PLXNA4,SEMA5A,HSD3B7,F2RL1,DPYSL2,ACKR4,NFIB,ZNF580,STX4,SAA1	up_VSAP_EC
GO:0042330	0.135	0.915	18	143	taxis	BP	1	ACKR3,ARHGEF5,C5AR2,ACKR2,ENPP2,SLC8B1,SLIT2,IL17RC,PLXNA4,SEMA5A,HSD3B7,F2RL1,DPYSL2,ACKR4,NFIB,ZNF580,STX4,SAA1	up_VSAP_EC
GO:0023056	0.135	0.918	15	462	positive regulation of signaling	BP	1	LEP,DLL1,F3,MLLT11,LMCD1,PLAGL2,GREM1,FAM53B,CLEC16A,CYLD,BVES,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0030900	0.135	0.92	14	101	forebrain development	BP	1	FGF13,BMP4,FGFR2,ATRX,TMEM108,NRP1,SLITRK5,FRS2,APP,PSEN1,CHD7,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:1902115	0.135	0.928	10	77	regulation of organelle assembly	BP	1	PLK2,MEF2C,EDN1,RALB,CNOT6,PROX1,SH3GLB1,SENP6,PAN3,FSCN1	up_VCAV_EC
GO:0009755	0.135	0.935	8	52	hormone-mediated signaling pathway	BP	1	LBH,SKP2,BMP4,MED14,LATS2,AR,CREBRF,PARK7	up_ACOR_VSMC
GO:0048704	0.135	0.942	6	46	embryonic skeletal system morphogenesis	BP	1	HOXB7,MEF2C,HOXB8,MDFI,HOXB5,ZEB1	up_VCAV_EC
GO:0007204	0.135	0.947	5	46	positive regulation of cytosolic calcium ion	BP	1	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0010675	0.135	0.947	5	46	regulation of cellular carbohydrate metabolic	BP	1	ENPP1,PGAM1,SESN2,SLC45A3,PTPN2	down_VSAP_EC
GO:0010927	0.135	0.949	5	28	cellular component assembly involved in	BP	1	ACTN2,NEBL,DAG1,EDN1,MYOZ2	up_ACOR_VSMC
GO:2000113	0.135	0.954	4	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC

GO:0046425	0.135	0.954	4	39	regulation of JAK-STAT cascade	BP	1	DCN,BGN,ASPN,ARL2BP	down_VCAV_EC
GO:0008306	0.135	0.956	4	21	associative learning	BP	1	HRH1,LRRN4,APP,CLN8	up_ACOR_VSMC
GO:0035637	0.135	0.956	4	21	multicellular organismal signaling	BP	1	KCNE3,GJA1,JUP,JAM3	up_ACOR_VSMC
GO:0050729	0.135	0.955	4	25	positive regulation of inflammatory response	BP	1	GBP5,TLR4,TLR3,PTGS2	up_VCAV_EC
GO:0070373	0.135	0.955	4	26	negative regulation of ERK1 and ERK2 cascade	BP	1	TNIP1,ATF3,RAPGEF1,TLR4	up_VCAV_EC
GO:0090049	0.135	0.956	4	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	ABL1,HDAC7,TBXA2R,HMOX1	up_VSAP_EC
GO:0035265	0.135	0.962	3	54	organ growth	BP	1	LEP,DLL1,ACACB	up_AFEM_EC
GO:0009790	0.135	0.963	3	335	embryo development	BP	1	TBX5,HOXA3,HOXA1	up_APUL_EC
GO:0009100	0.135	0.974	2	139	glycoprotein metabolic process	BP	1	SULF1,CSGALNACT1	down_ACOR_EC
GO:0045070	0.135	0.978	2	8	positive regulation of viral genome replication	BP	1	RAD23A,PPIH	down_ACOR_VSMC
GO:0044381	0.135	0.976	2	13	glucose import in response to insulin	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0048854	0.135	0.976	2	13	brain morphogenesis	BP	1	CDH2,FOXO3	down_VCAV_EC
GO:0043457	0.135	0.976	2	11	regulation of cellular respiration	BP	1	HIF1A,BNIP3	down_VSAP_EC
GO:0010712	0.135	0.978	2	7	regulation of collagen metabolic process	BP	1	BMP4,MFAP4	up_ACOR_VSMC
GO:0014911	0.135	0.979	2	6	positive regulation of smooth muscle cell	BP	1	SEMA6D,DOCK5	up_ACOR_VSMC
GO:1901213	0.135	0.978	2	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GATA5,BMP4	up_ACOR_VSMC
GO:0009410	0.135	0.974	2	27	response to xenobiotic stimulus	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0045445	0.135	0.974	2	27	myoblast differentiation	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0045682	0.135	0.974	2	27	regulation of epidermis development	BP	1	HOXA7,DLL1	up_AFEM_EC
GO:2000737	0.135	0.978	2	7	negative regulation of stem cell differentiation	BP	1	ZFP36L2,LBH	up_VSAP_EC
GO:0008625	0.135	0.991	1	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	STX4	down_ACOR_EC
GO:0071804	0.135	0.991	1	31	cellular potassium ion transport	BP	1	NEDD4	down_ACOR_EC
GO:0071805	0.135	0.991	1	31	potassium ion transmembrane transport	BP	1	NEDD4	down_ACOR_EC
GO:2000286	0.135	0.995	1	2	receptor internalization involved in canonical Wnt signaling pathway	BP	1	CAV1	down_ACOR_VSMC
GO:0072429	0.135	0.993	1	3	response to intra-S DNA damage checkpoint	BP	1	FBH1	down_VCAV_EC
GO:1901298	0.135	0.994	1	3	regulation of hydrogen peroxide-mediated	BP	1	PARK7	down_VCAV_EC
GO:1901299	0.135	0.994	1	3	negative regulation of hydrogen peroxide-mediated programmed	BP	1	PARK7	down_VCAV_EC
GO:0001955	0.135	0.994	1	3	blood vessel maturation	BP	1	RECK	down_VCAV_EC
GO:0045861	0.135	0.991	1	71	negative regulation of proteolysis	BP	1	CST3	down_VPOR_EC
GO:0071560	0.135	0.991	1	72	cellular response to transforming growth	BP	1	CITED2	down_VPOR_EC
GO:0045892	0.135	0.994	1	328	negative regulation of transcription, DNA-	BP	1	MOSPD1	down_VFEM_EC
GO:1902679	0.135	0.994	1	329	negative regulation of RNA biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:1903507	0.135	0.994	1	329	negative regulation of nucleic acid-templated	BP	1	MOSPD1	down_VFEM_EC
GO:0001771	0.135	0.995	1	2	immunological synapse formation	BP	1	MSN	down_VSAP_EC
GO:0003323	0.135	0.992	1	6	type B pancreatic cell development	BP	1	DLL1	up_AFEM_EC
GO:0003413	0.135	0.992	1	6	chondrocyte differentiation involved in endochondral bone	BP	1	AXIN2	up_AFEM_EC

GO:0010640	0.135	0.992	1	6	regulation of platelet-derived growth factor receptor signaling	BP	1	F3	up_AFEM_EC
GO:0021697	0.135	0.992	1	6	cerebellar cortex formation	BP	1	DLL1	up_AFEM_EC
GO:0030852	0.135	0.992	1	6	regulation of granulocyte differentiation	BP	1	EVI2B	up_AFEM_EC
GO:0032094	0.135	0.992	1	6	response to food	BP	1	LEP	up_AFEM_EC
GO:0035883	0.135	0.992	1	6	enteroendocrine cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0045981	0.135	0.992	1	6	positive regulation of nucleotide metabolic	BP	1	PPARGC1A	up_AFEM_EC
GO:0050909	0.135	0.992	1	6	sensory perception of taste	BP	1	REEP2	up_AFEM_EC
GO:0051447	0.135	0.992	1	6	negative regulation of meiotic cell cycle	BP	1	OVOL1	up_AFEM_EC
GO:0060676	0.135	0.992	1	6	ureteric bud formation	BP	1	GREM1	up_AFEM_EC
GO:0003309	0.135	0.992	1	6	type B pancreatic cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0070168	0.135	0.992	1	6	negative regulation of biomineral tissue	BP	1	GREM1	up_AFEM_EC
GO:0071549	0.135	0.992	1	6	cellular response to dexamethasone stimulus	BP	1	NR3C1	up_AFEM_EC
GO:0095500	0.135	0.992	1	6	acetylcholine receptor signaling pathway	BP	1	CHRM2	up_AFEM_EC
GO:0098869	0.135	0.992	1	6	cellular oxidant detoxification	BP	1	SOD1	up_AFEM_EC
GO:1900544	0.135	0.992	1	6	positive regulation of purine nucleotide	BP	1	PPARGC1A	up_AFEM_EC
GO:1903831	0.135	0.992	1	6	signal transduction involved in cellular response to ammonium	BP	1	CHRM2	up_AFEM_EC
GO:1904385	0.135	0.992	1	6	cellular response to angiotensin	BP	1	CAMK2A	up_AFEM_EC
GO:1905144	0.135	0.992	1	6	response to acetylcholine	BP	1	CHRM2	up_AFEM_EC
GO:1905145	0.135	0.992	1	6	cellular response to acetylcholine	BP	1	CHRM2	up_AFEM_EC
GO:1990000	0.135	0.992	1	6	amyloid fibril formation	BP	1	CRYAB	up_AFEM_EC
GO:1990776	0.135	0.992	1	6	response to angiotensin	BP	1	CAMK2A	up_AFEM_EC
GO:0098542	0.135	0.991	1	100	defense response to other organism	BP	1	TLR2	up_AFEM_VSMC
GO:0009306	0.135	0.992	1	127	protein secretion	BP	1	ARG2	up_AORT_VSMC
GO:0060759	0.135	0.991	1	37	regulation of response to cytokine stimulus	BP	1	NR1H4	up_APUL_EC
GO:1902904	0.135	0.991	1	38	negative regulation of supramolecular fiber	BP	1	TUBB4A	up_APUL_EC
GO:0008285	0.135	0.992	1	201	negative regulation of cell proliferation	BP	1	TBX5	up_APUL_VSMC
GO:0050801	0.135	0.992	1	200	ion homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0001558	0.135	0.991	1	101	regulation of cell growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0006790	0.135	0.992	1	99	sulfur compound metabolic process	BP	1	ENSCAFG00000028814	up_VCAV_VSMC
GO:0030879	0.135	0.991	1	34	mammary gland development	BP	1	HOXA9	up_VFEM_EC
GO:0006575	0.135	0.991	1	53	cellular modified amino acid metabolic process	BP	1	GATM	up_VFEM_VSMC
GO:0007259	0.135	0.991	1	42	JAK-STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:0030073	0.135	0.991	1	42	insulin secretion	BP	1	NR1H4	up_VPUL_EC
GO:0003018	0.135	0.991	1	42	vascular process in circulatory system	BP	1	HTR7	up_VPUL_EC
GO:0051048	0.135	0.991	1	42	negative regulation of secretion	BP	1	NR1H4	up_VPUL_EC
GO:0051592	0.135	0.991	1	33	response to calcium ion	BP	1	CAV1	up_VSAP_VSMC
GO:0021987	0.135	0.991	1	37	cerebral cortex development	BP	1	EMX2	up_VSAP_VSMC
GO:0032675	0.135	0.991	1	34	regulation of interleukin-6 production	BP	1	TLR2	up_VSAP_VSMC
GO:0042471	0.135	0.991	1	34	ear morphogenesis	BP	1	SALL1	up_VSAP_VSMC

GO:0048645	0.135	0.991	1	33	animal organ formation	BP	1	HOXA11	up_VSAP_VSMC
GO:0072078	0.135	0.991	1	33	nephron tubule morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:1900044	0.135230785	0.9923	1	5	regulation of protein K63-linked ubiquitination	BP	1	NOD2	up_ACOR_EC
GO:0021885	0.135468885	0.97434	2	24	forebrain cell migration	BP	1	DIXDC1,NRP1	up_ACOR_EC
GO:0032609	0.135565974	0.97425	2	25	interferon-gamma production	BP	1	NR1H4,FZD5	up_ACOR_EC
GO:1901564	0.135673611	0.89627	61	2053	organonitrogen compound metabolic process	BP	1	C7,NR1H4,BRSK1,PLCL1,PKIB,THNSL2,SOX9,NMNAT2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,IFI6,DUSP26,NOD2,ENSCAFG00000028814,SMAD6,B3GNT7,KLHL25,ZMYND8,NIT2,PAK3,GUCY1B1,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,LRRC15,KLHDC8B,PIGS,LRP4,SH3RF3,LRRC4,CLU,ALDOC,CHMP4B,TP53INP2,RARRES2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,HM13,PRKCD,PM20D1,PYGO2,DBNDD2,CCNYL1	up_ACOR_EC
GO:0031325	0.136	0.888	97	914	positive regulation of cellular metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PPARGC1B,PLEKHF1,IL6R,CRADD,HOXD3,CDH1,FGF7,ABL1,EMP2,DLL1,OSR1,MAP3K5,PDGFD,KLF15,C1QTNF2,ZBTB16,RARG,CCBE1,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,DDR2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,EEF2,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,PHF1,NPAS2,FBXO7,RNF166,RPUSD4,CDK9,PRMT2,PIP4K2B,OSBPL7,ZFP36L2,RAF1,TAF8,NFIB,ABHD14B,CYBA,ZNF205,NCOA2,SMARCA2,EIF3D,ACVRL1,UBQLN2,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0008283	0.136	0.899	39	545	cell proliferation	BP	1	ARHGEF2,VEGFA,SULF1,ETV6,SPARC,PTPN14,JCAD,HOOK3,ILK,TGFBR1,PTGS2,MSN,HIF1A,ZPR1,PTPN2,ESM1,ADAM17,SKAP2,CNOT7,MAGED1,CTNNB1,TFRC,APOE,LYN,STRAP,PDS5B,TAX1BP3,SDC4,REST,ENSCAFG00000017326,PRMT1,DISC1,INHBA,NR4A1,BTK,SIX4,CDKN1A,SPINK2,MARCKSL1	down_VSAP_EC
GO:0001934	0.136	0.903	32	274	positive regulation of protein phosphorylation	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,IL6R,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,PLPP3,CAMKK2,TNKS1BP1,F2RL1,DDR2,TRAF7,SASH1,MYD88,LRP4,CDK9,RAF1,ACVRL1,FLOT1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0002009	0.136	0.911	20	177	morphogenesis of an epithelium	BP	1	HOXB7,PODXL,MEF2C,DLL4,GATA3,EDN1,NTN4,MTSS1,MTOR,BMP2,HHEX,PROX1,BTBD7,EXOC5,TIMELESS,JAG1,BCL10,HIF1A,ALDH1A3,LUZP1	up_VCAV_EC
GO:1903827	0.136	0.918	14	164	regulation of cellular protein localization	BP	1	PLK3,PTPN14,PTPN11,SESN2,MYO1C,MSN,KIF5B,IWS1,ZPR1,CTNNB1,GSK3B,SH3GLB1,TAX1BP3,CDKN1A	down_VSAP_EC
GO:0007283	0.136	0.925	11	91	spermatogenesis	BP	1	NDC1,TRIP13,POC1A,HIST1H1A,HMGB2,SGPL1,ASPM,HOXA9,GLI1,H2AFX,TTLL1	down_ACOR_VSMC
GO:0001763	0.136	0.925	11	78	morphogenesis of a branching structure	BP	1	BMP4,FGFR2,SPINT1,CLSTN1,NRP1,NPNT,SPINT2,TBX20,FRS2,DAG1,EDN1	up_ACOR_VSMC
GO:0006887	0.136	0.924	11	99	exocytosis	BP	1	KIT,EXOC3L2,RAB11A,RAB27A,EXOC6,SNAP23,SCAMP1,RSC1A1,EXOC5,FES,STX11	up_VCAV_EC
GO:0048863	0.136	0.928	10	70	stem cell differentiation	BP	1	LBH,HTR2B,BMP4,FGFR2,CITED2,NRP1,GPM6A,CHD2,TBX5,EDN1	up_ACOR_VSMC
GO:0033157	0.136	0.933	8	82	regulation of intracellular protein transport	BP	1	PLK3,PTPN14,PTPN11,MYO1C,IWS1,ZPR1,GSK3B,CDKN1A	down_VSAP_EC
GO:0071310	0.136	0.934	8	634	cellular response to organic substance	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0010769	0.136	0.936	7	69	regulation of cell morphogenesis involved	BP	1	SIPA1L1,IFRD1,TNIK,UST,ENSCAFG00000002015,NRP1,YWHAH	down_VSAP_EC
GO:1905037	0.136	0.937	7	47	autophagosome organization	BP	1	FEZ1,TP53INP1,GABARAPL1,PSEN1,PIK3C3,ATG16L2,FEZ2	up_ACOR_VSMC
GO:0030155	0.136	0.936	7	180	regulation of cell adhesion	BP	1	LEP,HOXA7,DLL1,GPAM,GREM1,CYLD,KANK1	up_AFEM_EC
GO:0030010	0.136	0.942	6	41	establishment of cell polarity	BP	1	FSCN1,ZW10,CENPA,SLC29A1,NDC80,AMOTL1	down_ACOR_VSMC

GO:0002042	0.136	0.948	5	29	cell migration involved in sprouting angiogenesis	BP	1	SLIT2,ABL1,HDAC7,TBXA2R,HMOX1	up_VSAP_EC
GO:0051899	0.136	0.955	4	22	membrane depolarization	BP	1	TPC3,GJA1,PTPN3,PARK7	up_ACOR_VSMC
GO:0000288	0.136	0.955	4	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	CNOT6,PAN3,CNOT7,DCP2	up_VCAV_EC
GO:2000772	0.136	0.964	3	15	regulation of cellular senescence	BP	1	HMGA1,ARG2,RSL1D1	down_ACOR_VSMC
GO:0002711	0.136	0.965	3	14	positive regulation of T cell mediated immunity	BP	1	B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0035239	0.136	0.962	3	299	tube morphogenesis	BP	1	HOXA11,CAV1,SHOX2	up_VSAP_VSMC
GO:0033119	0.136	0.977	2	8	negative regulation of RNA splicing	BP	1	RNPS1,U2AF2	down_ACOR_VSMC
GO:0060628	0.136	0.977	2	8	regulation of ER to Golgi vesicle-mediated	BP	1	INSIG1,PREB	down_ACOR_VSMC
GO:0017145	0.136	0.975	2	13	stem cell division	BP	1	NUMBL,ZBTB16	down_VCAV_EC
GO:0042130	0.136	0.975	2	13	negative regulation of T cell proliferation	BP	1	PRNP,SDC4	down_VCAV_EC
GO:0070229	0.136	0.975	2	13	negative regulation of lymphocyte apoptotic	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0071242	0.136	0.976	2	11	cellular response to ammonium ion	BP	1	AGRN,GNAQ	down_VSAP_EC
GO:0002374	0.136	0.978	2	7	cytokine secretion involved in immune	BP	1	F2RL1,NOD2	up_ACOR_VSMC
GO:0034134	0.136	0.978	2	7	toll-like receptor 2 signaling pathway	BP	1	TLR1,F2RL1	up_ACOR_VSMC
GO:0045987	0.136	0.978	2	7	positive regulation of smooth muscle	BP	1	ADRA1B,NPNT	up_ACOR_VSMC
GO:0016079	0.136	0.974	2	27	synaptic vesicle exocytosis	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0014911	0.136	0.979	2	6	positive regulation of smooth muscle cell	BP	1	DOCK4,PDGFB	up_VCAV_EC
GO:0048246	0.136	0.977	2	9	macrophage chemotaxis	BP	1	EDNRB,MMP28	up_VCAV_EC
GO:0000289	0.136	0.978	2	7	nuclear-transcribed mRNA poly(A) tail shortening	BP	1	SAMD4B,TNRC6C	up_VSAP_EC
GO:0060439	0.136	0.978	2	7	trachea morphogenesis	BP	1	MAP2K2,TGFBR2	up_VSAP_EC
GO:0070723	0.136	0.978	2	7	response to cholesterol	BP	1	OSBPL7,TGFBR2	up_VSAP_EC
GO:1900746	0.136	0.978	2	7	regulation of vascular endothelial growth factor	BP	1	DLL1,CCBE1	up_VSAP_EC
GO:1902547	0.136	0.978	2	7	regulation of cellular response to vascular endothelial growth factor	BP	1	DLL1,CCBE1	up_VSAP_EC
GO:0032717	0.136	0.978	2	7	negative regulation of interleukin-8 production	BP	1	ANXA4,MAPKBP1	up_VSAP_EC
GO:0034377	0.136	0.978	2	7	plasma lipoprotein particle assembly	BP	1	LCAT,SOAT1	up_VSAP_EC
GO:0042554	0.136	0.978	2	7	superoxide anion generation	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0065005	0.136	0.978	2	7	protein-lipid complex assembly	BP	1	LCAT,SOAT1	up_VSAP_EC
GO:0001678	0.136	0.991	1	29	cellular glucose homeostasis	BP	1	STX4	down_ACOR_EC
GO:0072665	0.136	0.991	1	25	protein localization to vacuole	BP	1	NEDD4	down_ACOR_EC
GO:0031623	0.136	0.991	1	31	receptor internalization	BP	1	NEDD4	down_ACOR_EC
GO:0042776	0.136	0.995	1	2	mitochondrial ATP synthesis coupled proton	BP	1	CYC1	down_ACOR_VSMC
GO:0010646	0.136	1	1	945	regulation of cell communication	BP	1	GATA5	down_AFEM_VSMC
GO:0002265	0.136	0.993	1	3	astrocyte activation involved in immune	BP	1	LRP1	down_VCAV_EC
GO:0021631	0.136	0.993	1	3	optic nerve morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0030258	0.136	0.991	1	71	lipid modification	BP	1	GBGT1	down_VPOR_EC
GO:0007267	0.136	0.993	1	332	cell-cell signaling	BP	1	PLCL1	down_VFEM_EC
GO:0097709	0.136	0.995	1	2	connective tissue replacement	BP	1	HIF1A	down_VSAP_EC
GO:0071786	0.136	0.992	1	6	endoplasmic reticulum tubular network	BP	1	REEP2	up_AFEM_EC
GO:1900027	0.136	0.992	1	6	regulation of ruffle assembly	BP	1	KANK1	up_AFEM_EC

GO:0046006	0.136	0.992	1	6	regulation of activated T cell proliferation	BP	1	GPAM	up_AFEM_EC
GO:0003161	0.136	0.992	1	6	cardiac conduction system development	BP	1	BVES	up_AFEM_EC
GO:0060394	0.136	0.992	1	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	GREM1	up_AFEM_EC
GO:1905523	0.136	0.992	1	6	positive regulation of macrophage migration	BP	1	CMKLR1	up_AFEM_EC
GO:0008645	0.136	0.991	1	37	hexose transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0015749	0.136	0.991	1	37	monosaccharide transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0034219	0.136	0.991	1	37	carbohydrate transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0010975	0.136	0.991	1	103	regulation of neuron projection development	BP	1	LIMK1	up_VCAV_VSMC
GO:0002548	0.136	0.991	1	17	monocyte chemotaxis	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0030521	0.136	0.991	1	19	androgen receptor signaling pathway	BP	1	RNF6	up_VPOR_EC
GO:0043583	0.136	0.991	1	59	ear development	BP	1	EYA1	up_VFEM_VSMC
GO:0008064	0.136	0.991	1	72	regulation of actin polymerization or	BP	1	SLIT2	up_VPUL_VSMC
GO:0030832	0.136	0.991	1	72	regulation of actin filament length	BP	1	SLIT2	up_VPUL_VSMC
GO:0006629	0.136220339	0.91826	14	382	lipid metabolic process	BP	1	NR1H4,PLCL1,THNSL2,ENSCAFG00000004331,CCDC3,PLCE1,PTGDS,CFI,CHPT1,PIGS,RARRES2,AGPAT2,PRKCD,PM20D1	up_ACOR_EC
GO:0035306	0.136220716	0.97411	2	24	positive regulation of dephosphorylation	BP	1	DUSP26,PRKCD	up_ACOR_EC
GO:0071702	0.136531618	0.90823	23	687	organic substance transport	BP	1	SH3TC2,CA4,NR1H4,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,NOD2,PLS1,CFI,PTGER4,PREB,SLC25A42,MAVS,CHMP4B,RARRES2,VPS16,ABCB9,AZIN2,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0002062	0.136547384	0.96126	3	48	chondrocyte differentiation	BP	1	SOX9,PTH1R,EFEMP1	up_ACOR_EC
GO:0033209	0.136605931	0.974	2	24	tumor necrosis factor-mediated signaling	BP	1	NR1H4,CCDC3	up_ACOR_EC
GO:0009893	0.137	0.886	105	995	positive regulation of metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PTGFR,PPARGC1B,PLEKHF1,IL6R,CRADD,HOXD3,CDH1,SLC6A4,FGF7,ABL1,EBF2,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,KLF15,C1QTNF2,ZBTB16,RARG,CCBE1,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,DDR2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,ZC3H10,CIZ1,EEF2,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,PHF1,NPAS2,PRKAB1,FBXO7,RNF166,RPUSD4,CDK9,PRMT2,PIP4K2B,OSBPL7,ZFP36L2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,CYBA,ZNF205,NCOA2,SMARCA2,EIF3D,ACVRL1,UBQLN2,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,MAP2K2,TGFBR2,CITED2,BAG4,JCHAIN,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0051129	0.137	0.916	15	221	negative regulation of cellular component organization	BP	1	SLC35F6,PRNP,LMO4,CLIP3,CLSTN1,PRMT6,LRPAP1,THY1,TLX2,CLEC16A,PRKCSH,PLEKHH2,EVI5L,PACSIN3,RGMA	down_VCAV_EC
GO:0045785	0.137	0.919	14	107	positive regulation of cell adhesion	BP	1	CD274,ABL1,EMP2,ZBTB16,TFE3,ECM2,CD83,PNP,STX4,FLOT1,NCK1,TGFBR2,CITED2,BAG4	up_VSAP_EC
GO:0016482	0.137	0.933	8	63	cytosolic transport	BP	1	HOOK3,RAB6A,SNX2,GCC2,VPS54,DNAJC13,LMTK2,DOP1B	up_VCAV_EC
GO:0034250	0.137	0.938	7	45	positive regulation of cellular amide metabolic	BP	1	PRR16,PYM1,EEF2,LARP6,RPUSD4,EIF3D,NCK1	up_VSAP_EC
GO:0032869	0.137	0.941	6	57	cellular response to insulin stimulus	BP	1	NR1H4,ENPP1,PTPN11,TRIB3,MYO1C,PTPN2	down_VSAP_EC
GO:0007188	0.137	0.942	6	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	CALCRL,EDN1,ABCA1,AKAP12,GRM8,RAPGEF2	up_VCAV_EC
GO:1903555	0.137	0.942	6	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	CD274,C5AR2,PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC
GO:0060041	0.137	0.953	4	41	retina development in camera-type eye	BP	1	PDGFRB,THY1,IRX5,THRB	down_VCAV_EC

GO:0001947	0.137	0.955	4	21	heart looping	BP	1	GJA1,CITED2,TBX20,PSEN1	up_ACOR_VSMC
GO:0061371	0.137	0.955	4	21	determination of heart left/right asymmetry	BP	1	GJA1,CITED2,TBX20,PSEN1	up_ACOR_VSMC
GO:0044249	0.137	0.965	4	1851	cellular biosynthetic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0045005	0.137	0.955	4	21	DNA-dependent DNA replication maintenance	BP	1	THOC1,ETAA1,BLM,ATRX	up_VCAV_EC
GO:0072595	0.137	0.964	3	14	maintenance of protein localization in organelle	BP	1	OS9,SUN1,PARK7	up_ACOR_VSMC
GO:0048699	0.137	0.962	3	371	generation of neurons	BP	1	FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1905209	0.137	0.975	2	13	positive regulation of cardiocyte differentiation	BP	1	SEMA3C,GREM1	down_VCAV_EC
GO:0006536	0.137	0.976	2	10	glutamate metabolic process	BP	1	NR1H4,ALDH18A1	down_VSAP_EC
GO:0010033	0.137	0.979	2	772	response to organic substance	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0071621	0.137	0.974	2	27	granulocyte chemotaxis	BP	1	CMKLR1,CCL5	up_AFEM_EC
GO:0044089	0.137	0.974	2	170	positive regulation of cellular component	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0021511	0.137	0.978	2	7	spinal cord patterning	BP	1	RELN,DLL4	up_VCAV_EC
GO:0003009	0.137	0.976	2	9	skeletal muscle contraction	BP	1	KCNJ2,ATP2A1	up_VCAV_EC
GO:0071363	0.137	0.974	2	188	cellular response to growth factor stimulus	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0001938	0.137	0.991	1	34	positive regulation of endothelial cell	BP	1	ACVRL1	down_ACOR_EC
GO:0002377	0.137	0.991	1	26	immunoglobulin production	BP	1	STX4	down_ACOR_EC
GO:0070665	0.137	0.991	1	31	positive regulation of leukocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0014707	0.137	0.995	1	2	branchiomeric skeletal muscle development	BP	1	MSC	down_ACOR_VSMC
GO:1900154	0.137	0.995	1	2	regulation of bone trabecula formation	BP	1	GREM1	down_ACOR_VSMC
GO:1900155	0.137	0.995	1	2	negative regulation of bone trabecula formation	BP	1	GREM1	down_ACOR_VSMC
GO:0060579	0.137	0.993	1	3	ventral spinal cord interneuron fate	BP	1	GLI3	down_VCAV_EC
GO:0060581	0.137	0.993	1	3	cell fate commitment involved in pattern	BP	1	GLI3	down_VCAV_EC
GO:0060594	0.137	0.993	1	3	mammary gland specification	BP	1	GLI3	down_VCAV_EC
GO:0044340	0.137	0.995	1	2	canonical Wnt signaling pathway involved in regulation of cell	BP	1	CTNNB1	down_VSAP_EC
GO:2001280	0.137	0.995	1	2	positive regulation of unsaturated fatty acid	BP	1	PTGS2	down_VSAP_EC
GO:0002791	0.137	0.991	1	104	regulation of peptide secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0042692	0.137	0.991	1	105	muscle cell differentiation	BP	1	BEND2	up_AFEM_VSMC
GO:0044839	0.137	0.991	1	61	cell cycle G2/M phase transition	BP	1	TAOK1	up_AORT_EC
GO:0060562	0.137	0.991	1	120	epithelial tube morphogenesis	BP	1	ESR1	up_AORT_VSMC
GO:0090130	0.137	0.991	1	121	tissue migration	BP	1	WNT7A	up_AORT_VSMC
GO:0030282	0.137	0.991	1	37	bone mineralization	BP	1	HOXA3	up_APUL_EC
GO:0045667	0.137	0.991	1	38	regulation of osteoblast differentiation	BP	1	NPNT	up_APUL_EC
GO:0003158	0.137	0.991	1	38	endothelium development	BP	1	ARHGEF26	up_APUL_EC
GO:0048729	0.137	0.992	1	209	tissue morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0001973	0.137	0.995	1	2	adenosine receptor signaling pathway	BP	1	ACPP	up_VCAV_EC
GO:0051316	0.137	0.995	1	2	attachment of spindle microtubules to kinetochore involved in meiotic chromosome	BP	1	CENPC	up_VCAV_EC
GO:2000609	0.137	0.995	1	2	regulation of thyroid hormone generation	BP	1	GATA3	up_VCAV_EC
GO:2000611	0.137	0.995	1	2	positive regulation of thyroid hormone	BP	1	GATA3	up_VCAV_EC

GO:0035588	0.137	0.995	1	2	G protein-coupled purinergic receptor	BP	1	ACPP	up_VCAV_EC
GO:0035726	0.137	0.995	1	2	common myeloid progenitor cell	BP	1	ITPKB	up_VCAV_EC
GO:1903320	0.137	0.991	1	102	regulation of protein modification by small protein conjugation or	BP	1	LIMK1	up_VCAV_VSMC
GO:0048483	0.137	0.991	1	19	autonomic nervous system development	BP	1	SEMA3A	up_VPOR_EC
GO:1901215	0.137	0.991	1	57	negative regulation of neuron death	BP	1	CHL1	up_VPOR_VSMC
GO:0007179	0.137	0.991	1	57	transforming growth factor beta receptor	BP	1	BAMBI	up_VPOR_VSMC
GO:0044242	0.137	0.991	1	57	cellular lipid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001952	0.137	0.991	1	34	regulation of cell-matrix adhesion	BP	1	HOXA7	up_VFEM_EC
GO:0045580	0.137	0.991	1	35	regulation of T cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0072329	0.137	0.991	1	34	monocarboxylic acid catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:2001236	0.137	0.991	1	59	regulation of extrinsic apoptotic signaling	BP	1	EYA1	up_VFEM_VSMC
GO:0032271	0.137	0.991	1	73	regulation of protein polymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0048511	0.137	0.991	1	72	rhythmic process	BP	1	SLIT2	up_VPUL_VSMC
GO:1903321	0.137	0.991	1	33	negative regulation of protein modification by small protein conjugation	BP	1	CAV1	up_VSAP_VSMC
GO:0045638	0.137	0.991	1	33	negative regulation of myeloid cell	BP	1	HOXA9	up_VSAP_VSMC
GO:0090101	0.137	0.991	1	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0021537	0.137014108	0.95193	4	73	telencephalon development	BP	1	AQP1,DIXDC1,DCLK2,NRP1	up_ACOR_EC
GO:0003231	0.137094356	0.96104	3	48	cardiac ventricle development	BP	1	SMAD6,FOXC2,TBX5	up_ACOR_EC
GO:0042325	0.138	0.894	52	463	regulation of phosphorylation	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,LATS2,PDE5A,AR,SASH1,LMO4,FGF18,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,LRRC4,PRKAG3,DDIT4,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0046649	0.138	0.91	20	162	lymphocyte activation	BP	1	CD274,TBC1D10C,ABL1,DLL1,ZBTB16,TOX,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,PPP3CB,NCK1,TGFBR2	up_VSAP_EC
GO:0008219	0.138	0.911	19	611	cell death	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,THRB,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,AXIN2,PPARGC1A,CCL5,FAP,DMPK	up_AFEM_EC
GO:0051091	0.138	0.922	12	87	positive regulation of DNA-binding transcription factor activity	BP	1	TLR3,PPARGC1A,AR,JMY,APP,JUP,DDR2,EDN1,NOD2,ARID5B,PARK7,IL18R1	up_ACOR_VSMC
GO:0014706	0.138	0.925	10	112	striated muscle tissue development	BP	1	ACTN1,FLNB,IFRD1,FHL2,CTNNB1,KLF5,ATF3,NEXN,SIX4,HOMER1	down_VSAP_EC
GO:0032984	0.138	0.936	7	70	protein-containing complex disassembly	BP	1	ARHGEF2,SMARCA4,WDR1,KIF5B,BNIP3,CAPG,MID1	down_VSAP_EC
GO:0055088	0.138	0.942	6	37	lipid homeostasis	BP	1	HNF4A,LIPC,GOT1,ENSCAFG00000000071,LCAT,SOAT1	up_VSAP_EC
GO:0019933	0.138	0.947	5	32	cAMP-mediated signaling	BP	1	CALCRL,PDE4D,APLNR,ABCA1,RAPGEF2	up_VCAV_EC
GO:0009247	0.138	0.954	4	22	glycolipid biosynthetic process	BP	1	PIGN,PIGS,UGCG,PIGG	up_ACOR_VSMC
GO:0090596	0.138	0.952	4	84	sensory organ morphogenesis	BP	1	IRX5,COL8A2,DLL1,THRB	up_AFEM_EC
GO:0002090	0.138	0.964	3	14	regulation of receptor internalization	BP	1	PLCG2,ATXN2,LRPAP1	up_ACOR_VSMC
GO:0060359	0.138	0.964	3	14	response to ammonium ion	BP	1	PRKCE,AGRN,GNAQ	up_ACOR_VSMC
GO:0060445	0.138	0.964	3	13	branching involved in salivary gland	BP	1	FGFR2,NRP1,DAG1	up_ACOR_VSMC

GO:0010556	0.138	0.968	3	1137	regulation of macromolecule	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0097094	0.138	0.977	2	8	craniofacial suture morphogenesis	BP	1	INSIG1,MMP14	down_ACOR_VSMC
GO:2000515	0.138	0.977	2	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0045648	0.138	0.975	2	13	positive regulation of erythrocyte	BP	1	FOXO3,ANKRD54	down_VCAV_EC
GO:0009790	0.138	0.975	2	335	embryo development	BP	1	CITED2,TBX15	down_VPOR_EC
GO:1900026	0.138	0.975	2	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0070887	0.138	0.979	2	775	cellular response to chemical stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0034139	0.138	0.978	2	7	regulation of toll-like receptor 3 signaling	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0090335	0.138	0.978	2	7	regulation of brown fat cell differentiation	BP	1	LEP,FNDC5	up_ACOR_VSMC
GO:0045595	0.138	0.976	2	469	regulation of cell differentiation	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0010894	0.138	0.976	2	9	negative regulation of steroid biosynthetic	BP	1	BMP2,PROX1	up_VCAV_EC
GO:0035855	0.138	0.977	2	8	megakaryocyte development	BP	1	KIT,FLI1	up_VCAV_EC
GO:0045939	0.138	0.976	2	9	negative regulation of steroid metabolic process	BP	1	BMP2,PROX1	up_VCAV_EC
GO:0010647	0.138	0.976	2	460	positive regulation of cell communication	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0009725	0.138	0.974	2	188	response to hormone	BP	1	NR1H4,PTGER2	up_VPUL_EC
GO:0051493	0.138	0.973	2	188	regulation of cytoskeleton organization	BP	1	CCL24,ARHGEF2	up_VPUL_EC
GO:0019953	0.138	0.973	2	152	sexual reproduction	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0014033	0.138	0.991	1	30	neural crest cell differentiation	BP	1	NRP2	down_ACOR_EC
GO:0035282	0.138	0.991	1	30	segmentation	BP	1	NRP2	down_ACOR_EC
GO:1904888	0.138	0.991	1	31	cranial skeletal system development	BP	1	HOXA1	down_ACOR_EC
GO:0023051	0.138	1	1	954	regulation of signaling	BP	1	GATA5	down_AFEM_VSMC
GO:0061626	0.138	0.993	1	3	pharyngeal arch artery morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0071593	0.138	0.993	1	3	lymphocyte aggregation	BP	1	RAC2	down_VCAV_EC
GO:0072540	0.138	0.993	1	3	T-helper 17 cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:0071559	0.138	0.991	1	75	response to transforming growth factor beta	BP	1	CITED2	down_VPOR_EC
GO:0051241	0.138	0.993	1	336	negative regulation of multicellular organismal	BP	1	PLCL1	down_VFEM_EC
GO:0009794	0.138	0.995	1	2	regulation of mitotic cell cycle, embryonic	BP	1	CTNNB1	down_VSAP_EC
GO:0030050	0.138	0.995	1	2	vesicle transport along actin filament	BP	1	MYO1C	down_VSAP_EC
GO:0045448	0.138	0.995	1	2	mitotic cell cycle, embryonic	BP	1	CTNNB1	down_VSAP_EC
GO:0045976	0.138	0.995	1	2	negative regulation of mitotic cell cycle,	BP	1	CTNNB1	down_VSAP_EC
GO:0099515	0.138	0.995	1	2	actin filament-based transport	BP	1	MYO1C	down_VSAP_EC
GO:0150018	0.138	0.995	1	2	basal dendrite development	BP	1	NRP1	down_VSAP_EC
GO:0150019	0.138	0.995	1	2	basal dendrite morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0150020	0.138	0.995	1	2	basal dendrite arborization	BP	1	NRP1	down_VSAP_EC
GO:0019693	0.138	0.992	1	172	ribose phosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0030111	0.138	0.991	1	108	regulation of Wnt signaling pathway	BP	1	TLR2	up_AFEM_VSMC
GO:0006497	0.138	0.991	1	38	protein lipidation	BP	1	ZDHHC16	up_APUL_EC
GO:0048639	0.138	0.991	1	39	positive regulation of developmental growth	BP	1	TBX5	up_APUL_EC
GO:0071072	0.138	0.995	1	2	negative regulation of phospholipid biosynthetic	BP	1	PDGFB	up_VCAV_EC

GO:0072179	0.138	0.995	1	2	nephric duct formation	BP	1	GATA3	up_VCAV_EC
GO:0051604	0.138	0.991	1	102	protein maturation	BP	1	C6	up_VCAV_VSMC
GO:0035265	0.138	0.991	1	54	organ growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071482	0.138	0.991	1	34	cellular response to light stimulus	BP	1	MME	up_VFEM_EC
GO:0097696	0.138	0.991	1	43	STAT cascade	BP	1	FLRT3	up_VPUL_EC
GO:0010721	0.138	0.991	1	73	negative regulation of cell development	BP	1	SLIT2	up_VPUL_VSMC
GO:0051961	0.138	0.991	1	73	negative regulation of nervous system	BP	1	SLIT2	up_VPUL_VSMC
GO:0060541	0.138	0.991	1	73	respiratory system development	BP	1	TBX5	up_VPUL_VSMC
GO:0061138	0.138	0.991	1	73	morphogenesis of a branching epithelium	BP	1	SLIT2	up_VPUL_VSMC
GO:0043267	0.138182786	0.99163	1	6	negative regulation of potassium ion transport	BP	1	ACTN2	up_ACOR_EC
GO:0003208	0.138559383	0.9734	2	24	cardiac ventricle morphogenesis	BP	1	FOXC2,TBX5	up_ACOR_EC
GO:0001508	0.138561677	0.97334	2	25	action potential	BP	1	KCNB1,USP53	up_ACOR_EC
GO:0051179	0.139	0.896	48	1747	localization	BP	1	CMKLR1,TRAPPC3L,LEP,KCNC4,CRY2,VPS26C,RAB20,GAS1,ANGPT4,HOXA7,DLL1,CRYAB,KCND1,PLXNA4,GPAM,CHRM2,SLC17A5,TWIST2,MYO1D,ATP6V1B2,HCK,SLC6A6,GREM1,CAMK2A,CYLD,FXYD1,LRRC15,ICAM5,RECK,TBXA2R,REEP2,BVES,LGR6,RAB7A,AXIN2,ATP6V0B,ACACB,NIPAL1,SLC46A2,CCL5,FAP,DMPK,ADAM17,SLC43A1,CLIC4,KANK1,KXD1,ANXA11	up_AFEM_EC
GO:0051253	0.139	0.898	36	359	negative regulation of RNA metabolic process	BP	1	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,PPP3CA,TENT2,BMP2,HMG20A,HHEX,CREM,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,ELK3	up_VCAV_EC
GO:0000122	0.139	0.906	23	218	negative regulation of transcription by RNA polymerase II	BP	1	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,PROX1,HMBOX1,NCK1,TIMELESS,TCERG1,CNOT7,HMGB1,MTA2,KDM5A,ATRX,ARID5A	up_VCAV_EC
GO:0002696	0.139	0.923	11	80	positive regulation of leukocyte activation	BP	1	CD274,ZBTB16,TOX,STAT6,F2RL1,MYD88,CD83,PNP,STX4,NCK1,TGFBR2	up_VSAP_EC
GO:0031032	0.139	0.929	9	61	actomyosin structure organization	BP	1	EPB41L4A,ARHGAP28,ACTN2,NEBL,NRP1,EVL,EDN1,INPP5K,MYOZ2	up_ACOR_VSMC
GO:0034654	0.139	0.935	8	1236	nucleobase-containing compound biosynthetic	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0033673	0.139	0.935	7	84	negative regulation of kinase activity	BP	1	DCN,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1	down_VCAV_EC
GO:0007368	0.139	0.941	6	37	determination of left/right symmetry	BP	1	GJA1,CITED2,TBX20,PSEN1,PCSK6,PSKH1	up_ACOR_VSMC
GO:0006954	0.139	0.939	6	147	inflammatory response	BP	1	LEP,CD40,F3,TBXA2R,NAPEPLD,CCL5	up_AFEM_EC
GO:0071453	0.139	0.94	6	46	cellular response to oxygen levels	BP	1	CD34,MTOR,PTGS2,PMAIP1,HIF1A,HP1BP3	up_VCAV_EC
GO:0044093	0.139	0.939	6	437	positive regulation of molecular function	BP	1	HOXA3,ARHGEF2,ENSCAFG00000002015,MTDH,ABHD5,ENSCAFG00000032731	up_VPOR_EC
GO:0010558	0.139	0.952	4	392	negative regulation of macromolecule biosynthetic process	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0007612	0.139	0.952	4	33	learning	BP	1	HIF1A,UBA6,HTT,ARF4	down_VSAP_EC
GO:0051239	0.139	0.955	4	859	regulation of multicellular organismal process	BP	1	HOXC10,HOXA9,LNPEP,BPI	up_AORT_EC
GO:0045669	0.139	0.953	4	24	positive regulation of osteoblast differentiation	BP	1	MEF2C,BMP2,JAG1,FBXO5	up_VCAV_EC
GO:0051291	0.139	0.954	4	21	protein heterooligomerization	BP	1	C1QTNF2,CLDN1,HSD17B8,PCBD1	up_VSAP_EC
GO:0006766	0.139	0.963	3	16	vitamin metabolic process	BP	1	PDXP,GSTO1,ENSCAFG00000005637	down_ACOR_VSMC
GO:0008156	0.139	0.963	3	15	negative regulation of DNA replication	BP	1	SMC1A,GMNN,SMC3	down_ACOR_VSMC
GO:0007044	0.139	0.961	3	27	cell-substrate junction assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0044087	0.139	0.961	3	339	regulation of cellular component biogenesis	BP	1	TUBB4A,SLITRK5,NTRK2	up_APUL_EC

GO:0006884	0.139	0.964	3	14	cell volume homeostasis	BP	1	LRRC8D,LRRC8C,SLC12A7	up_VCAV_EC
GO:0070232	0.139	0.974	2	13	regulation of T cell apoptotic process	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0098659	0.139	0.974	2	13	inorganic cation import across plasma membrane	BP	1	PRNP,SLC39A6	down_VCAV_EC
GO:0099587	0.139	0.974	2	13	inorganic ion import across plasma membrane	BP	1	PRNP,SLC39A6	down_VCAV_EC
GO:0043243	0.139	0.975	2	11	positive regulation of protein complex	BP	1	WDR1,BNIP3	down_VSAP_EC
GO:0090322	0.139	0.977	2	7	regulation of superoxide metabolic process	BP	1	F2RL1,PARK7	up_ACOR_VSMC
GO:0002092	0.139	0.976	2	9	positive regulation of receptor internalization	BP	1	SELE,PLCG2	up_VCAV_EC
GO:0071044	0.139	0.976	2	8	histone mRNA catabolic process	BP	1	TENT2,DCP2	up_VCAV_EC
GO:0055012	0.139	0.977	2	8	ventricular cardiac muscle cell differentiation	BP	1	MEF2C,PROX1	up_VCAV_EC
GO:0070296	0.139	0.976	2	8	sarcoplasmic reticulum calcium ion transport	BP	1	PDE4D,CHD7	up_VCAV_EC
GO:0023056	0.139	0.976	2	462	positive regulation of signaling	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0034367	0.139	0.977	2	7	protein-containing complex remodeling	BP	1	LIPC,LCAT	up_VSAP_EC
GO:0034368	0.139	0.977	2	7	protein-lipid complex remodeling	BP	1	LIPC,LCAT	up_VSAP_EC
GO:0034369	0.139	0.977	2	7	plasma lipoprotein particle remodeling	BP	1	LIPC,LCAT	up_VSAP_EC
GO:0060546	0.139	0.977	2	7	negative regulation of necroptotic process	BP	1	RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0060547	0.139	0.977	2	7	negative regulation of necrotic cell death	BP	1	RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0008543	0.139	0.99	1	27	fibroblast growth factor receptor signaling	BP	1	SULF1	down_ACOR_EC
GO:0002702	0.139	0.99	1	28	positive regulation of production of molecular mediator of immune	BP	1	STX4	down_ACOR_EC
GO:0014066	0.139	0.99	1	26	regulation of phosphatidylinositol 3-	BP	1	NEDD4	down_ACOR_EC
GO:0015718	0.139	0.99	1	30	monocarboxylic acid transport	BP	1	ACSL3	down_ACOR_EC
GO:0042472	0.139	0.991	1	27	inner ear morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:1901888	0.139	0.99	1	29	regulation of cell junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0045654	0.139	0.995	1	2	positive regulation of megakaryocyte	BP	1	HMGB2	down_ACOR_VSMC
GO:0010557	0.139	0.995	1	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA5	down_VFEM_VSMC
GO:0045935	0.139	0.995	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA5	down_VFEM_VSMC
GO:0034382	0.139	0.993	1	3	chylomicron remnant clearance	BP	1	APOE	down_VSAP_EC
GO:0071830	0.139	0.993	1	3	triglyceride-rich lipoprotein particle	BP	1	APOE	down_VSAP_EC
GO:0007266	0.139	0.991	1	64	Rho protein signal transduction	BP	1	CTNNAL1	up_AORT_EC
GO:0002694	0.139	0.991	1	126	regulation of leukocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0048871	0.139	0.991	1	120	multicellular organismal homeostasis	BP	1	HOXC10	up_AORT_VSMC
GO:0048813	0.139	0.991	1	39	dendrite morphogenesis	BP	1	SLITRK5	up_APUL_EC
GO:0000395	0.139	0.995	1	2	mRNA 5'-splice site recognition	BP	1	PRPF39	up_VCAV_EC
GO:0010940	0.139	0.995	1	2	positive regulation of necrotic cell death	BP	1	RIPK1	up_VCAV_EC
GO:0051132	0.139	0.995	1	2	NK T cell activation	BP	1	ELF4	up_VCAV_EC
GO:1901652	0.139	0.991	1	105	response to peptide	BP	1	CA2	up_VCAV_VSMC
GO:0006096	0.139	0.991	1	18	glycolytic process	BP	1	FBP1	up_VPOR_EC
GO:0006165	0.139	0.991	1	18	nucleoside diphosphate phosphorylation	BP	1	FBP1	up_VPOR_EC
GO:0006757	0.139	0.991	1	18	ATP generation from ADP	BP	1	FBP1	up_VPOR_EC

GO:0042866	0.139	0.991	1	18	pyruvate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0048771	0.139	0.99	1	43	tissue remodeling	BP	1	HOXA3	up_VPUL_EC
GO:0021537	0.139	0.991	1	73	telencephalon development	BP	1	SLIT2	up_VPUL_VSMC
GO:0009953	0.139	0.99	1	34	dorsal/ventral pattern formation	BP	1	HOXA11	up_VSAP_VSMC
GO:1903169	0.139	0.99	1	34	regulation of calcium ion transmembrane transport	BP	1	STIM1	up_VSAP_VSMC
GO:0061041	0.139	0.99	1	34	regulation of wound healing	BP	1	CAV1	up_VSAP_VSMC
GO:0043588	0.139256842	0.95084	4	74	skin development	BP	1	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0048589	0.139644129	0.92986	8	188	developmental growth	BP	1	SOX9,PLS1,FOXC2,TBX5,LRP4,C23H3orf58,NRP1,PYGO2	up_ACOR_EC
GO:0051347	0.14	0.908	20	182	positive regulation of transferase activity	BP	1	IRAK1,HNRNPD,UBE2S,SLC29A1,RFC2,RFC5,RFC3,AURKB,EZH2,GREM1,MAP3K20,RFC4,NEK2,CKS2,EMP2,CLSPN,CDC20,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC
GO:0032269	0.14	0.908	20	306	negative regulation of cellular protein metabolic process	BP	1	CST3,KIRREL1,DCN,PRNP,BGN,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,PRMT6,ASPN,THY1,PARK7,ZFP36L1,CLEC16A,SPRED1,A2M,GREM1,EIF4EBP1	down_VCAV_EC
GO:0032870	0.14	0.908	20	162	cellular response to hormone stimulus	BP	1	FAM107A,PTGFR,PPARGC1B,SLIT2,GOT1,CHRM1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,CREBRF,PRMT2,ZFP36L2,NCOA2,NCK1,BGLAP,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0044262	0.14	0.92	12	89	cellular carbohydrate metabolic process	BP	1	ACACB,GOT1,INPP5E,C1QTNF2,PHKA2,PPIP5K1,PDK2,GALK1,PASK,TKFC,NCOA2,DDIT4	up_VSAP_EC
GO:0030198	0.14	0.922	11	81	extracellular matrix organization	BP	1	ABL1,CTSS,ADAMTSL4,RECK,DDR2,SULF2,LOX,ECM2,FBLN1,FLOT1,DPT	up_VSAP_EC
GO:0055085	0.14	0.924	10	284	transmembrane transport	BP	1	LEP,KCNC4,KCND1,ATP6V1B2,SLC6A6,FXYD1,ATP6V0B,SLC46A2,SLC43A1,CLIC4	up_AFEM_EC
GO:0032872	0.14	0.925	10	77	regulation of stress-activated MAPK cascade	BP	1	EPHB1,MAP3K11,TLR4,EDN1,MAP3K3,BMP2,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0051641	0.14	0.937	7	858	cellular localization	BP	1	LYN,SPG11,IPO7,ACSL3,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0098657	0.14	0.933	7	181	import into cell	BP	1	LEP,RAB20,DLL1,GREM1,ICAM5,RAB7A,ANXA11	up_AFEM_EC
GO:0006468	0.14	0.945	5	544	protein phosphorylation	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0072089	0.14	0.945	5	43	stem cell proliferation	BP	1	ARHGEF2,ETV6,HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0002824	0.14	0.946	5	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	TP53BP1,CD274,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051209	0.14	0.946	5	28	release of sequestered calcium ion into cytosol	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0051283	0.14	0.946	5	28	negative regulation of sequestering of calcium	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0062014	0.14	0.945	5	35	negative regulation of small molecule metabolic	BP	1	CDA,FAM3C,BMP2,PROX1,ENSCAFG00000010596	up_VCAV_EC
GO:0045444	0.14	0.95	4	84	fat cell differentiation	BP	1	CMKLR1,LEP,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:0019220	0.14	0.952	4	525	regulation of phosphate metabolic process	BP	1	NR1H4,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0051174	0.14	0.952	4	525	regulation of phosphorus metabolic process	BP	1	NR1H4,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0032760	0.14	0.953	4	22	positive regulation of tumor necrosis factor	BP	1	TLR4,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:1903557	0.14	0.953	4	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	TLR4,TLR3,RIPK1,ARHGEF2	up_VCAV_EC
GO:0032623	0.14	0.954	4	21	interleukin-2 production	BP	1	ABL1,HDAC7,CD83,PNP	up_VSAP_EC
GO:0043388	0.14	0.963	3	16	positive regulation of DNA binding	BP	1	HMGB1,FAM129B,HMGB2	down_ACOR_VSMC
GO:0046323	0.14	0.961	3	26	glucose import	BP	1	ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC
GO:2000401	0.14	0.964	3	13	regulation of lymphocyte migration	BP	1	APP,CCL5,WASL	up_ACOR_VSMC
GO:0060429	0.14	0.961	3	341	epithelium development	BP	1	TBX5,ARHGEF26,NPNT	up_APUL_EC
GO:0060421	0.14	0.963	3	14	positive regulation of heart growth	BP	1	MEF2C,EDN1,PROX1	up_VCAV_EC

GO:0070169	0.14	0.962	3	18	positive regulation of biomineral tissue	BP	1	MEF2C,BMP2,FBXO5	up_VCAV_EC
GO:0071364	0.14	0.963	3	14	cellular response to epidermal growth factor	BP	1	ZFP36L1,ZFP36L2,BAG4	up_VSAP_EC
GO:0002790	0.14	0.973	2	133	peptide secretion	BP	1	LYN,STX4	down_ACOR_EC
GO:0044260	0.14	1	2	2593	cellular macromolecule metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0003094	0.14	0.975	2	11	glomerular filtration	BP	1	SULF1,MYO1E	down_VSAP_EC
GO:0043114	0.14	0.977	2	7	regulation of vascular permeability	BP	1	HRH1,CLSTN1	up_ACOR_VSMC
GO:2000778	0.14	0.977	2	7	positive regulation of interleukin-6 secretion	BP	1	MBP,F2RL1	up_ACOR_VSMC
GO:0043069	0.14	0.974	2	262	negative regulation of programmed cell death	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0007264	0.14	0.973	2	164	small GTPase mediated signal transduction	BP	1	TIAM1,CDC42EP5	up_VFEM_EC
GO:0048589	0.14	0.973	2	188	developmental growth	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0001504	0.14	0.977	2	7	neurotransmitter uptake	BP	1	SLC6A4,FLOT1	up_VSAP_EC
GO:0015682	0.14	0.977	2	7	ferric iron transport	BP	1	RAB11B,STEAP3	up_VSAP_EC
GO:0072512	0.14	0.977	2	7	trivalent inorganic cation transport	BP	1	RAB11B,STEAP3	up_VSAP_EC
GO:0033194	0.14	0.977	2	7	response to hydroperoxide	BP	1	MGST1,STX4	up_VSAP_EC
GO:0032504	0.14	0.973	2	152	multicellular organism reproduction	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0048609	0.14	0.973	2	152	multicellular organismal reproductive process	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0097581	0.14	0.99	1	26	lamellipodium organization	BP	1	PDPN	down_ACOR_EC
GO:0030216	0.14	0.99	1	29	keratinocyte differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0034104	0.14	0.995	1	2	negative regulation of tissue remodeling	BP	1	GREM1	down_ACOR_VSMC
GO:0019800	0.14	0.993	1	3	peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	BP	1	DCN	down_VCAV_EC
GO:0002675	0.14	0.993	1	3	positive regulation of acute inflammatory	BP	1	PARK7	down_VCAV_EC
GO:2000380	0.14	0.993	1	3	regulation of mesoderm development	BP	1	BMPR1A	down_VCAV_EC
GO:0048014	0.14	0.993	1	3	Tie signaling pathway	BP	1	ANGPT1	down_VCAV_EC
GO:0061635	0.14	0.993	1	3	regulation of protein complex stability	BP	1	NCLN	down_VCAV_EC
GO:1902498	0.14	0.993	1	3	regulation of protein autoubiquitination	BP	1	SASH1	down_VCAV_EC
GO:2000191	0.14	0.993	1	3	regulation of fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:0060348	0.14	0.99	1	78	bone development	BP	1	CITED2	down_VPOR_EC
GO:0000414	0.14	0.995	1	2	regulation of histone H3-K36 methylation	BP	1	IWS1	down_VSAP_EC
GO:0003340	0.14	0.995	1	2	negative regulation of mesenchymal to epithelial transition involved in metanephros	BP	1	CTNNB1	down_VSAP_EC
GO:0019240	0.14	0.995	1	2	citrulline biosynthetic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0045741	0.14	0.995	1	2	positive regulation of epidermal growth factor-activated receptor activity	BP	1	ADAM17	down_VSAP_EC
GO:0097198	0.14	0.995	1	2	histone H3-K36 trimethylation	BP	1	IWS1	down_VSAP_EC
GO:0001525	0.14	0.991	1	173	angiogenesis	BP	1	TGFBI	down_VSAP_VSMC
GO:0006163	0.14	0.991	1	174	purine nucleotide metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:1904951	0.14	0.991	1	108	positive regulation of establishment of protein localization	BP	1	TLR2	up_AFEM_VSMC
GO:0048738	0.14	0.99	1	64	cardiac muscle tissue development	BP	1	SGCD	up_AORT_EC
GO:0009617	0.14	0.991	1	133	response to bacterium	BP	1	ARG2	up_AORT_VSMC

GO:0051896	0.14	0.99	1	39	regulation of protein kinase B signaling	BP	1	NTRK2	up_APUL_EC
GO:0009597	0.14	0.995	1	2	detection of virus	BP	1	SERINC5	up_VCAV_EC
GO:0034454	0.14	0.995	1	2	microtubule anchoring at centrosome	BP	1	HOOK3	up_VCAV_EC
GO:0042271	0.14	0.995	1	2	susceptibility to natural killer cell mediated	BP	1	NECTIN2	up_VCAV_EC
GO:0060370	0.14	0.995	1	2	susceptibility to T cell mediated cytotoxicity	BP	1	NECTIN2	up_VCAV_EC
GO:0072615	0.14	0.995	1	2	interleukin-17 secretion	BP	1	ARG2	up_VCAV_EC
GO:0007431	0.14	0.99	1	19	salivary gland development	BP	1	SEMA3A	up_VPOR_EC
GO:0070265	0.14	0.99	1	19	necrotic cell death	BP	1	ARHGEF2	up_VPOR_EC
GO:0007416	0.14	0.99	1	36	synapse assembly	BP	1	SIX1	up_VFEM_EC
GO:0002761	0.14	0.99	1	36	regulation of myeloid leukocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0055076	0.14	0.99	1	44	transition metal ion homeostasis	BP	1	NEO1	up_VPUL_EC
GO:0010975	0.140513694	0.94314	5	103	regulation of neuron projection development	BP	1	BRSK1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0022607	0.140665749	0.90014	31	969	cellular component assembly	BP	1	MYOZ2,NR1H4,TMOD1,TRPS1,KCTD12,CALY,SOX9,ARHGAP6,ATG16L2,SYNPO2,KCNB1,FZD5,SMAD6,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,PREB,LRP4,CLSTN1,CLU,CHMP4B,TP53INP2,VPS16,NRP1,ARHGEF26,PRKCD,ENSCAFG00000010493,MFAP4,TUBB4A	up_ACOR_EC
GO:0044281	0.141	0.894	43	622	small molecule metabolic process	BP	1	P4HB,ASNS,CARS,PLOD2,NR1H4,ENSCAFG00000000211,ERO1A,ENPP1,P4HA1,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,ALDH1L2,SESN2,PTGS2,CEMIP2,CHSY1,ENSCAFG00000008716,HIF1A,SLC45A3,NMNAT2,PTPN2,ALDH18A1,ENTPD4,YARS,TARS,NARS,ALDOC,PAPSS1,APOE,PLOD3,ATF3,AK5,GALE,REST,RAB11FIP1,BCAT1,KDM3A,CMPK1	down_VSAP_EC
GO:0031327	0.141	0.895	41	412	negative regulation of cellular biosynthetic process	BP	1	EDNRB,HCLS1,PDGFB,CD34,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,FAM3C,BMP2,HMG20A,HHEX,CREM,ENC1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,HMBOX1,SMARCA4,NCK1,TIMELESS,RAPGEF2,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,RAD17,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0002682	0.141	0.902	26	343	regulation of immune system process	BP	1	VEGFA,NR1H4,SERPINE1,SOCS5,FAM49B,MSN,HIF1A,PTPN2,EIF2B1,EVI2B,PVR,ADAM17,SKAP2,CNOT7,CTNNB1,TFRC,MMP28,LYN,CDC37,GBP5,SDC4,PRMT1,A2M,INHBA,BTK,CDKN1A	down_VSAP_EC
GO:0050789	0.141	0.928	16	3295	regulation of biological process	BP	1	NR1H4,TBX5,MAPK10,BPI,HOXA3,PLCL1,TUBB4A,PCSK1N,ARHGEF26,LZTS1,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,PDE1A	up_APUL_EC
GO:0042176	0.141	0.919	12	140	regulation of protein catabolic process	BP	1	PRICKLE1,PLK3,SOCS5,TRIB3,MSN,UCHL5,APOE,GSK3B,DISC1,RAD23A,TMTC3,USP14	down_VSAP_EC
GO:0043414	0.141	0.927	9	70	macromolecule methylation	BP	1	PRMT1,EZH2,FBL,THUMPD2,METTL1,PRMT5,WTAP,EMG1,MIS18A	down_ACOR_VSMC
GO:0050679	0.141	0.927	9	62	positive regulation of epithelial cell proliferation	BP	1	C5AR2,OSR2,FGF7,OSR1,STAT5A,MYC,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:0048562	0.141	0.929	8	102	embryonic organ morphogenesis	BP	1	FBN1,NAGLU,TBX15,HOXC4,GLI3,IFT57,IRX5,RDH10	down_VCAV_EC
GO:0050900	0.141	0.929	8	89	leukocyte migration	BP	1	VEGFA,SERPINE1,WDR1,MSN,CX3CL1,ADAM17,MMP28,LYN	down_VSAP_EC
GO:0034101	0.141	0.939	6	45	erythrocyte homeostasis	BP	1	HCLS1,ADGRF5,KIT,GATA3,HIF1A,TMOD3	up_VCAV_EC
GO:0045638	0.141	0.945	5	33	negative regulation of myeloid cell	BP	1	HSPA9,PRMT1,HMGB3,HOXA7,HOXA9	down_ACOR_VSMC
GO:0048864	0.141	0.945	5	29	stem cell development	BP	1	HTR2B,BMP4,CITED2,NRP1,EDN1	up_ACOR_VSMC
GO:0002792	0.141	0.946	5	29	negative regulation of peptide secretion	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1	up_VSAP_EC
GO:0050715	0.141	0.946	5	29	positive regulation of cytokine secretion	BP	1	CD274,ABL1,IL17RC,F2RL1,MAVS	up_VSAP_EC
GO:0070227	0.141	0.952	4	25	lymphocyte apoptotic process	BP	1	PRELID1,AURKB,ARG2,NOC2L	down_ACOR_VSMC
GO:0001706	0.141	0.961	3	20	endoderm formation	BP	1	CTNNB1,INHBA,COL12A1	down_VSAP_EC

GO:0043242	0.141	0.961	3	21	negative regulation of protein complex	BP	1	ARHGEF2,CAPG,MID1	down_VSAP_EC
GO:2000736	0.141	0.961	3	21	regulation of stem cell differentiation	BP	1	PRICKLE1,REST,KDM3A	down_VSAP_EC
GO:0043266	0.141	0.963	3	14	regulation of potassium ion transport	BP	1	ACTN2,KCNE3,AKAP6	up_ACOR_VSMC
GO:2001259	0.141	0.963	3	13	positive regulation of cation channel activity	BP	1	ACTN2,PLCG2,AKAP6	up_ACOR_VSMC
GO:0006913	0.141	0.972	2	124	nucleocytoplasmic transport	BP	1	IPO7,NEDD4	down_ACOR_EC
GO:0007268	0.141	0.972	2	130	chemical synaptic transmission	BP	1	SPG11,STX4	down_ACOR_EC
GO:0030099	0.141	0.972	2	133	myeloid cell differentiation	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0051169	0.141	0.972	2	124	nuclear transport	BP	1	IPO7,NEDD4	down_ACOR_EC
GO:0098660	0.141	0.972	2	141	inorganic ion transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0098916	0.141	0.972	2	130	anterograde trans-synaptic signaling	BP	1	SPG11,STX4	down_ACOR_EC
GO:0006085	0.141	0.976	2	8	acetyl-CoA biosynthetic process	BP	1	ACLY,PDHA1	down_ACOR_VSMC
GO:0006739	0.141	0.974	2	13	NADP metabolic process	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0060572	0.141	0.975	2	11	morphogenesis of an epithelial bud	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0060973	0.141	0.977	2	7	cell migration involved in heart development	BP	1	BMP4,BVES	up_ACOR_VSMC
GO:0060977	0.141	0.978	2	6	coronary vasculature morphogenesis	BP	1	SEC24B,NRP1	up_ACOR_VSMC
GO:0061323	0.141	0.977	2	7	cell proliferation involved in heart morphogenesis	BP	1	BMP4,TBX5	up_ACOR_VSMC
GO:1901881	0.141	0.977	2	7	positive regulation of protein depolymerization	BP	1	ACTN2,F2RL1	up_ACOR_VSMC
GO:0050869	0.141	0.976	2	8	negative regulation of B cell activation	BP	1	TNFAIP3,THOC1	up_VCAV_EC
GO:0071360	0.141	0.975	2	9	cellular response to exogenous dsRNA	BP	1	TMEM173,RALB	up_VCAV_EC
GO:0001963	0.141	0.977	2	7	synaptic transmission, dopaminergic	BP	1	SLC6A4,FLOT1	up_VSAP_EC
GO:0039531	0.141	0.977	2	7	regulation of viral-induced cytoplasmic pattern recognition receptor	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0010608	0.141	0.972	2	154	posttranscriptional regulation of gene	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0006355	0.141	1	1	974	regulation of transcription, DNA-	BP	1	GATA5	down_AFEM_VSMC
GO:1903506	0.141	1	1	977	regulation of nucleic acid-templated transcription	BP	1	GATA5	down_AFEM_VSMC
GO:0015031	0.141	0.995	1	510	protein transport	BP	1	SCAMP4	down_AORT_EC
GO:0042090	0.141	0.993	1	3	interleukin-12 biosynthetic process	BP	1	MAST2	down_VCAV_EC
GO:0045136	0.141	0.993	1	3	development of secondary sexual	BP	1	B4GALT1	down_VCAV_EC
GO:0010878	0.141	0.993	1	3	cholesterol storage	BP	1	SOAT1	down_VCAV_EC
GO:0021520	0.141	0.993	1	3	spinal cord motor neuron cell fate specification	BP	1	GLI3	down_VCAV_EC
GO:0045075	0.141	0.993	1	3	regulation of interleukin-12 biosynthetic process	BP	1	MAST2	down_VCAV_EC
GO:0045647	0.141	0.993	1	3	negative regulation of erythrocyte	BP	1	ZFP36L1	down_VCAV_EC
GO:0048251	0.141	0.993	1	3	elastic fiber assembly	BP	1	LOX	down_VCAV_EC
GO:0060174	0.141	0.993	1	3	limb bud formation	BP	1	SEMA3C	down_VCAV_EC
GO:0070208	0.141	0.993	1	3	protein heterotrimerization	BP	1	COL6A1	down_VCAV_EC
GO:1900122	0.141	0.993	1	3	positive regulation of receptor binding	BP	1	PLCL1	down_VCAV_EC
GO:0015031	0.141	0.995	1	510	protein transport	BP	1	JUP	down_VFEM_VSMC
GO:0014846	0.141	0.995	1	2	esophagus smooth muscle contraction	BP	1	SULF1	down_VSAP_EC
GO:0021649	0.141	0.995	1	2	vestibulocochlear nerve structural organization	BP	1	NRP1	down_VSAP_EC
GO:0061552	0.141	0.995	1	2	ganglion morphogenesis	BP	1	NRP1	down_VSAP_EC

GO:0097374	0.141	0.995	1	2	sensory neuron axon guidance	BP	1	NRP1	down_VSAP_EC
GO:1904835	0.141	0.995	1	2	dorsal root ganglion morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0086011	0.141	0.995	1	2	membrane repolarization during action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:0098903	0.141	0.995	1	2	regulation of membrane repolarization during action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:0016311	0.141	0.991	1	106	dephosphorylation	BP	1	EYA1	up_AFEM_VSMC
GO:0048514	0.141	0.992	1	214	blood vessel morphogenesis	BP	1	HOXA3	up_APUL_VSMC
GO:0001844	0.141	0.995	1	2	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	BP	1	SH3GLB1	up_VCAV_EC
GO:0051204	0.141	0.995	1	2	protein insertion into mitochondrial membrane	BP	1	SH3GLB1	up_VCAV_EC
GO:1900739	0.141	0.995	1	2	regulation of protein insertion into mitochondrial membrane involved in apoptotic	BP	1	SH3GLB1	up_VCAV_EC
GO:1900740	0.141	0.995	1	2	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic	BP	1	SH3GLB1	up_VCAV_EC
GO:0045765	0.141	0.991	1	105	regulation of angiogenesis	BP	1	C6	up_VCAV_VSMC
GO:1901880	0.141	0.99	1	19	negative regulation of protein depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0007569	0.141	0.99	1	36	cell aging	BP	1	MME	up_VFEM_EC
GO:0044272	0.141	0.99	1	35	sulfur compound biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:0010212	0.141	0.99	1	60	response to ionizing radiation	BP	1	EYA1	up_VFEM_VSMC
GO:0032273	0.141	0.99	1	44	positive regulation of protein polymerization	BP	1	CCL24	up_VPUL_EC
GO:0046474	0.141	0.99	1	44	glycerophospholipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0072089	0.141	0.99	1	43	stem cell proliferation	BP	1	ARHGEF2	up_VPUL_EC
GO:0061333	0.141	0.99	1	35	renal tubule morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:0042044	0.1410002	0.99127	1	6	fluid transport	BP	1	AQP1	up_ACOR_EC
GO:0072201	0.141277026	0.99123	1	6	negative regulation of mesenchymal cell	BP	1	CLSTN1	up_ACOR_EC
GO:0048525	0.141350613	0.97248	2	25	negative regulation of viral process	BP	1	TRIM8,MAVS	up_ACOR_EC
GO:0036010	0.141437025	0.99121	1	6	protein localization to endosome	BP	1	NRP1	up_ACOR_EC
GO:0008544	0.141910639	0.94954	4	75	epidermis development	BP	1	CDH3,SOX9,TNFRSF19,LRP4	up_ACOR_EC
GO:0009059	0.142	0.88	142	1563	macromolecule biosynthetic process	BP	1	ELK3,HMGB1,MCM6,SREBF1,MCM4,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,RRM1,MED17,POLA1,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,POLA2,MPDU1,SRRT,GINS4,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,RAD51,XYLT1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,SMARCC1,PLK3,PCNA,DHX33,HOXA7,TONSL,MCM10,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,FARSA,PPARD,CDC6,POLH,YBX3,NCL,NUP62,UGDH,MRPL37,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,PUM3,CDC45,MAST2,SMARCAL1,TBX15,GRWD1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,MRPL18,CDC5L,NUS1,HMGN1,CCT4,SIX4,NECAB3,MED16,EIF3M,ENSCAFG00000017103,GEN1,POLR1C	down_ACOR_VSMC

GO:0042127	0.142	0.891	50	452	regulation of cell proliferation	BP	1	VEGFD,SMAD6,LEP,LBH,CDC7,HTR2B,PRDX4,NACC2,FERMT1,BMP4,FGFR2,PDE5A,TP53INP1,RERG,CD274,MARCKSL1,AR,PTGIR,FGF18,NDRG2,CDKN2B,PLAC8B,LIMS2,CDKN1A,CLSTN1,PTPN22,SMARCD3,TBX20,TBX5,FZD3,FRS2,CCPG1,APP,TGFBR1,SYNJ2BP,JUP,DDR2,FOSL2,DUSP22,EDN1,SERPINB5,DISC1,TNFRSF11B,KLF11,RPRD1B,WDR48,SH3BP4,RREB1,CRKL,PTPN14	up_ACOR_VSMC
GO:0048872	0.142	0.929	8	85	homeostasis of number of cells	BP	1	CASP3,PTPN11,EXOC5,HIF1A,PTPN2,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0009966	0.142	0.935	7	868	regulation of signal transduction	BP	1	ACVRL1,LYN,IGF1R,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0031214	0.142	0.934	7	45	biomineral tissue development	BP	1	WNT11,AXIN2,OSR2,OSR1,DDR2,OMD,BGLAP	up_VSAP_EC
GO:0006497	0.142	0.939	6	38	protein lipidation	BP	1	ABCA1,PIGN,PIGS,PIGG,PIK3C3,ZDHHC21	up_ACOR_VSMC
GO:0062014	0.142	0.951	4	35	negative regulation of small molecule metabolic	BP	1	NR1H4,TRIB3,APOE,REST	down_VSAP_EC
GO:0110110	0.142	0.951	4	34	positive regulation of animal organ	BP	1	HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0030239	0.142	0.952	4	21	myofibril assembly	BP	1	ACTN2,NEBL,EDN1,MYOZ2	up_ACOR_VSMC
GO:1901576	0.142	0.963	4	1877	organic substance biosynthetic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0006970	0.142	0.952	4	23	response to osmotic stress	BP	1	LRRC8D,MAPK13,PTGS2,ARHGEF2	up_VCAV_EC
GO:0006720	0.142	0.96	3	25	isoprenoid metabolic process	BP	1	CYP1B1,RETSAT,RDH10	down_VCAV_EC
GO:0019219	0.142	0.967	3	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0021955	0.142	0.962	3	15	central nervous system neuron axonogenesis	BP	1	SLIT2,PLXNA4,NFIB	up_VSAP_EC
GO:0035384	0.142	0.962	3	14	thioester biosynthetic process	BP	1	ACACB,PDK2,ACSS2	up_VSAP_EC
GO:0071616	0.142	0.962	3	14	acyl-CoA biosynthetic process	BP	1	ACACB,PDK2,ACSS2	up_VSAP_EC
GO:0050994	0.142	0.962	3	14	regulation of lipid catabolic process	BP	1	ACACB,LONP2,IDH1	up_VSAP_EC
GO:2000727	0.142	0.976	2	7	positive regulation of cardiac muscle cell	BP	1	BMP4,EDN1	up_ACOR_VSMC
GO:0006814	0.142	0.972	2	28	sodium ion transport	BP	1	FXYD1,DMPK	up_AFEM_EC
GO:0046579	0.142	0.975	2	9	positive regulation of Ras protein signal	BP	1	GPR4,ITPKB	up_VCAV_EC
GO:0046794	0.142	0.995	1	2	transport of virus	BP	1	CAV1	down_ACOR_VSMC
GO:0046060	0.142	0.995	1	2	dATP metabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0046642	0.142	0.995	1	2	negative regulation of alpha-beta T cell	BP	1	ARG2	down_ACOR_VSMC
GO:1905397	0.142	0.995	1	2	activated CD8-positive, alpha-beta T cell	BP	1	ARG2	down_ACOR_VSMC
GO:1905402	0.142	0.995	1	2	regulation of activated CD8-positive, alpha-beta T cell apoptotic process	BP	1	ARG2	down_ACOR_VSMC
GO:2000562	0.142	0.995	1	2	negative regulation of CD4-positive, alpha-beta T cell proliferation	BP	1	ARG2	down_ACOR_VSMC
GO:0007051	0.142	0.99	1	70	spindle organization	BP	1	GPSM2	down_AFEM_EC
GO:2001141	0.142	1	1	979	regulation of RNA biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0031340	0.142	0.993	1	3	positive regulation of vesicle fusion	BP	1	AKT2	down_VCAV_EC
GO:0032891	0.142	0.993	1	3	negative regulation of organic acid transport	BP	1	AKT2	down_VCAV_EC
GO:0034380	0.142	0.993	1	3	high-density lipoprotein particle assembly	BP	1	LCAT	down_VCAV_EC
GO:0045792	0.142	0.993	1	3	negative regulation of cell size	BP	1	AKT1S1	down_VCAV_EC
GO:0048050	0.142	0.993	1	3	post-embryonic eye morphogenesis	BP	1	FBN1	down_VCAV_EC
GO:0060509	0.142	0.993	1	3	type I pneumocyte differentiation	BP	1	THRB	down_VCAV_EC
GO:0071472	0.142	0.993	1	3	cellular response to salt stress	BP	1	ZFP36L1	down_VCAV_EC
GO:1901569	0.142	0.993	1	3	fatty acid derivative catabolic process	BP	1	ACAT1	down_VCAV_EC

GO:1903553	0.142	0.993	1	3	positive regulation of extracellular exosome	BP	1	SDC4	down_VCAV_EC
GO:1903960	0.142	0.993	1	3	negative regulation of anion transmembrane	BP	1	AKT2	down_VCAV_EC
GO:2000121	0.142	0.993	1	3	regulation of removal of superoxide radicals	BP	1	PARK7	down_VCAV_EC
GO:0048762	0.142	0.99	1	77	mesenchymal cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:0010629	0.142	0.995	1	502	negative regulation of gene expression	BP	1	GATA5	down_VFEM_VSMC
GO:0040011	0.142	0.995	1	505	locomotion	BP	1	JUP	down_VFEM_VSMC
GO:0006419	0.142	0.995	1	2	alanyl-tRNA aminoacylation	BP	1	AARS	down_VSAP_EC
GO:0030643	0.142	0.995	1	2	cellular phosphate ion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0070933	0.142	0.995	1	2	histone H4 deacetylation	BP	1	REST	down_VSAP_EC
GO:0072501	0.142	0.995	1	2	cellular divalent inorganic anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0072502	0.142	0.995	1	2	cellular trivalent inorganic anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0051004	0.142	0.993	1	3	regulation of lipoprotein lipase activity	BP	1	ABHD5	down_VSAP_EC
GO:0060978	0.142	0.995	1	2	angiogenesis involved in coronary vascular	BP	1	NRP1	down_VSAP_EC
GO:0090259	0.142	0.995	1	2	regulation of retinal ganglion cell axon	BP	1	NRP1	down_VSAP_EC
GO:0009611	0.142	0.991	1	122	response to wounding	BP	1	WNT7A	up_AORT_VSMC
GO:0003130	0.142	0.995	1	2	BMP signaling pathway involved in heart	BP	1	BMP2	up_VCAV_EC
GO:0003133	0.142	0.995	1	2	endodermal-mesodermal cell signaling	BP	1	BMP2	up_VCAV_EC
GO:0003134	0.142	0.995	1	2	endodermal-mesodermal cell signaling involved in heart induction	BP	1	BMP2	up_VCAV_EC
GO:0033762	0.142	0.995	1	2	response to glucagon	BP	1	CREB1	up_VCAV_EC
GO:0003085	0.142	0.995	1	2	negative regulation of systemic arterial blood	BP	1	PRCP	up_VCAV_EC
GO:0030185	0.142	0.995	1	2	nitric oxide transport	BP	1	EDN1	up_VCAV_EC
GO:0035107	0.142	0.99	1	60	appendage morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0035108	0.142	0.99	1	60	limb morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0045766	0.142	0.99	1	63	positive regulation of angiogenesis	BP	1	C3AR1	up_VPOR_VSMC
GO:0035270	0.142	0.99	1	35	endocrine system development	BP	1	SIX1	up_VFEM_EC
GO:0050731	0.142	0.99	1	44	positive regulation of peptidyl-tyrosine	BP	1	ARHGEF2	up_VPUL_EC
GO:0050707	0.142	0.99	1	44	regulation of cytokine secretion	BP	1	NR1H4	up_VPUL_EC
GO:0110110	0.142	0.99	1	34	positive regulation of animal organ	BP	1	HOXA11	up_VSAP_VSMC
GO:0016197	0.142142252	0.94938	4	78	endosomal transport	BP	1	CALY,ACTN2,VPS16,ABCB9	up_ACOR_EC
GO:0007625	0.142601734	0.99106	1	6	grooming behavior	BP	1	CNTNAP4	up_ACOR_EC
GO:0060394	0.142672533	0.99106	1	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	SMAD6	up_ACOR_EC
GO:0045773	0.142870214	0.99103	1	6	positive regulation of axon extension	BP	1	NRP1	up_ACOR_EC
GO:0021854	0.142927401	0.99102	1	6	hypothalamus development	BP	1	NRP1	up_ACOR_EC
GO:0009063	0.142987757	0.97196	2	25	cellular amino acid catabolic process	BP	1	THNSL2,SARDH	up_ACOR_EC

GO:2000026	0.143	0.887	62	560	regulation of multicellular organismal development	BP	1	VEGFD,TMEM176B,TMEM176A,LEP,LBH,GATA5,CD83,RASSF2,MBP,MLLT3,ITM2C,FERMT1,BMP4,LNPK,FGFR2,TP53BP1,GJA1,TLR3,SEC24B,WASF3,CITED2,ISG15,ZNRF3,CD274,ZNF365,SASH1,FGF18,FAM210B,P4HTM,LIMS2,EGLN1,CLSTN1,NRP1,ULK2,SMARCD3,SLITRK5,TBX20,TBX5,FZD3,FRS2,DAG1,APP,LAMA3,PSEN1,TGFBR1,SYNJ2BP,CHD7,JUP,SIPA1L1,DDR2,SSH3,EDN1,ASAP1,B2M,DISC1,TNFRSF11B,CNOT4,ERAP1,SLC8A1,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0043065	0.143	0.904	23	188	positive regulation of apoptotic process	BP	1	WNT11,CD274,PLEKHF1,SLIT2,CRADD,ABL1,BTG1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,MFN2,TRAF7,RBCK1,MYC,PRMT2,ZNF205,HTRA2,NCK1,HMOX1,DEDD2,LATS2	up_VSAP_EC
GO:0097190	0.143	0.904	22	217	apoptotic signaling pathway	BP	1	TNFAIP3,ATF3,FIGNL1,CASP8,MADD,PAK2,SH3GLB1,TLR3,NCK1,PTGS2,BCL10,USP28,CTNNA1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,IVNS1ABP,ATP2A1,ARHGEF2	up_VCAV_EC
GO:0002684	0.143	0.91	16	239	positive regulation of immune system process	BP	1	GPAM,CFD,PRNP,CLSTN1,THY1,GLI3,PARK7,ZFP36L1,CYBA,MAVS,RAB7B,A2M,RAC2,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0003002	0.143	0.913	15	118	regionalization	BP	1	SMAD6,GATA5,MLLT3,BMP4,FGFR2,CITED2,CLSTN1,NRP1,SMARCD3,TBX20,FRS2,PSEN1,PCSK6,EDN1,CRKL	up_ACOR_VSMC
GO:0009719	0.143	0.915	13	395	response to endogenous stimulus	BP	1	LEP,LBH,CRY2,FIBIN,CHRM2,TMEM100,GREM1,AVPR1A,CAMK2A,GREM2,NR3C1,ADAM17,KANK1	up_AFEM_EC
GO:0043269	0.143	0.922	10	135	regulation of ion transport	BP	1	PRNP,FXYD1,TRPV2,AKT2,CACNB3,THY1,PARK7,CYBA,CLIC4,PACSIN3	down_VCAV_EC
GO:0048667	0.143	0.922	10	140	cell morphogenesis involved in neuron	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,ENSCAFG00000017708,UST,BRSK1	down_VCAV_EC
GO:0008154	0.143	0.923	10	81	actin polymerization or depolymerization	BP	1	HCLS1,BAIAP2L1,TMOD1,MTOR,NCKAP1,IQGAP2,SWAP70,NCK1,ARPC5L,TMOD3	up_VCAV_EC
GO:0003002	0.143	0.925	9	118	regionalization	BP	1	BMPR1A,HOXC4,CLSTN1,SEMA3C,GLI3,IFT57,PCSK6,GREM1,ZBTB16	down_VCAV_EC
GO:0043207	0.143	0.928	8	216	response to external biotic stimulus	BP	1	CD40,BPI,GPAM,CHRM2,SLC17A5,TBXA2R,CCL5,ADAM17	up_AFEM_EC
GO:0051707	0.143	0.928	8	216	response to other organism	BP	1	CD40,BPI,GPAM,CHRM2,SLC17A5,TBXA2R,CCL5,ADAM17	up_AFEM_EC
GO:0001817	0.143	0.932	7	182	regulation of cytokine production	BP	1	CMKLR1,LEP,DLL1,BPI,GPAM,ADAM17,AGPAT2	up_AFEM_EC
GO:0009605	0.143	0.933	7	538	response to external stimulus	BP	1	C3AR1,OAS3,SEMA3A,MTDH,SEMA3D,ENSCAFG00000032731,NAALADL2	up_VPOR_EC
GO:0031323	0.143	0.941	7	1788	regulation of cellular metabolic process	BP	1	EYA1,HOXA10,HOXA9,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042098	0.143	0.938	6	43	T cell proliferation	BP	1	HMGB1,ARG2,TFRC,CORO1A,ELF4,CTPS1	down_ACOR_VSMC
GO:0001841	0.143	0.943	5	44	neural tube formation	BP	1	PRICKLE1,PRKACB,TMED2,HIF1A,SDC4	down_VSAP_EC
GO:0008152	0.143	0.977	5	3714	metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0007286	0.143	0.95	4	34	spermatid development	BP	1	CELF1,CDYL,SPINK2,KDM3A	down_VSAP_EC
GO:0046128	0.143	0.952	4	23	purine ribonucleoside metabolic process	BP	1	ENPP4,PTGDR,ENSCAFG00000018611,NT5C2	up_ACOR_VSMC
GO:1901568	0.143	0.951	4	26	fatty acid derivative metabolic process	BP	1	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0034142	0.143	0.962	3	14	toll-like receptor 4 signaling pathway	BP	1	F2RL1,PTPN22,PRKCE	up_ACOR_VSMC
GO:0072074	0.143	0.975	2	8	kidney mesenchyme development	BP	1	SIX4,AMER1	down_ACOR_VSMC
GO:0031111	0.143	0.974	2	11	negative regulation of microtubule polymerization or	BP	1	ARHGEF2,MID1	down_VSAP_EC
GO:0061178	0.143	0.973	2	12	regulation of insulin secretion involved in cellular response to	BP	1	NR1H4,HIF1A	down_VSAP_EC
GO:0010633	0.143	0.972	2	28	negative regulation of epithelial cell migration	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:0140056	0.143	0.972	2	28	organelle localization by membrane tethering	BP	1	CAMK2A,BVES	up_AFEM_EC
GO:0051382	0.143	0.975	2	9	kinetochore assembly	BP	1	CENPC,SENP6	up_VCAV_EC
GO:0001816	0.143	0.972	2	194	cytokine production	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0034139	0.143	0.976	2	7	regulation of toll-like receptor 3 signaling	BP	1	F2RL1,FLOT1	up_VSAP_EC
GO:0120031	0.143	0.972	2	154	plasma membrane bounded cell projection	BP	1	EMP1,CAV1	up_VSAP_VSMC

GO:0007269	0.143	0.99	1	34	neurotransmitter secretion	BP	1	STX4	down_ACOR_EC
GO:0099643	0.143	0.99	1	34	signal release from synapse	BP	1	STX4	down_ACOR_EC
GO:0050796	0.143	0.99	1	33	regulation of insulin secretion	BP	1	STX4	down_ACOR_EC
GO:0048548	0.143	0.994	1	2	regulation of pinocytosis	BP	1	CAV1	down_ACOR_VSMC
GO:0060046	0.143	0.995	1	2	regulation of acrosome reaction	BP	1	B4GALT1	down_ACOR_VSMC
GO:0060353	0.143	0.994	1	2	regulation of cell adhesion molecule production	BP	1	CAV1	down_ACOR_VSMC
GO:0060355	0.143	0.994	1	2	positive regulation of cell adhesion molecule	BP	1	CAV1	down_ACOR_VSMC
GO:0006775	0.143	0.993	1	3	fat-soluble vitamin metabolic process	BP	1	VKORC1	down_VCAV_EC
GO:0009263	0.143	0.993	1	3	deoxyribonucleotide biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0032264	0.143	0.993	1	3	IMP salvage	BP	1	AMPD2	down_VCAV_EC
GO:0043173	0.143	0.993	1	3	nucleotide salvage	BP	1	AMPD2	down_VCAV_EC
GO:1900222	0.143	0.993	1	3	negative regulation of amyloid-beta clearance	BP	1	LRPAP1	down_VCAV_EC
GO:0016024	0.143	0.993	1	3	CDP-diacylglycerol biosynthetic process	BP	1	GPAM	down_VCAV_EC
GO:0032261	0.143	0.993	1	3	purine nucleotide salvage	BP	1	AMPD2	down_VCAV_EC
GO:0033240	0.143	0.993	1	3	positive regulation of cellular amine metabolic	BP	1	PARK7	down_VCAV_EC
GO:0042104	0.143	0.993	1	3	positive regulation of activated T cell	BP	1	GPAM	down_VCAV_EC
GO:0042416	0.143	0.993	1	3	dopamine biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0046341	0.143	0.993	1	3	CDP-diacylglycerol metabolic process	BP	1	GPAM	down_VCAV_EC
GO:0051583	0.143	0.993	1	3	dopamine uptake involved in synaptic	BP	1	PARK7	down_VCAV_EC
GO:0051934	0.143	0.993	1	3	catecholamine uptake involved in synaptic	BP	1	PARK7	down_VCAV_EC
GO:0090091	0.143	0.993	1	3	positive regulation of extracellular matrix	BP	1	DDR2	down_VCAV_EC
GO:0090493	0.143	0.993	1	3	catecholamine uptake	BP	1	PARK7	down_VCAV_EC
GO:0090494	0.143	0.993	1	3	dopamine uptake	BP	1	PARK7	down_VCAV_EC
GO:1901525	0.143	0.993	1	3	negative regulation of mitophagy	BP	1	CLEC16A	down_VCAV_EC
GO:0034330	0.143	0.99	1	80	cell junction organization	BP	1	HDAC7	down_VPOR_EC
GO:0051346	0.143	0.99	1	78	negative regulation of hydrolase activity	BP	1	CST3	down_VPOR_EC
GO:0007256	0.143	0.995	1	2	activation of JNKK activity	BP	1	TNIK	down_VSAP_EC
GO:0071500	0.143	0.993	1	3	cellular response to nitrosative stress	BP	1	DDIT3	down_VSAP_EC
GO:1903121	0.143	0.993	1	3	regulation of TRAIL-activated apoptotic	BP	1	ATF3	down_VSAP_EC
GO:0031223	0.143	0.995	1	2	auditory behavior	BP	1	HTT	down_VSAP_EC
GO:0090407	0.143	0.991	1	177	organophosphate biosynthetic process	BP	1	AK5	down_VSAP_VSMC
GO:1901988	0.143	0.99	1	63	negative regulation of cell cycle phase transition	BP	1	TAOK1	up_AORT_EC
GO:0002790	0.143	0.991	1	133	peptide secretion	BP	1	ARG2	up_AORT_VSMC
GO:0007268	0.143	0.991	1	130	chemical synaptic transmission	BP	1	WNT7A	up_AORT_VSMC
GO:0022604	0.143	0.991	1	122	regulation of cell morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0051656	0.143	0.991	1	129	establishment of organelle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0098916	0.143	0.991	1	130	anterograde trans-synaptic signaling	BP	1	WNT7A	up_AORT_VSMC
GO:0010565	0.143	0.99	1	40	regulation of cellular ketone metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0016202	0.143	0.99	1	39	regulation of striated muscle tissue	BP	1	TBX5	up_APUL_EC
GO:0002072	0.143	0.994	1	2	optic cup morphogenesis involved in camera-type	BP	1	ALDH1A3	up_VCAV_EC

GO:0030432	0.143	0.994	1	2	peristalsis	BP	1	P2RX2	up_VCAV_EC
GO:0002191	0.143	0.995	1	2	cap-dependent translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0070169	0.143	0.99	1	18	positive regulation of biomineral tissue	BP	1	ACVR2A	up_VPOR_EC
GO:0032874	0.143	0.99	1	57	positive regulation of stress-activated MAPK	BP	1	ANKRD6	up_VPOR_VSMC
GO:0016054	0.143	0.99	1	61	organic acid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0046395	0.143	0.99	1	61	carboxylic acid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0045216	0.143	0.99	1	44	cell-cell junction organization	BP	1	NR1H4	up_VPUL_EC
GO:0051494	0.143	0.99	1	44	negative regulation of cytoskeleton organization	BP	1	ARHGEF2	up_VPUL_EC
GO:0022412	0.143	0.99	1	76	cellular process involved in reproduction in multicellular organism	BP	1	SLIT2	up_VPUL_VSMC
GO:0051146	0.143	0.99	1	76	striated muscle cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0060402	0.143	0.99	1	35	calcium ion transport into cytosol	BP	1	CAV1	up_VSAP_VSMC
GO:0070301	0.143064787	0.97194	2	25	cellular response to hydrogen peroxide	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:1905523	0.143765472	0.99091	1	6	positive regulation of macrophage migration	BP	1	RARRES2	up_ACOR_EC
GO:0070168	0.143790392	0.99091	1	6	negative regulation of biomineral tissue	BP	1	SOX9	up_ACOR_EC
GO:0031323	0.144	0.877	158	1788	regulation of cellular metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,ADGRF5,KIT,SELE,PRCP,PPP2R5A,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,CD34,PDE4D,IWS1,MEF2C,ATF3,CHD7,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,FAM3C,SPTLC2,ARG2,CASP8,MTOR,TENT2,SAMD8,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,SLK,SH3BP5,CNOT6,DEPP1,RSC1A1,ENC1,CCAR1,PPP1R2,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,APOD,NCK1,ESCO1,DPH5,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,PTGS2,MMD,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,TAOK1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,PMAIP1,ZNF789,BLM,NUP133,SPTBN4,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,PDGFD,USP37,WTAP,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,IVNS1ABP,FKBP15,JCA	up_VCAV_EC
GO:0009891	0.144	0.888	57	521	positive regulation of biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,C1QTNF2,ZBTB16,RARG,PYM1,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,NPAS2,RPUSD4,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,CYBA,ZNF205,NCOA2,SMARCA2,EIF3D,ACVRL1,ASS1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0010557	0.144	0.888	54	492	positive regulation of macromolecule biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,C1QTNF2,ZBTB16,RARG,PYM1,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,NPAS2,RPUSD4,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,EIF3D,ACVRL1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0060627	0.144	0.906	20	165	regulation of vesicle-mediated transport	BP	1	EXPH5,DNAJC6,ACTN2,PLCG2,USP6NL,FBXL20,EVI5L,SEC24B,ATXN2,F2RL1,LRPAP1,SGSM2,SYNJ2BP,RAB11B,GTF2A1L,B2M,SCAMP5,RAB5C,PREPL,BVES	up_ACOR_VSMC

GO:0030001	0.144	0.913	14	172	metal ion transport	BP	1	SLC39A7,ERO1A,ATP2B1,REM1,KIF5B,CTNNB1,TFRC,LYN,DDIT3,NKAIN1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0051495	0.144	0.922	10	82	positive regulation of cytoskeleton organization	BP	1	NF2,POC1A,RAC1,NUP62,PDXP,PLK4,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0006810	0.144	0.929	9	1244	transport	BP	1	LYN,HOXA3,SPG11,PDPN,IPO7,ACSL3,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0022612	0.144	0.933	7	44	gland morphogenesis	BP	1	BMP4,FGFR2,LIMS2,NRP1,FRS2,DAG1,SERPINB5	up_ACOR_VSMC
GO:0010467	0.144	0.94	7	1787	gene expression	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0033865	0.144	0.938	6	43	nucleoside bisphosphate metabolic process	BP	1	ACLY,HMGCR,MVD,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0033875	0.144	0.938	6	43	ribonucleoside bisphosphate metabolic	BP	1	ACLY,HMGCR,MVD,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0034032	0.144	0.938	6	43	purine nucleoside bisphosphate metabolic	BP	1	ACLY,HMGCR,MVD,ELOVL1,ELOVL6,PDHA1	down_ACOR_VSMC
GO:0001843	0.144	0.938	6	38	neural tube closure	BP	1	FZD1,ABL1,FUZ,RARG,KDM2B,CITED2	up_VSAP_EC
GO:0048593	0.144	0.95	4	41	camera-type eye morphogenesis	BP	1	THY1,GLI3,IRX5,THRB	down_VCAV_EC
GO:1903169	0.144	0.95	4	34	regulation of calcium ion transmembrane transport	BP	1	REM1,LYN,HTT,CALM1	down_VSAP_EC
GO:0051058	0.144	0.952	4	21	negative regulation of small GTPase mediated signal transduction	BP	1	RAPGEF1,ARAP3,STMN1,TNFAIP1	up_VCAV_EC
GO:0045600	0.144	0.951	4	21	positive regulation of fat cell differentiation	BP	1	NAPEPLD,SAV1,ZBTB16,ZFP36L1	up_VSAP_EC
GO:0045595	0.144	0.95	4	469	regulation of cell differentiation	BP	1	HOXA11,HOXA9,CAV1,SHOX2	up_VSAP_VSMC
GO:0008037	0.144	0.96	3	22	cell recognition	BP	1	MSN,PVR,NRP1	down_VSAP_EC
GO:0032642	0.144	0.96	3	22	regulation of chemokine production	BP	1	NR1H4,SOCS5,ADAM17	down_VSAP_EC
GO:0034314	0.144	0.961	3	16	Arp2/3 complex-mediated actin nucleation	BP	1	NCKAP1,IQGAP2,ARPC5L	up_VCAV_EC
GO:0098655	0.144	0.971	2	142	cation transmembrane transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0099537	0.144	0.971	2	131	trans-synaptic signaling	BP	1	SPG11,STX4	down_ACOR_EC
GO:0035067	0.144	0.975	2	8	negative regulation of histone acetylation	BP	1	BRCA1,NOC2L	down_ACOR_VSMC
GO:0050685	0.144	0.975	2	8	positive regulation of mRNA processing	BP	1	THRAP3,SF3B4	down_ACOR_VSMC
GO:0060544	0.144	0.975	2	8	regulation of necroptotic process	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:2000758	0.144	0.975	2	8	positive regulation of peptidyl-lysine acetylation	BP	1	BRCA1,TADA2A	down_ACOR_VSMC
GO:0070647	0.144	0.973	2	311	protein modification by small protein conjugation	BP	1	IVNS1ABP,USP33	down_AFEM_EC
GO:0032024	0.144	0.973	2	12	positive regulation of insulin secretion	BP	1	NR1H4,HIF1A	down_VSAP_EC
GO:0090277	0.144	0.973	2	12	positive regulation of peptide hormone	BP	1	NR1H4,HIF1A	down_VSAP_EC
GO:0032232	0.144	0.976	2	7	negative regulation of actin filament bundle	BP	1	ARHGAP28,INPP5K	up_ACOR_VSMC
GO:0051497	0.144	0.976	2	7	negative regulation of stress fiber assembly	BP	1	ARHGAP28,INPP5K	up_ACOR_VSMC
GO:0051704	0.144	0.974	2	476	multi-organism process	BP	1	TLR2,HOXA9	up_AFEM_VSMC
GO:0060074	0.144	0.976	2	7	synapse maturation	BP	1	ARHGEF15,RELN	up_VCAV_EC
GO:2000516	0.144	0.976	2	7	positive regulation of CD4-positive, alpha-beta T cell activation	BP	1	CD83,TGFBR2	up_VSAP_EC
GO:0034134	0.144	0.976	2	7	toll-like receptor 2 signaling pathway	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0050851	0.144	0.99	1	34	antigen receptor-mediated signaling	BP	1	LYN	down_ACOR_EC
GO:0009893	0.144	1	1	995	positive regulation of metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0015833	0.144	0.994	1	521	peptide transport	BP	1	SCAMP4	down_AORT_EC
GO:0003257	0.144	0.993	1	3	positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	down_VCAV_EC
GO:0016197	0.144	0.99	1	78	endosomal transport	BP	1	RAB11B	down_VPOR_EC

GO:0031328	0.144	0.994	1	512	positive regulation of cellular biosynthetic	BP	1	GATA5	down_VFEM_VSMC
GO:0001654	0.144	0.99	1	110	eye development	BP	1	IRX5	up_AFEM_VSMC
GO:0006820	0.144	0.99	1	109	anion transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0048880	0.144	0.99	1	110	sensory system development	BP	1	IRX5	up_AFEM_VSMC
GO:0150063	0.144	0.99	1	110	visual system development	BP	1	IRX5	up_AFEM_VSMC
GO:0007254	0.144	0.99	1	67	JNK cascade	BP	1	TAOK1	up_AORT_EC
GO:0045165	0.144	0.99	1	65	cell fate commitment	BP	1	HOXC10	up_AORT_EC
GO:0099537	0.144	0.99	1	131	trans-synaptic signaling	BP	1	WNT7A	up_AORT_VSMC
GO:0006937	0.144	0.99	1	40	regulation of muscle contraction	BP	1	NPNT	up_APUL_EC
GO:0009743	0.144	0.99	1	40	response to carbohydrate	BP	1	NR1H4	up_APUL_EC
GO:0007202	0.144	0.994	1	2	activation of phospholipase C activity	BP	1	SELE	up_VCAV_EC
GO:0060155	0.144	1	1	1	platelet dense granule organization	BP	1	ABCA1	up_VCAV_EC
GO:1902954	0.144	1	1	1	regulation of early endosome to recycling	BP	1	DNAJC13	up_VCAV_EC
GO:0016338	0.144	0.994	1	2	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion	BP	1	BMP2	up_VCAV_EC
GO:0007200	0.144	0.99	1	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	C3AR1	up_VPOR_EC
GO:0008333	0.144	0.99	1	19	endosome to lysosome transport	BP	1	HOOK3	up_VPOR_EC
GO:0035150	0.144	0.99	1	36	regulation of tube size	BP	1	AVPR1A	up_VFEM_EC
GO:0050880	0.144	0.99	1	36	regulation of blood vessel size	BP	1	AVPR1A	up_VFEM_EC
GO:0008643	0.144	0.99	1	45	carbohydrate transport	BP	1	NR1H4	up_VPUL_EC
GO:0031214	0.144	0.99	1	45	biomineral tissue development	BP	1	HOXA3	up_VPUL_EC
GO:0043393	0.144	0.99	1	77	regulation of protein binding	BP	1	HOXA3	up_VPUL_VSMC
GO:0021564	0.144	0.994	1	2	vagus nerve development	BP	1	PLXNA4	up_VSAP_EC
GO:0032091	0.144	0.99	1	34	negative regulation of protein binding	BP	1	CAV1	up_VSAP_VSMC
GO:0032635	0.144	0.99	1	37	interleukin-6 production	BP	1	TLR2	up_VSAP_VSMC
GO:0007264	0.144186449	0.93085	7	164	small GTPase mediated signal transduction	BP	1	RHOU,PLCE1,PAK3,ARHGDIB,RAPGEF4,NRP1,ARHGEF26	up_ACOR_EC
GO:0051252	0.145	0.881	97	1051	regulation of RNA metabolic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,WTAP,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:1901700	0.145	0.891	42	364	response to oxygen-containing compound	BP	1	ACTN2,PLCG2,LEP,PRKAA2,ABCA1,CASTOR1,LPL,TP53INP1,GLRB,PTGIR,SASH1,SLC2A5,FAM210B,ADCY6,ANKRD1,DAPK1,EGLN1,AKAP6,P2RX7,UBR1,PTPN22,APLP1,PTGDR,SESN3,PRKCE,AGRN,APP,PSEN1,JUP,NR3C1,RAB11B,SESN1,OXR1,NOD2,DDIT4,TNFRSF11B,GNAQ,INPP5K,PFKL,CAT,SH3BP4,PARK7	up_ACOR_VSMC

GO:0006357	0.145	0.892	40	547	regulation of transcription by RNA polymerase II	BP	1	ARHGEF2,VEGFA,SULF1,NR1H4,PLK3,ETV6,CBX5,ILK,FHL2,PPP1R12A,SMARCA4,ANKRA2,SESN2,HIF1A,PTPN2,YES1,NEO1,PEG3,MTDH,BRD2,CNOT7,MAGED1,CTNNB1,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,ZMYND8,GLO1,INHBA,NR4A1,ENSCAFG00000018360,HIF1AN,ARF4,KDM3A	down_VSAP_EC
GO:0061061	0.145	0.903	22	179	muscle structure development	BP	1	TNNT2,ACTN2,BMP4,FGFR2,GJA1,CITED2,NEBL,ANKRD1,EGLN1,CHD2,DMPK,NPNT,SMARCD3,TBX20,TBX5,FRS2,CHD7,EDN1,ARID5B,ID3,BVES,MYOZ2	up_ACOR_VSMC
GO:0014070	0.145	0.903	21	172	response to organic cyclic compound	BP	1	FAM107A,PTGFR,PPARGC1B,SLIT2,CDH1,GOT1,ZFP36L1,ABAT,CREBRF,CD83,PRMT2,OSBPL7,ZFP36L2,NCOA2,PQBP1,FLOT1,MAVS,BGLAP,TGFBR2,LBH,DDIT4	up_VSAP_EC
GO:1901615	0.145	0.912	14	128	organic hydroxy compound metabolic process	BP	1	GK5,GATA3,SNCAIP,SPTLC2,BMP2,ABCA1,ITPKB,PROX1,RAPGEF2,PLCG2,GCH1,LBR,IMPA1,HIF1A	up_VCAV_EC
GO:0006979	0.145	0.919	11	130	response to oxidative stress	BP	1	P4HB,PLK3,SESN2,PTGS2,HIF1A,CTNNB1,CRYAB,APOE,KPNA4,EIF2S1,MSRB3	down_VSAP_EC
GO:0000075	0.145	0.919	11	91	cell cycle checkpoint	BP	1	PLK2,PROX1,THOC1,ETAA1,USP28,TAOK1,BLM,RAD17,CUL4A,ZW10,TOPBP1	up_VCAV_EC
GO:0051224	0.145	0.932	7	47	negative regulation of protein transport	BP	1	FERMT1,F2RL1,PTPN22,OS9,INPP5K,PFKL,PARK7	up_ACOR_VSMC
GO:1904950	0.145	0.932	7	47	negative regulation of establishment of protein localization	BP	1	FERMT1,F2RL1,PTPN22,OS9,INPP5K,PFKL,PARK7	up_ACOR_VSMC
GO:0030855	0.145	0.93	7	183	epithelial cell differentiation	BP	1	LBH,HOXA7,DLL1,THRB,TMEM100,GREM1,FOSL2	up_AFEM_EC
GO:0048839	0.145	0.932	7	50	inner ear development	BP	1	CHD7,GATA3,BMP2,PROX1,JAG1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0043903	0.145	0.936	6	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	P4HB,SMARCA4,CNOT7,APOE,REST,RAD23A	down_VSAP_EC
GO:0031399	0.145	0.943	5	559	regulation of protein modification process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0031345	0.145	0.942	5	46	negative regulation of cell projection organization	BP	1	DPYSL3,IFRD1,APOE,NRP1,YWHAH	down_VSAP_EC
GO:0042158	0.145	0.949	4	40	lipoprotein biosynthetic process	BP	1	CLIP3,LCAT,PIGS,WDR45	down_VCAV_EC
GO:1904892	0.145	0.949	4	40	regulation of STAT cascade	BP	1	DCN,BGN,ASPN,ARL2BP	down_VCAV_EC
GO:1901862	0.145	0.961	3	14	negative regulation of muscle tissue	BP	1	BMP4,TBX5,FRS2	up_ACOR_VSMC
GO:0006690	0.145	0.961	3	16	icosanoid metabolic process	BP	1	EDN1,PTGS1,PTGS2	up_VCAV_EC
GO:0120193	0.145	0.961	3	15	tight junction organization	BP	1	PRKCH,OCLN,TJP1	up_VCAV_EC
GO:0010628	0.145	0.96	3	527	positive regulation of gene expression	BP	1	NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0007155	0.145	0.959	3	324	cell adhesion	BP	1	HOXA7,TIAM1,RADIL	up_VFEM_EC
GO:0001825	0.145	0.961	3	14	blastocyst formation	BP	1	MFN2,CITED2,LATS2	up_VSAP_EC
GO:0043266	0.145	0.961	3	14	regulation of potassium ion transport	BP	1	AMIGO1,KCNE3,KLHL24	up_VSAP_EC
GO:0046606	0.145	0.975	2	8	negative regulation of centrosome cycle	BP	1	NEK2,RBM14	down_ACOR_VSMC
GO:0031268	0.145	0.974	2	9	pseudopodium organization	BP	1	CDC42EP4,ENSCAFG00000010224	down_ACOR_VSMC
GO:0031269	0.145	0.974	2	9	pseudopodium assembly	BP	1	CDC42EP4,ENSCAFG00000010224	down_ACOR_VSMC
GO:0098661	0.145	0.972	2	14	inorganic anion transmembrane transport	BP	1	PRNP,CLIC4	down_VCAV_EC
GO:0021799	0.145	0.973	2	11	cerebral cortex radially oriented cell migration	BP	1	CTNNB1,DISC1	down_VSAP_EC
GO:1902042	0.145	0.973	2	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	ARHGEF2,SERPINE1	down_VSAP_EC
GO:0046885	0.145	0.976	2	7	regulation of hormone biosynthetic process	BP	1	DKKL1,STC2	up_ACOR_VSMC
GO:2000136	0.145	0.976	2	7	regulation of cell proliferation involved in	BP	1	BMP4,TBX5	up_ACOR_VSMC
GO:0045935	0.145	0.974	2	491	positive regulation of nucleobase-containing compound metabolic	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0002009	0.145	0.971	2	177	morphogenesis of an epithelium	BP	1	TBX5,NPNT	up_APUL_EC

GO:2000352	0.145	0.975	2	8	negative regulation of endothelial cell apoptotic	BP	1	TNFAIP3,GATA3	up_VCAV_EC
GO:0007507	0.145	0.971	2	194	heart development	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0002507	0.145	0.976	2	7	tolerance induction	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0046633	0.145	0.976	2	7	alpha-beta T cell proliferation	BP	1	CD274,TGFBR2	up_VSAP_EC
GO:0060065	0.145	0.976	2	7	uterus development	BP	1	HOXA11,HOXA9	up_VSAP_EC
GO:0051895	0.145	0.976	2	7	negative regulation of focal adhesion assembly	BP	1	FAM107A,ACVRL1	up_VSAP_EC
GO:1903392	0.145	0.976	2	7	negative regulation of adherens junction	BP	1	FAM107A,ACVRL1	up_VSAP_EC
GO:0030031	0.145	0.971	2	155	cell projection assembly	BP	1	EMP1,CAV1	up_VSAP_VSMC
GO:0002705	0.145	0.99	1	31	positive regulation of leukocyte mediated	BP	1	STX4	down_ACOR_EC
GO:0042178	0.145	0.994	1	2	xenobiotic catabolic process	BP	1	GSTO1	down_ACOR_VSMC
GO:0030258	0.145	0.99	1	71	lipid modification	BP	1	ETFA	down_AFEM_EC
GO:0031346	0.145	0.99	1	73	positive regulation of cell projection organization	BP	1	FSCN1	down_AFEM_EC
GO:0042886	0.145	0.994	1	527	amide transport	BP	1	SCAMP4	down_AORT_EC
GO:0003350	0.145	0.993	1	3	pulmonary myocardium development	BP	1	SEMA3C	down_VCAV_EC
GO:1905292	0.145	0.993	1	3	regulation of neural crest cell differentiation	BP	1	SEMA3C	down_VCAV_EC
GO:1905294	0.145	0.993	1	3	positive regulation of neural crest cell	BP	1	SEMA3C	down_VCAV_EC
GO:1905310	0.145	0.993	1	3	regulation of cardiac neural crest cell migration involved in outflow tract	BP	1	SEMA3C	down_VCAV_EC
GO:1905312	0.145	0.993	1	3	positive regulation of cardiac neural crest cell migration involved in outflow tract	BP	1	SEMA3C	down_VCAV_EC
GO:0034137	0.145	0.993	1	3	positive regulation of toll-like receptor 2 signaling	BP	1	CYBA	down_VCAV_EC
GO:0034163	0.145	0.992	1	3	regulation of toll-like receptor 9 signaling	BP	1	RAB7B	down_VCAV_EC
GO:0071578	0.145	0.993	1	3	zinc ion import across plasma membrane	BP	1	SLC39A6	down_VCAV_EC
GO:0090280	0.145	0.993	1	3	positive regulation of calcium ion import	BP	1	TRPV2	down_VCAV_EC
GO:0015833	0.145	0.994	1	521	peptide transport	BP	1	JUP	down_VFEM_VSMC
GO:0030099	0.145	0.99	1	133	myeloid cell differentiation	BP	1	HOXA9	up_AORT_VSMC
GO:0061564	0.145	0.99	1	119	axon development	BP	1	WNT7A	up_AORT_VSMC
GO:0071407	0.145	0.99	1	129	cellular response to organic cyclic compound	BP	1	ESR1	up_AORT_VSMC
GO:0017015	0.145	0.99	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	NPNT	up_APUL_EC
GO:0035051	0.145	0.99	1	41	cardiocyte differentiation	BP	1	TBX5	up_APUL_EC
GO:0042158	0.145	0.99	1	40	lipoprotein biosynthetic process	BP	1	ZDHHC16	up_APUL_EC
GO:0045834	0.145	0.99	1	41	positive regulation of lipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0060041	0.145	0.99	1	41	retina development in camera-type eye	BP	1	NTRK2	up_APUL_EC
GO:1903844	0.145	0.99	1	40	regulation of cellular response to transforming growth factor beta	BP	1	NPNT	up_APUL_EC
GO:0002638	0.145	0.994	1	2	negative regulation of immunoglobulin	BP	1	THOC1	up_VCAV_EC
GO:2001200	0.145	0.994	1	2	positive regulation of dendritic cell	BP	1	HMGB1	up_VCAV_EC
GO:0048865	0.145	0.994	1	2	stem cell fate commitment	BP	1	SOX18	up_VCAV_EC
GO:0048866	0.145	0.994	1	2	stem cell fate specification	BP	1	SOX18	up_VCAV_EC
GO:0010720	0.145	0.99	1	110	positive regulation of cell development	BP	1	LIMK1	up_VCAV_VSMC

GO:0021795	0.145	0.99	1	20	cerebral cortex cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0031032	0.145	0.99	1	61	actomyosin structure organization	BP	1	NKX2-5	up_VPOR_VSMC
GO:0070304	0.145	0.99	1	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0006941	0.145	0.99	1	36	striated muscle contraction	BP	1	MAP2K6	up_VFEM_EC
GO:0048588	0.145	0.99	1	44	developmental cell growth	BP	1	FLRT3	up_VPUL_EC
GO:0055002	0.145	0.99	1	45	striated muscle cell development	BP	1	MYBPC2	up_VPUL_EC
GO:0048762	0.145	0.99	1	77	mesenchymal cell differentiation	BP	1	GATA5	up_VPUL_VSMC
GO:0044332	0.145	0.994	1	2	Wnt signaling pathway involved in dorsal/ventral	BP	1	LRP4	up_VSAP_EC
GO:0010984	0.14512706	0.99074	1	6	regulation of lipoprotein particle clearance	BP	1	NR1H4	up_ACOR_EC
GO:0030335	0.145571329	0.93001	7	165	positive regulation of cell migration	BP	1	SOX9,AQP1,SEMA6D,FOXC2,LRRC15,RARRES2,NRP1	up_ACOR_EC
GO:0031328	0.146	0.886	56	512	positive regulation of cellular biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,C1QTNF2,ZBTB16,RARG,PYM1,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,NPAS2,RPUSD4,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,SMARCA2,EIF3D,ACVRL1,ASS1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0016192	0.146	0.89	43	452	vesicle-mediated transport	BP	1	KIT,SELE,CXCL8,CALCRL,ATP8A1,EXOC3L2,RAB11A,RAB27A,EXOC6,IRF8,PIK3C2A,PPP3CA,HOOK3,SNAP23,RAB6A,CAV2,BMP2K,RALBP1,SCAMP1,RSC1A1,ANKRD50,ABCA1,ELMO1,SNX2,EXOC5,FES,HIST1H1A,EHD4,PLCG2,GCC2,STX11,VPS54,HMGB1,TBC1D1,CHIC2,DNAJC13,ZW10,ALS2,LMTK2,DOP1B,RABGAP1,PEAR1,USP6NL	up_VCAV_EC
GO:0007018	0.146	0.927	8	82	microtubule-based movement	BP	1	RPGR,KIF5B,HIF1A,DYNLL1,TRAK1,KPNB1,HTT,AP3S1	down_VSAP_EC
GO:0045637	0.146	0.93	7	73	regulation of myeloid cell differentiation	BP	1	HIF1A,PTPN2,EVI2B,CTNNB1,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0003206	0.146	0.931	7	51	cardiac chamber morphogenesis	BP	1	MEF2C,CHD7,DLL4,GATA3,PROX1,JAG1,HIF1A	up_VCAV_EC
GO:0002040	0.146	0.932	7	46	sprouting angiogenesis	BP	1	SLIT2,ABL1,HDAC7,DLL1,EPN2,TBXA2R,HMOX1	up_VSAP_EC
GO:0035305	0.146	0.937	6	37	negative regulation of dephosphorylation	BP	1	SH3RF2,MARF1,PPP1R26,INPP5K,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0002699	0.146	0.942	5	46	positive regulation of immune effector process	BP	1	SOCS5,FAM49B,PVR,TFRC,LYN	down_VSAP_EC
GO:0032231	0.146	0.943	5	32	regulation of actin filament bundle assembly	BP	1	ARHGEF15,ARHGAP28,MTOR,STMN1,SWAP70	up_VCAV_EC
GO:2001243	0.146	0.942	5	33	negative regulation of intrinsic apoptotic	BP	1	FIGNL1,PTGS2,HIF1A,IVNS1ABP,ARHGEF2	up_VCAV_EC
GO:0070167	0.146	0.943	5	29	regulation of biomineral tissue development	BP	1	OSR2,OSR1,DDR2,OMD,BGLAP	up_VSAP_EC
GO:0098656	0.146	0.948	4	42	anion transmembrane transport	BP	1	PRNP,FOLR2,AKT2,CLIC4	down_VCAV_EC
GO:1902531	0.146	0.95	4	536	regulation of intracellular signal transduction	BP	1	NR1H4,ARHGEF26,NPNT,NTRK2	up_APUL_EC
GO:0007584	0.146	0.95	4	24	response to nutrient	BP	1	P2RX7,SELL,MTOR,P2RX2	up_VCAV_EC
GO:2000107	0.146	0.96	3	16	negative regulation of leukocyte apoptotic	BP	1	AURKB,ARG2,NOC2L	down_ACOR_VSMC
GO:0006900	0.146	0.959	3	21	vesicle budding from membrane	BP	1	SEC24D,SEC23A,SEC13	down_VSAP_EC
GO:0001569	0.146	0.961	3	14	branching involved in blood vessel	BP	1	NRP1,TBX20,EDN1	up_ACOR_VSMC
GO:0032613	0.146	0.961	3	14	interleukin-10 production	BP	1	CD83,CD274,F2RL1	up_ACOR_VSMC
GO:0048635	0.146	0.961	3	14	negative regulation of muscle organ	BP	1	BMP4,TBX5,FRS2	up_ACOR_VSMC
GO:0003209	0.146	0.961	3	14	cardiac atrium morphogenesis	BP	1	GATA4,TBX20,TBX5	up_ACOR_VSMC
GO:0003230	0.146	0.961	3	14	cardiac atrium development	BP	1	GATA4,TBX20,TBX5	up_ACOR_VSMC
GO:0060191	0.146	0.961	3	14	regulation of lipase activity	BP	1	HTR2B,FGFR2,LMF1	up_ACOR_VSMC

GO:0001838	0.146	0.957	3	56	embryonic epithelial tube formation	BP	1	IRX3,GREM1,LUZP1	up_AFEM_EC
GO:0090313	0.146	0.972	2	14	regulation of protein targeting to membrane	BP	1	PRNP,AKT2	down_VCAV_EC
GO:2000378	0.146	0.973	2	12	negative regulation of reactive oxygen species	BP	1	HIF1A,BNIP3	down_VSAP_EC
GO:0021846	0.146	0.973	2	11	cell proliferation in forebrain	BP	1	HOOK3,DISC1	down_VSAP_EC
GO:0060193	0.146	0.973	2	11	positive regulation of lipase activity	BP	1	ABHD5,ARF4	down_VSAP_EC
GO:0007205	0.146	0.975	2	7	protein kinase C-activating G protein-coupled receptor signaling	BP	1	HTR2B,EDN1	up_ACOR_VSMC
GO:0010829	0.146	0.975	2	7	negative regulation of glucose transmembrane	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:0034312	0.146	0.975	2	8	diol biosynthetic process	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0048468	0.146	0.975	2	553	cell development	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0001501	0.146	0.971	2	178	skeletal system development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0040007	0.146	0.972	2	276	growth	BP	1	FBP1,HOXA11	up_VFEM_VSMC
GO:0010043	0.146	0.975	2	7	response to zinc ion	BP	1	ENSCAFG00000009113,MT2A	up_VSAP_EC
GO:0022406	0.146	0.989	1	35	membrane docking	BP	1	STX4	down_ACOR_EC
GO:0061732	0.146	0.994	1	2	mitochondrial acetyl-CoA biosynthetic process from pyruvate	BP	1	PDHA1	down_ACOR_VSMC
GO:0071543	0.146	0.994	1	2	diphosphoinositol polyphosphate metabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:1901906	0.146	0.994	1	2	diadenosine pentaphosphate	BP	1	NUDT3	down_ACOR_VSMC
GO:1901907	0.146	0.994	1	2	diadenosine pentaphosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:1901908	0.146	0.994	1	2	diadenosine hexaphosphate metabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:1901909	0.146	0.994	1	2	diadenosine hexaphosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:1901910	0.146	0.994	1	2	adenosine 5'-(hexahydrogen pentaphosphate)	BP	1	NUDT3	down_ACOR_VSMC
GO:1901911	0.146	0.994	1	2	adenosine 5'-(hexahydrogen pentaphosphate)	BP	1	NUDT3	down_ACOR_VSMC
GO:0009120	0.146	0.994	1	2	deoxyribonucleoside metabolic process	BP	1	TK1	down_ACOR_VSMC
GO:0015961	0.146	0.994	1	2	diadenosine polyphosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0045637	0.146	0.99	1	73	regulation of myeloid cell differentiation	BP	1	GABPA	down_AFEM_EC
GO:0042221	0.146	1	1	1012	response to chemical	BP	1	GATA5	down_AFEM_VSMC
GO:0042221	0.146	1	1	1012	response to chemical	BP	1	MXRA5	down_AORT_VSMC
GO:0033869	0.146	0.992	1	3	nucleoside bisphosphate catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0034031	0.146	0.992	1	3	ribonucleoside bisphosphate catabolic	BP	1	ACAT1	down_VCAV_EC
GO:0034034	0.146	0.992	1	3	purine nucleoside bisphosphate catabolic	BP	1	ACAT1	down_VCAV_EC
GO:0003175	0.146	0.992	1	3	tricuspid valve development	BP	1	BMPR1A	down_VCAV_EC
GO:0090647	0.146	0.992	1	3	modulation of age-related behavioral decline	BP	1	PRNP	down_VCAV_EC
GO:0006574	0.146	0.992	1	3	valine catabolic process	BP	1	ENSCAFG00000002977	down_VCAV_EC
GO:0061450	0.146	0.992	1	3	trophoblast cell migration	BP	1	SYDE1	down_VCAV_EC
GO:1901163	0.146	0.992	1	3	regulation of trophoblast cell migration	BP	1	SYDE1	down_VCAV_EC
GO:0042886	0.146	0.994	1	527	amide transport	BP	1	JUP	down_VFEM_VSMC
GO:0007276	0.146	0.99	1	130	gamete generation	BP	1	HOXA9	up_AORT_VSMC
GO:0032535	0.146	0.99	1	128	regulation of cellular component size	BP	1	WNT7A	up_AORT_VSMC
GO:0051090	0.146	0.99	1	134	regulation of DNA-binding transcription factor	BP	1	ESR1	up_AORT_VSMC

GO:0099536	0.146	0.99	1	133	synaptic signaling	BP	1	WNT7A	up_AORT_VSMC
GO:0002274	0.146	0.989	1	40	myeloid leukocyte activation	BP	1	BPI	up_APUL_EC
GO:0016241	0.146	0.989	1	41	regulation of macroautophagy	BP	1	LZTS1	up_APUL_EC
GO:0048634	0.146	0.989	1	40	regulation of muscle organ development	BP	1	TBX5	up_APUL_EC
GO:0061326	0.146	0.989	1	41	renal tubule development	BP	1	NPNT	up_APUL_EC
GO:0072080	0.146	0.989	1	41	nephron tubule development	BP	1	NPNT	up_APUL_EC
GO:0072708	0.146	0.994	1	2	response to sorbitol	BP	1	MAPK13	up_VCAV_EC
GO:0072739	0.146	0.994	1	2	response to anisomycin	BP	1	MAPK13	up_VCAV_EC
GO:1901033	0.146	0.994	1	2	positive regulation of response to reactive	BP	1	RIPK1	up_VCAV_EC
GO:1903677	0.146	0.994	1	2	regulation of cap-independent translational	BP	1	NCK1	up_VCAV_EC
GO:1903679	0.146	0.994	1	2	positive regulation of cap-independent translational initiation	BP	1	NCK1	up_VCAV_EC
GO:1904688	0.146	0.994	1	2	regulation of cytoplasmic translational initiation	BP	1	NCK1	up_VCAV_EC
GO:1904690	0.146	0.994	1	2	positive regulation of cytoplasmic translational	BP	1	NCK1	up_VCAV_EC
GO:0006820	0.146	0.99	1	109	anion transport	BP	1	CA2	up_VCAV_VSMC
GO:0007405	0.146	0.989	1	21	neuroblast proliferation	BP	1	ARHGEF2	up_VPOR_EC
GO:0031122	0.146	0.99	1	21	cytoplasmic microtubule organization	BP	1	HOOK3	up_VPOR_EC
GO:0046939	0.146	0.989	1	19	nucleotide phosphorylation	BP	1	FBP1	up_VPOR_EC
GO:0051058	0.146	0.989	1	21	negative regulation of small GTPase mediated signal transduction	BP	1	FBP1	up_VPOR_EC
GO:0006006	0.146	0.99	1	61	glucose metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0098742	0.146	0.99	1	44	cell-cell adhesion via plasma-membrane	BP	1	FLRT3	up_VPUL_EC
GO:0048704	0.146	0.989	1	46	embryonic skeletal system morphogenesis	BP	1	HOXA3	up_VPUL_EC
GO:0043567	0.146075042	0.99061	1	6	regulation of insulin-like growth factor receptor	BP	1	CDH3	up_ACOR_EC
GO:0010640	0.146092554	0.99061	1	6	regulation of platelet-derived growth factor receptor signaling	BP	1	PTGIR	up_ACOR_EC
GO:0006595	0.146121378	0.9906	1	6	polyamine metabolic process	BP	1	AZIN2	up_ACOR_EC
GO:0034110	0.146220305	0.99059	1	6	regulation of homotypic cell-cell adhesion	BP	1	PRKCD	up_ACOR_EC
GO:0072109	0.146519169	0.99055	1	6	glomerular mesangium development	BP	1	FOXC2	up_ACOR_EC
GO:0035774	0.146675362	0.99053	1	6	positive regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_ACOR_EC
GO:0003161	0.146744841	0.99052	1	6	cardiac conduction system development	BP	1	TBX5	up_ACOR_EC
GO:0010941	0.146978747	0.9051	18	524	regulation of cell death	BP	1	NR1H4,SOX9,AQP1,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,CHMP4B,NRP1,PRKCD,PM20D1	up_ACOR_EC
GO:0009892	0.147	0.884	58	835	negative regulation of metabolic process	BP	1	PRICKLE1,NR1H4,PLK3,SERPINE1,SOCS5,ETV6,ENPP1,ERRFI1,SNX25,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTGS2,HIF1A,DYNLL1,DNAJC10,NXN,PTPN2,UCHL5,MORF4L2,SPOPL,PLCL1,PEG3,SMG7,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,APOE,WWC3,KLF5,LYN,BNIP3,STRAP,DDIT3,CBLC,ATF3,VLDLR,REST,ZMYND8,EIF2S1,ARFGEF3,CDYL,PAK2,LRRTM2,A2M,HIF1AN,SIX4,CDKN1A,SPINK2,USP14,KDM3A	down_VSAP_EC
GO:0050865	0.147	0.907	17	135	regulation of cell activation	BP	1	CD274,TBC1D10C,ABL1,ZBTB16,TOX,STAT6,F2RL1,ZFP36L1,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,STX4,NCK1,TGFBR2	up_VSAP_EC
GO:0016042	0.147	0.918	11	80	lipid catabolic process	BP	1	PLCG2,LEP,PLCL1,LPL,ACAD11,LIPE,SMPD1,PRKCE,NEU3,CFI,ENSCAFG00000029553	up_ACOR_VSMC

GO:0071560	0.147	0.93	7	72	cellular response to transforming growth	BP	1	HSPA5,SNX25,TGFBR1,YES1,ADAM17,ENSCAFG00000002015,STRAP	down_VSAP_EC
GO:1901576	0.147	0.945	6	1877	organic substance biosynthetic process	BP	1	HDAC7,CITED2,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0030433	0.147	0.936	6	38	ubiquitin-dependent ERAD pathway	BP	1	OS9,STT3B,HERPUD1,FAF2,WFS1,DZIP3	up_ACOR_VSMC
GO:0006275	0.147	0.936	6	38	regulation of DNA replication	BP	1	ESCO1,BLM,RAD17,USP37,ATRX,RBBP6	up_VCAV_EC
GO:0065008	0.147	0.939	6	1056	regulation of biological quality	BP	1	HOXA3,NR1H4,CCL24,HTR7,FLRT3,NEO1	up_VPUL_EC
GO:0071887	0.147	0.942	5	34	leukocyte apoptotic process	BP	1	PRELID1,AURKB,ARG2,NOC2L,PIK3CD	down_ACOR_VSMC
GO:0043467	0.147	0.948	4	35	regulation of generation of precursor metabolites	BP	1	ENPP1,PGAM1,HIF1A,BNIP3	down_VSAP_EC
GO:0090101	0.147	0.948	4	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:0032608	0.147	0.95	4	24	interferon-beta production	BP	1	TMEM173,TLR4,RIOK3,TLR3	up_VCAV_EC
GO:0045844	0.147	0.95	4	24	positive regulation of striated muscle tissue	BP	1	MEF2C,EDN1,CREB1,CDON	up_VCAV_EC
GO:0048636	0.147	0.95	4	24	positive regulation of muscle organ	BP	1	MEF2C,EDN1,CREB1,CDON	up_VCAV_EC
GO:0062013	0.147	0.949	4	27	positive regulation of small molecule metabolic	BP	1	PDGFB,PTGS2,NOS2,PMAIP1	up_VCAV_EC
GO:0006412	0.147	0.947	4	245	translation	BP	1	RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:0032760	0.147	0.95	4	22	positive regulation of tumor necrosis factor	BP	1	PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC
GO:1903557	0.147	0.95	4	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC
GO:0055085	0.147	0.958	3	284	transmembrane transport	BP	1	LYN,PDPN,NEDD4	down_ACOR_EC
GO:0015918	0.147	0.958	3	27	sterol transport	BP	1	LCAT,SCP2,SOAT1	down_VCAV_EC
GO:0030301	0.147	0.958	3	27	cholesterol transport	BP	1	LCAT,SCP2,SOAT1	down_VCAV_EC
GO:2000826	0.147	0.96	3	14	regulation of heart morphogenesis	BP	1	GATA5,BMP4,TBX5	up_ACOR_VSMC
GO:0022409	0.147	0.957	3	56	positive regulation of cell-cell adhesion	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0008283	0.147	0.959	3	545	cell proliferation	BP	1	HOXA3,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0022610	0.147	0.958	3	326	biological adhesion	BP	1	HOXA7,TIAM1,RADIL	up_VFEM_EC
GO:0006357	0.147	0.959	3	547	regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9,SHOX2	up_VFEM_VSMC
GO:0032722	0.147	0.961	3	14	positive regulation of chemokine production	BP	1	IL6R,MYD88,MAVS	up_VSAP_EC
GO:0099536	0.147	0.97	2	133	synaptic signaling	BP	1	SPG11,STX4	down_ACOR_EC
GO:0048646	0.147	0.972	2	349	anatomical structure formation involved in	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0090199	0.147	0.972	2	15	regulation of release of cytochrome c from	BP	1	BNIP3,FAM162A	down_VSAP_EC
GO:0014904	0.147	0.973	2	12	myotube cell development	BP	1	ACTN1,HOMER1	down_VSAP_EC
GO:0048741	0.147	0.973	2	12	skeletal muscle fiber development	BP	1	ACTN1,HOMER1	down_VSAP_EC
GO:2001275	0.147	0.973	2	11	positive regulation of glucose import in response to insulin	BP	1	NR1H4,PTPN11	down_VSAP_EC
GO:0034377	0.147	0.975	2	7	plasma lipoprotein particle assembly	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0065005	0.147	0.975	2	7	protein-lipid complex assembly	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:2000404	0.147	0.975	2	7	regulation of T cell migration	BP	1	APP,CCL5	up_ACOR_VSMC
GO:0010557	0.147	0.973	2	492	positive regulation of macromolecule biosynthetic process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0000904	0.147	0.97	2	181	cell morphogenesis involved in differentiation	BP	1	ARHGEF26,SLITRK5	up_APUL_EC
GO:0090066	0.147	0.97	2	162	regulation of anatomical structure size	BP	1	AVPR1A,CDC42EP5	up_VFEM_EC
GO:0046365	0.147	0.975	2	7	monosaccharide catabolic process	BP	1	DHDH,GALK1	up_VSAP_EC

GO:0002224	0.147	0.989	1	34	toll-like receptor signaling pathway	BP	1	LYN	down_ACOR_EC
GO:0034332	0.147	0.989	1	32	adherens junction organization	BP	1	ACVRL1	down_ACOR_EC
GO:0003057	0.147	0.994	1	2	regulation of the force of heart contraction by	BP	1	CAV1	down_ACOR_VSMC
GO:0031077	0.147	0.994	1	2	post-embryonic camera-type eye development	BP	1	HMGN1	down_ACOR_VSMC
GO:0070507	0.147	0.99	1	73	regulation of microtubule cytoskeleton organization	BP	1	GPSM2	down_AFEM_EC
GO:0045184	0.147	0.994	1	532	establishment of protein localization	BP	1	SCAMP4	down_AORT_EC
GO:0050790	0.147	0.994	1	532	regulation of catalytic activity	BP	1	CST3	down_AORT_EC
GO:0019336	0.147	0.992	1	3	phenol-containing compound catabolic	BP	1	MAOA	down_VCAV_EC
GO:0019614	0.147	0.992	1	3	catechol-containing compound catabolic	BP	1	MAOA	down_VCAV_EC
GO:0042424	0.147	0.992	1	3	catecholamine catabolic process	BP	1	MAOA	down_VCAV_EC
GO:0042420	0.147	0.992	1	3	dopamine catabolic process	BP	1	MAOA	down_VCAV_EC
GO:0051253	0.147	0.992	1	359	negative regulation of RNA metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0009891	0.147	0.994	1	521	positive regulation of biosynthetic process	BP	1	GATA5	down_VFEM_VSMC
GO:0045184	0.147	0.994	1	532	establishment of protein localization	BP	1	JUP	down_VFEM_VSMC
GO:0044502	0.147	0.992	1	3	positive regulation of signal transduction in	BP	1	CALM1	down_VSAP_EC
GO:0052470	0.147	0.992	1	3	modulation by host of symbiont signal	BP	1	CALM1	down_VSAP_EC
GO:0052525	0.147	0.992	1	3	positive regulation by host of symbiont signal transduction pathway	BP	1	CALM1	down_VSAP_EC
GO:0052526	0.147	0.992	1	3	positive regulation by organism of signal transduction in other organism involved in	BP	1	CALM1	down_VSAP_EC
GO:0075205	0.147	0.992	1	3	modulation by host of symbiont cAMP-mediated signal transduction	BP	1	CALM1	down_VSAP_EC
GO:0075206	0.147	0.992	1	3	positive regulation by host of symbiont cAMP-mediated signal	BP	1	CALM1	down_VSAP_EC
GO:0071895	0.147	0.992	1	3	odontoblast differentiation	BP	1	SERPINE1	down_VSAP_EC
GO:0050865	0.147	0.99	1	135	regulation of cell activation	BP	1	ARG2	up_AORT_VSMC
GO:0060993	0.147	0.989	1	42	kidney morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0003226	0.147	1	1	1	right ventricular compact myocardium	BP	1	CHD7	up_VCAV_EC
GO:0045634	0.147	0.994	1	2	regulation of melanocyte differentiation	BP	1	ADAMTS9	up_VCAV_EC
GO:0045636	0.147	0.994	1	2	positive regulation of melanocyte	BP	1	ADAMTS9	up_VCAV_EC
GO:0048087	0.147	0.994	1	2	positive regulation of developmental	BP	1	ADAMTS9	up_VCAV_EC
GO:0050932	0.147	0.994	1	2	regulation of pigment cell differentiation	BP	1	ADAMTS9	up_VCAV_EC
GO:0050942	0.147	0.994	1	2	positive regulation of pigment cell	BP	1	ADAMTS9	up_VCAV_EC
GO:0061074	0.147	0.994	1	2	regulation of neural retina development	BP	1	DLL4	up_VCAV_EC
GO:1902866	0.147	0.994	1	2	regulation of retina development in camera-	BP	1	DLL4	up_VCAV_EC
GO:0021553	0.147	1	1	1	olfactory nerve development	BP	1	CHD7	up_VCAV_EC
GO:0044057	0.147	0.99	1	110	regulation of system process	BP	1	GATA5	up_VCAV_VSMC
GO:0051321	0.147	0.989	1	61	meiotic cell cycle	BP	1	CYP26B1	up_VPOR_VSMC
GO:0007163	0.147	0.989	1	60	establishment or maintenance of cell	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001764	0.147	0.989	1	45	neuron migration	BP	1	ARHGEF2	up_VPUL_EC
GO:0031348	0.147	0.989	1	46	negative regulation of defense response	BP	1	NR1H4	up_VPUL_EC

GO:0002221	0.147	0.989	1	46	pattern recognition receptor signaling	BP	1	NR1H4	up_VPUL_EC
GO:0002758	0.147	0.989	1	46	innate immune response-activating signal	BP	1	NR1H4	up_VPUL_EC
GO:0001763	0.147	0.99	1	78	morphogenesis of a branching structure	BP	1	SLIT2	up_VPUL_VSMC
GO:0010959	0.147	0.989	1	79	regulation of metal ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0001892	0.147	0.989	1	35	embryonic placenta development	BP	1	GJB5	up_VSAP_VSMC
GO:0050770	0.147	0.989	1	39	regulation of axonogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:1904591	0.147170094	0.97064	2	25	positive regulation of protein import	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0032496	0.147290927	0.94689	4	77	response to lipopolysaccharide	BP	1	NR1H4,PTGIR,NOD2,PTGER4	up_ACOR_EC
GO:0048679	0.147441637	0.99043	1	6	regulation of axon regeneration	BP	1	RGMA	up_ACOR_EC
GO:0048856	0.148	0.873	160	1533	anatomical structure development	BP	1	EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,LGR6,PLCG2,LEP,LBH,AFF3,GATA5,GATA4,CD83,CDC7,ANGPT1,EPYC,HTR2B,RASSF2,MBP,ZRANB1,PRDX4,RECK,SHROOM3,FEZ1,MLLT3,ITM2C,FERMT1,BMP4,LNPK,TBX18,FGFR2,TP53BP1,GJA1,ATRX,TLR3,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,SPINT1,GLRB,ISG15,ACSL6,ZNRF3,CD274,ZNF365,SASH1,LMO4,TMEM108,FGF18,FAM210B,ARHGEF26,NDRG2,ATRN,P4HTM,NEBL,CDKN2B,EBF4,ZMYM2,ITPR1,LIMS2,ANKRD1,F2RL1,CAMK2D,MARCH5,CTSB,BNIP3,EGLN1,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,GPM6A,CHD2,ULK2,DMPK,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,PTGDR,TBX20,BBX,TBX5,MARF1,FZD3,AFF4,FRS2,CPAMD8,RND1,DAG1,POMK,APP,LAMA3,PSEN1,SEMA6D,TGFBR1,PCSK6,SYNJ2BP,CHD7,JUP,SPINK2,SIPA1L1,DDR2,CLN8,FOSL2,PERP,PSKH1,RTKN2,SIAH1,SSH3,C10H2orf49,EDN1,NID1,HPGD,ARID5B,ASAP1,DMC1,SERPINB5,JAM3,B2M,DISC1,AP2B1,TNFRSF11B,TACC1,GAA,ATXN10,FEZ2,SUN1,INPP5K,CNOT4,LHX9,WFS1,WDR48,WASL,ATP2C1,DOCK5,ACP2,ERAP1,ID3,SLC8A1,TEAD1,ENSCAFG00000003530,IL18R1,BVES,RREB1,ZDH	up_ACOR_VSMC
GO:0006811	0.148	0.893	32	330	ion transport	BP	1	CP,CALCRL,ATP8A1,LRRC8D,PDGFB,ATP2B1,RELN,PDE4D,MEF2C,CHD7,SLC35A3,STC1,APLNR,SLC39A8,SLCO2A1,PPP3CA,SLC38A1,SNAP23,LRRC8C,RALBP1,ABCA1,KCNJ3,SLCO3A1,KCNJ2,SLC25A25,PLCG2,NOS2,SPTBN4,RIPK1,MCU,LMTK2,ATP2A1	up_VCAV_EC
GO:0070302	0.148	0.92	10	78	regulation of stress-activated protein kinase	BP	1	EPHB1,MAP3K11,TLR4,EDN1,MAP3K3,BMP2,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0045766	0.148	0.923	9	63	positive regulation of angiogenesis	BP	1	ABL1,BTG1,HDAC7,DLL1,CCBE1,SASH1,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0002440	0.148	0.93	7	51	production of molecular mediator of immune	BP	1	IL7R,KIT,TLR4,GATA3,THOC1,SWAP70,TLR3	up_VCAV_EC
GO:0030100	0.148	0.934	6	70	regulation of endocytosis	BP	1	LRP1,CLIP3,LRPAP1,CYBA,GREM1,PACSIN3	down_VCAV_EC
GO:0048519	0.148	0.942	6	1554	negative regulation of biological process	BP	1	HOXC10,DKK2,HOXA9,LNPEP,TAOK1,BPI	up_AORT_EC
GO:0010631	0.148	0.939	5	118	epithelial cell migration	BP	1	ANGPT4,GREM1,TBXA2R,FAP,ADAM17	up_AFEM_EC
GO:0090132	0.148	0.939	5	118	epithelium migration	BP	1	ANGPT4,GREM1,TBXA2R,FAP,ADAM17	up_AFEM_EC
GO:0048844	0.148	0.942	5	30	artery morphogenesis	BP	1	WNT11,HPGD,ACVRL1,NPRL3,CITED2	up_VSAP_EC
GO:0032481	0.148	0.949	4	24	positive regulation of type I interferon production	BP	1	IRAK1,DHX33,HMGB2,POLR3F	down_ACOR_VSMC
GO:0032414	0.148	0.95	4	21	positive regulation of ion transmembrane transporter activity	BP	1	ACTN2,PLCG2,TCAF1,AKAP6	up_ACOR_VSMC
GO:0010771	0.148	0.958	3	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	IFRD1,NRP1,YWHAH	down_VSAP_EC
GO:0048640	0.148	0.958	3	21	negative regulation of developmental growth	BP	1	IFRD1,WWC3,NRP1	down_VSAP_EC
GO:1905515	0.148	0.958	3	22	non-motile cilium assembly	BP	1	EXOC5,DYNLL1,DISC1	down_VSAP_EC
GO:0045806	0.148	0.96	3	15	negative regulation of endocytosis	BP	1	ATXN2,LRPAP1,SCAMP5	up_ACOR_VSMC

GO:0015849	0.148	0.957	3	56	organic acid transport	BP	1	LEP,SLC17A5,SLC6A6	up_AFEM_EC
GO:0046942	0.148	0.957	3	56	carboxylic acid transport	BP	1	LEP,SLC17A5,SLC6A6	up_AFEM_EC
GO:0031326	0.148	0.965	3	1176	regulation of cellular biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0048646	0.148	0.957	3	349	anatomical structure formation involved in	BP	1	TBX5,HOXA3,HOXA1	up_APUL_EC
GO:0002444	0.148	0.959	3	18	myeloid leukocyte mediated immunity	BP	1	KIT,SNAP23,FES	up_VCAV_EC
GO:0048468	0.148	0.959	3	553	cell development	BP	1	EYA1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060071	0.148	0.96	3	14	Wnt signaling pathway, planar cell polarity	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0072595	0.148	0.96	3	14	maintenance of protein localization in organelle	BP	1	MORC3,CIZ1,TAF8	up_VSAP_EC
GO:0032757	0.148	0.96	3	14	positive regulation of interleukin-8 production	BP	1	F2RL1,ZNF580,MAVS	up_VSAP_EC
GO:0050778	0.148	0.97	2	141	positive regulation of immune response	BP	1	LYN,STX4	down_ACOR_EC
GO:0009988	0.148	0.974	2	8	cell-cell recognition	BP	1	B4GALT1,CCT4	down_ACOR_VSMC
GO:0043954	0.148	0.972	2	14	cellular component maintenance	BP	1	PRNP,RASSF8	down_VCAV_EC
GO:0010524	0.148	0.972	2	12	positive regulation of calcium ion transport into	BP	1	HTT,CALM1	down_VSAP_EC
GO:1900077	0.148	0.972	2	11	negative regulation of cellular response to	BP	1	ENPP1,PTPN2	down_VSAP_EC
GO:0007399	0.148	0.974	2	564	nervous system development	BP	1	HOXC10,WNT7A	up_AORT_VSMC
GO:0035872	0.148	0.974	2	8	nucleotide-binding domain, leucine rich repeat containing	BP	1	TNFAIP3,TLR4	up_VCAV_EC
GO:0070423	0.148	0.974	2	8	nucleotide-binding oligomerization domain containing signaling	BP	1	TNFAIP3,TLR4	up_VCAV_EC
GO:0070431	0.148	0.974	2	8	nucleotide-binding oligomerization domain containing 2 signaling	BP	1	TNFAIP3,TLR4	up_VCAV_EC
GO:0046649	0.148	0.97	2	162	lymphocyte activation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0002429	0.148	0.989	1	35	immune response-activating cell surface receptor signaling	BP	1	LYN	down_ACOR_EC
GO:0010923	0.148	0.989	1	30	negative regulation of phosphatase activity	BP	1	MYO1D	down_ACOR_EC
GO:2001245	0.148	0.994	1	2	regulation of phosphatidylcholine	BP	1	ACSL3	down_ACOR_VSMC
GO:0060541	0.148	0.989	1	73	respiratory system development	BP	1	SRSF6	down_AFEM_EC
GO:2000027	0.148	0.989	1	72	regulation of animal organ morphogenesis	BP	1	SRSF6	down_AFEM_EC
GO:0001547	0.148	0.992	1	3	antral ovarian follicle growth	BP	1	FOXO3	down_VCAV_EC
GO:0003183	0.148	0.992	1	3	mitral valve morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0060391	0.148	0.992	1	3	positive regulation of SMAD protein signal	BP	1	BMPR1A	down_VCAV_EC
GO:0003376	0.148	0.992	1	3	sphingosine-1-phosphate receptor signaling	BP	1	SPNS1	down_VCAV_EC
GO:0009134	0.148	0.992	1	3	nucleoside diphosphate catabolic process	BP	1	ENTPD3	down_VCAV_EC
GO:0034379	0.148	0.992	1	3	very-low-density lipoprotein particle	BP	1	SOAT1	down_VCAV_EC
GO:0080154	0.148	0.992	1	3	regulation of fertilization	BP	1	B4GALT1	down_VCAV_EC
GO:0140115	0.148	0.992	1	3	export across plasma membrane	BP	1	FXYD1	down_VCAV_EC
GO:0010628	0.148	0.994	1	527	positive regulation of gene expression	BP	1	GATA5	down_VFEM_VSMC
GO:0030855	0.148	0.99	1	183	epithelial cell differentiation	BP	1	GATA5	down_VSAP_VSMC
GO:0072521	0.148	0.99	1	185	purine-containing compound metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0098609	0.148	0.99	1	181	cell-cell adhesion	BP	1	GATA5	down_VSAP_VSMC
GO:0007567	0.148	0.994	1	2	parturition	BP	1	HPGD	up_ACOR_VSMC
GO:0001655	0.148	0.99	1	116	urogenital system development	BP	1	EYA1	up_AFEM_VSMC

GO:0044057	0.148	0.99	1	110	regulation of system process	BP	1	IRX5	up_AFEM_VSMC
GO:0006473	0.148	0.989	1	66	protein acetylation	BP	1	TAOK1	up_AORT_EC
GO:0007548	0.148	0.989	1	68	sex differentiation	BP	1	HOXA9	up_AORT_EC
GO:0050890	0.148	0.989	1	67	cognition	BP	1	GPR155	up_AORT_EC
GO:0060840	0.148	0.989	1	42	artery development	BP	1	HOXA1	up_APUL_EC
GO:0001821	0.148	0.992	1	3	histamine secretion	BP	1	SNAP23	up_VCAV_EC
GO:0002349	0.148	0.992	1	3	histamine production involved in inflammatory	BP	1	SNAP23	up_VCAV_EC
GO:0002441	0.148	0.992	1	3	histamine secretion involved in inflammatory	BP	1	SNAP23	up_VCAV_EC
GO:0002553	0.148	0.992	1	3	histamine secretion by mast cell	BP	1	SNAP23	up_VCAV_EC
GO:0035526	0.148	0.994	1	2	retrograde transport, plasma membrane to	BP	1	USP6NL	up_VCAV_EC
GO:0051608	0.148	0.992	1	3	histamine transport	BP	1	SNAP23	up_VCAV_EC
GO:0045646	0.148	0.989	1	19	regulation of erythrocyte differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0030838	0.148	0.989	1	37	positive regulation of actin filament	BP	1	CDC42EP5	up_VFEM_EC
GO:1904062	0.148	0.989	1	62	regulation of cation transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0006479	0.148	0.989	1	45	protein methylation	BP	1	NR1H4	up_VPUL_EC
GO:0008213	0.148	0.989	1	45	protein alkylation	BP	1	NR1H4	up_VPUL_EC
GO:0008360	0.148	0.989	1	46	regulation of cell shape	BP	1	CCL24	up_VPUL_EC
GO:0045598	0.148	0.989	1	47	regulation of fat cell differentiation	BP	1	WIF1	up_VPUL_EC
GO:0097529	0.148108548	0.95633	3	52	myeloid leukocyte migration	BP	1	MMP28,PTGER4,RARRES2	up_ACOR_EC
GO:0003091	0.148238737	0.99032	1	6	renal water homeostasis	BP	1	AQP1	up_ACOR_EC
GO:0048584	0.148314605	0.90194	20	592	positive regulation of response to stimulus	BP	1	C7,CDH3,NR1H4,SOX9,ENSCAFG00000004331,EDEM2,FZD5,DIXDC1,NOD2,IL33,ESM1,TNFRSF19,PTGER4,MAVS,FOXC2,SH3RF3,CLU,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0070262	0.148460784	0.99029	1	6	peptidyl-serine dephosphorylation	BP	1	DUSP26	up_ACOR_EC
GO:0016486	0.148524374	0.99028	1	6	peptide hormone processing	BP	1	PCSK1N	up_ACOR_EC
GO:0095500	0.14861062	0.99027	1	6	acetylcholine receptor signaling pathway	BP	1	AGRN	up_ACOR_EC
GO:1903831	0.14861062	0.99027	1	6	signal transduction involved in cellular response to ammonium	BP	1	AGRN	up_ACOR_EC
GO:1905144	0.14861062	0.99027	1	6	response to acetylcholine	BP	1	AGRN	up_ACOR_EC
GO:1905145	0.14861062	0.99027	1	6	cellular response to acetylcholine	BP	1	AGRN	up_ACOR_EC
GO:0021543	0.148610696	0.9562	3	49	pallium development	BP	1	DIXDC1,DCLK2,NRP1	up_ACOR_EC
GO:0032070	0.148740085	0.99025	1	6	regulation of deoxyribonuclease	BP	1	PRKCD	up_ACOR_EC
GO:0043933	0.149	0.881	64	698	protein-containing complex subunit organization	BP	1	TEK,HCLS1,GBP5,SELP,CDA,MX2,BAIAP2L1,VWF,TLR4,SMAD1,PSME4,IRF8,SNAP91,TMOD1,NASP,MTOR,ACPP,SNAP23,LRRC8C,LNX2,SCAF11,CNOT6,ABCA1,NCKAP1,MZT1,RIOK3,IQGAP2,STMN1,SNX2,SWAP70,SMARCA4,CENPC,NCK1,KCNJ2,FES,MRRF,HIST1H1A,EHD4,BCL10,SENP6,PAN3,TAOK1,PRPF39,CNOT7,GCH1,ASF1A,HMGB1,PMAIP1,ARPC5L,BLM,NUP133,RIPK1,LSM14A,MCU,ZW10,ATRX,ALDH1A3,HP1BP3,P2RX2,TNFAIP1,TMOD3,ARHGEF2,FSCN1,FBXO5	up_VCAV_EC

GO:0048513	0.149	0.885	52	906	animal organ development	BP	1	ADAMTS2,NOTCH2,PDGFRB,SMAD9,NAB2,SDC4,VASN,FBN1,GLIPR2,KANK2,THBS3,BMPR1A,LOX,LMO4,NUMBL,NAGLU,CHRDL1,TBX15,TFE3,ENSCAFG00000018277,HOXC4,CLSTN1,PKD1,SEMA3C,ASPN,THY1,TEAD1,PEX5,B4GALT1,GLI3,EEF2,ZFP36L1,IFT57,CDH2,LOXL3,GSDME,SPRED1,RAB7B,IRX5,TSC22D3,GLIS2,PRKCSH,DDR2,SHC1,RDH10,OMD,GREM1,FOXO3,THRB,ZBTB16,ANKRD54,SEC61A1	down_VCAV_EC
GO:0065009	0.149	0.884	51	735	regulation of molecular function	BP	1	ARHGEF2,VEGFA,NR1H4,SERPINE1,SOCS5,ERRFI1,NUAK1,PTPN11,TRIB3,BHLHE40,PPP1R12A,SMARCA4,SESN2,PTGS2,REM1,HIF1A,DYNLL1,DNAJC10,TNIK,PTPN2,PLCL1,MTDH,ADAM17,MAGED1,CTNNB1,CRYAB,ENSCAFG00000000002015,APOE,LYN,DDIT3,FAM162A,CCNYL1,MMD,CBLC,GSK3B,VLDLR,SH3GLB1,TAX1BP3,HTT,REST,ABHD5,ARFGEF3,CALM1,DISC1,PAK2,CDKN1A,SPINK2,ARF4,YWHAH,MADD,HOMER1	down_VSAP_EC
GO:0006631	0.149	0.916	11	93	fatty acid metabolic process	BP	1	SCD,SREBF1,INSIG1,CAV1,BRCA1,ELOVL1,PPARD,ELOVL6,SGPL1,LIPC,ACADL	down_ACOR_VSMC
GO:0006875	0.149	0.916	11	129	cellular metal ion homeostasis	BP	1	SLC39A7,ERO1A,ATP2B1,HIF1A,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0034599	0.149	0.917	11	81	cellular response to oxidative stress	BP	1	FZD1,PPARGC1B,ABL1,MAP3K5,MGST1,NFE2L2,PDK2,FXN,FBXO7,ZNF580,HTRA2	up_VSAP_EC
GO:1901653	0.149	0.924	8	84	cellular response to peptide	BP	1	ARHGEF2,NR1H4,ENPP1,PTPN11,TRIB3,MYO1C,PTPN2,NR4A1	down_VSAP_EC
GO:2000027	0.149	0.933	6	72	regulation of animal organ morphogenesis	BP	1	BMPR1A,SEMA3C,ASPN,B4GALT1,GREM1,THRB	down_VCAV_EC
GO:0022898	0.149	0.94	5	48	regulation of transmembrane	BP	1	REM1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0030534	0.149	0.941	5	33	adult behavior	BP	1	CHD7,HOXB8,TMOD1,PREX2,SPTBN4	up_VCAV_EC
GO:0042752	0.149	0.941	5	34	regulation of circadian rhythm	BP	1	PPARG,PROX1,ENSCAFG00000010596,TIMELESS,NR1D2	up_VCAV_EC
GO:0010648	0.149	0.948	4	407	negative regulation of cell communication	BP	1	LYN,IGF1R,SULF1,ASPN	down_ACOR_EC
GO:0009058	0.149	0.96	4	1910	biosynthetic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0034333	0.149	0.948	4	25	adherens junction assembly	BP	1	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0045597	0.149	0.947	4	253	positive regulation of cell differentiation	BP	1	ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A	up_VPOR_EC
GO:0006101	0.149	0.959	3	16	citrate metabolic process	BP	1	ACLY,SUCLG1,PDHA1	down_ACOR_VSMC
GO:0030510	0.149	0.957	3	27	regulation of BMP signaling pathway	BP	1	FBN1,CHRDL1,GREM1	down_VCAV_EC
GO:1904064	0.149	0.957	3	27	positive regulation of cation transmembrane	BP	1	FXYD1,THY1,PARK7	down_VCAV_EC
GO:0032835	0.149	0.958	3	21	glomerulus development	BP	1	SULF1,ACTA2,MYO1E	down_VSAP_EC
GO:0033173	0.149	0.959	3	17	calcineurin-NFAT signaling cascade	BP	1	HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0097720	0.149	0.959	3	17	calcineurin-mediated signaling	BP	1	HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0050869	0.149	0.974	2	8	negative regulation of B cell activation	BP	1	MNDA,HMGB3	down_ACOR_VSMC
GO:0051171	0.149	0.986	2	1697	regulation of nitrogen compound metabolic	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0001910	0.149	0.972	2	12	regulation of leukocyte mediated cytotoxicity	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0045685	0.149	0.972	2	11	regulation of glial cell differentiation	BP	1	SLC45A3,CTNNB1	down_VSAP_EC
GO:0036475	0.149	0.972	2	11	neuron death in response to oxidative stress	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:0070670	0.149	0.972	2	11	response to interleukin-4	BP	1	HSPA5,PTPN2	down_VSAP_EC
GO:0071353	0.149	0.972	2	11	cellular response to interleukin-4	BP	1	HSPA5,PTPN2	down_VSAP_EC
GO:1903203	0.149	0.972	2	11	regulation of oxidative stress-induced neuron	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:2000008	0.149	0.972	2	12	regulation of protein localization to cell surface	BP	1	CTNNB1,TAX1BP3	down_VSAP_EC
GO:2001169	0.149	0.972	2	11	regulation of ATP biosynthetic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0008038	0.149	0.975	2	7	neuron recognition	BP	1	NRP1,APP	up_ACOR_VSMC
GO:0006029	0.149	0.97	2	29	proteoglycan metabolic process	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC

GO:0061061	0.149	0.97	2	179	muscle structure development	BP	1	TBX5,NPNT	up_APUL_EC
GO:0035270	0.149	0.989	1	35	endocrine system development	BP	1	HOXA3	down_ACOR_EC
GO:0007605	0.149	0.989	1	27	sensory perception of sound	BP	1	HOXA1	down_ACOR_EC
GO:0071962	0.149	0.994	1	2	mitotic sister chromatid cohesion, centromeric	BP	1	SGO1	down_ACOR_VSMC
GO:1903311	0.149	0.989	1	72	regulation of mRNA metabolic process	BP	1	SRSF6	down_AFEM_EC
GO:0002693	0.149	0.992	1	3	positive regulation of cellular extravasation	BP	1	THY1	down_VCAV_EC
GO:0016255	0.149	0.992	1	3	attachment of GPI anchor to protein	BP	1	PIGS	down_VCAV_EC
GO:0046835	0.149	0.992	1	3	carbohydrate phosphorylation	BP	1	ADK	down_VCAV_EC
GO:0008202	0.149	0.989	1	80	steroid metabolic process	BP	1	HSD3B7	down_VPOR_EC
GO:0030163	0.149	0.992	1	365	protein catabolic process	BP	1	USP12	down_VFEM_EC
GO:0046907	0.149	0.994	1	536	intracellular transport	BP	1	JUP	down_VFEM_VSMC
GO:0034144	0.149	0.992	1	3	negative regulation of toll-like receptor 4 signaling	BP	1	LYN	down_VSAP_EC
GO:0090037	0.149	0.992	1	3	positive regulation of protein kinase C signaling	BP	1	VEGFA	down_VSAP_EC
GO:0050778	0.149	0.99	1	141	positive regulation of immune response	BP	1	ESR1	up_AORT_VSMC
GO:0001657	0.149	0.989	1	42	ureteric bud development	BP	1	NPNT	up_APUL_EC
GO:0072163	0.149	0.989	1	42	mesonephric epithelium development	BP	1	NPNT	up_APUL_EC
GO:0072164	0.149	0.989	1	42	mesonephric tubule development	BP	1	NPNT	up_APUL_EC
GO:1903531	0.149	0.989	1	41	negative regulation of secretion by cell	BP	1	NR1H4	up_APUL_EC
GO:0072602	0.149	0.994	1	2	interleukin-4 secretion	BP	1	GATA3	up_VCAV_EC
GO:0060816	0.149	0.994	1	2	random inactivation of X chromosome	BP	1	CDYL	up_VCAV_EC
GO:0032527	0.149	0.989	1	19	protein exit from endoplasmic reticulum	BP	1	GCC2	up_VPOR_EC
GO:1901224	0.149	0.989	1	20	positive regulation of NIK/NF-kappaB signaling	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0051402	0.149	0.989	1	64	neuron apoptotic process	BP	1	CHL1	up_VPOR_VSMC
GO:0048738	0.149	0.989	1	64	cardiac muscle tissue development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051224	0.149	0.989	1	47	negative regulation of protein transport	BP	1	NR1H4	up_VPUL_EC
GO:1904950	0.149	0.989	1	47	negative regulation of establishment of protein localization	BP	1	NR1H4	up_VPUL_EC
GO:0008104	0.149019919	0.89716	25	763	protein localization	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,AGRN,NOD2,PLS1,ACTN2,TRIM8,PTGER4,PREB,DCLK2,MAVS,LRRC15,LRP4,LRRC4,CHMP4B,TP53INP2,VPS16,ABCB9,NRP1,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0070373	0.149026619	0.96998	2	26	negative regulation of ERK1 and ERK2 cascade	BP	1	NDRG2,DUSP26	up_ACOR_EC
GO:0071549	0.149038066	0.99021	1	6	cellular response to dexamethasone stimulus	BP	1	AQP1	up_ACOR_EC
GO:0032332	0.149104967	0.9902	1	6	positive regulation of chondrocyte	BP	1	SOX9	up_ACOR_EC
GO:0035563	0.149207532	0.99019	1	6	positive regulation of chromatin binding	BP	1	PYGO2	up_ACOR_EC
GO:0050482	0.149239074	0.99019	1	6	arachidonic acid secretion	BP	1	CFI	up_ACOR_EC
GO:1903963	0.149239074	0.99019	1	6	arachidonate transport	BP	1	CFI	up_ACOR_EC
GO:0051491	0.149510369	0.99015	1	6	positive regulation of filopodium assembly	BP	1	NRP1	up_ACOR_EC
GO:1904152	0.149567393	0.99014	1	6	regulation of retrograde protein transport, ER to	BP	1	EDEM2	up_ACOR_EC
GO:0051346	0.149729504	0.94567	4	78	negative regulation of hydrolase activity	BP	1	PCSK1N,IFI6,CST3,PPP1R26	up_ACOR_EC
GO:0042692	0.1498028	0.93813	5	105	muscle cell differentiation	BP	1	MYOZ2,TMOD1,ACTN2,TBX5,RBM38	up_ACOR_EC

GO:0030001	0.15	0.903	18	172	metal ion transport	BP	1	CP,CALCRL,PDGFB,ATP2B1,PDE4D,CHD7,STC1,APLNR,SLC39A8,PPP3CA,KCNJ3,KCNJ2,SLC25A25,PLCG2,SPTBN4,MCU,LMTK2,ATP2A1	up_VCAV_EC
GO:0048562	0.15	0.913	12	102	embryonic organ morphogenesis	BP	1	EIF4A3,HOXA3,INSIG1,MMP14,HOXA7,HOXB7,HOXB5,HOXC4,PHACTR4,TBX15,GLI1,SIX4	down_ACOR_VSMC
GO:0007423	0.15	0.915	11	155	sensory organ development	BP	1	PDGFRB,SDC4,FBN1,NAGLU,CHRDL1,THY1,GLI3,GSDME,IRX5,RDH10,THRB	down_VCAV_EC
GO:0048638	0.15	0.916	11	82	regulation of developmental growth	BP	1	ACACB,SLC6A4,ABL1,DLL1,SAV1,PLXNA4,FXN,DPYSL2,TTL,HTRA2,LATS2	up_VSAP_EC
GO:0032259	0.15	0.922	9	71	methylation	BP	1	PRMT1,EZH2,FBL,THUMPD2,METTL1,PRMT5,WTAP,EMG1,MIS18A	down_ACOR_VSMC
GO:2001252	0.15	0.925	8	61	positive regulation of chromosome organization	BP	1	SREBF1,HNRNPD,AURKB,NEK2,FEN1,BRCA1,TADA2A,CCT4	down_ACOR_VSMC
GO:0070588	0.15	0.926	8	54	calcium ion transmembrane transport	BP	1	PLCG2,HTR2B,MICU2,ITPR1,CACNB3,PRKCE,CHD7,SLC8A1	up_ACOR_VSMC
GO:0071216	0.15	0.925	8	61	cellular response to biotic stimulus	BP	1	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,TLR4,IRF8,ABCA1	up_VCAV_EC
GO:0019438	0.15	0.929	8	1258	aromatic compound biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0006665	0.15	0.929	7	48	sphingolipid metabolic process	BP	1	UGCG,ORMDL3,SMPD1,CLN8,SERINC3,NEU3,SERINC1	up_ACOR_VSMC
GO:0007596	0.15	0.93	7	47	blood coagulation	BP	1	HNF4A,KLKB1,PDGFD,HPSE,F2RL1,HPS4,FBLN1	up_VSAP_EC
GO:1904062	0.15	0.933	6	62	regulation of cation transmembrane transport	BP	1	REM1,LYN,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0003158	0.15	0.934	6	38	endothelium development	BP	1	BTG1,DLL1,F2RL1,ZEB1,MYD88,ACVRL1	up_VSAP_EC
GO:0045667	0.15	0.934	6	38	regulation of osteoblast differentiation	BP	1	TWIST2,AXIN2,ZHX3,HDAC7,DDR2,LIMD1	up_VSAP_EC
GO:0031397	0.15	0.941	5	30	negative regulation of protein ubiquitination	BP	1	SH3RF2,ISG15,PRKCE,PSEN1,PARK7	up_ACOR_VSMC
GO:0046620	0.15	0.941	5	30	regulation of organ growth	BP	1	ACACB,SLC6A4,SAV1,FXN,LATS2	up_VSAP_EC
GO:0023057	0.15	0.947	4	409	negative regulation of signaling	BP	1	LYN,IGF1R,SULF1,ASPN	down_ACOR_EC
GO:0090398	0.15	0.948	4	24	cellular senescence	BP	1	HMGA1,ARG2,RSL1D1,SMC6	down_ACOR_VSMC
GO:0051261	0.15	0.947	4	33	protein depolymerization	BP	1	ARHGEF2,WDR1,CAPG,MID1	down_VSAP_EC
GO:2001243	0.15	0.947	4	33	negative regulation of intrinsic apoptotic	BP	1	ARHGEF2,HYOU1,PTGS2,HIF1A	down_VSAP_EC
GO:0032233	0.15	0.949	4	21	positive regulation of actin filament bundle	BP	1	SYNPO2L,SYNPO2,NRP1,EVL	up_ACOR_VSMC
GO:0009605	0.15	0.948	4	538	response to external stimulus	BP	1	NR1H4,BPI,PCSK1N,NPNT	up_APUL_EC
GO:0043043	0.15	0.946	4	247	peptide biosynthetic process	BP	1	RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:0043154	0.15	0.957	3	23	negative regulation of cysteine-type endopeptidase activity	BP	1	PTGS2,CRYAB,PAK2	down_VSAP_EC
GO:0007265	0.15	0.97	2	121	Ras protein signal transduction	BP	1	PDPN,USP28	down_ACOR_EC
GO:0061564	0.15	0.969	2	119	axon development	BP	1	SPG11,NRP2	down_ACOR_EC
GO:0000578	0.15	0.972	2	11	embryonic axis specification	BP	1	TMED2,CTNNB1	down_VSAP_EC
GO:0010883	0.15	0.972	2	11	regulation of lipid storage	BP	1	PTPN2,ABHD5	down_VSAP_EC
GO:0045687	0.15	0.974	2	7	positive regulation of glial cell differentiation	BP	1	ZNF365,APP	up_ACOR_VSMC
GO:0030216	0.15	0.97	2	29	keratinocyte differentiation	BP	1	HOXA7,FOSL2	up_AFEM_EC
GO:0002042	0.15	0.97	2	29	cell migration involved in sprouting angiogenesis	BP	1	GREM1,TBXA2R	up_AFEM_EC
GO:0051570	0.15	0.974	2	7	regulation of histone H3-K9 methylation	BP	1	KDM3A,ATRX	up_VCAV_EC
GO:0000902	0.15	0.971	2	266	cell morphogenesis	BP	1	CHL1,BAMBI	up_VPOR_VSMC
GO:0051231	0.15	0.994	1	2	spindle elongation	BP	1	AURKB	down_ACOR_VSMC
GO:0035711	0.15	0.994	1	2	T-helper 1 cell activation	BP	1	HMGB1	down_ACOR_VSMC
GO:0051988	0.15	0.994	1	2	regulation of attachment of spindle microtubules to kinetochore	BP	1	NEK2	down_ACOR_VSMC
GO:0031115	0.15	0.992	1	3	negative regulation of microtubule	BP	1	CLIP3	down_VCAV_EC

GO:0034144	0.15	0.992	1	3	negative regulation of toll-like receptor 4 signaling	BP	1	RAB7B	down_VCAV_EC
GO:0018193	0.15	0.992	1	368	peptidyl-amino acid modification	BP	1	PLCL1	down_VFEM_EC
GO:0009605	0.15	0.994	1	538	response to external stimulus	BP	1	JUP	down_VFEM_VSMC
GO:0001818	0.15	0.989	1	65	negative regulation of cytokine production	BP	1	BPI	up_AORT_EC
GO:0071396	0.15	0.99	1	134	cellular response to lipid	BP	1	ESR1	up_AORT_VSMC
GO:0003018	0.15	0.989	1	42	vascular process in circulatory system	BP	1	HTR7	up_APUL_EC
GO:1901861	0.15	0.989	1	41	regulation of muscle tissue development	BP	1	TBX5	up_APUL_EC
GO:0006812	0.15	0.99	1	222	cation transport	BP	1	HOXA3	up_APUL_VSMC
GO:0032707	0.15	0.994	1	2	negative regulation of interleukin-23 production	BP	1	TLR4	up_VCAV_EC
GO:0038146	0.15	0.994	1	2	chemokine (C-X-C motif) ligand 12 signaling	BP	1	CXCR4	up_VCAV_EC
GO:0039692	0.15	0.994	1	2	single stranded viral RNA replication via double stranded DNA	BP	1	CXCL8	up_VCAV_EC
GO:0042421	0.15	0.994	1	2	norepinephrine biosynthetic process	BP	1	GATA3	up_VCAV_EC
GO:0042415	0.15	0.994	1	2	norepinephrine metabolic process	BP	1	GATA3	up_VCAV_EC
GO:0045091	0.15	0.994	1	2	regulation of single stranded viral RNA replication via double	BP	1	CXCL8	up_VCAV_EC
GO:0050679	0.15	0.989	1	62	positive regulation of epithelial cell proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:0030509	0.15	0.989	1	47	BMP signaling pathway	BP	1	NEO1	up_VPUL_EC
GO:0002296	0.15	0.994	1	2	T-helper 1 cell lineage commitment	BP	1	STAT6	up_VSAP_EC
GO:0001570	0.15	0.989	1	37	vasculogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:0009886	0.150148618	0.99006	1	6	post-embryonic animal morphogenesis	BP	1	EFEMP1	up_ACOR_EC
GO:0032400	0.150441817	0.99002	1	6	melanosome localization	BP	1	CDH3	up_ACOR_EC
GO:0032401	0.150441817	0.99002	1	6	establishment of melanosome localization	BP	1	CDH3	up_ACOR_EC
GO:0051875	0.150441817	0.99002	1	6	pigment granule localization	BP	1	CDH3	up_ACOR_EC
GO:0051905	0.150441817	0.99002	1	6	establishment of pigment granule localization	BP	1	CDH3	up_ACOR_EC
GO:0071219	0.150802461	0.95523	3	50	cellular response to molecule of bacterial	BP	1	NR1H4,FZD5,NOD2	up_ACOR_EC
GO:0046890	0.150934135	0.95515	3	51	regulation of lipid biosynthetic process	BP	1	NR1H4,CCDC3,PRKCD	up_ACOR_EC
GO:0048519	0.151	0.87	161	1554	negative regulation of biological process	BP	1	FGF13,TMEM176B,TMEM176A,SMAD6,ARHGAP28,ACTN2,PLCG2,LEP,PLCL1,LBH,DCBLD2,MID1,KCNE3,GATA5,BCL2,CD83,HTR2B,RASSF2,TCAF1,MBP,PRDX4,RECK,FEZ1,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,EVI5L,TUBB4A,TM7SF3,FGFR2,TP53BP1,MX1,EIF4A2,GJA1,ELF1,ATRX,CASTOR1,TRPS1,SH3RF2,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,ATXN2,RERG,ISG15,ZNRF3,CD274,ZNF365,AR,PTGIR,LMO4,PTPN3,NDRG2,CDKN2B,ITPR1,CST3,ZNF174,PLAC8B,KLHL20,LIMS2,ANKRD1,F2RL1,FAM129A,MARCH5,DAPK1,BNIP3,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,LRPAP1,ULK2,OS9,UNC5B,ORMDL3,EVL,SMPD1,APLP1,SPINT2,TBX20,SESN3,SH3RF1,TBX5,CCDC3,PRKCE,CCNT1,MARF1,FZD3,DKKL1,FRS2,RND1,RGS2,RNLS,DAG1,PPP1R26,PARP9,APP,PSEN1,SEMA6D,SYNJ2BP,MXI1,CHD7,JUP,SPINK2,CLN8,NR3C1,WWC2,DUSP22,EDN1,SESN1,OXR1,HPGD,DUSP26,CBX7,LRRC4,ASAP1,FAM107A,DDIT4,B2M,SCAMP5,TNFRSF11B,KLF11,HERPUD1,FEZ2,INPP5K,CNOT4,BMT2,PFKL,WFS1,AZIN2,WASL,CTIF,NAIF1,DOCK5,SH3BP4,ENSCAFG00000029553,ID3,PARK7,GPATCH2,STC2,ZFYVE1,IL18R1,HMB	up_ACOR_VSMC

GO:0050776	0.151	0.899	21	173	regulation of immune response	BP	1	TLR1,PLCG2,LEP,COCH,TP53BP1,ELF1,TLR3,CD274,F2RL1,C1S,PTPN22,C7,PRKCE,PARP9,PSEN1,DUSP22,NOD2,B2M,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0008610	0.151	0.899	21	177	lipid biosynthetic process	BP	1	PIP5K1B,PLCG2,LEP,HTR2B,PRKAA2,LCAT,CHPT1,FAXDC2,PIGN,PIGS,UGCG,PIGG,GGPS1,SCP2,ORMDL3,SMPD1,CCDC3,CRLS1,DKKL1,EDN1,ELOVL7	up_ACOR_VSMC
GO:0008283	0.151	0.904	17	545	cell proliferation	BP	1	LEP,LBH,COL8A2,CD40,DLL1,F3,GPAM,MAB21L1,LGI4,HCK,GREM1,OVOL1,AXIN2,FAP,ADAM17,FOSL2,TNC	up_AFEM_EC
GO:0009260	0.151	0.918	10	83	ribonucleotide biosynthetic process	BP	1	ACLY,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0046390	0.151	0.918	10	83	ribose phosphate biosynthetic process	BP	1	ACLY,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0046879	0.151	0.921	9	63	hormone secretion	BP	1	HNF4A,SLC8B1,RAB11B,PASK,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0006464	0.151	0.932	7	1162	cellular protein modification process	BP	1	NR1H4,MAPK10,PLCL1,GALNT17,ZDHHC16,NPNT,NTRK2	up_APUL_EC
GO:0036211	0.151	0.932	7	1162	protein modification process	BP	1	NR1H4,MAPK10,PLCL1,GALNT17,ZDHHC16,NPNT,NTRK2	up_APUL_EC
GO:0090092	0.151	0.932	6	72	regulation of transmembrane receptor protein serine/threonine	BP	1	VASN,FBN1,BMPR1A,CHRDL1,ASPN,GREM1	down_VCAV_EC
GO:1903008	0.151	0.939	5	47	organelle disassembly	BP	1	PLK3,KIF5B,HIF1A,CDC37,HTT	down_VSAP_EC
GO:1902882	0.151	0.941	5	29	regulation of response to oxidative stress	BP	1	SESN3,FUT8,SESN1,OXR1,PARK7	up_ACOR_VSMC
GO:0035150	0.151	0.94	5	36	regulation of tube size	BP	1	EDNRB,DOCK4,EDN1,GUCY1A1,NOS2	up_VCAV_EC
GO:0050880	0.151	0.94	5	36	regulation of blood vessel size	BP	1	EDNRB,DOCK4,EDN1,GUCY1A1,NOS2	up_VCAV_EC
GO:0030183	0.151	0.94	5	30	B cell differentiation	BP	1	ABL1,DLL1,ZFP36L1,PIK3R1,ZFP36L2	up_VSAP_EC
GO:0009749	0.151	0.947	4	34	response to glucose	BP	1	NR1H4,SMARCA4,SESN2,HIF1A	down_VSAP_EC
GO:0034121	0.151	0.948	4	22	regulation of toll-like receptor signaling	BP	1	TLR1,TLR3,F2RL1,PTPN22	up_ACOR_VSMC
GO:0045935	0.151	0.947	4	491	positive regulation of nucleobase-containing compound metabolic	BP	1	HOXA11,HOXA9,SALL1,SHOX2	up_VSAP_VSMC
GO:0008152	0.151	1	3	3714	metabolic process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0048259	0.151	0.957	3	24	regulation of receptor-mediated endocytosis	BP	1	VEGFA,SERPINE1,LRRTM2	down_VSAP_EC
GO:1903510	0.151	0.957	3	22	mucopolysaccharide metabolic process	BP	1	ENSCAFG00000032470,CEMIP2,CHSY1	down_VSAP_EC
GO:0098927	0.151	0.958	3	17	vesicle-mediated transport between endosomal compartments	BP	1	HOOK3,DNAJC13,LMTK2	up_VCAV_EC
GO:0032757	0.151	0.971	2	14	positive regulation of interleukin-8 production	BP	1	PARK7,MAVS	down_VCAV_EC
GO:0042398	0.151	0.971	2	12	cellular modified amino acid biosynthetic process	BP	1	PLOD2,PLOD3	down_VSAP_EC
GO:0090207	0.151	0.972	2	11	regulation of triglyceride metabolic process	BP	1	APOE,ABHD5	down_VSAP_EC
GO:0032946	0.151	0.969	2	29	positive regulation of mononuclear cell	BP	1	LEP,GPAM	up_AFEM_EC
GO:0050671	0.151	0.969	2	29	positive regulation of lymphocyte proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0060008	0.151	0.974	2	7	Sertoli cell differentiation	BP	1	ARID4B,ATRX	up_VCAV_EC
GO:0086004	0.151	0.972	2	10	regulation of cardiac muscle cell contraction	BP	1	PDE4D,STC1	up_VCAV_EC
GO:2000171	0.151	0.973	2	8	negative regulation of dendrite development	BP	1	PPP3CA,RAPGEF2	up_VCAV_EC
GO:0030003	0.151	0.969	2	157	cellular cation homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0006939	0.151	0.989	1	32	smooth muscle contraction	BP	1	SULF1	down_ACOR_EC
GO:0000720	0.151	0.994	1	2	pyrimidine dimer repair by nucleotide-excision	BP	1	HMGN1	down_ACOR_VSMC
GO:0086103	0.151	0.994	1	2	G protein-coupled receptor signaling pathway involved in heart	BP	1	CAV1	down_ACOR_VSMC
GO:0032769	0.151	0.994	1	2	negative regulation of monooxygenase activity	BP	1	CAV1	down_ACOR_VSMC

GO:0051001	0.151	0.994	1	2	negative regulation of nitric-oxide synthase	BP	1	CAV1	down_ACOR_VSMC
GO:0043588	0.151	0.989	1	74	skin development	BP	1	SRSF6	down_AFEM_EC
GO:0030154	0.151	1	1	1040	cell differentiation	BP	1	GATA5	down_AFEM_VSMC
GO:0002138	0.151	0.992	1	3	retinoic acid biosynthetic process	BP	1	RDH10	down_VCAV_EC
GO:0046351	0.151	0.992	1	3	disaccharide biosynthetic process	BP	1	B4GALT1	down_VCAV_EC
GO:0090191	0.151	0.992	1	3	negative regulation of branching involved in ureteric bud	BP	1	GREM1	down_VCAV_EC
GO:2001268	0.151	0.992	1	3	negative regulation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	PARK7	down_VCAV_EC
GO:0005984	0.151	0.992	1	3	disaccharide metabolic process	BP	1	B4GALT1	down_VCAV_EC
GO:0016102	0.151	0.992	1	3	diterpenoid biosynthetic process	BP	1	RDH10	down_VCAV_EC
GO:0016114	0.151	0.992	1	3	terpenoid biosynthetic process	BP	1	RDH10	down_VCAV_EC
GO:0030091	0.151	0.992	1	3	protein repair	BP	1	PARK7	down_VCAV_EC
GO:0034370	0.151	0.992	1	3	triglyceride-rich lipoprotein particle	BP	1	LCAT	down_VCAV_EC
GO:0034372	0.151	0.992	1	3	very-low-density lipoprotein particle	BP	1	LCAT	down_VCAV_EC
GO:0046007	0.151	0.992	1	3	negative regulation of activated T cell	BP	1	PRNP	down_VCAV_EC
GO:0071500	0.151	0.992	1	3	cellular response to nitrosative stress	BP	1	PARK7	down_VCAV_EC
GO:0071609	0.151	0.992	1	3	chemokine (C-C motif) ligand 5 production	BP	1	MAVS	down_VCAV_EC
GO:0071649	0.151	0.992	1	3	regulation of chemokine (C-C motif) ligand 5	BP	1	MAVS	down_VCAV_EC
GO:1903121	0.151	0.992	1	3	regulation of TRAIL-activated apoptotic	BP	1	PARK7	down_VCAV_EC
GO:0090596	0.151	0.989	1	84	sensory organ morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0008283	0.151	0.994	1	545	cell proliferation	BP	1	JUP	down_VFEM_VSMC
GO:0033700	0.151	0.992	1	3	phospholipid efflux	BP	1	APOE	down_VSAP_EC
GO:0035313	0.151	0.99	1	7	wound healing, spreading of epidermal cells	BP	1	ADAM17	up_AFEM_EC
GO:0036166	0.151	0.994	1	2	phenotypic switching	BP	1	PDGFB	up_VCAV_EC
GO:1900239	0.151	0.994	1	2	regulation of phenotypic switching	BP	1	PDGFB	up_VCAV_EC
GO:1904425	0.151	0.994	1	2	negative regulation of GTP binding	BP	1	ARHGAP28	up_VCAV_EC
GO:0045862	0.151	0.989	1	112	positive regulation of proteolysis	BP	1	C6	up_VCAV_VSMC
GO:0002027	0.151	0.989	1	20	regulation of heart rate	BP	1	SEMA3A	up_VPOR_EC
GO:0060393	0.151	0.989	1	19	regulation of pathway-restricted SMAD protein	BP	1	ACVR2A	up_VPOR_EC
GO:0007498	0.151	0.989	1	38	mesoderm development	BP	1	EYA1	up_VFEM_EC
GO:0008217	0.151	0.989	1	38	regulation of blood pressure	BP	1	AVPR1A	up_VFEM_EC
GO:0008584	0.151	0.989	1	39	male gonad development	BP	1	HOXA9	up_VFEM_EC
GO:0032092	0.151	0.989	1	38	positive regulation of protein binding	BP	1	TIAM1	up_VFEM_EC
GO:0043524	0.151	0.989	1	39	negative regulation of neuron apoptotic process	BP	1	SIX1	up_VFEM_EC
GO:0046546	0.151	0.989	1	39	development of primary male sexual	BP	1	HOXA9	up_VFEM_EC
GO:0010769	0.151	0.989	1	69	regulation of cell morphogenesis involved	BP	1	SHOX2	up_VFEM_VSMC
GO:0051092	0.151	0.989	1	47	positive regulation of NF-kappaB transcription	BP	1	ARHGEF2	up_VPUL_EC
GO:0055001	0.151	0.989	1	47	muscle cell development	BP	1	MYBPC2	up_VPUL_EC
GO:1902107	0.151	0.989	1	47	positive regulation of leukocyte differentiation	BP	1	EVI2B	up_VPUL_EC

GO:0035150	0.151	0.989	1	36	regulation of tube size	BP	1	CAV1	up_VSAP_VSMC
GO:0050880	0.151	0.989	1	36	regulation of blood vessel size	BP	1	CAV1	up_VSAP_VSMC
GO:0002088	0.151033025	0.96933	2	26	lens development in camera-type eye	BP	1	TMOD1,PYGO2	up_ACOR_EC
GO:0097106	0.151047075	0.98994	1	6	postsynaptic density organization	BP	1	LRRC4	up_ACOR_EC
GO:0099084	0.151047075	0.98994	1	6	postsynaptic specialization	BP	1	LRRC4	up_ACOR_EC
GO:0035295	0.151114044	0.90952	13	356	tube development	BP	1	GATA4,SOX9,AQP1,ENSCAFG00000004331,FZD5,SMAD6,ESM1,ADAMTSL2,FOXC2,TBX5,CLSTN1,RARRES2,NRP1	up_ACOR_EC
GO:0032692	0.151119149	0.98993	1	6	negative regulation of interleukin-1 production	BP	1	NR1H4	up_ACOR_EC
GO:0055090	0.151123614	0.98993	1	6	acylglycerol homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0070328	0.151123614	0.98993	1	6	triglyceride homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0032494	0.15114053	0.98993	1	6	response to peptidoglycan	BP	1	NOD2	up_ACOR_EC
GO:0032906	0.151194548	0.98992	1	6	transforming growth factor beta2 production	BP	1	CDH3	up_ACOR_EC
GO:0032909	0.151194548	0.98992	1	6	regulation of transforming growth factor beta2	BP	1	CDH3	up_ACOR_EC
GO:0044255	0.151626197	0.91342	11	293	cellular lipid metabolic process	BP	1	NR1H4,THNSL2,ENSCAFG00000004331,PTGDS,CFI,CHPT1,PIGS,RARRES2,AGPAT2,PRKCD,PM20D1	up_ACOR_EC
GO:1901361	0.152	0.901	19	154	organic cyclic compound catabolic process	BP	1	AXIN2,GDA,TENT5C,HSD17B14,ALDH6A1,EXOSC7,PYM1,DFFB,ZFP36L1,GALK1,ENTPD3,SMG9,SAMD4B,ZFP36L2,PNP,TNRC6C,HMOX1,DDIT4,IDO2	up_VSAP_EC
GO:0051179	0.152	0.907	18	1747	localization	BP	1	C3AR1,MZT1,HOOK3,XPOT,HOXA3,ARHGEF2,ENSCAFG00000002015,SLC7A11,SEMA3A,ENSCAFG00000005494,GOLT1B,GCC2,ABHD5,SLC25A16,SRP54,TMEM87B,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:0042981	0.152	0.905	15	471	regulation of apoptotic process	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,PPARGC1A,FAP	up_AFEM_EC
GO:0009967	0.152	0.907	14	435	positive regulation of signal transduction	BP	1	LEP,DLL1,F3,MLLT11,LMCD1,PLAGL2,GREM1,FAM53B,CLEC16A,CYLD,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0015711	0.152	0.914	11	81	organic anion transport	BP	1	LEP,SLC26A7,ABCA1,SLC17A5,SCP2,SLCO1A2,PSEN1,CLN8,PLIN2,CFI,SLC25A12	up_ACOR_VSMC
GO:0050896	0.152	0.925	11	2346	response to stimulus	BP	1	NR1H4,RGS1,IL18BP,MRC1,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1,MXRA5	up_VPUL_EC
GO:0030336	0.152	0.923	8	86	negative regulation of cell migration	BP	1	SULF1,SERPINE1,DPYSL3,STARD13,APOE,MMP28,STRAP,ZMYND8	down_VSAP_EC
GO:1903037	0.152	0.923	8	65	regulation of leukocyte cell-cell adhesion	BP	1	IL7R,GATA3,PELI1,ARG2,ITPKB,NCK1,BCL10,HMGB1	up_VCAV_EC
GO:0018130	0.152	0.927	8	1261	heterocycle biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0009987	0.152	1	6	5086	cellular process	BP	1	TGFBI,AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:1903555	0.152	0.934	6	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	TLR1,LEP,TLR3,CD274,PTPN22,NOD2	up_ACOR_VSMC
GO:0007498	0.152	0.934	6	38	mesoderm development	BP	1	HOXA11,WNT11,OSR1,ZFP36L1,IRX3,CITED2	up_VSAP_EC
GO:0032479	0.152	0.939	5	33	regulation of type I interferon production	BP	1	IRAK1,DHX33,CACTIN,HMGB2,POLR3F	down_ACOR_VSMC
GO:0007179	0.152	0.938	5	57	transforming growth factor beta receptor	BP	1	SMAD9,VASN,FBN1,ASPN,FUT8	down_VCAV_EC
GO:0032869	0.152	0.938	5	57	cellular response to insulin stimulus	BP	1	ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:1903706	0.152	0.937	5	119	regulation of hemopoiesis	BP	1	HOXA9,HOXA7,DLL1,CYLD,EVI2B	up_AFEM_EC
GO:0072091	0.152	0.947	4	24	regulation of stem cell proliferation	BP	1	NF2,PDCD2,HMGB2,ASPM	down_ACOR_VSMC
GO:0048660	0.152	0.946	4	35	regulation of smooth muscle cell proliferation	BP	1	SULF1,CTNNB1,ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:0001889	0.152	0.948	4	22	liver development	BP	1	HNF4A,LIMS2,SULF2,CITED2	up_VSAP_EC
GO:0051704	0.152	0.946	4	476	multi-organism process	BP	1	HOXA11,HOXA9,TLR2,CAV1	up_VSAP_VSMC
GO:0032212	0.152	0.958	3	16	positive regulation of telomere maintenance via	BP	1	AURKB,NEK2,CCT4	down_ACOR_VSMC

GO:1904358	0.152	0.958	3	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	AURKB,NEK2,CCT4	down_ACOR_VSMC
GO:0014031	0.152	0.956	3	27	mesenchymal cell development	BP	1	BMPR1A,SEMA3C,RDH10	down_VCAV_EC
GO:0014032	0.152	0.956	3	27	neural crest cell development	BP	1	BMPR1A,SEMA3C,RDH10	down_VCAV_EC
GO:0031122	0.152	0.957	3	21	cytoplasmic microtubule organization	BP	1	PLK3,HOOK3,KPNB1	down_VSAP_EC
GO:1901616	0.152	0.958	3	15	organic hydroxy compound catabolic	BP	1	MAOA,MOXD1,INPP5K	up_ACOR_VSMC
GO:0046847	0.152	0.957	3	17	filopodium assembly	BP	1	ENSCAFG00000010224,ITGA6,FSCN1	up_VCAV_EC
GO:0030182	0.152	0.956	3	327	neuron differentiation	BP	1	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0019538	0.152	0.985	2	1713	protein metabolic process	BP	1	PLCL1,USP12	down_VFEM_EC
GO:1900006	0.152	0.971	2	11	positive regulation of dendrite development	BP	1	APOE,VLDLR	down_VSAP_EC
GO:0007026	0.152	0.973	2	8	negative regulation of microtubule	BP	1	TAOK1,ARHGEF2	up_VCAV_EC
GO:0033081	0.152	0.973	2	8	regulation of T cell differentiation in thymus	BP	1	IL7R,ZEB1	up_VCAV_EC
GO:0060326	0.152	0.968	2	84	cell chemotaxis	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0090066	0.152	0.969	2	162	regulation of anatomical structure size	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0120035	0.152	0.969	2	160	regulation of plasma membrane bounded cell projection organization	BP	1	CAV1,SHOX2	up_VSAP_VSMC
GO:0009051	0.152	0.994	1	2	pentose-phosphate shunt, oxidative branch	BP	1	PGD	down_ACOR_VSMC
GO:0042816	0.152	0.994	1	2	vitamin B6 metabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0042822	0.152	0.994	1	2	pyridoxal phosphate metabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0051252	0.152	1	1	1051	regulation of RNA metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0009438	0.152	0.992	1	3	methylglyoxal metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0035461	0.152	0.992	1	3	vitamin transmembrane transport	BP	1	FOLR2	down_VCAV_EC
GO:0000188	0.152	0.992	1	3	inactivation of MAPK activity	BP	1	SPRED1	down_VCAV_EC
GO:0051901	0.152	0.992	1	3	positive regulation of mitochondrial	BP	1	DCN	down_VCAV_EC
GO:1904181	0.152	0.992	1	3	positive regulation of membrane depolarization	BP	1	DCN	down_VCAV_EC
GO:1905446	0.152	0.992	1	3	regulation of mitochondrial ATP synthesis coupled	BP	1	PARK7	down_VCAV_EC
GO:0009642	0.152	0.992	1	3	response to light intensity	BP	1	AKT2	down_VCAV_EC
GO:0015884	0.152	0.992	1	3	folic acid transport	BP	1	FOLR2	down_VCAV_EC
GO:0033216	0.152	0.992	1	3	ferric iron import	BP	1	ARHGAP1	down_VCAV_EC
GO:0046348	0.152	0.992	1	3	amino sugar catabolic process	BP	1	CHID1	down_VCAV_EC
GO:0097283	0.152	0.992	1	3	keratinocyte apoptotic process	BP	1	ZFP36L1	down_VCAV_EC
GO:1900084	0.152	0.992	1	3	regulation of peptidyl-tyrosine	BP	1	GREM1	down_VCAV_EC
GO:1902172	0.152	0.992	1	3	regulation of keratinocyte apoptotic process	BP	1	ZFP36L1	down_VCAV_EC
GO:0009888	0.152	0.994	1	545	tissue development	BP	1	GATA5	down_VFEM_VSMC
GO:0060754	0.152	0.992	1	3	positive regulation of mast cell chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0009435	0.152	0.992	1	3	NAD biosynthetic process	BP	1	NMNAT2	down_VSAP_EC
GO:0080154	0.152	0.992	1	3	regulation of fertilization	BP	1	SPINK2	down_VSAP_EC
GO:0048245	0.152	0.994	1	2	eosinophil chemotaxis	BP	1	HRH1	up_ACOR_VSMC
GO:0048732	0.152	0.989	1	116	gland development	BP	1	HOXA9	up_AFEM_VSMC
GO:0002572	0.152	0.994	1	2	pro-T cell differentiation	BP	1	GATA3	up_VCAV_EC

GO:0001911	0.152	0.994	1	2	negative regulation of leukocyte mediated	BP	1	IL7R	up_VCAV_EC
GO:2000625	0.152	0.994	1	2	regulation of miRNA catabolic process	BP	1	TENT2	up_VCAV_EC
GO:0001915	0.152	0.994	1	2	negative regulation of T cell mediated cytotoxicity	BP	1	IL7R	up_VCAV_EC
GO:0031342	0.152	0.994	1	2	negative regulation of cell killing	BP	1	IL7R	up_VCAV_EC
GO:1901342	0.152	0.989	1	114	regulation of vasculature development	BP	1	C6	up_VCAV_VSMC
GO:0051893	0.152	0.989	1	20	regulation of focal adhesion assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0051897	0.152	0.989	1	20	positive regulation of protein kinase B signaling	BP	1	MTDH	up_VPOR_EC
GO:0090109	0.152	0.989	1	20	regulation of cell-substrate junction	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0032103	0.152	0.989	1	69	positive regulation of response to external	BP	1	C3AR1	up_VPOR_VSMC
GO:0046328	0.152	0.989	1	61	regulation of JNK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030010	0.152	0.988	1	41	establishment of cell polarity	BP	1	CYP26B1	up_VFEM_EC
GO:0003205	0.152	0.989	1	67	cardiac chamber development	BP	1	SHOX2	up_VFEM_VSMC
GO:0035023	0.152	0.989	1	46	regulation of Rho protein signal transduction	BP	1	ARHGEF2	up_VPUL_EC
GO:0008154	0.152	0.989	1	81	actin polymerization or depolymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0006941	0.152	0.989	1	36	striated muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0030836	0.152176414	0.98978	1	6	positive regulation of actin filament	BP	1	ACTN2	up_ACOR_EC
GO:0061136	0.152230473	0.94442	4	78	regulation of proteasomal protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0002367	0.152293456	0.96892	2	26	cytokine production involved in immune	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0050996	0.152339726	0.98976	1	6	positive regulation of lipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0044550	0.152342795	0.98976	1	6	secondary metabolite biosynthetic process	BP	1	CDH3	up_ACOR_EC
GO:0003413	0.15234798	0.98976	1	6	chondrocyte differentiation involved in endochondral bone	BP	1	SOX9	up_ACOR_EC
GO:0045776	0.152417692	0.98975	1	6	negative regulation of blood pressure	BP	1	RNLS	up_ACOR_EC
GO:0048731	0.152562625	0.88727	39	1247	system development	BP	1	SH3TC2,CPAMD8,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TBX18,SOX9,PTH1R,NDRG2,AQP1,ENSCAFG00000004331,FZD5,SEMA6D,DIXDC1,PDLIM3,RGMA,LHX9,SMAD6,ACTN2,ESM1,PAK3,DLX3,TNFRSF19,PTGER4,DCLK2,ADAMTSL2,MAPK8IP2,FOXC2,TBX5,LRP4,CLSTN1,C23H3orf58,RARRES2,NRP1,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:0033622	0.152794031	0.9897	1	6	integrin activation	BP	1	PTGER4	up_ACOR_EC
GO:0070307	0.152825798	0.98969	1	6	lens fiber cell development	BP	1	TMOD1	up_ACOR_EC

GO:0043170	0.153	0.867	262	2980	macromolecule metabolic process	BP	1	ELK3,HMGB1,MCM6,RNPS1,SREBF1,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,HOXA3,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,RAD54L,POLE,DDX23,NAB2,SLC35C2,MRPS18B,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,EDC4,AURKB,NONO,MMP14,HNRNPL,TK1,CDKN2C,TOPBP1,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,RNF152,DIS3,GMNN,DHCR24,BRCA1,NOC4L,WDR62,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,PRCP,FARSA,TFRC,DDX51,ENSCAFG00000015065,PPARD,CDC6,POLH,NEIL3,RAP2C,YBX3,HNRNPF,UBE2J2,YWHAB,CYCS,NCL,RAC1,NUP62,UGDH,	down_ACOR_VSMC
GO:0019222	0.153	0.868	170	1934	regulation of metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,IL7R,ADGRF5,KIT,SELE,PRCP,PPP2R5A,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,TSPAN8,RELN,CD34,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,FAM3C,ODC1,SPTLC2,ARG2,CASP8,MTOR,TENT2,SAMD8,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,TUT7,SLK,SH3BP5,CNOT6,DEPP1,RSC1A1,ENC1,CCAR1,PPP1R2,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,APOD,NCK1,ESCO1,DPH5,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,PTGS2,MMD,TOP1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,PAN3,TAOK1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,ADIPOR2,HMGB1,AHR,NOS2,PMAIP1,ZNF789,BLM,NUP133,SPTBN4,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,PDGFD,USP37,WTAP,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,H	up_VCAV_EC
GO:0007423	0.153	0.9	19	155	sensory organ development	BP	1	THRB,CDON,OSR2,INSIG2,MAB21L1,LRIG3,IRX5,DLL1,OSR1,RARG,MFN2,ZEB1,CTNS,CLCN2,SMG9,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0019216	0.153	0.919	9	101	regulation of lipid metabolic process	BP	1	NR1H4,TRIB3,PTGS2,SLC45A3,APOE,LYN,SH3GLB1,REST,ABHD5	down_VSAP_EC
GO:0043406	0.153	0.92	9	62	positive regulation of MAP kinase activity	BP	1	HTR2B,BMP4,PDE5A,SASH1,FGF18,FRS2,PSEN1,EDN1,MAP3K7	up_ACOR_VSMC
GO:0000077	0.153	0.923	8	60	DNA damage checkpoint	BP	1	THOC1,ETAA1,USP28,TAOK1,BLM,RAD17,CUL4A,TOPBP1	up_VCAV_EC
GO:0019827	0.153	0.923	8	59	stem cell population maintenance	BP	1	HOOK3,PROX1,MMP24,LDB2,JAG1,CUL4A,KDM3A,ZC3H13	up_VCAV_EC
GO:0072330	0.153	0.923	8	68	monocarboxylic acid biosynthetic process	BP	1	EDN1,PTGS1,PROX1,ELOVL7,ENSCAFG00000024323,PTGS2,HIF1A,ALDH1A3	up_VCAV_EC
GO:0006936	0.153	0.926	7	74	muscle contraction	BP	1	SULF1,TPM4,HTR7,ACTA2,CALM1,MYBPC2,HOMER1	down_VSAP_EC
GO:0033993	0.153	0.925	7	186	response to lipid	BP	1	LBH,CRY2,CD40,FIBIN,NR3C1,TBXA2R,ADAM17	up_AFEM_EC
GO:0060047	0.153	0.927	7	57	heart contraction	BP	1	PDE4D,STC1,EDN1,MTOR,KCNJ2,GCH1,SPTBN4	up_VCAV_EC
GO:0042742	0.153	0.933	6	39	defense response to bacterium	BP	1	TLR1,COCH,ISG15,PLAC8B,F2RL1,NOD2	up_ACOR_VSMC
GO:0045934	0.153	0.945	4	407	negative regulation of nucleobase-containing compound metabolic	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0035710	0.153	0.947	4	22	CD4-positive, alpha-beta T cell activation	BP	1	CD274,STAT6,CD83,TGFBR2	up_VSAP_EC

GO:0061005	0.153	0.955	3	28	cell differentiation involved in kidney	BP	1	GLI3,GLIS2,GREM1	down_VCAV_EC
GO:0035914	0.153	0.956	3	22	skeletal muscle cell differentiation	BP	1	KLF5,ATF3,SIX4	down_VSAP_EC
GO:0006749	0.153	0.958	3	14	glutathione metabolic process	BP	1	CTNS,IDH1,ENSCAFG00000006478	up_VSAP_EC
GO:0035295	0.153	0.97	2	356	tube development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0030225	0.153	0.971	2	12	macrophage differentiation	BP	1	VEGFA,PTPN2	down_VSAP_EC
GO:0071480	0.153	0.971	2	12	cellular response to gamma radiation	BP	1	CRYAB,CDKN1A	down_VSAP_EC
GO:0043254	0.153	0.969	2	164	regulation of protein complex assembly	BP	1	TRIM9,CDC42EP5	up_VFEM_EC
GO:0031344	0.153	0.968	2	161	regulation of cell projection organization	BP	1	CAV1,SHOX2	up_VSAP_VSMC
GO:0045087	0.153	0.968	2	161	innate immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0051209	0.153	0.988	1	28	release of sequestered calcium ion into cytosol	BP	1	LYN	down_ACOR_EC
GO:0051283	0.153	0.988	1	28	negative regulation of sequestering of calcium	BP	1	LYN	down_ACOR_EC
GO:0032707	0.153	0.994	1	2	negative regulation of interleukin-23 production	BP	1	RAC1	down_ACOR_VSMC
GO:0051132	0.153	0.994	1	2	NK T cell activation	BP	1	ELF4	down_ACOR_VSMC
GO:1901386	0.153	0.994	1	2	negative regulation of voltage-gated calcium	BP	1	REM1	down_ACOR_VSMC
GO:1901841	0.153	0.994	1	2	regulation of high voltage-gated calcium channel	BP	1	REM1	down_ACOR_VSMC
GO:1901842	0.153	0.994	1	2	negative regulation of high voltage-gated calcium channel activity	BP	1	REM1	down_ACOR_VSMC
GO:0008544	0.153	0.989	1	75	epidermis development	BP	1	SRSF6	down_AFEM_EC
GO:0016197	0.153	0.989	1	78	endosomal transport	BP	1	ANKRD50	down_AFEM_EC
GO:2001234	0.153	0.989	1	75	negative regulation of apoptotic signaling	BP	1	IVNS1ABP	down_AFEM_EC
GO:0038033	0.153	0.992	1	3	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular	BP	1	VEGFA	down_VSAP_EC
GO:0006694	0.153	0.988	1	42	steroid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0030073	0.153	0.988	1	42	insulin secretion	BP	1	NR1H4	up_APUL_EC
GO:0048771	0.153	0.988	1	43	tissue remodeling	BP	1	HOXA3	up_APUL_EC
GO:0051048	0.153	0.988	1	42	negative regulation of secretion	BP	1	NR1H4	up_APUL_EC
GO:0003307	0.153	0.994	1	2	regulation of Wnt signaling pathway involved in heart	BP	1	BMP2	up_VCAV_EC
GO:0014041	0.153	0.994	1	2	regulation of neuron maturation	BP	1	EDNRB	up_VCAV_EC
GO:0090209	0.153	0.994	1	2	negative regulation of triglyceride metabolic	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:1902308	0.153	0.994	1	2	regulation of peptidyl-serine dephosphorylation	BP	1	SWAP70	up_VCAV_EC
GO:0032956	0.153	0.989	1	116	regulation of actin cytoskeleton organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0035272	0.153	0.988	1	21	exocrine system development	BP	1	SEMA3A	up_VPOR_EC
GO:0072666	0.153	0.988	1	21	establishment of protein localization to vacuole	BP	1	GCC2	up_VPOR_EC
GO:1904018	0.153	0.988	1	69	positive regulation of vasculature development	BP	1	C3AR1	up_VPOR_VSMC
GO:0060349	0.153	0.988	1	38	bone morphogenesis	BP	1	CYP26B1	up_VFEM_EC
GO:0030072	0.153	0.988	1	48	peptide hormone secretion	BP	1	NR1H4	up_VPUL_EC
GO:0071901	0.153	0.988	1	37	negative regulation of protein serine/threonine	BP	1	CAV1	up_VSAP_VSMC
GO:0033135	0.153	0.988	1	40	regulation of peptidyl-serine phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0055088	0.153	0.988	1	37	lipid homeostasis	BP	1	CAV1	up_VSAP_VSMC
GO:0050805	0.153039346	0.98966	1	6	negative regulation of synaptic transmission	BP	1	KCNB1	up_ACOR_EC

GO:1901879	0.153102209	0.96866	2	26	regulation of protein depolymerization	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0085029	0.153169003	0.98964	1	6	extracellular matrix assembly	BP	1	MFAP4	up_ACOR_EC
GO:1900017	0.153184005	0.98964	1	6	positive regulation of cytokine production involved in inflammatory	BP	1	NOD2	up_ACOR_EC
GO:0060433	0.153202821	0.98964	1	6	bronchus development	BP	1	ADAMTSL2	up_ACOR_EC
GO:2000117	0.153495562	0.96847	2	27	negative regulation of cysteine-type	BP	1	IFI6,CST3	up_ACOR_EC
GO:0035455	0.153705934	0.98957	1	6	response to interferon-alpha	BP	1	IFIT2	up_ACOR_EC
GO:0019098	0.153759179	0.98956	1	6	reproductive behavior	BP	1	MAPK8IP2	up_ACOR_EC
GO:0035728	0.153896484	0.98954	1	6	response to hepatocyte growth factor	BP	1	NRP1	up_ACOR_EC
GO:0035729	0.153896484	0.98954	1	6	cellular response to hepatocyte growth factor	BP	1	NRP1	up_ACOR_EC
GO:0070887	0.154	0.874	83	775	cellular response to chemical stimulus	BP	1	VEGFD,SMAD6,ACTN2,IFNGR1,LEP,LBH,GATA5,SKP2,PRKAA2,FERMT1,BMP4,TM7SF3,FGFR2,ABCA1,EIF4A2,ATRX,MED14,HRH1,CASTOR1,PPARGC1A,LATS2,CITED2,TP53INP1,AR,SASH1,SLC2A5,TMEM108,FGF18,FAM210B,CDKN2B,ADCY6,ANKRD1,F2RL1,DAPK1,CTSB,BNIP3,NCEH1,AKAP6,CREBRF,NRP1,UBR1,PTPN22,NPNT,EVL,APLP1,PTGDR,SESN3,CCDC3,PRKCE,FRS2,AGRN,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,JUP,CCL5,NR3C1,DUSP22,RAB11B,SESN1,OXR1,HPGD,NOD2,LRRC4,ARID5B,FAM107A,DDIT4,JAM3,B2M,ENSCAFG00000018360,HERPUD1,GNAQ,INPP5K,WFS1,DZIP3,SH3BP4,ENSCAFG00000029553,PARK7,STC2,CRKL	up_ACOR_VSMC
GO:0043068	0.154	0.894	23	190	positive regulation of programmed cell death	BP	1	WNT11,CD274,PLEKHF1,SLIT2,CRADD,ABL1,BTG1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,MFN2,TRAF7,RBCK1,MYC,PRMT2,ZNF205,HTRA2,NCK1,HMOX1,DEDD2,LATS2	up_VSAP_EC
GO:0051098	0.154	0.906	14	129	regulation of binding	BP	1	PDGFB,TMEM173,MEF2C,GATA3,RALB,ARHGAP28,PPP3CA,BMP2,STMN1,MFNG,NSD1,RAPGEF2,HMGB1,CDON	up_VCAV_EC
GO:0010467	0.154	0.917	12	1787	gene expression	BP	1	ACVRL1,YEATS2,HOXA3,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,WDR12,NEDD4	down_ACOR_EC
GO:0065008	0.154	0.926	8	1056	regulation of biological quality	BP	1	ACVRL1,LYN,HOXA3,PDPN,NRP2,USP28,STX4,NEDD4	down_ACOR_EC
GO:0070661	0.154	0.922	8	63	leukocyte proliferation	BP	1	HMGB1,MNDA,GREM1,ARG2,TFRC,CORO1A,ELF4,CTPS1	down_ACOR_VSMC
GO:0016236	0.154	0.925	7	88	macroautophagy	BP	1	DCN,GABARAP,POLDIP2,WDR45,CLEC16A,RETREG1,EMC6	down_VCAV_EC
GO:0052548	0.154	0.925	7	80	regulation of endopeptidase activity	BP	1	PTGS2,CRYAB,LYN,FAM162A,REST,PAK2,SPINK2	down_VSAP_EC
GO:0002221	0.154	0.927	7	46	pattern recognition receptor signaling	BP	1	F2RL1,MYD88,NLRX1,TKFC,CYBA,UNC93B1,FLOT1	up_VSAP_EC
GO:0002758	0.154	0.927	7	46	innate immune response-activating signal	BP	1	F2RL1,MYD88,NLRX1,TKFC,CYBA,UNC93B1,FLOT1	up_VSAP_EC
GO:0048771	0.154	0.932	6	43	tissue remodeling	BP	1	HMGB1,HOXA3,CAV1,GREM1,B4GALT1,TFRC	down_ACOR_VSMC
GO:0051168	0.154	0.931	6	57	nuclear export	BP	1	PTPN14,PTPN11,IWS1,SMG7,DDX39B,GSK3B	down_VSAP_EC
GO:0008217	0.154	0.933	6	38	regulation of blood pressure	BP	1	RNPEP,EMP2,DLL1,F2RL1,TBXA2R,ACVRL1	up_VSAP_EC
GO:0097305	0.154	0.938	5	31	response to alcohol	BP	1	PTGFR,SLIT2,CDH1,OSBPL7,TGFBR2	up_VSAP_EC
GO:0006468	0.154	0.946	4	544	protein phosphorylation	BP	1	MAPK10,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0048468	0.154	0.946	4	553	cell development	BP	1	MAPK10,ARHGEF26,SLITRK5,NTRK2	up_APUL_EC
GO:0000902	0.154	0.944	4	266	cell morphogenesis	BP	1	ARHGEF2,ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0045582	0.154	0.947	4	22	positive regulation of T cell differentiation	BP	1	ZBTB16,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0044706	0.154	0.955	3	27	multi-multicellular organism process	BP	1	RECK,SYDE1,B4GALT1	down_VCAV_EC
GO:0010522	0.154	0.955	3	24	regulation of calcium ion transport into cytosol	BP	1	LYN,HTT,CALM1	down_VSAP_EC
GO:0032502	0.154	0.968	3	1661	developmental process	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0060071	0.154	0.958	3	14	Wnt signaling pathway, planar cell polarity	BP	1	MLLT3,ZNRF3,FZD3	up_ACOR_VSMC

GO:0071356	0.154	0.954	3	57	cellular response to tumor necrosis factor	BP	1	CYLD,CCL5,ADAM17	up_AFEM_EC
GO:1904894	0.154	0.957	3	17	positive regulation of STAT cascade	BP	1	HCLS1,IL7R,KIT	up_VCAV_EC
GO:0007166	0.154	0.958	3	686	cell surface receptor signaling pathway	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0006721	0.154	0.958	3	14	terpenoid metabolic process	BP	1	DHRS4,RETSAT,DHRS9	up_VSAP_EC
GO:0072657	0.154	0.968	2	144	protein localization to membrane	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0032506	0.154	0.972	2	8	cytokinetic process	BP	1	AURKB,NUP62	down_ACOR_VSMC
GO:0050994	0.154	0.97	2	14	regulation of lipid catabolic process	BP	1	AKT2,LONP2	down_VCAV_EC
GO:0072595	0.154	0.97	2	14	maintenance of protein localization in organelle	BP	1	PARK7,ARL2BP	down_VCAV_EC
GO:0032715	0.154	0.971	2	11	negative regulation of interleukin-6 production	BP	1	NR1H4,SOCS5	down_VSAP_EC
GO:0042634	0.154	0.971	2	11	regulation of hair cycle	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0050819	0.154	0.97	2	12	negative regulation of coagulation	BP	1	SERPINE1,APOE	down_VSAP_EC
GO:1902110	0.154	0.97	2	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:1902686	0.154	0.97	2	12	mitochondrial outer membrane permeabilization involved	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:1903307	0.154	0.972	2	8	positive regulation of regulated secretory	BP	1	F2RL1,SCAMP5	up_ACOR_VSMC
GO:0043032	0.154	0.972	2	8	positive regulation of macrophage activation	BP	1	TLR4,CD200	up_VCAV_EC
GO:0051091	0.154	0.968	2	87	positive regulation of DNA-binding transcription factor activity	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0006873	0.154	0.968	2	160	cellular ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0044272	0.154	0.988	1	35	sulfur compound biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0046824	0.154	0.988	1	30	positive regulation of nucleocytoplasmic	BP	1	NEDD4	down_ACOR_EC
GO:1903862	0.154	0.994	1	2	positive regulation of oxidative phosphorylation	BP	1	CDK1	down_ACOR_VSMC
GO:1905448	0.154	0.994	1	2	positive regulation of mitochondrial ATP synthesis coupled	BP	1	CDK1	down_ACOR_VSMC
GO:0052548	0.154	0.988	1	80	regulation of endopeptidase activity	BP	1	CST3	down_VPOR_EC
GO:0006357	0.154	0.994	1	547	regulation of transcription by RNA polymerase II	BP	1	GATA5	down_VFEM_VSMC
GO:0002420	0.154	0.992	1	3	natural killer cell mediated cytotoxicity directed against tumor	BP	1	PVR	down_VSAP_EC
GO:0002423	0.154	0.992	1	3	natural killer cell mediated immune	BP	1	PVR	down_VSAP_EC
GO:0002857	0.154	0.992	1	3	positive regulation of natural killer cell mediated immune	BP	1	PVR	down_VSAP_EC
GO:0002858	0.154	0.992	1	3	regulation of natural killer cell mediated cytotoxicity directed against tumor	BP	1	PVR	down_VSAP_EC
GO:0002860	0.154	0.992	1	3	positive regulation of natural killer cell mediated cytotoxicity	BP	1	PVR	down_VSAP_EC
GO:0046476	0.154	0.991	1	3	glycosylceramide biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0002855	0.154	0.992	1	3	regulation of natural killer cell mediated immune response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:0000289	0.154	0.989	1	7	nuclear-transcribed mRNA poly(A) tail shortening	BP	1	SAMD4B	up_AFEM_EC
GO:0032717	0.154	0.989	1	7	negative regulation of interleukin-8 production	BP	1	BPI	up_AFEM_EC
GO:0032814	0.154	0.989	1	7	regulation of natural killer cell activation	BP	1	LEP	up_AFEM_EC
GO:0034377	0.154	0.989	1	7	plasma lipoprotein particle assembly	BP	1	PLAGL2	up_AFEM_EC
GO:0048643	0.154	0.989	1	7	positive regulation of skeletal muscle tissue	BP	1	DLL1	up_AFEM_EC

GO:0060638	0.154	0.989	1	7	mesenchymal-epithelial cell signaling	BP	1	TNC	up_AFEM_EC
GO:0065005	0.154	0.989	1	7	protein-lipid complex assembly	BP	1	PLAGL2	up_AFEM_EC
GO:1900746	0.154	0.989	1	7	regulation of vascular endothelial growth factor	BP	1	DLL1	up_AFEM_EC
GO:1902547	0.154	0.989	1	7	regulation of cellular response to vascular endothelial growth factor	BP	1	DLL1	up_AFEM_EC
GO:2000737	0.154	0.989	1	7	negative regulation of stem cell differentiation	BP	1	LBH	up_AFEM_EC
GO:0032984	0.154	0.988	1	70	protein-containing complex disassembly	BP	1	TAOK1	up_AORT_EC
GO:0006954	0.154	0.989	1	147	inflammatory response	BP	1	ESR1	up_AORT_VSMC
GO:0009266	0.154	0.988	1	43	response to temperature stimulus	BP	1	PCSK1N	up_APUL_EC
GO:0002246	0.154	0.994	1	2	wound healing involved in inflammatory response	BP	1	HIF1A	up_VCAV_EC
GO:0090594	0.154	0.994	1	2	inflammatory response to wounding	BP	1	HIF1A	up_VCAV_EC
GO:0043242	0.154	0.988	1	21	negative regulation of protein complex	BP	1	ARHGEF2	up_VPOR_EC
GO:0045995	0.154	0.988	1	40	regulation of embryonic development	BP	1	SIX1	up_VFEM_EC
GO:0010038	0.154	0.988	1	62	response to metal ion	BP	1	FBP1	up_VFEM_VSMC
GO:0003231	0.154	0.988	1	48	cardiac ventricle development	BP	1	TBX5	up_VPUL_EC
GO:0003279	0.154	0.988	1	48	cardiac septum development	BP	1	TBX5	up_VPUL_EC
GO:0030917	0.154	0.994	1	2	midbrain-hindbrain boundary development	BP	1	KDM2B	up_VSAP_EC
GO:0051668	0.154	0.988	1	39	localization within membrane	BP	1	NETO1	up_VSAP_VSMC
GO:0060041	0.154	0.988	1	41	retina development in camera-type eye	BP	1	IRX5	up_VSAP_VSMC
GO:0060322	0.154138454	0.92074	8	193	head development	BP	1	NDRG2,AQP1,SEMA6D,DIXDC1,IL11RA,DCLK2,NRP1,PYGO2	up_ACOR_EC
GO:0021604	0.154250784	0.98949	1	6	cranial nerve structural organization	BP	1	NRP1	up_ACOR_EC
GO:0021612	0.154250784	0.98949	1	6	facial nerve structural organization	BP	1	NRP1	up_ACOR_EC
GO:1904424	0.154327152	0.98948	1	6	regulation of GTP binding	BP	1	ARHGAP28	up_ACOR_EC
GO:0006516	0.154365061	0.98948	1	6	glycoprotein catabolic process	BP	1	EDEM2	up_ACOR_EC
GO:0033599	0.154501097	0.98946	1	6	regulation of mammary gland epithelial cell	BP	1	PYGO2	up_ACOR_EC
GO:0021800	0.154524502	0.98945	1	6	cerebral cortex tangential migration	BP	1	NRP1	up_ACOR_EC
GO:0044848	0.15453302	0.98945	1	6	biological phase	BP	1	CDH3	up_ACOR_EC
GO:0044851	0.15453302	0.98945	1	6	hair cycle phase	BP	1	CDH3	up_ACOR_EC
GO:0048819	0.15453302	0.98945	1	6	regulation of hair follicle maturation	BP	1	CDH3	up_ACOR_EC
GO:0051764	0.154605978	0.98944	1	6	actin crosslink formation	BP	1	PLS1	up_ACOR_EC
GO:0032530	0.154717241	0.98943	1	6	regulation of microvillus organization	BP	1	PLS1	up_ACOR_EC
GO:0003184	0.154783493	0.98942	1	6	pulmonary valve morphogenesis	BP	1	SMAD6	up_ACOR_EC
GO:0014066	0.154795634	0.9681	2	26	regulation of phosphatidylinositol 3-	BP	1	SOX9,C23H3orf58	up_ACOR_EC
GO:0014911	0.154970727	0.98939	1	6	positive regulation of smooth muscle cell	BP	1	SEMA6D	up_ACOR_EC

GO:0034645	0.155	0.868	140	1546	cellular macromolecule biosynthetic process	BP	1	ELK3,HMGB1,MCM6,SREBF1,MCM4,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,NEDD4,RRM1,MED17,POLA1,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,POLA2,MPDU1,SRRT,GINS4,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,RAD51,XYLT1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,TK1,TOPBP1,EZH2,GREM1,RFC4,NEK2,FEN1,SMARCC1,PLK3,PCNA,DHX33,HOXA7,TONSL,MCM10,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,FARSA,PPARD,CDC6,POLH,YBX3,NCL,NUP62,MRPL37,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,PUM3,CDC45,SMARCAL1,TBX15,GRWD1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,MRPL18,CDC5L,NUS1,HMGN1,CCT4,SIX4,NECAB3,MED16,EIF3M,ENSCAFG00000017103,GEN1,POLR1C	down_ACOR_VSMC
GO:0072358	0.155	0.888	31	268	cardiovascular system development	BP	1	HOXA7,WNT11,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,WARS2,HPSE,CCBE1,RECK,PLPP3,DLX3,ZFP36L1,TBXA2R,SASH1,LOX,HPGD,ZFAND5,ANPEP,ACVRL1,PPP3CB,HMOX1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0044283	0.155	0.896	21	201	small molecule biosynthetic process	BP	1	SCD,LSS,SREBF1,BCAT1,HMGCR,INSIG1,DHCR24,BRCA1,MVD,ELOVL1,ELOVL6,FDFT1,PRPS1,CTH,LIPC,NUDT1,PGD,NUS1,CTPS1,PDSS1,NUDT3	down_ACOR_VSMC
GO:0090407	0.155	0.898	19	177	organophosphate biosynthetic process	BP	1	ACSL3,PRPSAP1,ACLY,RRM1,PFAS,TKT,MVD,ELOVL1,VAC14,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,NUS1,GK5,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0032101	0.155	0.905	14	173	regulation of response to external stimulus	BP	1	VEGFA,NR1H4,SERPINE1,SOCS5,PTGS2,PTPN2,ADAM17,APOE,MMP28,LYN,GBP5,A2M,NRP1,USP14	down_VSAP_EC
GO:0098542	0.155	0.908	13	100	defense response to other organism	BP	1	TLR1,COCH,MX1,TLR3,ISG15,PLAC8B,F2RL1,BNIP3,PTPN22,PARP9,NOD2,DDIT4,SERINC3	up_ACOR_VSMC
GO:0051402	0.155	0.918	9	64	neuron apoptotic process	BP	1	PPARGC1A,USP53,NRP1,UNC5B,APP,PSEN1,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0006351	0.155	0.929	7	1069	transcription, DNA-templated	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0061138	0.155	0.93	6	73	morphogenesis of a branching epithelium	BP	1	CLSTN1,SEMA3C,B4GALT1,GLI3,RDH10,GREM1	down_VCAV_EC
GO:0009267	0.155	0.93	6	60	cellular response to starvation	BP	1	ASNS,HSPA5,SESN2,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0007187	0.155	0.931	6	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	CALCRL,EDN1,ABCA1,AKAP12,GRM8,RAPGEF2	up_VCAV_EC
GO:0048754	0.155	0.936	5	57	branching morphogenesis of an epithelial tube	BP	1	CLSTN1,B4GALT1,GLI3,RDH10,GREM1	down_VCAV_EC
GO:0001764	0.155	0.936	5	45	neuron migration	BP	1	ARHGEF2,VEGFA,CTNNB1,DISC1,NRP1	down_VSAP_EC
GO:0051208	0.155	0.938	5	29	sequestering of calcium ion	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0051282	0.155	0.938	5	29	regulation of sequestering of calcium ion	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0042303	0.155	0.938	5	30	molting cycle	BP	1	FGF7,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0042633	0.155	0.938	5	30	hair cycle	BP	1	FGF7,SAV1,HPSE,LRP4,TRADD	up_VSAP_EC
GO:0001704	0.155	0.944	4	43	formation of primary germ layer	BP	1	BMPR1A,COL6A1,LAMA3,TLX2	down_VCAV_EC
GO:0003143	0.155	0.946	4	22	embryonic heart tube morphogenesis	BP	1	GJA1,CITED2,TBX20,PSEN1	up_ACOR_VSMC
GO:0045839	0.155	0.946	4	25	negative regulation of mitotic nuclear division	BP	1	RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0032880	0.155	0.954	3	266	regulation of protein localization	BP	1	LYN,ACSL3,STX4	down_ACOR_EC
GO:0006826	0.155	0.957	3	15	iron ion transport	BP	1	RAB11B,LMTK2,B2M	up_ACOR_VSMC

GO:0060043	0.155	0.958	3	14	regulation of cardiac muscle cell proliferation	BP	1	FGFR2,TBX20,TBX5	up_ACOR_VSMC
GO:0009893	0.155	0.96	3	995	positive regulation of metabolic process	BP	1	TLR2,EYA1,HOXA9	up_AFEM_VSMC
GO:0012501	0.155	0.956	3	561	programmed cell death	BP	1	CHL1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0071396	0.155	0.968	2	134	cellular response to lipid	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0080090	0.155	0.985	2	1734	regulation of primary metabolic process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0043552	0.155	0.97	2	11	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	LYN,SH3GLB1	down_VSAP_EC
GO:0090218	0.155	0.97	2	11	positive regulation of lipid kinase activity	BP	1	LYN,SH3GLB1	down_VSAP_EC
GO:0048668	0.155	0.973	2	7	collateral sprouting	BP	1	ULK2,APP	up_ACOR_VSMC
GO:0042273	0.155	0.988	1	35	ribosomal large subunit biogenesis	BP	1	WDR12	down_ACOR_EC
GO:0071887	0.155	0.988	1	34	leukocyte apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0090101	0.155	0.988	1	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ASPN	down_ACOR_EC
GO:0035928	0.155	0.993	1	2	rRNA import into mitochondrion	BP	1	MRPL18	down_ACOR_VSMC
GO:0045901	0.155	0.993	1	2	positive regulation of translational elongation	BP	1	EIF5A	down_ACOR_VSMC
GO:0072367	0.155	0.993	1	2	regulation of lipid transport by regulation of transcription from RNA	BP	1	SREBF2	down_ACOR_VSMC
GO:0072368	0.155	0.993	1	2	regulation of lipid transport by negative regulation of transcription from RNA polymerase II	BP	1	SREBF2	down_ACOR_VSMC
GO:0090370	0.155	0.993	1	2	negative regulation of cholesterol efflux	BP	1	SREBF2	down_ACOR_VSMC
GO:0007341	0.155	0.994	1	2	penetration of zona pellucida	BP	1	B4GALT1	down_ACOR_VSMC
GO:0010885	0.155	0.993	1	2	regulation of cholesterol storage	BP	1	SREBF2	down_ACOR_VSMC
GO:0010886	0.155	0.993	1	2	positive regulation of cholesterol storage	BP	1	SREBF2	down_ACOR_VSMC
GO:0016093	0.155	0.993	1	2	polyprenol metabolic process	BP	1	NUS1	down_ACOR_VSMC
GO:0016094	0.155	0.993	1	2	polyprenol biosynthetic process	BP	1	NUS1	down_ACOR_VSMC
GO:0034418	0.155	0.993	1	2	urate biosynthetic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0036065	0.155	0.993	1	2	fucosylation	BP	1	SLC35C2	down_ACOR_VSMC
GO:0036066	0.155	0.993	1	2	protein O-linked fucosylation	BP	1	SLC35C2	down_ACOR_VSMC
GO:0046415	0.155	0.993	1	2	urate metabolic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0051029	0.155	0.993	1	2	rRNA transport	BP	1	MRPL18	down_ACOR_VSMC
GO:0006351	0.155	1	1	1069	transcription, DNA-templated	BP	1	GATA5	down_AFEM_VSMC
GO:0032774	0.155	1	1	1073	RNA biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0097659	0.155	1	1	1072	nucleic acid-templated transcription	BP	1	GATA5	down_AFEM_VSMC
GO:0009642	0.155	0.991	1	3	response to light intensity	BP	1	RDH11	down_VSAP_EC
GO:0010635	0.155	0.991	1	3	regulation of mitochondrial fusion	BP	1	BNIP3	down_VSAP_EC
GO:0010637	0.155	0.991	1	3	negative regulation of mitochondrial fusion	BP	1	BNIP3	down_VSAP_EC
GO:0045653	0.155	0.991	1	3	negative regulation of megakaryocyte	BP	1	PRMT1	down_VSAP_EC
GO:1902956	0.155	0.994	1	2	regulation of mitochondrial electron transport, NADH to	BP	1	PARK7	up_ACOR_VSMC
GO:0006654	0.155	0.989	1	7	phosphatidic acid biosynthetic process	BP	1	AGPAT2	up_AFEM_EC
GO:0010659	0.155	0.989	1	7	cardiac muscle cell apoptotic process	BP	1	CAMK2A	up_AFEM_EC

GO:0010665	0.155	0.989	1	7	regulation of cardiac muscle cell apoptotic	BP	1	CAMK2A	up_AFEM_EC
GO:0010829	0.155	0.989	1	7	negative regulation of glucose transmembrane	BP	1	LEP	up_AFEM_EC
GO:0046473	0.155	0.989	1	7	phosphatidic acid metabolic process	BP	1	AGPAT2	up_AFEM_EC
GO:0051154	0.155	0.989	1	7	negative regulation of striated muscle cell	BP	1	DLL1	up_AFEM_EC
GO:0055089	0.155	0.989	1	7	fatty acid homeostasis	BP	1	GPAM	up_AFEM_EC
GO:0060487	0.155	0.989	1	7	lung epithelial cell differentiation	BP	1	THRB	up_AFEM_EC
GO:0060973	0.155	0.989	1	7	cell migration involved in heart development	BP	1	BVES	up_AFEM_EC
GO:0090136	0.155	0.989	1	7	epithelial cell-cell adhesion	BP	1	BVES	up_AFEM_EC
GO:1900120	0.155	0.989	1	7	regulation of receptor binding	BP	1	GREM2	up_AFEM_EC
GO:2000727	0.155	0.989	1	7	positive regulation of cardiac muscle cell	BP	1	GREM1	up_AFEM_EC
GO:0048871	0.155	0.989	1	120	multicellular organismal homeostasis	BP	1	HOXC10	up_AFEM_VSMC
GO:1903706	0.155	0.989	1	119	regulation of hemopoiesis	BP	1	HOXA9	up_AFEM_VSMC
GO:0016055	0.155	0.989	1	134	Wnt signaling pathway	BP	1	WNT7A	up_AORT_VSMC
GO:0198738	0.155	0.989	1	134	cell-cell signaling by wnt	BP	1	WNT7A	up_AORT_VSMC
GO:0006479	0.155	0.988	1	45	protein methylation	BP	1	NR1H4	up_APUL_EC
GO:0008213	0.155	0.988	1	45	protein alkylation	BP	1	NR1H4	up_APUL_EC
GO:0035023	0.155	0.988	1	46	regulation of Rho protein signal transduction	BP	1	ARHGEF26	up_APUL_EC
GO:0051494	0.155	0.988	1	44	negative regulation of cytoskeleton organization	BP	1	TUBB4A	up_APUL_EC
GO:0021814	0.155	0.994	1	2	cell motility involved in cerebral cortex radial glia	BP	1	ENSCAFG00000010224	up_VCAV_EC
GO:0021815	0.155	0.994	1	2	modulation of microtubule cytoskeleton involved in cerebral	BP	1	ENSCAFG00000010224	up_VCAV_EC
GO:0010744	0.155	0.994	1	2	positive regulation of macrophage derived foam	BP	1	PRKCH	up_VCAV_EC
GO:1903377	0.155	0.994	1	2	negative regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	HIF1A	up_VCAV_EC
GO:1903715	0.155	0.994	1	2	regulation of aerobic respiration	BP	1	HIF1A	up_VCAV_EC
GO:0021536	0.155	0.988	1	21	diencephalon development	BP	1	SEMA3A	up_VPOR_EC
GO:0048538	0.155	0.988	1	20	thymus development	BP	1	HOXA3	up_VPOR_EC
GO:0048736	0.155	0.988	1	66	appendage development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0060173	0.155	0.988	1	66	limb development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0016051	0.155	0.988	1	63	carbohydrate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0045666	0.155	0.988	1	68	positive regulation of neuron differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0046578	0.155	0.988	1	77	regulation of Ras protein signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0001936	0.155	0.988	1	49	regulation of endothelial cell proliferation	BP	1	CCL24	up_VPUL_EC
GO:0048638	0.155	0.988	1	82	regulation of developmental growth	BP	1	TBX5	up_VPUL_VSMC
GO:0016202	0.155	0.988	1	39	regulation of striated muscle tissue	BP	1	SHOX2	up_VSAP_VSMC
GO:0006650	0.155005842	0.94303	4	78	glycerophospholipid metabolic process	BP	1	NR1H4,ENSCAFG00000004331,PIGS,AGPAT2	up_ACOR_EC
GO:0071696	0.155173526	0.98936	1	6	ectodermal placode development	BP	1	NRP1	up_ACOR_EC
GO:0002252	0.155243701	0.92412	7	166	immune effector process	BP	1	C7,FZD5,PTGER4,MAVS,IFIT2,AGBL5,PRKCD	up_ACOR_EC
GO:0048468	0.155357898	0.8977	19	553	cell development	BP	1	SH3TC2,MYOZ2,TMOD1,BRSK1,SOX9,PTH1R,FZD5,DIXDC1,RGMA,ACTN2,PAK3,DCLK2,MAPK8IP2,FOXC2,LRP4,NRP1,ARHGEF26,PYGO2,DBNDD2	up_ACOR_EC
GO:0032637	0.155694832	0.9678	2	26	interleukin-8 production	BP	1	NOD2,MAVS	up_ACOR_EC

GO:0021954	0.155866121	0.96774	2	26	central nervous system neuron development	BP	1	DCLK2,NRP1	up_ACOR_EC
GO:0009595	0.155888058	0.98926	1	6	detection of biotic stimulus	BP	1	NOD2	up_ACOR_EC
GO:0033160	0.155993455	0.98924	1	6	positive regulation of protein import into	BP	1	MAVS	up_ACOR_EC
GO:0051241	0.156	0.884	38	336	negative regulation of multicellular organismal process	BP	1	THRB,HOXA7,TWIST2,HOXA9,WNT11,CD274,AXIN2,C5AR2,LIMS2,SLIT2,SLC6A4,HDAC7,KLKB1,KCNE3,DLL1,EPN2,OSR1,SAV1,ANXA4,ZBTB16,RARG,F2RL1,ZFP36L1,FXN,PIK3R1,MYC,IRX3,TBXA2R,RTN4RL1,HOXC10,LRP4,FBXO7,LIMD1,NLRX1,CD83,MAPKBP1,NFIB,ACVRL1	up_VSAP_EC
GO:0040012	0.156	0.885	35	303	regulation of locomotion	BP	1	VEGFD,LGR6,TCAF1,RECK,BMP4,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,EVL,SPINT2,TBX5,PRKCE,DAG1,APP,LAMA3,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,FAM107A,JAM3,WASL,DOCK5,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0010942	0.156	0.892	24	200	positive regulation of cell death	BP	1	WNT11,CD274,AXIN2,PLEKHF1,SLIT2,CRADD,ABL1,BTG1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,MFN2,TRAF7,RBCK1,MYC,PRMT2,ZNF205,HTRA2,NCK1,HMOX1,DEDD2,LATS2	up_VSAP_EC
GO:0030335	0.156	0.896	20	165	positive regulation of cell migration	BP	1	TWIST2,WNT11,FAM107A,ENPP2,FGF7,ABL1,HDAC7,PDGFD,CCBE1,STAT5A,F2RL1,DDR2,PIK3R1,TIAM1,SASH1,ZNF580,STX4,HMOX1,TGFBR2,BAG4	up_VSAP_EC
GO:0043549	0.156	0.9	16	244	regulation of kinase activity	BP	1	PDGFRB,DCN,PRNP,BGN,LMO4,ENSCAFG00000014978,AKT1S1,CSPG4,ASPN,THY1,PARK7,SASH1,SPRED1,MAPRE3,DDR2,SHC1	down_VCAV_EC
GO:0071495	0.156	0.908	12	365	cellular response to endogenous stimulus	BP	1	LEP,LBH,CRY2,CHRM2,TMEM100,GREM1,AVPR1A,CAMK2A,GREM2,NR3C1,ADAM17,KANK1	up_AFEM_EC
GO:0050896	0.156	0.92	12	2346	response to stimulus	BP	1	NR1H4,MAPK10,BPI,PLCL1,PCSK1N,ARHGEF26,ZDHHC16,SLITRK5,NPNT,NTRK2,HOXA1,PDE1A	up_APUL_EC
GO:0018209	0.156	0.911	11	125	peptidyl-serine modification	BP	1	VEGFA,SGK1,BCAR3,ILK,PTGS2,GALNT1,NAA10,PLCL1,GSK3B,PAK2,CAMK2D	down_VSAP_EC
GO:0043270	0.156	0.922	8	56	positive regulation of ion transport	BP	1	ACTN2,PLCG2,TCAF1,AKAP6,PSEN1,FXYD1,WFS1,PARK7	up_ACOR_VSMC
GO:0048589	0.156	0.924	7	188	developmental growth	BP	1	LEP,GAS1,DLL1,PLXNA4,GPAM,LGR6,ACACB	up_AFEM_EC
GO:0097659	0.156	0.928	7	1072	nucleic acid-templated transcription	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0051250	0.156	0.931	6	38	negative regulation of lymphocyte activation	BP	1	BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0002821	0.156	0.937	5	30	positive regulation of adaptive immune	BP	1	TP53BP1,CD274,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0008625	0.156	0.937	5	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	PIK3R1,RAF1,STX4,HMOX1,DEDD2	up_VSAP_EC
GO:2001237	0.156	0.944	4	33	negative regulation of extrinsic apoptotic	BP	1	ARHGEF2,SERPINE1,HTT,NRP1	down_VSAP_EC
GO:0006401	0.156	0.943	4	88	RNA catabolic process	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0032088	0.156	0.945	4	26	negative regulation of NF-kappaB transcription	BP	1	TNFAIP3,NLRC5,PELI1,CD200	up_VCAV_EC
GO:1900407	0.156	0.946	4	24	regulation of cellular response to oxidative	BP	1	TLR4,GCH1,RIPK1,HIF1A	up_VCAV_EC
GO:0033866	0.156	0.946	4	22	nucleoside bisphosphate biosynthetic process	BP	1	ACACB,PDK2,ACSS2,DCAKD	up_VSAP_EC
GO:0034030	0.156	0.946	4	22	ribonucleoside bisphosphate biosynthetic	BP	1	ACACB,PDK2,ACSS2,DCAKD	up_VSAP_EC
GO:0034033	0.156	0.946	4	22	purine nucleoside bisphosphate biosynthetic	BP	1	ACACB,PDK2,ACSS2,DCAKD	up_VSAP_EC
GO:0051049	0.156	0.944	4	479	regulation of transport	BP	1	NETO1,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0021545	0.156	0.955	3	21	cranial nerve development	BP	1	CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0034446	0.156	0.955	3	23	substrate adhesion-dependent cell spreading	BP	1	ILK,ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0030595	0.156	0.953	3	57	leukocyte chemotaxis	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:0055010	0.156	0.957	3	15	ventricular cardiac muscle tissue morphogenesis	BP	1	CHD7,DLL4,PROX1	up_VCAV_EC
GO:0009312	0.156	0.971	2	9	oligosaccharide biosynthetic process	BP	1	MPDU1,B4GALT1	down_ACOR_VSMC
GO:0002090	0.156	0.969	2	14	regulation of receptor internalization	BP	1	LRPAP1,GREM1	down_VCAV_EC

GO:0010676	0.156	0.969	2	13	positive regulation of cellular carbohydrate	BP	1	SLC45A3,PTPN2	down_VSAP_EC
GO:0042417	0.156	0.971	2	9	dopamine metabolic process	BP	1	SNCAIP,GCH1	up_VCAV_EC
GO:0051208	0.156	0.988	1	29	sequestering of calcium ion	BP	1	LYN	down_ACOR_EC
GO:0051282	0.156	0.988	1	29	regulation of sequestering of calcium ion	BP	1	LYN	down_ACOR_EC
GO:0048660	0.156	0.988	1	35	regulation of smooth muscle cell proliferation	BP	1	SULF1	down_ACOR_EC
GO:2000278	0.156	0.988	1	37	regulation of DNA biosynthetic process	BP	1	ACVRL1	down_ACOR_EC
GO:0009403	0.156	0.993	1	2	toxin biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0070814	0.156	0.993	1	2	hydrogen sulfide biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:1901301	0.156	0.993	1	2	regulation of cargo loading into COPII-coated	BP	1	INSIG1	down_ACOR_VSMC
GO:1904211	0.156	0.993	1	2	membrane protein proteolysis involved in retrograde protein	BP	1	HM13	down_ACOR_VSMC
GO:0090068	0.156	0.988	1	78	positive regulation of cell cycle process	BP	1	GPSM2	down_AFEM_EC
GO:0006629	0.156	0.991	1	382	lipid metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0006928	0.156	0.993	1	557	movement of cell or subcellular component	BP	1	JUP	down_VFEM_VSMC
GO:0090091	0.156	0.991	1	3	positive regulation of extracellular matrix	BP	1	FSCN1	down_VSAP_EC
GO:1902993	0.156	0.991	1	3	positive regulation of amyloid precursor protein catabolic process	BP	1	LYN	down_VSAP_EC
GO:1905936	0.156	0.993	1	2	regulation of germ cell proliferation	BP	1	PRDX4	up_ACOR_VSMC
GO:2000254	0.156	0.993	1	2	regulation of male germ cell proliferation	BP	1	PRDX4	up_ACOR_VSMC
GO:0071281	0.156	0.993	1	2	cellular response to iron ion	BP	1	B2M	up_ACOR_VSMC
GO:0007218	0.156	0.989	1	7	neuropeptide signaling pathway	BP	1	GPR1	up_AFEM_EC
GO:0032594	0.156	0.989	1	7	protein transport within lipid bilayer	BP	1	REEP2	up_AFEM_EC
GO:0045987	0.156	0.989	1	7	positive regulation of smooth muscle	BP	1	TBXA2R	up_AFEM_EC
GO:0060065	0.156	0.989	1	7	uterus development	BP	1	HOXA9	up_AFEM_EC
GO:0003272	0.156	0.989	1	7	endocardial cushion formation	BP	1	TMEM100	up_AFEM_EC
GO:0072172	0.156	0.989	1	7	mesonephric tubule formation	BP	1	GREM1	up_AFEM_EC
GO:1901213	0.156	0.989	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GREM1	up_AFEM_EC
GO:0060562	0.156	0.989	1	120	epithelial tube morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0042228	0.156	0.993	1	2	interleukin-8 biosynthetic process	BP	1	BCL10	up_VCAV_EC
GO:0046426	0.156	0.988	1	20	negative regulation of JAK-STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:1904893	0.156	0.988	1	20	negative regulation of STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:0050890	0.156	0.988	1	67	cognition	BP	1	CHL1	up_VPOR_VSMC
GO:0021537	0.156	0.988	1	73	telencephalon development	BP	1	EMX2	up_VFEM_VSMC
GO:0043433	0.156	0.988	1	49	negative regulation of DNA-binding transcription factor activity	BP	1	NR1H4	up_VPUL_EC
GO:0046883	0.156	0.988	1	49	regulation of hormone secretion	BP	1	NR1H4	up_VPUL_EC
GO:0060326	0.156	0.988	1	84	cell chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0007498	0.156	0.988	1	38	mesoderm development	BP	1	HOXA11	up_VSAP_VSMC
GO:0017015	0.156	0.988	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0032092	0.156	0.988	1	38	positive regulation of protein binding	BP	1	CAV1	up_VSAP_VSMC

GO:1903844	0.156	0.988	1	40	regulation of cellular response to transforming growth factor beta	BP	1	CAV1	up_VSAP_VSMC
GO:0061550	0.156372983	0.98919	1	6	cranial ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0050892	0.156434336	0.98918	1	6	intestinal absorption	BP	1	PLS1	up_ACOR_EC
GO:0000920	0.15645129	0.98889	1	7	septum digestion after cytokinesis	BP	1	CHMP4B	up_ACOR_EC
GO:0035542	0.15662528	0.98915	1	6	regulation of SNARE complex assembly	BP	1	VPS16	up_ACOR_EC
GO:1900120	0.156639176	0.98886	1	7	regulation of receptor binding	BP	1	PLCL1	up_ACOR_EC
GO:0006928	0.15692466	0.89651	19	557	movement of cell or subcellular component	BP	1	SOX9,AQP1,ENSCAFG00000004331,SEMA6D,DIXDC1,DYNC1I1,ZMYND8,PAK3,MMP28,PTGER4,ARHGDIB,ELMO2,FOXC2,LRRC15,TBX5,RARRES2,NRP1,PRKCD,CCNYL1	up_ACOR_EC
GO:0048522	0.157	0.883	41	1484	positive regulation of cellular process	BP	1	HOXA9,CMKLR1,IRX3,LEP,LBH,PRR16,ANGPT4,DLL1,F3,GPAM,MLLT11,LMCD1,TWIST2,MAB21L1,THRB,TMEM100,PLAGL2,GREM1,NFE2L1,OVOL1,FAM53B,CAMK2A,CLEC16A,CYLD,LRRC15,MYBL1,EVI2B,DCUN1D3,BVES,LGR6,RAB7A,AXIN2,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,FAP,ADAM17,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0035295	0.157	0.882	40	356	tube development	BP	1	HOXA11,FZD1,THRB,HOXA7,WNT11,ACKR3,ENPP2,SLIT2,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,FUZ,WARS2,SAV1,HPSE,RARG,CCBE1,AMBRA1,ZFP36L1,IRX3,ZEB1,TBXA2R,SHOX2,SASH1,LOX,KDM2B,HPGD,NFIB,ANPEP,ACVRL1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0007417	0.157	0.896	19	235	central nervous system development	BP	1	HSPA5,PTPN11,AARS,HOOK3,HIF1A,SLC45A3,UBA6,ZPR1,UCHL5,EIF2B1,CDH11,CTNNB1,LYN,GSK3B,VLDLR,EXT1,DISC1,INHBA,NRP1	down_VSAP_EC
GO:0001667	0.157	0.898	18	146	ameboidal-type cell migration	BP	1	WNT11,ENPP2,SLIT2,FGF7,ABL1,HDAC7,EMP2,CCBE1,STAT5A,DDR2,TBXA2R,SASH1,ZNF580,ZFAND5,ACVRL1,HMOX1,TGFBR2,BAG4	up_VSAP_EC
GO:0050673	0.157	0.9	17	135	epithelial cell proliferation	BP	1	C5AR2,OSR2,LIMS2,FGF7,PEX2,OSR1,SAV1,STAT5A,STAT6,ZFP36L1,MYC,SULF2,NFIB,ZNF580,ACVRL1,HMOX1,MAP2K2	up_VSAP_EC
GO:0033044	0.157	0.902	15	127	regulation of chromosome organization	BP	1	IWS1,GATA3,UHRF2,HMBOX1,PRKD2,NSD1,SENP6,SMC5,RAD21,ZW10,KDM5A,KDM3A,ATRX,DCP2,FBXO5	up_VCAV_EC
GO:0050678	0.157	0.903	15	117	regulation of epithelial cell proliferation	BP	1	C5AR2,OSR2,LIMS2,FGF7,PEX2,OSR1,SAV1,STAT5A,ZFP36L1,MYC,SULF2,NFIB,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:0034641	0.157	0.932	8	2171	cellular nitrogen compound metabolic	BP	1	EYA1,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0061448	0.157	0.923	7	89	connective tissue development	BP	1	SMAD9,THBS3,BMPR1A,HOXC4,GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:0071695	0.157	0.925	7	45	anatomical structure maturation	BP	1	RECK,FERMT1,GJA1,RND1,DAG1,APP,DMC1	up_ACOR_VSMC
GO:2001251	0.157	0.925	7	49	negative regulation of chromosome organization	BP	1	RAD21,ZW10,KDM5A,KDM3A,ATRX,DCP2,FBXO5	up_VCAV_EC
GO:0032774	0.157	0.928	7	1073	RNA biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0009058	0.157	0.94	6	1910	biosynthetic process	BP	1	HDAC7,CITED2,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0009156	0.157	0.935	5	50	ribonucleoside monophosphate	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:0010921	0.157	0.936	5	46	regulation of phosphatase activity	BP	1	NUAK1,PPP1R12A,HTT,ARFGEF3,CALM1	down_VSAP_EC
GO:0010976	0.157	0.935	5	47	positive regulation of neuron projection	BP	1	DPYSL3,APOE,LYN,VLDLR,NRP1	down_VSAP_EC
GO:0043244	0.157	0.936	5	34	regulation of protein complex disassembly	BP	1	TMOD1,SWAP70,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0031327	0.157	0.944	4	412	negative regulation of cellular biosynthetic	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0032649	0.157	0.945	4	23	regulation of interferon-gamma production	BP	1	TLR3,ISG15,CD274,IL18R1	up_ACOR_VSMC
GO:0061097	0.157	0.944	4	27	regulation of protein tyrosine kinase activity	BP	1	PDGFB,RELN,NEDD9,SH3BP5	up_VCAV_EC
GO:2001244	0.157	0.953	3	27	positive regulation of intrinsic apoptotic	BP	1	PARK7,GSDME,FBH1	down_VCAV_EC
GO:0006940	0.157	0.957	3	14	regulation of smooth muscle contraction	BP	1	ADRA1B,NPNT,DOCK5	up_ACOR_VSMC

GO:0060612	0.157	0.956	3	14	adipose tissue development	BP	1	LEP,PPARGC1A,ARID5B	up_ACOR_VSMC
GO:0007080	0.157	0.955	3	18	mitotic metaphase plate congression	BP	1	RAB11A,CENPC,ZW10	up_VCAV_EC
GO:0014909	0.157	0.969	2	15	smooth muscle cell migration	BP	1	PDGFRB,BMPR1A	down_VCAV_EC
GO:0043462	0.157	0.969	2	13	regulation of ATPase activity	BP	1	DYNLL1,DNAJC10	down_VSAP_EC
GO:2000403	0.157	0.972	2	7	positive regulation of lymphocyte migration	BP	1	APP,CCL5	up_ACOR_VSMC
GO:0031328	0.157	0.97	2	512	positive regulation of cellular biosynthetic	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0001817	0.157	0.967	2	182	regulation of cytokine production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0030154	0.157	0.975	2	1040	cell differentiation	BP	1	TBX5,HOXB5	up_APUL_VSMC
GO:0033137	0.157	0.97	2	10	negative regulation of peptidyl-serine	BP	1	PDE4D,NCK1	up_VCAV_EC
GO:0051235	0.157	0.967	2	90	maintenance of location	BP	1	ENSCAFG00000005494,ABHD5	up_VPOR_EC
GO:0010717	0.157	0.988	1	32	regulation of epithelial to mesenchymal transition	BP	1	PDPN	down_ACOR_EC
GO:0021954	0.157	0.988	1	26	central nervous system neuron development	BP	1	NRP2	down_ACOR_EC
GO:0060326	0.157	0.988	1	84	cell chemotaxis	BP	1	HSD3B7	down_VPOR_EC
GO:2000113	0.157	0.991	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:1902260	0.157	0.993	1	2	negative regulation of delayed rectifier potassium channel	BP	1	KCNE3	up_ACOR_VSMC
GO:2000341	0.157	0.993	1	2	regulation of chemokine (C-X-C motif) ligand 2	BP	1	MBP	up_ACOR_VSMC
GO:0018205	0.157	0.988	1	122	peptidyl-lysine modification	BP	1	EYA1	up_AFEM_VSMC
GO:0050678	0.157	0.988	1	117	regulation of epithelial cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0007249	0.157	0.988	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	ERC1	up_AORT_EC
GO:0032386	0.157	0.989	1	137	regulation of intracellular transport	BP	1	WNT7A	up_AORT_VSMC
GO:0001764	0.157	0.988	1	45	neuron migration	BP	1	NTRK2	up_APUL_EC
GO:1903093	0.157	0.993	1	2	regulation of protein K48-linked deubiquitination	BP	1	OTUD4	up_VCAV_EC
GO:0061072	0.157	0.993	1	2	iris morphogenesis	BP	1	HIF1A	up_VCAV_EC
GO:1903706	0.157	0.988	1	119	regulation of hemopoiesis	BP	1	LRRC17	up_VCAV_VSMC
GO:0032760	0.157	0.988	1	22	positive regulation of tumor necrosis factor	BP	1	ARHGEF2	up_VPOR_EC
GO:1903557	0.157	0.988	1	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	up_VPOR_EC
GO:0030217	0.157	0.988	1	65	T cell differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0050863	0.157	0.988	1	69	regulation of T cell activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001935	0.157	0.988	1	50	endothelial cell proliferation	BP	1	CCL24	up_VPUL_EC
GO:0006816	0.157	0.988	1	84	calcium ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0031999	0.157	0.993	1	2	negative regulation of fatty acid beta-oxidation	BP	1	ACACB	up_VSAP_EC
GO:0042475	0.15710039	0.96733	2	26	odontogenesis of dentin-containing tooth	BP	1	DLX3,LRP4	up_ACOR_EC
GO:0048846	0.157556205	0.98902	1	6	axon extension involved in axon guidance	BP	1	NRP1	up_ACOR_EC
GO:1902284	0.157556205	0.98902	1	6	neuron projection extension involved in neuron projection	BP	1	NRP1	up_ACOR_EC
GO:0000302	0.157884806	0.9521	3	52	response to reactive oxygen species	BP	1	AQP1,GUCY1B1,PRKCD	up_ACOR_EC
GO:0017144	0.158	0.891	24	199	drug metabolic process	BP	1	DLST,COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,ENSCAFG00000016140,CLYBL,NDUFS2,NT5C2,PCBD1,ACSS2,DHRS9,PNPO,ENSCAFG00000013366,MPST,ZNF205,IDH1,IDH3A,ENSCAFG00000006639,ASS1,NDUFV1,DDIT4	up_VSAP_EC

GO:1901698	0.158	0.893	21	266	response to nitrogen compound	BP	1	ARHGEF2,NR1H4,SOCS5,HM13,HSP90B1,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,SEL1L,DNAJC10,PTPN2,AGRN,DNAJB9,GNAQ,CTNNB1,APOE,NR4A1,USP14,HOMER1	down_VSAP_EC
GO:0042110	0.158	0.904	14	109	T cell activation	BP	1	CD274,ABL1,ZBTB16,STAT6,PATZ1,F2RL1,ZFP36L1,ZEB1,CD83,ZFP36L2,PNP,PPP3CB,NCK1,TGFBR2	up_VSAP_EC
GO:0060541	0.158	0.913	10	73	respiratory system development	BP	1	THRB,WNT11,FGF7,SAV1,RARG,CCBE1,LOX,NFIB,MAP2K2,TGFBR2	up_VSAP_EC
GO:0007266	0.158	0.92	8	64	Rho protein signal transduction	BP	1	ENSCAFG00000030005,STMN1,ARHGDIA,CDC42EP4,PHACTR4,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0010506	0.158	0.919	8	86	regulation of autophagy	BP	1	PLK3,SESN2,HIF1A,MTDH,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0060606	0.158	0.93	6	39	tube closure	BP	1	FZD1,ABL1,FUZ,RARG,KDM2B,CITED2	up_VSAP_EC
GO:0014033	0.158	0.937	5	30	neural crest cell differentiation	BP	1	HTR2B,BMP4,CITED2,NRP1,EDN1	up_ACOR_VSMC
GO:0048701	0.158	0.944	4	25	embryonic cranial skeleton morphogenesis	BP	1	EIF4A3,MMP14,TBX15,SIX4	down_ACOR_VSMC
GO:0001657	0.158	0.942	4	42	ureteric bud development	BP	1	SMAD9,CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0050870	0.158	0.942	4	42	positive regulation of T cell activation	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:0072163	0.158	0.942	4	42	mesonephric epithelium development	BP	1	SMAD9,CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0072164	0.158	0.942	4	42	mesonephric tubule development	BP	1	SMAD9,CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0071383	0.158	0.952	3	58	cellular response to steroid hormone stimulus	BP	1	LBH,CRY2,NR3C1	up_AFEM_EC
GO:0032728	0.158	0.955	3	16	positive regulation of interferon-beta	BP	1	TLR4,RIOK3,TLR3	up_VCAV_EC
GO:1905207	0.158	0.955	3	17	regulation of cardiocyte differentiation	BP	1	MEF2C,EDN1,BMP2	up_VCAV_EC
GO:0031935	0.158	0.971	2	8	regulation of chromatin silencing	BP	1	ATAD2,UHRF1	down_ACOR_VSMC
GO:0034405	0.158	0.969	2	11	response to fluid shear stress	BP	1	SOCS5,PTGS2	down_VSAP_EC
GO:0050435	0.158	0.971	2	8	amyloid-beta metabolic process	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0071801	0.158	0.972	2	7	regulation of podosome assembly	BP	1	ASAP1,KIF9	up_ACOR_VSMC
GO:0030183	0.158	0.967	2	30	B cell differentiation	BP	1	DLL1,CYLD	up_AFEM_EC
GO:0032732	0.158	0.97	2	9	positive regulation of interleukin-1 production	BP	1	TLR4,HMGB1	up_VCAV_EC
GO:0002768	0.158	0.988	1	37	immune response-regulating cell surface receptor signaling	BP	1	LYN	down_ACOR_EC
GO:0019852	0.158	0.993	1	2	L-ascorbic acid metabolic process	BP	1	GSTO1	down_ACOR_VSMC
GO:0033567	0.158	0.993	1	2	DNA replication, Okazaki fragment processing	BP	1	FEN1	down_ACOR_VSMC
GO:0043137	0.158	0.993	1	2	DNA replication, removal of RNA primer	BP	1	FEN1	down_ACOR_VSMC
GO:2000650	0.158	0.993	1	2	negative regulation of sodium ion transmembrane	BP	1	NEDD4	down_ACOR_VSMC
GO:0048583	0.158	1	1	1095	regulation of response to stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0043542	0.158	0.988	1	86	endothelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0048872	0.158	0.988	1	85	homeostasis of number of cells	BP	1	CITED2	down_VPOR_EC
GO:0052547	0.158	0.988	1	82	regulation of peptidase activity	BP	1	CST3	down_VPOR_EC
GO:0017144	0.158	0.989	1	199	drug metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0001819	0.158	0.988	1	120	positive regulation of cytokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0008015	0.158	0.988	1	120	blood circulation	BP	1	IRX5	up_AFEM_VSMC
GO:0070507	0.158	0.988	1	73	regulation of microtubule cytoskeleton organization	BP	1	TAOK1	up_AORT_EC
GO:0002695	0.158	0.988	1	44	negative regulation of leukocyte activation	BP	1	BPI	up_APUL_EC
GO:0045216	0.158	0.988	1	44	cell-cell junction organization	BP	1	NR1H4	up_APUL_EC
GO:0042310	0.158	0.988	1	21	vasoconstriction	BP	1	HTR7	up_VPOR_EC

GO:0097756	0.158	0.988	1	21	negative regulation of blood vessel diameter	BP	1	HTR7	up_VPOR_EC
GO:0001101	0.158	0.988	1	65	response to acid chemical	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003205	0.158	0.988	1	67	cardiac chamber development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0001704	0.158	0.988	1	43	formation of primary germ layer	BP	1	EYA1	up_VFEM_EC
GO:0048634	0.158	0.988	1	40	regulation of muscle organ development	BP	1	SHOX2	up_VSAP_VSMC
GO:0030178	0.158365737	0.95189	3	52	negative regulation of Wnt signaling pathway	BP	1	SOX9,LRP4,CLSTN1	up_ACOR_EC
GO:0060977	0.158534896	0.98888	1	6	coronary vasculature morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0006811	0.15856059	0.90631	12	330	ion transport	BP	1	CA4,CLIC3,AQP1,KCNB1,ACTN2,CFI,SLC25A42,MAPK8IP2,SLC9A9,PRKCD,PM20D1,ATP7B	up_ACOR_EC
GO:2000147	0.158904616	0.92184	7	169	positive regulation of cell motility	BP	1	SOX9,AQP1,SEMA6D,FOXC2,LRRC15,RARRES2,NRP1	up_ACOR_EC
GO:0051338	0.159	0.891	22	288	regulation of transferase activity	BP	1	VEGFA,SOCS5,ERRFI1,PTPN11,TRIB3,SESN2,TNIK,PTPN2,ADAM17,MAGED1,CTNNB1,APOE,LYN,CCNYL1,MMD,CBLC,VLDLR,SH3GLB1,HTT,PAK2,CDKN1A,MADD	down_VSAP_EC
GO:0007015	0.159	0.896	18	144	actin filament organization	BP	1	SYNPO2L,PDLIM3,ARHGAP28,ACTN2,SYNPO2,NEBL,F2RL1,JMY,NRP1,EVL,PRKCE,MYO1B,TTC17,RND1,SSH3,FAM107A,INPP5K,WASL	up_ACOR_VSMC
GO:0022409	0.159	0.92	8	56	positive regulation of cell-cell adhesion	BP	1	CD274,ZBTB16,CD83,PNP,FLOT1,NCK1,TGFBR2,CITED2	up_VSAP_EC
GO:0048731	0.159	0.94	5	1247	system development	BP	1	HOXC10,HOXA9,HOXC6,SGCD,TAOK1	up_AORT_EC
GO:0032479	0.159	0.935	5	33	regulation of type I interferon production	BP	1	TMEM173,TLR4,RIOK3,TLR3,PLCG2	up_VCAV_EC
GO:0051149	0.159	0.944	4	25	positive regulation of muscle cell differentiation	BP	1	MMP14,GREM1,RBM14,CTH	down_ACOR_VSMC
GO:0002831	0.159	0.942	4	42	regulation of response to biotic stimulus	BP	1	RNF216,SASH1,CYBA,MAVS	down_VCAV_EC
GO:0032371	0.159	0.955	3	15	regulation of sterol transport	BP	1	LEP,ABCA1,SCP2	up_ACOR_VSMC
GO:0032374	0.159	0.955	3	15	regulation of cholesterol transport	BP	1	LEP,ABCA1,SCP2	up_ACOR_VSMC
GO:0006810	0.159	0.961	3	1244	transport	BP	1	SLC20A2,WNT7A,ARG2	up_AORT_VSMC
GO:0002275	0.159	0.954	3	18	myeloid cell activation involved in immune	BP	1	KIT,SNAP23,FES	up_VCAV_EC
GO:0030042	0.159	0.955	3	17	actin filament depolymerization	BP	1	TMOD1,SWAP70,TMOD3	up_VCAV_EC
GO:0030834	0.159	0.955	3	17	regulation of actin filament depolymerization	BP	1	TMOD1,SWAP70,TMOD3	up_VCAV_EC
GO:0031572	0.159	0.955	3	15	G2 DNA damage checkpoint	BP	1	TAOK1,BLM,TOPBP1	up_VCAV_EC
GO:0043647	0.159	0.955	3	17	inositol phosphate metabolic process	BP	1	ITPKB,PLCG2,IMPA1	up_VCAV_EC
GO:0006213	0.159	0.97	2	9	pyrimidine nucleoside metabolic process	BP	1	TK1,CTPS1	down_ACOR_VSMC
GO:0035384	0.159	0.968	2	14	thioester biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0071616	0.159	0.968	2	14	acyl-CoA biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0031099	0.159	0.967	2	30	regeneration	BP	1	LGR6,TNC	up_AFEM_EC
GO:1903670	0.159	0.966	2	30	regulation of sprouting angiogenesis	BP	1	DLL1,TBXA2R	up_AFEM_EC
GO:0090344	0.159	0.971	2	8	negative regulation of cell aging	BP	1	PLK2,MAP3K3	up_VCAV_EC
GO:0003151	0.159	0.987	1	34	outflow tract morphogenesis	BP	1	NRP2	down_ACOR_EC
GO:0007044	0.159	0.987	1	27	cell-substrate junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0009749	0.159	0.987	1	34	response to glucose	BP	1	STX4	down_ACOR_EC
GO:0006348	0.159	0.993	1	2	chromatin silencing at telomere	BP	1	HAT1	down_ACOR_VSMC
GO:0051754	0.159	0.993	1	2	meiotic sister chromatid cohesion, centromeric	BP	1	SGO2	down_ACOR_VSMC
GO:0006404	0.159	0.993	1	2	RNA import into nucleus	BP	1	RAN	down_ACOR_VSMC
GO:0044771	0.159	0.993	1	2	meiotic cell cycle phase transition	BP	1	TTK	down_ACOR_VSMC

GO:0048209	0.159	0.993	1	2	regulation of vesicle targeting, to, from or	BP	1	PREB	down_ACOR_VSMC
GO:0051030	0.159	0.993	1	2	snRNA transport	BP	1	RAN	down_ACOR_VSMC
GO:0051177	0.159	0.993	1	2	meiotic sister chromatid cohesion	BP	1	SGO2	down_ACOR_VSMC
GO:0061015	0.159	0.993	1	2	snRNA import into nucleus	BP	1	RAN	down_ACOR_VSMC
GO:0071650	0.159	0.993	1	2	negative regulation of chemokine (C-C motif)	BP	1	ARG2	down_ACOR_VSMC
GO:1901993	0.159	0.993	1	2	regulation of meiotic cell cycle phase transition	BP	1	TTK	down_ACOR_VSMC
GO:1901994	0.159	0.993	1	2	negative regulation of meiotic cell cycle phase	BP	1	TTK	down_ACOR_VSMC
GO:0010558	0.159	0.991	1	392	negative regulation of macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0070244	0.159	0.991	1	3	negative regulation of thymocyte apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0071593	0.159	0.991	1	3	lymphocyte aggregation	BP	1	MSN	down_VSAP_EC
GO:0018202	0.159	0.991	1	3	peptidyl-histidine modification	BP	1	HIF1AN	down_VSAP_EC
GO:0010915	0.159	0.993	1	2	regulation of very-low-density lipoprotein	BP	1	LRPAP1	up_ACOR_VSMC
GO:0010916	0.159	0.993	1	2	negative regulation of very-low-density lipoprotein particle	BP	1	LRPAP1	up_ACOR_VSMC
GO:0010985	0.159	0.993	1	2	negative regulation of lipoprotein particle	BP	1	LRPAP1	up_ACOR_VSMC
GO:0030049	0.159	0.993	1	2	muscle filament sliding	BP	1	TNNT2	up_ACOR_VSMC
GO:1900426	0.159	0.993	1	2	positive regulation of defense response to	BP	1	F2RL1	up_ACOR_VSMC
GO:0003013	0.159	0.988	1	121	circulatory system process	BP	1	IRX5	up_AFEM_VSMC
GO:0001823	0.159	0.987	1	45	mesonephros development	BP	1	NPNT	up_APUL_EC
GO:0046474	0.159	0.987	1	44	glycerophospholipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0050707	0.159	0.987	1	44	regulation of cytokine secretion	BP	1	NR1H4	up_APUL_EC
GO:0021684	0.159	0.993	1	2	cerebellar granular layer formation	BP	1	PROX1	up_VCAV_EC
GO:0021707	0.159	0.993	1	2	cerebellar granule cell differentiation	BP	1	PROX1	up_VCAV_EC
GO:0034165	0.159	0.993	1	2	positive regulation of toll-like receptor 9 signaling	BP	1	HMGB1	up_VCAV_EC
GO:0035745	0.159	0.993	1	2	T-helper 2 cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:0055005	0.159	0.993	1	2	ventricular cardiac myofibril assembly	BP	1	PROX1	up_VCAV_EC
GO:0072603	0.159	0.993	1	2	interleukin-5 secretion	BP	1	GATA3	up_VCAV_EC
GO:2000551	0.159	0.993	1	2	regulation of T-helper 2 cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:2000553	0.159	0.993	1	2	positive regulation of T-helper 2 cell cytokine	BP	1	GATA3	up_VCAV_EC
GO:2000662	0.159	0.993	1	2	regulation of interleukin-5 secretion	BP	1	GATA3	up_VCAV_EC
GO:2000664	0.159	0.993	1	2	positive regulation of interleukin-5 secretion	BP	1	GATA3	up_VCAV_EC
GO:2000667	0.159	0.993	1	2	positive regulation of interleukin-13 secretion	BP	1	GATA3	up_VCAV_EC
GO:0032736	0.159	0.993	1	2	positive regulation of interleukin-13 production	BP	1	GATA3	up_VCAV_EC
GO:0070309	0.159	0.993	1	2	lens fiber cell morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0070858	0.159	0.993	1	2	negative regulation of bile acid biosynthetic process	BP	1	PROX1	up_VCAV_EC
GO:1904252	0.159	0.993	1	2	negative regulation of bile acid metabolic process	BP	1	PROX1	up_VCAV_EC
GO:0022604	0.159	0.988	1	122	regulation of cell morphogenesis	BP	1	LIMK1	up_VCAV_VSMC
GO:0007032	0.159	0.987	1	22	endosome organization	BP	1	HOOK3	up_VPOR_EC
GO:0045666	0.159	0.987	1	68	positive regulation of neuron differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0016125	0.159	0.987	1	41	sterol metabolic process	BP	1	CYP26B1	up_VFEM_EC

GO:0071772	0.159	0.987	1	50	response to BMP	BP	1	NEO1	up_VPUL_EC
GO:0071773	0.159	0.987	1	50	cellular response to BMP stimulus	BP	1	NEO1	up_VPUL_EC
GO:1990845	0.159056721	0.95161	3	51	adaptive thermogenesis	BP	1	PLCL1,FOXC2,PM20D1	up_ACOR_EC
GO:0008285	0.159271047	0.91742	8	201	negative regulation of cell proliferation	BP	1	SOX9,PTH1R,NDRG2,FZD5,PTGIR,SMAD6,TBX5,CLSTN1	up_ACOR_EC
GO:0030154	0.159846381	0.88385	33	1040	cell differentiation	BP	1	SH3TC2,MYOZ2,CDH3,TMOD1,GATA4,BRSK1,TRPS1,SOX9,PTH1R,FZD5,CCDC3,DIXDC1,RGMA,SMAD6,ACTN2,PAK3,DLX3,PTGER4,PIAS1,DCLK2,MAPK8IP2,FOXC2,FIGNL1,TBX5,LRP4,CLSTN1,RBM38,TP53INP2,NRP1,ARHGEF26,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:0030111	0.159937712	0.93253	5	108	regulation of Wnt signaling pathway	BP	1	CDH3,SOX9,DIXDC1,LRP4,CLSTN1	up_ACOR_EC
GO:0010556	0.16	0.866	104	1137	regulation of macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,SAMD8,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,ENC1,CCAR1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0006915	0.16	0.896	17	550	apoptotic process	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,THRB,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,PPARGC1A,FAP,DMPK	up_AFEM_EC
GO:0042060	0.16	0.906	12	103	wound healing	BP	1	ELK3,TFPI,TFPI2,SDC1,CAV1,EZH2,ADIPOR2,B4GALT1,PRCP,PPARD,ITGB3,PIK3CD	down_ACOR_VSMC
GO:0043588	0.16	0.912	10	74	skin development	BP	1	HOXA7,FGF7,DLL1,SAV1,HPSE,CLDN1,ZFP36L1,LRP4,TRADD,LATS2	up_VSAP_EC
GO:0043393	0.16	0.915	9	77	regulation of protein binding	BP	1	PDGFB,TMEM173,MEF2C,RALB,BMP2,STMN1,MFNG,RAPGEF2,CDON	up_VCAV_EC
GO:0061138	0.16	0.915	9	73	morphogenesis of a branching epithelium	BP	1	HOXB7,DLL4,EDN1,NTN4,BMP2,HHEX,PROX1,BTBD7,TIMELESS	up_VCAV_EC
GO:0030324	0.16	0.915	9	64	lung development	BP	1	THRB,WNT11,FGF7,SAV1,CCBE1,LOX,NFIB,MAP2K2,TGFBR2	up_VSAP_EC
GO:0007409	0.16	0.917	8	109	axonogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,GLI3,UST,BRSK1	down_VCAV_EC
GO:0051348	0.16	0.918	8	90	negative regulation of transferase activity	BP	1	SOCS5,ERRFI1,TRIB3,PTPN2,APOE,LYN,CBLC,CDKN1A	down_VSAP_EC
GO:0007626	0.16	0.919	8	53	locomotory behavior	BP	1	GLRB,PRKCE,APP,CHD7,CLN8,OXR1,GAA,PARK7	up_ACOR_VSMC
GO:0001838	0.16	0.919	8	56	embryonic epithelial tube formation	BP	1	FZD1,ABL1,OSR1,FUZ,RARG,IRX3,KDM2B,CITED2	up_VSAP_EC
GO:0071363	0.16	0.921	7	188	cellular response to growth factor stimulus	BP	1	GAS1,DLL1,TMEM100,GREM1,GREM2,NR3C1,ADAM17	up_AFEM_EC
GO:0021915	0.16	0.928	6	58	neural tube development	BP	1	PRICKLE1,PRKACB,TMED2,HIF1A,PLOD3,SDC4	down_VSAP_EC
GO:0046879	0.16	0.927	6	63	hormone secretion	BP	1	NR1H4,PTPN11,HIF1A,REST,RAB11FIP1,INHBA	down_VSAP_EC
GO:2001242	0.16	0.927	6	62	regulation of intrinsic apoptotic signaling	BP	1	ARHGEF2,P4HB,HYOU1,PTGS2,HIF1A,PTPN2	down_VSAP_EC
GO:0090130	0.16	0.933	5	121	tissue migration	BP	1	ANGPT4,GREM1,TBXA2R,FAP,ADAM17	up_AFEM_EC
GO:0007259	0.16	0.942	4	42	JAK-STAT cascade	BP	1	DCN,BGN,ASPN,ARL2BP	down_VCAV_EC
GO:0002367	0.16	0.943	4	26	cytokine production involved in immune	BP	1	KIT,TLR4,GATA3,TLR3	up_VCAV_EC
GO:0032642	0.16	0.944	4	22	regulation of chemokine production	BP	1	IL6R,F2RL1,MYD88,MAVS	up_VSAP_EC
GO:0048878	0.16	0.952	3	283	chemical homeostasis	BP	1	LYN,HOXA3,STX4	down_ACOR_EC
GO:0008589	0.16	0.952	3	28	regulation of smoothened signaling pathway	BP	1	EVC,GLI3,GLIS2	down_VCAV_EC
GO:0032602	0.16	0.953	3	23	chemokine production	BP	1	NR1H4,SOCS5,ADAM17	down_VSAP_EC
GO:0017157	0.16	0.951	3	58	regulation of exocytosis	BP	1	CHRM2,CAMK2A,RAB7A	up_AFEM_EC

GO:0008283	0.16	0.954	3	545	cell proliferation	BP	1	EYA1,EMX2,SHOX2	up_VFEM_VSMC
GO:0018279	0.16	0.968	2	14	protein N-linked glycosylation via	BP	1	DDOST,FUT8	down_VCAV_EC
GO:0061045	0.16	0.968	2	12	negative regulation of wound healing	BP	1	SERPINE1,APOE	down_VSAP_EC
GO:1901889	0.16	0.97	2	8	negative regulation of cell junction assembly	BP	1	DUSP22,FAM107A	up_ACOR_VSMC
GO:0071711	0.16	0.97	2	8	basement membrane organization	BP	1	LAMC2,FERMT1	up_VCAV_EC
GO:0090162	0.16	0.97	2	9	establishment of epithelial cell polarity	BP	1	FRMD4B,FERMT1	up_VCAV_EC
GO:0044264	0.16	0.987	1	32	cellular polysaccharide metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0044344	0.16	0.987	1	33	cellular response to fibroblast growth factor	BP	1	SULF1	down_ACOR_EC
GO:0071774	0.16	0.987	1	33	response to fibroblast growth factor	BP	1	SULF1	down_ACOR_EC
GO:0006813	0.16	0.987	1	37	potassium ion transport	BP	1	NEDD4	down_ACOR_EC
GO:0048659	0.16	0.987	1	36	smooth muscle cell proliferation	BP	1	SULF1	down_ACOR_EC
GO:0003085	0.16	0.993	1	2	negative regulation of systemic arterial blood	BP	1	PRCP	down_ACOR_VSMC
GO:0051316	0.16	0.993	1	2	attachment of spindle microtubules to kinetochore involved in meiotic chromosome	BP	1	DSN1	down_ACOR_VSMC
GO:0071705	0.16	0.993	1	582	nitrogen compound transport	BP	1	SCAMP4	down_AORT_EC
GO:0034613	0.16	0.993	1	576	cellular protein localization	BP	1	JUP	down_VFEM_VSMC
GO:0060768	0.16	0.991	1	3	regulation of epithelial cell proliferation involved in prostate gland	BP	1	CTNNB1	down_VSAP_EC
GO:2000644	0.16	0.991	1	3	regulation of receptor catabolic process	BP	1	APOE	down_VSAP_EC
GO:2000646	0.16	0.991	1	3	positive regulation of receptor catabolic process	BP	1	APOE	down_VSAP_EC
GO:0046689	0.16	0.993	1	2	response to mercury ion	BP	1	PARK7	up_ACOR_VSMC
GO:0071798	0.16	0.993	1	2	response to prostaglandin D	BP	1	PTGDR	up_ACOR_VSMC
GO:0071799	0.16	0.993	1	2	cellular response to prostaglandin D stimulus	BP	1	PTGDR	up_ACOR_VSMC
GO:0045354	0.16	0.993	1	2	regulation of interferon-alpha biosynthetic	BP	1	TLR3	up_VCAV_EC
GO:1905064	0.16	0.993	1	2	negative regulation of vascular smooth muscle	BP	1	PDGFB	up_VCAV_EC
GO:0045349	0.16	0.993	1	2	interferon-alpha biosynthetic process	BP	1	TLR3	up_VCAV_EC
GO:1903391	0.16	0.987	1	21	regulation of adherens junction organization	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0042063	0.16	0.987	1	67	gliogenesis	BP	1	TRPC4	up_VPOR_VSMC
GO:0051216	0.16	0.987	1	70	cartilage development	BP	1	HOXA3	up_VPOR_VSMC
GO:0034764	0.16	0.987	1	50	positive regulation of transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0043542	0.16	0.987	1	86	endothelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0046425	0.16	0.987	1	39	regulation of JAK-STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0045017	0.160180759	0.95109	3	52	glycerolipid biosynthetic process	BP	1	NR1H4,PIGS,AGPAT2	up_ACOR_EC
GO:0050920	0.160222275	0.95104	3	53	regulation of chemotaxis	BP	1	MMP28,RARRES2,NRP1	up_ACOR_EC
GO:0045732	0.160378891	0.94031	4	78	positive regulation of protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0071229	0.160420559	0.95101	3	51	cellular response to acid chemical	BP	1	NR1H4,AQP1,PTGER4	up_ACOR_EC
GO:0000003	0.161	0.881	34	295	reproduction	BP	1	LEP,GATA4,PRDX4,RECK,BMP4,FGFR2,ATRX,PDE5A,CITED2,SPINT1,GLRB,CTSB,EGLN1,ENSCAFG00000006238,CREBRF,SPINT2,PTGDR,MARF1,AFF4,DKKL1,FRS2,APP,CHD7,SPINK2,HPGD,ARID5B,DMC1,SERPINB5,JAM3,SUN1,HERPUD2,LHX9,WDR48,MMP23	up_ACOR_VSMC
GO:1901615	0.161	0.898	16	128	organic hydroxy compound metabolic process	BP	1	PLCG2,LEP,LCAT,PCBD1,ABCA1,MAOA,PPIP5K1,LIPE,MOXD1,DKKL1,APP,CLN8,INPP5K,PTS,PARK7,LMF1	up_ACOR_VSMC

GO:0032956	0.161	0.899	15	116	regulation of actin cytoskeleton organization	BP	1	SYNPO2L,ARHGAP28,ACTN2,SYNPO2,F2RL1,JMY,NRP1,EVL,PRKCE,SSH3,EDN1,FAM107A,JAM3,INPP5K,WASL	up_ACOR_VSMC
GO:0031589	0.161	0.906	12	93	cell-substrate adhesion	BP	1	HOXA7,FAM107A,RADIL,HOXD3,ABL1,EMP2,HPSE,PIK3R1,TIAM1,ECM2,FBLN1,ACVRL1	up_VSAP_EC
GO:0002697	0.161	0.911	10	85	regulation of immune effector process	BP	1	IL7R,TMEM173,TLR4,GATA3,NECTIN2,RIOK3,THOC1,TLR3,FES,HMGB1	up_VCAV_EC
GO:0002262	0.161	0.922	7	54	myeloid cell homeostasis	BP	1	HMGB1,HSPA9,PRMT1,HMGB2,BAP1,JMJD6,PIK3CD	down_ACOR_VSMC
GO:0061138	0.161	0.921	7	73	morphogenesis of a branching epithelium	BP	1	SULF1,ILK,HOXB7,MAGED1,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0034220	0.161	0.92	7	188	ion transmembrane transport	BP	1	KCNC4,KCND1,ATP6V1B2,SLC6A6,FXYD1,ATP6V0B,CLIC4	up_AFEM_EC
GO:0043244	0.161	0.934	5	34	regulation of protein complex disassembly	BP	1	CAPG,LIMA1,EIF5A,PDXP,ARHGEF2	down_ACOR_VSMC
GO:0042471	0.161	0.935	5	34	ear morphogenesis	BP	1	CHD7,GATA3,EDN1,ALDH1A3,ZEB1	up_VCAV_EC
GO:0035150	0.161	0.942	4	36	regulation of tube size	BP	1	HTR7,ACTA2,APOE,PLOD3	down_VSAP_EC
GO:0050880	0.161	0.942	4	36	regulation of blood vessel size	BP	1	HTR7,ACTA2,APOE,PLOD3	down_VSAP_EC
GO:0030048	0.161	0.943	4	23	actin filament-based movement	BP	1	TNNT2,KCNE3,MYO1B,JUP	up_ACOR_VSMC
GO:0098927	0.161	0.954	3	17	vesicle-mediated transport between endosomal compartments	BP	1	EMP2,EZR,CORO1A	down_ACOR_VSMC
GO:0009880	0.161	0.952	3	22	embryonic pattern specification	BP	1	TMED2,CTNNB1,NRP1	down_VSAP_EC
GO:0051171	0.161	0.965	3	1697	regulation of nitrogen compound metabolic	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0090304	0.161	0.965	3	1694	nucleic acid metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0006928	0.161	0.954	3	557	movement of cell or subcellular component	BP	1	CHL1,BAMBI,C3AR1	up_VPOR_VSMC
GO:0055065	0.161	0.966	2	145	metal ion homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:1901016	0.161	0.969	2	9	regulation of potassium ion transmembrane transporter activity	BP	1	NEDD4,CAV1	down_ACOR_VSMC
GO:0072359	0.161	0.968	2	368	circulatory system development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0001893	0.161	0.97	2	8	maternal placenta development	BP	1	CITED2,CTSB	up_ACOR_VSMC
GO:0086091	0.161	0.97	2	8	regulation of heart rate by cardiac conduction	BP	1	KCNE3,JUP	up_ACOR_VSMC
GO:2000105	0.161	0.971	2	7	positive regulation of DNA-dependent DNA	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0000291	0.161	0.969	2	10	nuclear-transcribed mRNA catabolic process,	BP	1	CNOT6,CNOT7	up_VCAV_EC
GO:0034453	0.161	0.97	2	8	microtubule anchoring	BP	1	HOOK3,GCC2	up_VCAV_EC
GO:0000050	0.161	0.993	1	2	urea cycle	BP	1	ARG2	down_ACOR_VSMC
GO:0043988	0.161	0.993	1	2	histone H3-S28 phosphorylation	BP	1	AURKB	down_ACOR_VSMC
GO:0006072	0.161	0.993	1	2	glycerol-3-phosphate metabolic process	BP	1	GK5	down_ACOR_VSMC
GO:0031507	0.161	0.993	1	2	heterochromatin assembly	BP	1	HMGA1	down_ACOR_VSMC
GO:0032696	0.161	0.993	1	2	negative regulation of interleukin-13 production	BP	1	ARG2	down_ACOR_VSMC
GO:0034969	0.161	0.993	1	2	histone arginine methylation	BP	1	PRMT1	down_ACOR_VSMC
GO:0046166	0.161	0.993	1	2	glyceraldehyde-3-phosphate biosynthetic	BP	1	TKT	down_ACOR_VSMC
GO:0097350	0.161	0.993	1	2	neutrophil clearance	BP	1	HMGB1	down_ACOR_VSMC
GO:0034330	0.161	0.987	1	80	cell junction organization	BP	1	FSCN1	down_AFEM_EC
GO:0070727	0.161	0.993	1	579	cellular macromolecule localization	BP	1	JUP	down_VFEM_VSMC
GO:0071705	0.161	0.993	1	582	nitrogen compound transport	BP	1	JUP	down_VFEM_VSMC
GO:0036023	0.161	0.991	1	3	embryonic skeletal limb joint morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0002861	0.161	0.993	1	2	regulation of inflammatory response to	BP	1	PARK7	up_ACOR_VSMC
GO:0001667	0.161	0.988	1	146	ameboidal-type cell migration	BP	1	WNT7A	up_AORT_VSMC

GO:0010921	0.161	0.987	1	46	regulation of phosphatase activity	BP	1	NPNT	up_APUL_EC
GO:0001743	0.161	0.993	1	2	optic placode formation	BP	1	PROX1	up_VCAV_EC
GO:0044154	0.161	0.993	1	2	histone H3-K14 acetylation	BP	1	GATA3	up_VCAV_EC
GO:0071440	0.161	0.993	1	2	regulation of histone H3-K14 acetylation	BP	1	GATA3	up_VCAV_EC
GO:2000819	0.161	0.993	1	2	regulation of nucleotide-excision repair	BP	1	CUL4A	up_VCAV_EC
GO:0044854	0.161	0.991	1	3	plasma membrane raft assembly	BP	1	CAV2	up_VCAV_EC
GO:0044857	0.161	0.991	1	3	plasma membrane raft organization	BP	1	CAV2	up_VCAV_EC
GO:0046619	0.161	0.993	1	2	optic placode formation involved in camera-type	BP	1	PROX1	up_VCAV_EC
GO:2000394	0.161	0.993	1	2	positive regulation of lamellipodium	BP	1	ENPP2	up_VSAP_EC
GO:0010565	0.161	0.987	1	40	regulation of cellular ketone metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0051100	0.16115007	0.95063	3	53	negative regulation of binding	BP	1	ARHGAP28,IFIT2,CLSTN1	up_ACOR_EC
GO:0051895	0.161620126	0.98811	1	7	negative regulation of focal adhesion assembly	BP	1	ARHGAP6	up_ACOR_EC
GO:1903392	0.161620126	0.98811	1	7	negative regulation of adherens junction	BP	1	ARHGAP6	up_ACOR_EC
GO:0014031	0.161757935	0.9657	2	27	mesenchymal cell development	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0014032	0.161757935	0.9657	2	27	neural crest cell development	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0007267	0.162	0.886	25	332	cell-cell signaling	BP	1	PRICKLE1,SULF1,NR1H4,PTPN11,ILK,SMARCA4,KIF5B,HIF1A,HTR7,NXN,PLCL1,CDH11,CTNNB1,APOE,KLF5,DDIT3,GSK3B,TAX1BP3,KPNA1,REST,RAB11FIP1,DISC1,LRRTM2,INHBA,USP14	down_VSAP_EC
GO:0031347	0.162	0.904	12	144	regulation of defense response	BP	1	NR1H4,SERPINE1,SOCS5,PTGS2,PTPN2,PVR,CNOT7,APOE,LYN,CDC37,GBP5,A2M	down_VSAP_EC
GO:0046578	0.162	0.91	10	77	regulation of Ras protein signal transduction	BP	1	ARHGEF5,ARHGEF6,ABL1,F2RL1,MFN2,TIAM1,DLC1,FGD4,PSD4,FLOT1	up_VSAP_EC
GO:0009914	0.162	0.914	9	64	hormone transport	BP	1	HNF4A,SLC8B1,RAB11B,PASK,KCNB1,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:1902107	0.162	0.923	7	47	positive regulation of leukocyte differentiation	BP	1	PPARGC1B,ZBTB16,TOX,ZFP36L1,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0007423	0.162	0.925	6	155	sensory organ development	BP	1	IRX5,COL8A2,DLL1,CRYAB,MAB21L1,THRB	up_AFEM_EC
GO:0023052	0.162	0.934	6	1602	signaling	BP	1	DKK2,LNPEP,ERC1,TAOK1,CTNNAL1,GPR155	up_AORT_EC
GO:0008219	0.162	0.934	5	611	cell death	BP	1	LYN,IGF1R,PDPN,USP28,STX4	down_ACOR_EC
GO:0120162	0.162	0.934	5	31	positive regulation of cold-induced thermogenesis	BP	1	PPARGC1B,EBF2,STAT6,MFN2,PRKAB1	up_VSAP_EC
GO:0007601	0.162	0.943	4	22	visual perception	BP	1	GLRB,ABCA4,CLN8,WFS1	up_ACOR_VSMC
GO:0050953	0.162	0.943	4	22	sensory perception of light stimulus	BP	1	GLRB,ABCA4,CLN8,WFS1	up_ACOR_VSMC
GO:0060395	0.162	0.951	3	27	SMAD protein signal transduction	BP	1	SMAD9,BMPR1A,ENSCAFG00000017708	down_VCAV_EC
GO:0046849	0.162	0.952	3	23	bone remodeling	BP	1	CTNNB1,TFRC,P3H4	down_VSAP_EC
GO:0001954	0.162	0.953	3	17	positive regulation of cell-matrix adhesion	BP	1	TEK,FERMT1,ENSCAFG00000002015	up_VCAV_EC
GO:0060255	0.162	0.983	2	1782	regulation of macromolecule metabolic	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:1990748	0.162	0.97	2	8	cellular detoxification	BP	1	SESN1,PARK7	up_ACOR_VSMC
GO:0009891	0.162	0.969	2	521	positive regulation of biosynthetic process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:1904031	0.162	0.969	2	10	positive regulation of cyclin-dependent protein	BP	1	PDGFB,PROX1	up_VCAV_EC
GO:1903169	0.162	0.987	1	34	regulation of calcium ion transmembrane transport	BP	1	LYN	down_ACOR_EC
GO:0009746	0.162	0.987	1	35	response to hexose	BP	1	STX4	down_ACOR_EC
GO:0034284	0.162	0.987	1	35	response to monosaccharide	BP	1	STX4	down_ACOR_EC
GO:0050954	0.162	0.987	1	30	sensory perception of mechanical stimulus	BP	1	HOXA1	down_ACOR_EC
GO:0060411	0.162	0.987	1	33	cardiac septum morphogenesis	BP	1	NRP2	down_ACOR_EC

GO:0032202	0.162	0.993	1	2	telomere assembly	BP	1	TINF2	down_ACOR_VSMC
GO:0045472	0.162	0.993	1	2	response to ether	BP	1	CDK4	down_ACOR_VSMC
GO:0071362	0.162	0.993	1	2	cellular response to ether	BP	1	CDK4	down_ACOR_VSMC
GO:1904636	0.162	0.993	1	2	response to ionomycin	BP	1	CDK4	down_ACOR_VSMC
GO:1904637	0.162	0.993	1	2	cellular response to ionomycin	BP	1	CDK4	down_ACOR_VSMC
GO:0006972	0.162	0.993	1	2	hyperosmotic response	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0030174	0.162	0.993	1	2	regulation of DNA-dependent DNA	BP	1	CDK2	down_ACOR_VSMC
GO:0032298	0.162	0.993	1	2	positive regulation of DNA-dependent DNA replication initiation	BP	1	CDK2	down_ACOR_VSMC
GO:0051006	0.162	0.993	1	2	positive regulation of lipoprotein lipase activity	BP	1	ABHD5	down_ACOR_VSMC
GO:0061365	0.162	0.993	1	2	positive regulation of triglyceride lipase activity	BP	1	ABHD5	down_ACOR_VSMC
GO:0071474	0.162	0.993	1	2	cellular hyperosmotic response	BP	1	ARHGEF2	down_ACOR_VSMC
GO:1901029	0.162	0.993	1	2	negative regulation of mitochondrial outer membrane permeabilization involved	BP	1	SLC25A5	down_ACOR_VSMC
GO:0032886	0.162	0.987	1	81	regulation of microtubule-based process	BP	1	GPSM2	down_AFEM_EC
GO:0048869	0.162	1	1	1119	cellular developmental process	BP	1	GATA5	down_AFEM_VSMC
GO:2000112	0.162	1	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0019388	0.162	0.991	1	3	galactose catabolic process	BP	1	GALE	down_VSAP_EC
GO:0046642	0.162	0.993	1	2	negative regulation of alpha-beta T cell	BP	1	CD274	up_ACOR_VSMC
GO:0071435	0.162	0.993	1	2	potassium ion export	BP	1	KCNE3	up_ACOR_VSMC
GO:0097623	0.162	0.993	1	2	potassium ion export across plasma membrane	BP	1	KCNE3	up_ACOR_VSMC
GO:1905397	0.162	0.993	1	2	activated CD8-positive, alpha-beta T cell	BP	1	CD274	up_ACOR_VSMC
GO:1905402	0.162	0.993	1	2	regulation of activated CD8-positive, alpha-beta T cell apoptotic process	BP	1	CD274	up_ACOR_VSMC
GO:2000562	0.162	0.993	1	2	negative regulation of CD4-positive, alpha-beta T cell proliferation	BP	1	CD274	up_ACOR_VSMC
GO:0045637	0.162	0.987	1	73	regulation of myeloid cell differentiation	BP	1	HOXA9	up_AORT_EC
GO:0014719	0.162	0.993	1	2	skeletal muscle satellite cell activation	BP	1	EPHB1	up_VCAV_EC
GO:0006972	0.162	0.993	1	2	hyperosmotic response	BP	1	ARHGEF2	up_VCAV_EC
GO:0071474	0.162	0.993	1	2	cellular hyperosmotic response	BP	1	ARHGEF2	up_VCAV_EC
GO:1903365	0.162	0.993	1	2	regulation of fear response	BP	1	MEF2C	up_VCAV_EC
GO:2000822	0.162	0.993	1	2	regulation of behavioral fear response	BP	1	MEF2C	up_VCAV_EC
GO:0034762	0.162	0.988	1	122	regulation of transmembrane transport	BP	1	CA2	up_VCAV_VSMC
GO:0009880	0.162	0.987	1	22	embryonic pattern specification	BP	1	SEMA3A	up_VPOR_EC
GO:0051341	0.162	0.987	1	22	regulation of oxidoreductase activity	BP	1	ACVR2A	up_VPOR_EC
GO:0030522	0.162	0.987	1	67	intracellular receptor signaling pathway	BP	1	CYP26B1	up_VPOR_VSMC
GO:0030856	0.162	0.987	1	41	regulation of epithelial cell differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0046890	0.162	0.987	1	51	regulation of lipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0061351	0.162	0.987	1	50	neural precursor cell proliferation	BP	1	ARHGEF2	up_VPUL_EC
GO:0001704	0.162	0.987	1	43	formation of primary germ layer	BP	1	HOXA11	up_VSAP_VSMC
GO:0048593	0.162	0.987	1	41	camera-type eye morphogenesis	BP	1	IRX5	up_VSAP_VSMC

GO:0042742	0.162	0.987	1	39	defense response to bacterium	BP	1	TLR2	up_VSAP_VSMC
GO:0061326	0.162	0.987	1	41	renal tubule development	BP	1	HOXA11	up_VSAP_VSMC
GO:0072080	0.162	0.987	1	41	nephron tubule development	BP	1	HOXA11	up_VSAP_VSMC
GO:1901861	0.162	0.987	1	41	regulation of muscle tissue development	BP	1	SHOX2	up_VSAP_VSMC
GO:0007009	0.162308443	0.96551	2	27	plasma membrane organization	BP	1	SH3TC2,PRKCD	up_ACOR_EC
GO:0051272	0.162367988	0.91969	7	170	positive regulation of cellular component	BP	1	SOX9,AQP1,SEMA6D,FOXC2,LRRC15,RARRES2,NRP1	up_ACOR_EC
GO:0039702	0.162514188	0.98798	1	7	viral budding via host ESCRT complex	BP	1	CHMP4B	up_ACOR_EC
GO:0021761	0.162581518	0.96542	2	27	limbic system development	BP	1	DCLK2,NRP1	up_ACOR_EC
GO:0051788	0.162597106	0.98796	1	7	response to misfolded protein	BP	1	CLU	up_ACOR_EC
GO:0044248	0.163	0.874	48	691	cellular catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,ENPP1,SNX25,PGK1,TPI1,TRIB3,PGAM1,ALDH1L2,SESN2,CEMIP2,MSN,SEL1L,HIF1A,USP12,DNAJC10,UBA6,ZPR1,ENTPD4,UCHL5,SPOPL,SMG7,MTDH,CNOT7,DNAJB9,ALDOC,SND1,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CDC37,CUL2,SH3GLB1,HTT,ABHD5,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0006812	0.163	0.889	22	222	cation transport	BP	1	CP,CALCRL,PDGFB,ATP2B1,RELN,PDE4D,MEF2C,CHD7,STC1,APLNR,SLC39A8,PPP3CA,SNAP23,RALBP1,KCNJ3,KCNJ2,SLC25A25,PLCG2,SPTBN4,MCU,LMTK2,ATP2A1	up_VCAV_EC
GO:0001934	0.163	0.89	21	274	positive regulation of protein phosphorylation	BP	1	ARHGEF2,VEGFA,JCAD,BCAR3,PTPN11,ILK,PTGS2,TNIK,YES1,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0097435	0.163	0.897	15	230	supramolecular fiber organization	BP	1	ADAMTS2,KIRREL1,LUM,LOX,CLIP3,RHOD,ENSCAFG00000014978,WIPF1,MYO1B,LOXL3,ACTR3B,DDR2,GREM1,PLEKHH2,RAC2	down_VCAV_EC
GO:0048583	0.163	0.907	12	1095	regulation of response to stimulus	BP	1	C3AR1,BARX1,CXHXorf57,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0071214	0.163	0.907	11	93	cellular response to abiotic stimulus	BP	1	NEDD4,INTS7,RAD51,CASP2,AURKB,MAP3K20,PCNA,NOC2L,POLH,ARHGEF2,CDC25A	down_ACOR_VSMC
GO:0104004	0.163	0.907	11	93	cellular response to environmental stimulus	BP	1	NEDD4,INTS7,RAD51,CASP2,AURKB,MAP3K20,PCNA,NOC2L,POLH,ARHGEF2,CDC25A	down_ACOR_VSMC
GO:0048522	0.163	0.918	9	1484	positive regulation of cellular process	BP	1	EYA1,HOXA9,TOX,MAP2K6,SIX1,MAB21L1,TIAM1,CYP26B1,CDC42EP5	up_VFEM_EC
GO:0031570	0.163	0.917	8	61	DNA integrity checkpoint	BP	1	THOC1,ETAA1,USP28,TAOK1,BLM,RAD17,CUL4A,TOPBP1	up_VCAV_EC
GO:0051302	0.163	0.922	7	47	regulation of cell division	BP	1	LBH,HTR2B,FGFR2,PKP4,PRKCE,PIK3C3,CAT	up_ACOR_VSMC
GO:0043065	0.163	0.919	7	188	positive regulation of apoptotic process	BP	1	F3,MLLT11,PLAGL2,CAMK2A,CYLD,DCUN1D3,FAP	up_AFEM_EC
GO:0003015	0.163	0.921	7	58	heart process	BP	1	PDE4D,STC1,EDN1,MTOR,KCNJ2,GCH1,SPTBN4	up_VCAV_EC
GO:0007599	0.163	0.922	7	48	hemostasis	BP	1	HNF4A,KLKB1,PDGFD,HPSE,F2RL1,HPS4,FBLN1	up_VSAP_EC
GO:0009746	0.163	0.941	4	35	response to hexose	BP	1	NR1H4,SMARCA4,SESN2,HIF1A	down_VSAP_EC
GO:0034284	0.163	0.941	4	35	response to monosaccharide	BP	1	NR1H4,SMARCA4,SESN2,HIF1A	down_VSAP_EC
GO:0090276	0.163	0.94	4	36	regulation of peptide hormone secretion	BP	1	NR1H4,PTPN11,HIF1A,REST	down_VSAP_EC
GO:0007565	0.163	0.942	4	23	female pregnancy	BP	1	RECK,CITED2,CTSB,HPGD	up_ACOR_VSMC
GO:0050900	0.163	0.939	4	89	leukocyte migration	BP	1	CMKLR1,HOXA7,CCL5,ADAM17	up_AFEM_EC
GO:2000142	0.163	0.953	3	17	regulation of DNA-templated transcription,	BP	1	HMGB1,FOSL1,PSMC1	down_ACOR_VSMC
GO:0050818	0.163	0.951	3	24	regulation of coagulation	BP	1	SERPINE1,APOE,LYN	down_VSAP_EC
GO:0006884	0.163	0.954	3	14	cell volume homeostasis	BP	1	CLCN3,SLC12A7,LRRC8C	up_ACOR_VSMC
GO:0072006	0.163	0.95	3	59	nephron development	BP	1	IRX3,DLL1,GREM1	up_AFEM_EC
GO:0071495	0.163	0.951	3	365	cellular response to endogenous stimulus	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0046622	0.163	0.954	3	15	positive regulation of organ growth	BP	1	MEF2C,EDN1,PROX1	up_VCAV_EC
GO:0098751	0.163	0.967	2	15	bone cell development	BP	1	NOTCH2,FBN1	down_VCAV_EC

GO:0031323	0.163	0.983	2	1788	regulation of cellular metabolic process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0050884	0.163	0.97	2	8	neuromuscular process controlling posture	BP	1	CLN8,GAA	up_ACOR_VSMC
GO:1904645	0.163	0.97	2	7	response to amyloid-beta	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0034122	0.163	0.969	2	9	negative regulation of toll-like receptor signaling	BP	1	TNFAIP3,OTUD4	up_VCAV_EC
GO:1900745	0.163	0.969	2	9	positive regulation of p38MAPK cascade	BP	1	MAP3K3,BMP2	up_VCAV_EC
GO:1903524	0.163	0.968	2	11	positive regulation of blood circulation	BP	1	EDN1,GCH1	up_VCAV_EC
GO:0035690	0.163	0.965	2	91	cellular response to drug	BP	1	ARHGEF2,FBP1	up_VPOR_EC
GO:0044703	0.163	0.965	2	172	multi-organism reproductive process	BP	1	HOXA9,CYP26B1	up_VFEM_EC
GO:0007040	0.163	0.987	1	33	lysosome organization	BP	1	SPG11	down_ACOR_EC
GO:0080171	0.163	0.987	1	33	lytic vacuole organization	BP	1	SPG11	down_ACOR_EC
GO:0000495	0.163	0.993	1	2	box H/ACA snoRNA 3'-end processing	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0017126	0.163	0.993	1	2	nucleologenesis	BP	1	EMG1	down_ACOR_VSMC
GO:0019520	0.163	0.993	1	2	aldonic acid metabolic process	BP	1	PGD	down_ACOR_VSMC
GO:0021590	0.163	0.993	1	2	cerebellum maturation	BP	1	ARCN1	down_ACOR_VSMC
GO:0021626	0.163	0.993	1	2	central nervous system maturation	BP	1	ARCN1	down_ACOR_VSMC
GO:0033979	0.163	0.993	1	2	box H/ACA snoRNA metabolic process	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0034964	0.163	0.993	1	2	box H/ACA snoRNA processing	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0043415	0.163	0.993	1	2	positive regulation of skeletal muscle tissue	BP	1	PPARD	down_ACOR_VSMC
GO:0043416	0.163	0.993	1	2	regulation of skeletal muscle tissue	BP	1	PPARD	down_ACOR_VSMC
GO:0009111	0.163	0.993	1	2	vitamin catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0010159	0.163	0.993	1	2	specification of animal organ position	BP	1	HOXA3	down_ACOR_VSMC
GO:0016128	0.163	0.993	1	2	phytosteroid metabolic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0016129	0.163	0.993	1	2	phytosteroid biosynthetic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0019521	0.163	0.993	1	2	D-gluconate metabolic process	BP	1	PGD	down_ACOR_VSMC
GO:0021578	0.163	0.993	1	2	hindbrain maturation	BP	1	ARCN1	down_ACOR_VSMC
GO:0021699	0.163	0.993	1	2	cerebellar cortex maturation	BP	1	ARCN1	down_ACOR_VSMC
GO:0002072	0.163	0.993	1	2	optic cup morphogenesis involved in camera-type	BP	1	PHACTR4	down_ACOR_VSMC
GO:0036089	0.163	0.993	1	2	cleavage furrow formation	BP	1	AURKB	down_ACOR_VSMC
GO:0051126	0.163	0.993	1	2	negative regulation of actin nucleation	BP	1	CORO1A	down_ACOR_VSMC
GO:0060054	0.163	0.993	1	2	positive regulation of epithelial cell proliferation involved in wound healing	BP	1	B4GALT1	down_ACOR_VSMC
GO:0072615	0.163	0.993	1	2	interleukin-17 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:1902339	0.163	0.993	1	2	positive regulation of apoptotic process involved in	BP	1	B4GALT1	down_ACOR_VSMC
GO:1904747	0.163	0.993	1	2	positive regulation of apoptotic process	BP	1	B4GALT1	down_ACOR_VSMC
GO:2001200	0.163	0.993	1	2	positive regulation of dendritic cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0051495	0.163	0.987	1	82	positive regulation of cytoskeleton organization	BP	1	GPSM2	down_AFEM_EC
GO:0016042	0.163	0.987	1	80	lipid catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0090287	0.163	0.987	1	91	regulation of cellular response to growth factor	BP	1	CITED2	down_VPOR_EC
GO:0006366	0.163	0.993	1	583	transcription by RNA polymerase II	BP	1	GATA5	down_VFEM_VSMC
GO:0034370	0.163	0.99	1	3	triglyceride-rich lipoprotein particle	BP	1	APOE	down_VSAP_EC

GO:0034372	0.163	0.99	1	3	very-low-density lipoprotein particle	BP	1	APOE	down_VSAP_EC
GO:0045059	0.163	0.99	1	3	positive thymic T cell selection	BP	1	PTPN2	down_VSAP_EC
GO:1903975	0.163	0.993	1	2	regulation of glial cell migration	BP	1	CRKL	up_ACOR_VSMC
GO:0060046	0.163	0.993	1	2	regulation of acrosome reaction	BP	1	SPINK2	up_ACOR_VSMC
GO:0032872	0.163	0.987	1	77	regulation of stress-activated MAPK cascade	BP	1	TAOK1	up_AORT_EC
GO:0034204	0.163	0.993	1	2	lipid translocation	BP	1	ATP8A1	up_VCAV_EC
GO:0048266	0.163	0.993	1	2	behavioral response to pain	BP	1	P2RX2	up_VCAV_EC
GO:0016049	0.163	0.987	1	124	cell growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0008037	0.163	0.987	1	22	cell recognition	BP	1	SEMA3A	up_VPOR_EC
GO:0019915	0.163	0.987	1	22	lipid storage	BP	1	ABHD5	up_VPOR_EC
GO:0030326	0.163	0.987	1	51	embryonic limb morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0035113	0.163	0.987	1	51	embryonic appendage morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0097529	0.163	0.987	1	52	myeloid leukocyte migration	BP	1	CCL24	up_VPUL_EC
GO:0009416	0.163	0.987	1	88	response to light stimulus	BP	1	LRRN4	up_VPUL_VSMC
GO:1903034	0.163	0.987	1	40	regulation of response to wounding	BP	1	CAV1	up_VSAP_VSMC
GO:0098655	0.163119104	0.92435	6	142	cation transmembrane transport	BP	1	AQP1,KCNB1,ACTN2,MAPK8IP2,SLC9A9,PM20D1	up_ACOR_EC
GO:0048167	0.163219727	0.96513	2	28	regulation of synaptic plasticity	BP	1	BRSK1,KCNB1	up_ACOR_EC
GO:0051259	0.163576451	0.92409	6	140	protein complex oligomerization	BP	1	TRPS1,KCTD12,KCNB1,ACTN2,CLU,CHMP4B	up_ACOR_EC
GO:0007417	0.164	0.884	27	235	central nervous system development	BP	1	EMX2,PCDH19,SEZ6L,CDON,WASF3,SLIT2,SLC6A4,ABL1,DLL1,PLXNA4,ZBTB16,PLPP3,ZEB1,CTNS,RTN4RL1,HOXC10,DPYSL2,GDPD5,SMG9,MCPH1,KIF27,KDM2B,NFIB,QARS,HTRA2,TGFBR2,CITED2	up_VSAP_EC
GO:0031400	0.164	0.886	24	205	negative regulation of protein modification process	BP	1	SMAD6,RASSF2,PRKAA2,BMP4,SH3RF2,LATS2,ISG15,NDRG2,F2RL1,FAM129A,CDKN1A,PTPN22,SMPD1,PRKCE,DAG1,PSEN1,SYNJ2BP,DUSP22,OXR1,DUSP26,LRRC4,INPP5K,PARK7,CRKL	up_ACOR_VSMC
GO:0001558	0.164	0.901	13	101	regulation of cell growth	BP	1	DCBLD2,CRIM1,GJA1,RERG,CDKN1A,CRLF3,NRP1,ULK2,EDN1,FAM107A,IGFBP7,NAIF1,SH3BP4	up_ACOR_VSMC
GO:0040013	0.164	0.901	13	100	negative regulation of locomotion	BP	1	TCAF1,RECK,TP53INP1,NRP1,EVL,SPINT2,TBX5,DAG1,SEMA6D,SYNJ2BP,JUP,DUSP22,WASL	up_ACOR_VSMC
GO:0051234	0.164	0.917	9	1283	establishment of localization	BP	1	LYN,HOXA3,SPG11,PDPN,IPO7,ACSL3,STX4,MYO1D,NEDD4	down_ACOR_EC
GO:0007165	0.164	0.918	9	1496	signal transduction	BP	1	EYA1,MAP2K6,ENSCAFG00000018194,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,ADCY3	up_VFEM_EC
GO:0043401	0.164	0.921	7	46	steroid hormone mediated signaling	BP	1	LBH,SKP2,BMP4,MED14,AR,CREBRF,PARK7	up_ACOR_VSMC
GO:0031623	0.164	0.933	5	31	receptor internalization	BP	1	PLCG2,HTR2B,ATXN2,LRPAP1,AP2B1	up_ACOR_VSMC
GO:0071804	0.164	0.933	5	31	cellular potassium ion transport	BP	1	ACTN2,KCNE3,AKAP6,KCNJ4,KCNC4	up_ACOR_VSMC
GO:0071805	0.164	0.933	5	31	potassium ion transmembrane transport	BP	1	ACTN2,KCNE3,AKAP6,KCNJ4,KCNC4	up_ACOR_VSMC
GO:0071495	0.164	0.931	5	365	cellular response to endogenous stimulus	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,RNF6	up_VPOR_EC
GO:0110020	0.164	0.933	5	31	regulation of actomyosin structure organization	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,BAG4	up_VSAP_EC
GO:0009890	0.164	0.94	4	420	negative regulation of biosynthetic process	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0048659	0.164	0.94	4	36	smooth muscle cell proliferation	BP	1	SULF1,CTNNB1,ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:2000026	0.164	0.941	4	560	regulation of multicellular organismal development	BP	1	NR1H4,TBX5,SLITRK5,NTRK2	up_APUL_EC
GO:0030334	0.164	0.939	4	267	regulation of cell migration	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0009966	0.164	0.943	4	868	regulation of signal transduction	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC

GO:0046847	0.164	0.953	3	17	filopodium assembly	BP	1	FSCN1,EZR,ENSCAFG00000010224	down_ACOR_VSMC
GO:0031128	0.164	0.953	3	15	developmental induction	BP	1	GATA5,BMP4,FRS2	up_ACOR_VSMC
GO:0050885	0.164	0.954	3	14	neuromuscular process controlling balance	BP	1	APP,CLN8,GAA	up_ACOR_VSMC
GO:0034654	0.164	0.959	3	1236	nucleobase-containing compound biosynthetic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0098751	0.164	0.953	3	15	bone cell development	BP	1	KIT,FLI1,TJP2	up_VCAV_EC
GO:0045717	0.164	0.969	2	9	negative regulation of fatty acid biosynthetic	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:0030970	0.164	0.967	2	14	retrograde protein transport, ER to cytosol	BP	1	SEC61B,HM13	down_VCAV_EC
GO:1903513	0.164	0.967	2	14	endoplasmic reticulum to cytosol transport	BP	1	SEC61B,HM13	down_VCAV_EC
GO:0051239	0.164	0.972	2	859	regulation of multicellular organismal process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0007183	0.164	0.969	2	8	SMAD protein complex assembly	BP	1	SMAD6,TBX20	up_ACOR_VSMC
GO:0000212	0.164	0.97	2	7	meiotic spindle organization	BP	1	ATRX,FBXO5	up_VCAV_EC
GO:0061437	0.164	0.968	2	10	renal system vasculature development	BP	1	PDGFB,GPR4	up_VCAV_EC
GO:0061440	0.164	0.968	2	10	kidney vasculature development	BP	1	PDGFB,GPR4	up_VCAV_EC
GO:0048729	0.164	0.965	2	209	tissue morphogenesis	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0050921	0.164	0.986	1	39	positive regulation of chemotaxis	BP	1	STX4	down_ACOR_EC
GO:0070193	0.164	0.993	1	2	synaptonemal complex organization	BP	1	TRIP13	down_ACOR_VSMC
GO:0071034	0.164	0.993	1	2	CUT catabolic process	BP	1	DIS3	down_ACOR_VSMC
GO:0071043	0.164	0.993	1	2	CUT metabolic process	BP	1	DIS3	down_ACOR_VSMC
GO:0021814	0.164	0.993	1	2	cell motility involved in cerebral cortex radial glia	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0021815	0.164	0.993	1	2	modulation of microtubule cytoskeleton involved in cerebral	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0010556	0.164	1	1	1137	regulation of macromolecule	BP	1	GATA5	down_AFEM_VSMC
GO:0048584	0.164	0.993	1	592	positive regulation of response to stimulus	BP	1	GATA5	down_VFEM_VSMC
GO:0006621	0.164	0.99	1	3	protein retention in ER lumen	BP	1	KDELR2	down_VSAP_EC
GO:0051016	0.164	0.99	1	3	barbed-end actin filament capping	BP	1	CAPG	down_VSAP_EC
GO:1902031	0.164	0.99	1	3	regulation of NADP metabolic process	BP	1	PGAM1	down_VSAP_EC
GO:0006561	0.164	0.99	1	3	proline biosynthetic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0055129	0.164	0.99	1	3	L-proline biosynthetic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0072393	0.164	0.99	1	3	microtubule anchoring at microtubule organizing	BP	1	HOOK3	down_VSAP_EC
GO:0010511	0.164	0.993	1	2	regulation of phosphatidylinositol	BP	1	HTR2B	up_ACOR_VSMC
GO:0036476	0.164	0.993	1	2	neuron death in response to hydrogen peroxide	BP	1	PARK7	up_ACOR_VSMC
GO:0038107	0.164	0.993	1	2	nodal signaling pathway involved in determination of left/right asymmetry	BP	1	CITED2	up_ACOR_VSMC
GO:0110095	0.164	0.993	1	2	cellular detoxification of aldehyde	BP	1	PARK7	up_ACOR_VSMC
GO:0110096	0.164	0.993	1	2	cellular response to aldehyde	BP	1	PARK7	up_ACOR_VSMC
GO:1900094	0.164	0.993	1	2	regulation of transcription from RNA polymerase II promoter involved in determination of	BP	1	CITED2	up_ACOR_VSMC
GO:1900164	0.164	0.993	1	2	nodal signaling pathway involved in determination of lateral mesoderm	BP	1	CITED2	up_ACOR_VSMC
GO:1903207	0.164	0.993	1	2	regulation of hydrogen peroxide-induced neuron	BP	1	PARK7	up_ACOR_VSMC
GO:1903208	0.164	0.993	1	2	negative regulation of hydrogen peroxide-	BP	1	PARK7	up_ACOR_VSMC

GO:0008643	0.164	0.987	1	45	carbohydrate transport	BP	1	NR1H4	up_APUL_EC
GO:0031214	0.164	0.987	1	45	biomineral tissue development	BP	1	HOXA3	up_APUL_EC
GO:0031333	0.164	0.986	1	46	negative regulation of protein complex assembly	BP	1	TUBB4A	up_APUL_EC
GO:0071222	0.164	0.987	1	46	cellular response to lipopolysaccharide	BP	1	NR1H4	up_APUL_EC
GO:0020027	0.164	0.993	1	2	hemoglobin metabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0032423	0.164	0.993	1	2	regulation of mismatch repair	BP	1	HMGB1	up_VCAV_EC
GO:0042541	0.164	0.993	1	2	hemoglobin biosynthetic process	BP	1	HIF1A	up_VCAV_EC
GO:0097411	0.164	0.993	1	2	hypoxia-inducible factor-1alpha signaling pathway	BP	1	HIF1A	up_VCAV_EC
GO:1902903	0.164	0.987	1	125	regulation of supramolecular fiber	BP	1	LIMK1	up_VCAV_VSMC
GO:0030168	0.164	0.987	1	23	platelet activation	BP	1	SLC7A11	up_VPOR_EC
GO:0060389	0.164	0.987	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	ACVR2A	up_VPOR_EC
GO:0048863	0.164	0.987	1	70	stem cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035023	0.164	0.986	1	46	regulation of Rho protein signal transduction	BP	1	TIAM1	up_VFEM_EC
GO:1901605	0.164	0.987	1	67	alpha-amino acid metabolic process	BP	1	GATM	up_VFEM_VSMC
GO:0003206	0.164	0.987	1	51	cardiac chamber morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0050900	0.164	0.987	1	89	leukocyte migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0051056	0.164	0.987	1	87	regulation of small GTPase mediated signal	BP	1	SLIT2	up_VPUL_VSMC
GO:0090090	0.164	0.986	1	44	negative regulation of canonical Wnt signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0022612	0.164	0.986	1	44	gland morphogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:1904892	0.164	0.987	1	40	regulation of STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0033194	0.16424295	0.98771	1	7	response to hydroperoxide	BP	1	PRKCD	up_ACOR_EC
GO:0048523	0.165	0.858	145	1399	negative regulation of cellular process	BP	1	FGF13,TMEM176B,TMEM176A,SMAD6,ARHGAP28,ACTN2,PLCG2,LEP,LBH,DCBLD2,MID1,KCNE3,BCL2,HTR2B,RASSF2,TCAF1,MBP,PRDX4,RECK,FEZ1,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,EVI5L,TUBB4A,TM7SF3,FGFR2,TP53BP1,EIF4A2,GJA1,ELF1,ATRX,CASTOR1,TRPS1,SH3RF2,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,ATXN2,RERG,ISG15,ZNRF3,CD274,ZNF365,AR,PTGIR,LMO4,PTPN3,NDRG2,CDKN2B,ITPR1,CST3,ZNF174,PLAC8B,KLHL20,LIMS2,ANKRD1,F2RL1,FAM129A,MARCH5,DAPK1,BNIP3,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,LRPAP1,ULK2,OS9,UNC5B,ORMDL3,EVL,SMPD1,APLP1,SPINT2,TBX20,SESN3,SH3RF1,TBX5,CCDC3,PRKCE,CCNT1,MARF1,FZD3,DKKL1,FRS2,RND1,RGS2,DAG1,PPP1R26,PARP9,APP,PSEN1,SEMA6D,SYNJ2BP,MXI1,CHD7,JUP,SPINK2,CLN8,NR3C1,WWC2,DUSP22,EDN1,SESN1,OXR1,HPGD,DUSP26,CBX7,LRRC4,ASAP1,FAM107A,DDIT4,B2M,SCAMP5,KLF11,HERPUD1,FEZ2,INPP5K,BMT2,PFKL,WFS1,WASL,NAIF1,SH3BP4,ENSCAFG00000029553,ID3,PARK7,GPATCH2,ZFYVE1,HMBOX1,RREB1,PAG1,CRKL,PTPN14	up_ACOR_VSMC
GO:0051130	0.165	0.878	34	342	positive regulation of cellular component organization	BP	1	FSCN1,SREBF1,ANLN,HNRNPD,COLGALT1,SDC1,BIRC5,CAV1,NF2,AURKB,GREM1,NEK2,FEN1,DHX33,POC1A,BRCA1,EIF5A,HIST1H1A,RAC1,NUP62,PDXP,FOSL1,PLK4,IQGAP2,CDC42EP4,ENSCAFG00000005299,CORO1A,CDC20,ARPC1B,PSMC1,TADA2A,UBE2C,CCT4,TPBG	down_ACOR_VSMC
GO:0009100	0.165	0.894	17	139	glycoprotein metabolic process	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,ITM2C,B3GNT7,CCDC126,MAGT1,STT3B,FUT11,FUT8,POMK,PSEN1,PCSK6,EOGT,PARK7,LMF1	up_ACOR_VSMC

GO:0032990	0.165	0.898	14	167	cell part morphogenesis	BP	1	SIPA1L1,SGK1,PTPN11,IFRD1,KIF5B,TNIK,NEO1,UST,CDH11,CTNNB1,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0051656	0.165	0.898	14	129	establishment of organelle localization	BP	1	KIT,RAB11A,KIF3C,RAB27A,NECTIN2,HOOK3,SNAP23,HHEX,CENPC,FES,STX11,ZW10,HIF1A,SHROOM2	up_VCAV_EC
GO:0007507	0.165	0.9	13	194	heart development	BP	1	NOTCH2,PDGFRB,FBN1,BMPR1A,LOX,LMO4,SEMA3C,GLI3,ZFP36L1,IFT57,SPRED1,SHC1,GREM1	down_VCAV_EC
GO:0031346	0.165	0.911	9	73	positive regulation of cell projection organization	BP	1	RELN,RAPGEF1,RAB11A,MTOR,NCKAP1,NCK1,FES,RAPGEF2,FSCN1	up_VCAV_EC
GO:0098727	0.165	0.916	8	60	maintenance of cell number	BP	1	HOOK3,PROX1,MMP24,LDB2,JAG1,CUL4A,KDM3A,ZC3H13	up_VCAV_EC
GO:0007411	0.165	0.921	7	45	axon guidance	BP	1	FEZ1,NRP1,UNC5B,FZD3,DAG1,APP,FEZ2	up_ACOR_VSMC
GO:0097485	0.165	0.921	7	45	neuron projection guidance	BP	1	FEZ1,NRP1,UNC5B,FZD3,DAG1,APP,FEZ2	up_ACOR_VSMC
GO:0033002	0.165	0.92	7	55	muscle cell proliferation	BP	1	EPHB1,CALCRL,TNFAIP3,PDGFB,MEF2C,EDN1,APOD	up_VCAV_EC
GO:0050793	0.165	0.927	6	731	regulation of developmental process	BP	1	ACVRL1,LYN,PDPN,HOXA7,SULF1,ASPN	down_ACOR_EC
GO:0010467	0.165	0.935	6	1787	gene expression	BP	1	IVNS1ABP,DARS,EIF3M,SRSF6,GABPA,TSEN15	down_AFEM_EC
GO:0034612	0.165	0.924	6	63	response to tumor necrosis factor	BP	1	ARHGEF2,NR1H4,ILK,PTPN2,ADAM17,ENSCAFG00000002015	down_VSAP_EC
GO:0034762	0.165	0.93	5	122	regulation of transmembrane transport	BP	1	LEP,KCNC4,KCND1,FXYD1,CLIC4	up_AFEM_EC
GO:0061333	0.165	0.932	5	35	renal tubule morphogenesis	BP	1	HOXB7,MEF2C,GATA3,MTSS1,BMP2	up_VCAV_EC
GO:0030038	0.165	0.933	5	31	contractile actin filament bundle assembly	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,BAG4	up_VSAP_EC
GO:0043149	0.165	0.933	5	31	stress fiber assembly	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,BAG4	up_VSAP_EC
GO:0003151	0.165	0.94	4	34	outflow tract morphogenesis	BP	1	ILK,HIF1A,CTNNB1,NRP1	down_VSAP_EC
GO:0002456	0.165	0.941	4	23	T cell mediated immunity	BP	1	DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0048144	0.165	0.941	4	23	fibroblast proliferation	BP	1	TP53INP1,CDKN1A,DDR2,FOSL2	up_ACOR_VSMC
GO:0048145	0.165	0.941	4	23	regulation of fibroblast proliferation	BP	1	TP53INP1,CDKN1A,DDR2,FOSL2	up_ACOR_VSMC
GO:1901863	0.165	0.941	4	25	positive regulation of muscle tissue	BP	1	MEF2C,EDN1,CREB1,CDON	up_VCAV_EC
GO:0010827	0.165	0.95	3	28	regulation of glucose transmembrane transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0048699	0.165	0.95	3	371	generation of neurons	BP	1	MAPK10,SLITRK5,NTRK2	up_APUL_EC
GO:0000904	0.165	0.949	3	181	cell morphogenesis involved in differentiation	BP	1	ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0002762	0.165	0.953	3	15	negative regulation of myeloid leukocyte	BP	1	HOXA7,PIK3R1,MYC	up_VSAP_EC
GO:0070849	0.165	0.953	3	15	response to epidermal growth factor	BP	1	ZFP36L1,ZFP36L2,BAG4	up_VSAP_EC
GO:0045892	0.165	0.95	3	328	negative regulation of transcription, DNA-	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0035337	0.165	0.968	2	9	fatty-acyl-CoA metabolic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:1902745	0.165	0.968	2	9	positive regulation of lamellipodium	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:0072376	0.165	0.967	2	11	protein activation cascade	BP	1	PRCP,A2M	down_VSAP_EC
GO:0061298	0.165	0.969	2	8	retina vasculature development in camera-	BP	1	ARHGEF15,HIF1A	up_VCAV_EC
GO:0090287	0.165	0.964	2	91	regulation of cellular response to growth factor	BP	1	ASPN,ACVR2A	up_VPOR_EC
GO:0060349	0.165	0.986	1	38	bone morphogenesis	BP	1	CSGALNACT1	down_ACOR_EC
GO:0000389	0.165	0.993	1	2	mRNA 3'-splice site recognition	BP	1	SF3A1	down_ACOR_VSMC
GO:0070202	0.165	0.993	1	2	regulation of establishment of protein localization to	BP	1	CCT4	down_ACOR_VSMC
GO:0070203	0.165	0.993	1	2	regulation of establishment of protein	BP	1	CCT4	down_ACOR_VSMC
GO:0090666	0.165	0.993	1	2	scaRNA localization to Cajal body	BP	1	CCT4	down_ACOR_VSMC
GO:1904851	0.165	0.993	1	2	positive regulation of establishment of protein localization to telomere	BP	1	CCT4	down_ACOR_VSMC

GO:1904714	0.165	0.993	1	2	regulation of chaperone-mediated autophagy	BP	1	PLK3	down_ACOR_VSMC
GO:0030198	0.165	0.987	1	81	extracellular matrix organization	BP	1	FSCN1	down_AFEM_EC
GO:0045934	0.165	0.99	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0031120	0.165	0.99	1	3	snRNA pseudouridine synthesis	BP	1	MRPL1	down_VSAP_EC
GO:0019627	0.165	0.99	1	3	urea metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:1900122	0.165	0.99	1	3	positive regulation of receptor binding	BP	1	PLCL1	down_VSAP_EC
GO:0009117	0.165	0.988	1	208	nucleotide metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0036481	0.165	0.993	1	2	intrinsic apoptotic signaling pathway in response to hydrogen	BP	1	PARK7	up_ACOR_VSMC
GO:0060971	0.165	0.993	1	2	embryonic heart tube left/right pattern	BP	1	CITED2	up_ACOR_VSMC
GO:1903862	0.165	0.993	1	2	positive regulation of oxidative phosphorylation	BP	1	PARK7	up_ACOR_VSMC
GO:1905448	0.165	0.993	1	2	positive regulation of mitochondrial ATP synthesis coupled	BP	1	PARK7	up_ACOR_VSMC
GO:0045664	0.165	0.987	1	144	regulation of neuron differentiation	BP	1	WNT7A	up_AORT_VSMC
GO:0010976	0.165	0.986	1	47	positive regulation of neuron projection	BP	1	NTRK2	up_APUL_EC
GO:0042445	0.165	0.986	1	46	hormone metabolic process	BP	1	PCSK1N	up_APUL_EC
GO:0001568	0.165	0.988	1	252	blood vessel development	BP	1	HOXA3	up_APUL_VSMC
GO:0021502	0.165	0.993	1	2	neural fold elevation formation	BP	1	HIF1A	up_VCAV_EC
GO:0048102	0.165	0.99	1	3	autophagic cell death	BP	1	SH3GLB1	up_VCAV_EC
GO:0007186	0.165	0.987	1	124	G protein-coupled receptor signaling	BP	1	CA2	up_VCAV_VSMC
GO:0007254	0.165	0.987	1	67	JNK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0003018	0.165	0.986	1	42	vascular process in circulatory system	BP	1	AVPR1A	up_VFEM_EC
GO:0031346	0.165	0.986	1	73	positive regulation of cell projection organization	BP	1	SHOX2	up_VFEM_VSMC
GO:0045017	0.165	0.986	1	52	glycerolipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0061448	0.165	0.987	1	89	connective tissue development	BP	1	HOXA3	up_VPUL_VSMC
GO:0021784	0.165	0.993	1	2	postganglionic parasympathetic fiber	BP	1	PLXNA4	up_VSAP_EC
GO:0061643	0.165	0.993	1	2	chemorepulsion of axon	BP	1	PLXNA4	up_VSAP_EC
GO:1901628	0.165	0.993	1	2	positive regulation of postsynaptic membrane organization	BP	1	LRP4	up_VSAP_EC
GO:1901629	0.165	0.993	1	2	regulation of presynaptic membrane organization	BP	1	LRP4	up_VSAP_EC
GO:1903909	0.165	0.993	1	2	regulation of receptor clustering	BP	1	LRP4	up_VSAP_EC
GO:1904393	0.165	0.993	1	2	regulation of skeletal muscle acetylcholine-gated channel clustering	BP	1	LRP4	up_VSAP_EC
GO:0006937	0.165	0.986	1	40	regulation of muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0032509	0.165420446	0.98753	1	7	endosome transport via multivesicular body sorting pathway	BP	1	ABCB9	up_ACOR_EC
GO:0043114	0.165523381	0.98751	1	7	regulation of vascular permeability	BP	1	CLSTN1	up_ACOR_EC

GO:0002376	0.166	0.866	67	622	immune system process	BP	1	VEGFD,TMEM176B,TLR1,TMEM176A,SMAD6,PLCG2,LEP,CD83,RASSF2,COCH,BMP4,FGFR2,TP53BP1,MX1,ELF1,HRH1,TLR3,PDE5A,CITED2,ISG15,CD274,CTSS,LMO4,FAM210B,P4HTM,CDKN2B,TINAGL1,BLNK,F2RL1,HRH2,DAPK1,BNIP3,CDKN1A,C1S,EDA,TNFSF10,CLSTN1,PTPN22,CHD2,EVL,C7,PRKCE,PARP9,APP,PSEN1,CHD7,CCL5,RTKN2,DUSP22,NOD2,DLA88,DDIT4,JAM3,B2M,SERINC3,TNFRSF11B,MAP3K7,CNOT4,WASL,ERAP1,PARK7,ENSCAFG00000003530,IL18R1,BVES,PAG1,TAPBPL,CRKL	up_ACOR_VSMC
GO:0009057	0.166	0.877	34	473	macromolecule catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,SNX25,TRIB3,CEMIP2,MSN,SEL1L,USP12,DNAJC10,UBA6,ZPR1,UCHL5,SPOPL,SMG7,CNOT7,DNAJB9,SND1,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:0046700	0.166	0.891	18	147	heterocycle catabolic process	BP	1	AXIN2,GDA,TENT5C,ALDH6A1,EXOSC7,PYM1,DFFB,ZFP36L1,GALK1,ENTPD3,SMG9,SAMD4B,ZFP36L2,PNP,TNRC6C,HMOX1,DDIT4,IDO2	up_VSAP_EC
GO:0001558	0.166	0.9	13	101	regulation of cell growth	BP	1	WNT11,HNF4A,FAM107A,SLIT2,ABL1,PLXNA4,DPYSL2,WISP2,KDM2B,IGFBP6,TTL,SMARCA2,ACVRL1	up_VSAP_EC
GO:0019216	0.166	0.9	13	101	regulation of lipid metabolic process	BP	1	HNF4A,INSIG2,ACACB,C1QTNF2,ENSCAFG00000000071,AMBRA1,RBL2,LMF1,PDK2,PIK3R1,PIK3IP1,LONP2,IDH1	up_VSAP_EC
GO:0045165	0.166	0.911	9	65	cell fate commitment	BP	1	HOXA11,CDON,WNT11,EBF2,DLL1,STAT6,GAS1,HOXC10,LATS2	up_VSAP_EC
GO:0006066	0.166	0.918	7	89	alcohol metabolic process	BP	1	LCAT,CYB5R3,CYP1B1,RETSAT,PARK7,NAPEPLD,SOAT1	down_VCAV_EC
GO:1901991	0.166	0.919	7	56	negative regulation of mitotic cell cycle phase	BP	1	TAOK1,BLM,RAD21,RAD17,ZW10,TOPBP1,FBXO5	up_VCAV_EC
GO:0045619	0.166	0.925	6	44	regulation of lymphocyte differentiation	BP	1	IL7R,GATA3,ITPKB,HMGB1,ATP11C,ZEB1	up_VCAV_EC
GO:0007596	0.166	0.931	5	47	blood coagulation	BP	1	SERPINE1,APOE,LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0010923	0.166	0.932	5	30	negative regulation of phosphatase activity	BP	1	SH3RF2,MARF1,PPP1R26,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0009967	0.166	0.939	4	435	positive regulation of signal transduction	BP	1	ACVRL1,LYN,SULF1,NEDD4	down_ACOR_EC
GO:0014031	0.166	0.94	4	27	mesenchymal cell development	BP	1	EDNRB,EDN1,JAG1,HIF1A	up_VCAV_EC
GO:0014032	0.166	0.94	4	27	neural crest cell development	BP	1	EDNRB,EDN1,JAG1,HIF1A	up_VCAV_EC
GO:0007017	0.166	0.938	4	273	microtubule-based process	BP	1	MZT1,HOOK3,ARHGEF2,GCC2	up_VPOR_EC
GO:0051173	0.166	0.942	4	874	positive regulation of nitrogen compound	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0001909	0.166	0.951	3	18	leukocyte mediated cytotoxicity	BP	1	FAM49B,EMP2,CORO1A	down_ACOR_VSMC
GO:0046632	0.166	0.949	3	29	alpha-beta T cell differentiation	BP	1	GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0045022	0.166	0.952	3	15	early endosome to late endosome transport	BP	1	PIK3C3,AKTIP,LMTK2	up_ACOR_VSMC
GO:0001525	0.166	0.948	3	173	angiogenesis	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0022008	0.166	0.95	3	406	neurogenesis	BP	1	FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1902679	0.166	0.949	3	329	negative regulation of RNA biosynthetic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:1903507	0.166	0.949	3	329	negative regulation of nucleic acid-templated	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0050999	0.166	0.968	2	9	regulation of nitric-oxide synthase activity	BP	1	CAV1,NUS1	down_ACOR_VSMC
GO:0019637	0.166	0.966	2	342	organophosphate metabolic process	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0044087	0.166	0.966	2	339	regulation of cellular component biogenesis	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0051241	0.166	0.966	2	336	negative regulation of multicellular organismal	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:1901654	0.166	0.964	2	31	response to ketone	BP	1	FIBIN,NR3C1	up_AFEM_EC
GO:0060322	0.166	0.964	2	193	head development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0022414	0.166	0.965	2	294	reproductive process	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:1903599	0.166	0.969	2	8	positive regulation of autophagy of	BP	1	MFN2,FBXO7	up_VSAP_EC

GO:0005976	0.166	0.986	1	34	polysaccharide metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0042471	0.166	0.986	1	34	ear morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0090276	0.166	0.986	1	36	regulation of peptide hormone secretion	BP	1	STX4	down_ACOR_EC
GO:0001951	0.166	0.992	1	2	intestinal D-glucose absorption	BP	1	EZR	down_ACOR_VSMC
GO:0042758	0.166	0.993	1	2	long-chain fatty acid catabolic process	BP	1	ACADL	down_ACOR_VSMC
GO:0043622	0.166	0.993	1	2	cortical microtubule organization	BP	1	EZR	down_ACOR_VSMC
GO:0044210	0.166	0.992	1	2	'de novo' CTP biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0071139	0.166	0.992	1	2	resolution of recombination	BP	1	GEN1	down_ACOR_VSMC
GO:0071140	0.166	0.992	1	2	resolution of mitotic recombination	BP	1	GEN1	down_ACOR_VSMC
GO:0032274	0.166	0.992	1	2	gonadotropin secretion	BP	1	FAM129B	down_ACOR_VSMC
GO:0032532	0.166	0.992	1	2	regulation of microvillus length	BP	1	EZR	down_ACOR_VSMC
GO:0034165	0.166	0.992	1	2	positive regulation of toll-like receptor 9 signaling	BP	1	HMGB1	down_ACOR_VSMC
GO:0106001	0.166	0.992	1	2	intestinal hexose absorption	BP	1	EZR	down_ACOR_VSMC
GO:1902896	0.166	0.992	1	2	terminal web assembly	BP	1	EZR	down_ACOR_VSMC
GO:1904781	0.166	0.993	1	2	positive regulation of protein localization to	BP	1	NUP62	down_ACOR_VSMC
GO:0031334	0.166	0.986	1	84	positive regulation of protein complex assembly	BP	1	FSCN1	down_AFEM_EC
GO:0097091	0.166	0.989	1	4	synaptic vesicle clustering	BP	1	CDH2	down_VCAV_EC
GO:0071569	0.166	0.99	1	3	protein ufmylation	BP	1	UBA5	down_VSAP_EC
GO:1990564	0.166	0.99	1	3	protein polyufmylation	BP	1	UBA5	down_VSAP_EC
GO:1990592	0.166	0.99	1	3	protein K69-linked ufmylation	BP	1	UBA5	down_VSAP_EC
GO:0034374	0.166	0.99	1	3	low-density lipoprotein particle remodeling	BP	1	APOE	down_VSAP_EC
GO:1903589	0.166	0.99	1	3	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	JCAD	down_VSAP_EC
GO:2000576	0.166	0.989	1	4	positive regulation of microtubule motor	BP	1	DYNLL1	down_VSAP_EC
GO:2000580	0.166	0.989	1	4	regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNLL1	down_VSAP_EC
GO:2000582	0.166	0.989	1	4	positive regulation of ATP-dependent microtubule motor activity, plus-end-	BP	1	DYNLL1	down_VSAP_EC
GO:0098909	0.166	0.992	1	2	regulation of cardiac muscle cell action potential involved in	BP	1	FGF13	up_ACOR_VSMC
GO:0043309	0.166	0.993	1	2	regulation of eosinophil degranulation	BP	1	F2RL1	up_ACOR_VSMC
GO:0043311	0.166	0.993	1	2	positive regulation of eosinophil degranulation	BP	1	F2RL1	up_ACOR_VSMC
GO:0086036	0.166	0.993	1	2	regulation of cardiac muscle cell membrane	BP	1	FXYD1	up_ACOR_VSMC
GO:1902566	0.166	0.993	1	2	regulation of eosinophil activation	BP	1	F2RL1	up_ACOR_VSMC
GO:1902568	0.166	0.993	1	2	positive regulation of eosinophil activation	BP	1	F2RL1	up_ACOR_VSMC
GO:0002683	0.166	0.987	1	126	negative regulation of immune system process	BP	1	HOXA9	up_AFEM_VSMC
GO:0070302	0.166	0.986	1	78	regulation of stress-activated protein kinase	BP	1	TAOK1	up_AORT_EC
GO:0031348	0.166	0.986	1	46	negative regulation of defense response	BP	1	NR1H4	up_APUL_EC
GO:0035898	0.166	0.993	1	2	parathyroid hormone secretion	BP	1	GATA3	up_VCAV_EC
GO:0044313	0.166	0.992	1	2	protein K6-linked deubiquitination	BP	1	USP13	up_VCAV_EC
GO:2000660	0.166	0.992	1	2	negative regulation of interleukin-1-mediated	BP	1	OTUD4	up_VCAV_EC

GO:0006575	0.166	0.986	1	53	cellular modified amino acid metabolic process	BP	1	ENSCAFG00000028814	up_VPUL_EC
GO:0050663	0.166	0.986	1	52	cytokine secretion	BP	1	NR1H4	up_VPUL_EC
GO:0044789	0.166	0.992	1	2	modulation by host of viral release from host cell	BP	1	PC	up_VSAP_EC
GO:0044791	0.166	0.992	1	2	positive regulation by host of viral release from	BP	1	PC	up_VSAP_EC
GO:0045727	0.166	0.986	1	40	positive regulation of translation	BP	1	PRR16	up_VSAP_VSMC
GO:0071548	0.166239933	0.9874	1	7	response to dexamethasone	BP	1	AQP1	up_ACOR_EC
GO:0006820	0.166630433	0.92876	5	109	anion transport	BP	1	CA4,CLIC3,CFI,SLC25A42,PRKCD	up_ACOR_EC
GO:0009890	0.167	0.873	41	420	negative regulation of biosynthetic process	BP	1	EDNRB,HCLS1,PDGFB,CD34,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,FAM3C,BMP2,HMG20A,HHEX,CREM,ENC1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,HMBOX1,SMARCA4,NCK1,TIMELESS,RAPGEF2,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,RAD17,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0034660	0.167	0.885	22	211	ncRNA metabolic process	BP	1	VARS,INTS7,SRRT,NOP56,FBL,DIS3,NOC4L,FARSA,NCL,RSL1D1,THUMPD2,RRP1,OSGEP,ENSCAFG00000019620,RARS,NOP14,NOP58,ENSCAFG00000015189,EMG1,RTCB,EXOSC5,NOB1	down_ACOR_VSMC
GO:0042327	0.167	0.885	22	289	positive regulation of phosphorylation	BP	1	ARHGEF2,VEGFA,JCAD,BCAR3,PTPN11,ILK,PTGS2,TNIK,YES1,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,SH3GLB1,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0010243	0.167	0.889	19	238	response to organonitrogen compound	BP	1	ARHGEF2,NR1H4,SOCS5,HM13,HSP90B1,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,SEL1L,DNAJC10,PTPN2,DNAJB9,CTNNB1,APOE,NR4A1,USP14,HOMER1	down_VSAP_EC
GO:0044270	0.167	0.891	18	147	cellular nitrogen compound catabolic process	BP	1	AXIN2,GDA,TENT5C,ALDH6A1,EXOSC7,PYM1,DFFB,ZFP36L1,GALK1,ENTPD3,SMG9,SAMD4B,ZFP36L2,PNP,TNRC6C,HMOX1,DDIT4,IDO2	up_VSAP_EC
GO:0007610	0.167	0.893	16	146	behavior	BP	1	PLK2,PTCHD1,ATP8A1,RELN,MEF2C,CHD7,HOXB8,TMOD1,NAV2,PREX2,CREB1,SPTBN4,HIF1A,ALS2,ALDH1A3,P2RX2	up_VCAV_EC
GO:0043067	0.167	0.894	15	479	regulation of programmed cell death	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,PPARGC1A,FAP	up_AFEM_EC
GO:0050867	0.167	0.904	11	83	positive regulation of cell activation	BP	1	CD274,ZBTB16,TOX,STAT6,F2RL1,MYD88,CD83,PNP,STX4,NCK1,TGFBR2	up_VSAP_EC
GO:0035265	0.167	0.915	8	54	organ growth	BP	1	LEP,FGFR2,LATS2,TBX20,TBX5,DDR2,WWC2,EDN1	up_ACOR_VSMC
GO:0034250	0.167	0.924	6	45	positive regulation of cellular amide metabolic	BP	1	EIF4A3,HNRNPD,TRUB2,PLK3,FASTKD3,EIF5A	down_ACOR_VSMC
GO:0009124	0.167	0.93	5	51	nucleoside monophosphate	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC	down_VSAP_EC
GO:1903707	0.167	0.93	5	48	negative regulation of hemopoiesis	BP	1	SOCS5,PTPN2,CTNNB1,LYN,PRMT1	down_VSAP_EC
GO:0008277	0.167	0.932	5	31	regulation of G protein-coupled receptor signaling	BP	1	HTR2B,APLP1,RGS2,EDN1,USP20	up_ACOR_VSMC
GO:0090100	0.167	0.932	5	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FERMT1,BMP4,CITED2,CDKN2B,NPNT	up_ACOR_VSMC
GO:0006865	0.167	0.95	3	23	amino acid transport	BP	1	SLC7A5,SLC38A1,SLC7A11	down_VSAP_EC
GO:0097194	0.167	0.95	3	23	execution phase of apoptosis	BP	1	CASP3,PAK2,MADD	down_VSAP_EC
GO:0018193	0.167	0.949	3	368	peptidyl-amino acid modification	BP	1	NR1H4,PLCL1,NTRK2	up_APUL_EC
GO:0120036	0.167	0.949	3	373	plasma membrane bounded cell projection	BP	1	ARHGEF26,SLITRK5,NTRK2	up_APUL_EC
GO:0014909	0.167	0.952	3	15	smooth muscle cell migration	BP	1	DOCK4,PDGFB,MEF2C	up_VCAV_EC
GO:0032386	0.167	0.964	2	137	regulation of intracellular transport	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0010939	0.167	0.967	2	9	regulation of necrotic cell death	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:0070131	0.167	0.967	2	9	positive regulation of mitochondrial translation	BP	1	TRUB2,FASTKD3	down_ACOR_VSMC
GO:0051130	0.167	0.965	2	342	positive regulation of cellular component	BP	1	GPSM2,FSCN1	down_AFEM_EC

GO:0000060	0.167	0.965	2	15	protein import into nucleus, translocation	BP	1	MAVS,SEC61B	down_VCAV_EC
GO:0006509	0.167	0.965	2	15	membrane protein ectodomain proteolysis	BP	1	TIMP2,PACSIN3	down_VCAV_EC
GO:0045620	0.167	0.965	2	15	negative regulation of lymphocyte	BP	1	GLI3,LOXL3	down_VCAV_EC
GO:0040036	0.167	0.966	2	11	regulation of fibroblast growth factor receptor	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0097205	0.167	0.966	2	12	renal filtration	BP	1	SULF1,MYO1E	down_VSAP_EC
GO:0055070	0.167	0.968	2	8	copper ion homeostasis	BP	1	ATP7A,APP	up_ACOR_VSMC
GO:0009062	0.167	0.964	2	31	fatty acid catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0048469	0.167	0.964	2	31	cell maturation	BP	1	IRX5,LGI4	up_AFEM_EC
GO:1902106	0.167	0.964	2	31	negative regulation of leukocyte differentiation	BP	1	HOXA7,CYLD	up_AFEM_EC
GO:0071310	0.167	0.968	2	634	cellular response to organic substance	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:1905517	0.167	0.967	2	10	macrophage migration	BP	1	EDNRB,MMP28	up_VCAV_EC
GO:0007283	0.167	0.963	2	91	spermatogenesis	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0060548	0.167	0.965	2	294	negative regulation of cell death	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0000003	0.167	0.965	2	295	reproduction	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0071495	0.167	0.966	2	365	cellular response to endogenous stimulus	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0007520	0.167	0.968	2	8	myoblast fusion	BP	1	CDON,FLOT1	up_VSAP_EC
GO:0097553	0.167	0.986	1	32	calcium ion transmembrane import	BP	1	LYN	down_ACOR_EC
GO:0014834	0.167	0.992	1	2	skeletal muscle satellite cell maintenance involved in skeletal muscle	BP	1	EZH2	down_ACOR_VSMC
GO:0032466	0.167	0.992	1	2	negative regulation of cytokinesis	BP	1	E2F8	down_ACOR_VSMC
GO:0006420	0.167	0.992	1	2	arginyl-tRNA aminoacylation	BP	1	RARS	down_ACOR_VSMC
GO:0008582	0.167	0.992	1	2	regulation of synaptic growth at neuromuscular	BP	1	SIX4	down_ACOR_VSMC
GO:0030910	0.167	0.992	1	2	olfactory placode formation	BP	1	SIX4	down_ACOR_VSMC
GO:0031339	0.167	0.992	1	2	negative regulation of vesicle fusion	BP	1	CORO1A	down_ACOR_VSMC
GO:0032825	0.167	0.992	1	2	positive regulation of natural killer cell	BP	1	TOX	down_ACOR_VSMC
GO:0035281	0.167	0.992	1	2	pre-miRNA export from nucleus	BP	1	RAN	down_ACOR_VSMC
GO:0003025	0.167	0.992	1	2	regulation of systemic arterial blood pressure by baroreceptor feedback	BP	1	NAV2	down_ACOR_VSMC
GO:0051255	0.167	0.992	1	2	spindle midzone assembly	BP	1	AURKB	down_ACOR_VSMC
GO:0060717	0.167	0.992	1	2	chorion development	BP	1	E2F8	down_ACOR_VSMC
GO:0060718	0.167	0.992	1	2	chorionic trophoblast cell differentiation	BP	1	E2F8	down_ACOR_VSMC
GO:0061055	0.167	0.992	1	2	myotome development	BP	1	SIX4	down_ACOR_VSMC
GO:0071698	0.167	0.992	1	2	olfactory placode development	BP	1	SIX4	down_ACOR_VSMC
GO:0071699	0.167	0.992	1	2	olfactory placode morphogenesis	BP	1	SIX4	down_ACOR_VSMC
GO:1903651	0.167	0.992	1	2	positive regulation of cytoplasmic transport	BP	1	EZR	down_ACOR_VSMC
GO:2000643	0.167	0.992	1	2	positive regulation of early endosome to late endosome transport	BP	1	EZR	down_ACOR_VSMC
GO:0009615	0.167	0.986	1	83	response to virus	BP	1	IVNS1ABP	down_AFEM_EC
GO:0019219	0.167	1	1	1151	regulation of nucleobase-containing compound metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0021819	0.167	0.989	1	4	layer formation in cerebral cortex	BP	1	GLI3	down_VCAV_EC
GO:0097104	0.167	0.989	1	4	postsynaptic membrane assembly	BP	1	CDH2	down_VCAV_EC

GO:0099068	0.167	0.989	1	4	postsynapse assembly	BP	1	CDH2	down_VCAV_EC
GO:0031327	0.167	0.99	1	412	negative regulation of cellular biosynthetic	BP	1	MOSPD1	down_VFEM_EC
GO:0045893	0.167	0.99	1	413	positive regulation of transcription, DNA-	BP	1	MOSPD1	down_VFEM_EC
GO:0045722	0.167	0.99	1	3	positive regulation of gluconeogenesis	BP	1	PTPN2	down_VSAP_EC
GO:1903969	0.167	0.99	1	3	regulation of response to macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:1903972	0.167	0.99	1	3	regulation of cellular response to macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:0031033	0.167	0.99	1	3	myosin filament organization	BP	1	MYBPC2	down_VSAP_EC
GO:0042220	0.167	0.99	1	3	response to cocaine	BP	1	HOMER1	down_VSAP_EC
GO:0006753	0.167	0.988	1	211	nucleoside phosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0048389	0.167	0.992	1	2	intermediate mesoderm development	BP	1	BMP4	up_ACOR_VSMC
GO:0061227	0.167	0.992	1	2	pattern specification involved in mesonephros	BP	1	BMP4	up_ACOR_VSMC
GO:0072098	0.167	0.992	1	2	anterior/posterior pattern specification involved in kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:0072190	0.167	0.992	1	2	ureter urothelium development	BP	1	BMP4	up_ACOR_VSMC
GO:0090155	0.167	0.992	1	2	negative regulation of sphingolipid biosynthetic	BP	1	ORMDL3	up_ACOR_VSMC
GO:0090156	0.167	0.992	1	2	cellular sphingolipid homeostasis	BP	1	ORMDL3	up_ACOR_VSMC
GO:1900060	0.167	0.992	1	2	negative regulation of ceramide biosynthetic	BP	1	ORMDL3	up_ACOR_VSMC
GO:0009306	0.167	0.987	1	127	protein secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0002758	0.167	0.986	1	46	innate immune response-activating signal	BP	1	NR1H4	up_APUL_EC
GO:0002221	0.167	0.986	1	46	pattern recognition receptor signaling	BP	1	NR1H4	up_APUL_EC
GO:0072009	0.167	0.986	1	48	nephron epithelium development	BP	1	NPNT	up_APUL_EC
GO:0045597	0.167	0.988	1	253	positive regulation of cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:0002683	0.167	0.987	1	126	negative regulation of immune system process	BP	1	LRRC17	up_VCAV_VSMC
GO:0032535	0.167	0.987	1	128	regulation of cellular component size	BP	1	LIMK1	up_VCAV_VSMC
GO:0001736	0.167	0.986	1	23	establishment of planar polarity	BP	1	PTK7	up_VPOR_EC
GO:0006970	0.167	0.986	1	23	response to osmotic stress	BP	1	ARHGEF2	up_VPOR_EC
GO:0007164	0.167	0.986	1	23	establishment of tissue polarity	BP	1	PTK7	up_VPOR_EC
GO:0009311	0.167	0.986	1	21	oligosaccharide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0022029	0.167	0.986	1	23	telencephalon cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0034446	0.167	0.986	1	23	substrate adhesion-dependent cell spreading	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0072330	0.167	0.986	1	68	monocarboxylic acid biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:2001234	0.167	0.986	1	75	negative regulation of apoptotic signaling	BP	1	EYA1	up_VFEM_VSMC
GO:0051924	0.167	0.986	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0003012	0.167	0.986	1	90	muscle system process	BP	1	GATA5	up_VPUL_VSMC
GO:0042478	0.167	0.992	1	2	regulation of eye photoreceptor cell	BP	1	THRB	up_VSAP_EC
GO:0030856	0.167	0.986	1	41	regulation of epithelial cell differentiation	BP	1	CAV1	up_VSAP_VSMC
GO:0032660	0.167507246	0.9872	1	7	regulation of interleukin-17 production	BP	1	NOD2	up_ACOR_EC
GO:0006807	0.168	0.904	19	3221	nitrogen compound metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,TNRC6B,ASPN,NEDD4	down_ACOR_EC

GO:0044255	0.168	0.888	19	293	cellular lipid metabolic process	BP	1	GPAM,PDGFRB,ENSCAFG00000014978,AKT2,LCAT,ACAA1,THNSL2,PIGS,CYP1B1,PEX5,RETSAT,ABHD15,ORMDL3,ENSCAFG00000017708,RDH10,LONP2,NAPEPLD,SOAT1,ACAT1	down_VCAV_EC
GO:0070201	0.168	0.894	15	187	regulation of establishment of protein localization	BP	1	NR1H4,PLK3,PTPN14,PTPN11,MYO1C,HIF1A,IWS1,ZPR1,LYN,GSK3B,SH3GLB1,REST,RAB11FIP1,CDKN1A,RHBDF2	down_VSAP_EC
GO:0072331	0.168	0.918	7	49	signal transduction by p53 class mediator	BP	1	ATRX,ANKRD1,CDKN1A,JMY,PERP,DDIT4,ZMAT3	up_ACOR_VSMC
GO:0009914	0.168	0.922	6	64	hormone transport	BP	1	NR1H4,PTPN11,HIF1A,REST,RAB11FIP1,INHBA	down_VSAP_EC
GO:0051173	0.168	0.925	6	874	positive regulation of nitrogen compound	BP	1	HOXA11,HOXA9,SALL1,PRR16,CAV1,SHOX2	up_VSAP_VSMC
GO:0043583	0.168	0.929	5	59	ear development	BP	1	SDC4,NAGLU,GLI3,GSDME,RDH10	down_VCAV_EC
GO:1903039	0.168	0.937	4	43	positive regulation of leukocyte cell-cell	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:0048515	0.168	0.938	4	36	spermatid differentiation	BP	1	CELF1,CDYL,SPINK2,KDM3A	down_VSAP_EC
GO:0030203	0.168	0.939	4	27	glycosaminoglycan metabolic process	BP	1	PDGFB,LYVE1,CHST7,CHST1	up_VCAV_EC
GO:0050871	0.168	0.94	4	24	positive regulation of B cell activation	BP	1	MEF2C,TLR4,PELI1,ATP11C	up_VCAV_EC
GO:1901888	0.168	0.949	3	29	regulation of cell junction assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0045744	0.168	0.951	3	15	negative regulation of G protein-coupled receptor signaling pathway	BP	1	HTR2B,APLP1,RGS2	up_ACOR_VSMC
GO:0032435	0.168	0.965	2	15	negative regulation of proteasomal ubiquitin-dependent protein	BP	1	PARK7,CLEC16A	down_VCAV_EC
GO:0002260	0.168	0.965	2	15	lymphocyte homeostasis	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0046635	0.168	0.965	2	15	positive regulation of alpha-beta T cell	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:0006891	0.168	0.966	2	12	intra-Golgi vesicle-mediated transport	BP	1	RAB6A,COPB2	down_VSAP_EC
GO:0008631	0.168	0.966	2	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	P4HB,HIF1A	down_VSAP_EC
GO:0030947	0.168	0.966	2	12	regulation of vascular endothelial growth factor receptor signaling	BP	1	VEGFA,HIF1A	down_VSAP_EC
GO:0035794	0.168	0.966	2	13	positive regulation of mitochondrial membrane permeability	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0050771	0.168	0.966	2	11	negative regulation of axonogenesis	BP	1	IFRD1,NRP1	down_VSAP_EC
GO:1905710	0.168	0.966	2	13	positive regulation of membrane permeability	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0002115	0.168	0.968	2	8	store-operated calcium entry	BP	1	SARAF,STC2	up_ACOR_VSMC
GO:0010822	0.168	0.963	2	31	positive regulation of mitochondrion	BP	1	MLLT11,PPARGC1A	up_AFEM_EC
GO:0070665	0.168	0.963	2	31	positive regulation of leukocyte proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:1904888	0.168	0.963	2	31	cranial skeletal system development	BP	1	TBX15,IRX5	up_AFEM_EC
GO:0019752	0.168	0.965	2	283	carboxylic acid metabolic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0048514	0.168	0.964	2	214	blood vessel morphogenesis	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:0071494	0.168	0.992	1	2	cellular response to UV-C	BP	1	POLH	down_ACOR_VSMC
GO:1902036	0.168	0.992	1	2	regulation of hematopoietic stem cell	BP	1	HSPA9	down_ACOR_VSMC
GO:0010891	0.168	0.992	1	2	negative regulation of sequestering of	BP	1	ABHD5	down_ACOR_VSMC
GO:0032423	0.168	0.992	1	2	regulation of mismatch repair	BP	1	HMGB1	down_ACOR_VSMC
GO:0098528	0.168	0.992	1	2	skeletal muscle fiber differentiation	BP	1	SIX4	down_ACOR_VSMC
GO:0003007	0.168	0.986	1	94	heart morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0050900	0.168	0.986	1	89	leukocyte migration	BP	1	HSD3B7	down_VPOR_EC
GO:0001932	0.168	0.99	1	416	regulation of protein phosphorylation	BP	1	PLCL1	down_VFEM_EC

GO:1902680	0.168	0.99	1	415	positive regulation of RNA biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:1903508	0.168	0.99	1	415	positive regulation of nucleic acid-templated	BP	1	MOSPD1	down_VFEM_EC
GO:0043589	0.168	0.99	1	3	skin morphogenesis	BP	1	ERRFI1	down_VSAP_EC
GO:0045627	0.168	0.99	1	3	positive regulation of T-helper 1 cell	BP	1	SOCS5	down_VSAP_EC
GO:0018307	0.168	0.992	1	2	enzyme active site formation	BP	1	PARK7	up_ACOR_VSMC
GO:1903789	0.168	0.992	1	2	regulation of amino acid transmembrane transport	BP	1	PSEN1	up_ACOR_VSMC
GO:1990168	0.168	0.992	1	2	protein K33-linked deubiquitination	BP	1	ZRANB1	up_ACOR_VSMC
GO:0007276	0.168	0.987	1	130	gamete generation	BP	1	HOXA9	up_AFEM_VSMC
GO:0048667	0.168	0.987	1	140	cell morphogenesis involved in neuron	BP	1	WNT7A	up_AORT_VSMC
GO:0021953	0.168	0.986	1	49	central nervous system neuron differentiation	BP	1	NTRK2	up_APUL_EC
GO:0002676	0.168	0.992	1	2	regulation of chronic inflammatory response	BP	1	TNFAIP3	up_VCAV_EC
GO:0051103	0.168	0.992	1	2	DNA ligation involved in DNA repair	BP	1	HMGB1	up_VCAV_EC
GO:0006936	0.168	0.986	1	74	muscle contraction	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071560	0.168	0.986	1	72	cellular response to transforming growth	BP	1	BAMBI	up_VPOR_VSMC
GO:0090092	0.168	0.986	1	72	regulation of transmembrane receptor protein serine/threonine	BP	1	BAMBI	up_VPOR_VSMC
GO:2001022	0.168	0.986	1	42	positive regulation of response to DNA damage	BP	1	EYA1	up_VFEM_EC
GO:0008544	0.168	0.986	1	75	epidermis development	BP	1	SPINK5	up_VFEM_VSMC
GO:0002218	0.168	0.986	1	53	activation of innate immune response	BP	1	NR1H4	up_VPUL_EC
GO:0060211	0.168	0.992	1	2	regulation of nuclear-transcribed mRNA poly(A)	BP	1	TNRC6C	up_VSAP_EC
GO:0060213	0.168	0.992	1	2	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	BP	1	TNRC6C	up_VSAP_EC
GO:0090259	0.168	0.992	1	2	regulation of retinal ganglion cell axon	BP	1	SLIT2	up_VSAP_EC
GO:0001657	0.168	0.986	1	42	ureteric bud development	BP	1	HOXA11	up_VSAP_VSMC
GO:0007259	0.168	0.986	1	42	JAK-STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0072163	0.168	0.986	1	42	mesonephric epithelium development	BP	1	HOXA11	up_VSAP_VSMC
GO:0072164	0.168	0.986	1	42	mesonephric tubule development	BP	1	HOXA11	up_VSAP_VSMC
GO:0002218	0.168372245	0.94738	3	53	activation of innate immune response	BP	1	NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0008154	0.168630457	0.93601	4	81	actin polymerization or depolymerization	BP	1	TMOD1,ACTN2,PAK3,PRKCD	up_ACOR_EC
GO:0010463	0.168664775	0.96324	2	28	mesenchymal cell proliferation	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0032682	0.168671085	0.98701	1	7	negative regulation of chemokine production	BP	1	NR1H4	up_ACOR_EC
GO:0007165	0.169	0.874	41	1496	signal transduction	BP	1	CMKLR1,LEP,LBH,CRY2,GAS1,ANGPT4,CD40,DLL1,F3,PLXNA4,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,HCK,TMEM100,PLAGL2,GREM1,HTR1D,FAM53B,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,RECK,PTHLH,TBXA2R,LGR6,RAB7A,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0002253	0.169	0.9	12	92	activation of immune response	BP	1	TLR1,PLCG2,ELF1,TLR3,F2RL1,C1S,PTPN22,C7,PRKCE,PSEN1,DUSP22,NOD2	up_ACOR_VSMC
GO:0006091	0.169	0.902	11	139	generation of precursor metabolites and energy	BP	1	ENPP1,PGK1,TPI1,PGAM1,ENSCAFG00000007260,HIF1A,NDUFA4L2,ALDOC,PPP1R3C,BNIP3,GSK3B	down_VSAP_EC
GO:0060537	0.169	0.904	10	117	muscle tissue development	BP	1	ACTN1,FLNB,IFRD1,FHL2,CTNNB1,KLF5,ATF3,NEXN,SIX4,HOMER1	down_VSAP_EC
GO:0043068	0.169	0.916	7	190	positive regulation of programmed cell death	BP	1	F3,MLLT11,PLAGL2,CAMK2A,CYLD,DCUN1D3,FAP	up_AFEM_EC
GO:0097529	0.169	0.928	5	52	myeloid leukocyte migration	BP	1	VEGFA,SERPINE1,WDR1,MMP28,LYN	down_VSAP_EC

GO:0050731	0.169	0.937	4	44	positive regulation of peptidyl-tyrosine	BP	1	PRNP,CSPG4,ARL2BP,GREM1	down_VCAV_EC
GO:0090287	0.169	0.936	4	91	regulation of cellular response to growth factor	BP	1	DLL1,GREM1,GREM2,ADAM17	up_AFEM_EC
GO:0097194	0.169	0.939	4	23	execution phase of apoptosis	BP	1	DFFB,XKR8,CASP12,DEDD2	up_VSAP_EC
GO:0006023	0.169	0.95	3	17	aminoglycan biosynthetic process	BP	1	B3GNT2,XYLT1,UGDH	down_ACOR_VSMC
GO:0051172	0.169	0.951	3	663	negative regulation of nitrogen compound	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0080090	0.169	0.963	3	1734	regulation of primary metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0072073	0.169	0.947	3	60	kidney epithelium development	BP	1	IRX3,DLL1,GREM1	up_AFEM_EC
GO:0072175	0.169	0.947	3	60	epithelial tube formation	BP	1	IRX3,GREM1,LUZP1	up_AFEM_EC
GO:0006366	0.169	0.95	3	583	transcription by RNA polymerase II	BP	1	EYA1,HOXA9,SHOX2	up_VFEM_VSMC
GO:0090050	0.169	0.951	3	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	ABL1,HDAC7,HMOX1	up_VSAP_EC
GO:0006801	0.169	0.965	2	15	superoxide metabolic process	BP	1	PARK7,CYBA	down_VCAV_EC
GO:0051173	0.169	0.97	2	874	positive regulation of nitrogen compound	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0048873	0.169	0.967	2	9	homeostasis of number of cells within a tissue	BP	1	EXOC5,VPS54	up_VCAV_EC
GO:0010628	0.169	0.966	2	527	positive regulation of gene expression	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0050900	0.169	0.963	2	89	leukocyte migration	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0002009	0.169	0.963	2	177	morphogenesis of an epithelium	BP	1	HOXA11,SALL1	up_VSAP_VSMC
GO:0006910	0.169	0.992	1	2	phagocytosis, recognition	BP	1	JMJD6	down_ACOR_VSMC
GO:0007084	0.169	0.992	1	2	mitotic nuclear envelope reassembly	BP	1	REEP4	down_ACOR_VSMC
GO:0010767	0.169	0.992	1	2	regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage	BP	1	NEDD4	down_ACOR_VSMC
GO:0030997	0.169	0.992	1	2	regulation of centriole-centriole cohesion	BP	1	NEK2	down_ACOR_VSMC
GO:0043654	0.169	0.992	1	2	recognition of apoptotic cell	BP	1	JMJD6	down_ACOR_VSMC
GO:0051103	0.169	0.992	1	2	DNA ligation involved in DNA repair	BP	1	HMGB1	down_ACOR_VSMC
GO:0098722	0.169	0.992	1	2	asymmetric stem cell division	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0046034	0.169	0.986	1	88	ATP metabolic process	BP	1	NDUFA10	down_AFEM_EC
GO:0032104	0.169	0.989	1	4	regulation of response to extracellular stimulus	BP	1	KANK2	down_VCAV_EC
GO:0032107	0.169	0.989	1	4	regulation of response to nutrient levels	BP	1	KANK2	down_VCAV_EC
GO:0007296	0.169	0.99	1	3	vitellogenesis	BP	1	ETV6	down_VSAP_EC
GO:0035973	0.169	0.99	1	3	aggrephagy	BP	1	HTT	down_VSAP_EC
GO:0048729	0.169	0.987	1	209	tissue morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0001999	0.169	0.992	1	2	renal response to blood flow involved in circulatory renin-angiotensin regulation of	BP	1	F2RL1	up_ACOR_VSMC
GO:0002528	0.169	0.992	1	2	regulation of vascular permeability involved in acute inflammatory	BP	1	CLSTN1	up_ACOR_VSMC
GO:0007341	0.169	0.992	1	2	penetration of zona pellucida	BP	1	DKKL1	up_ACOR_VSMC
GO:0019355	0.169	0.992	1	2	nicotinamide nucleotide biosynthetic process from aspartate	BP	1	NMNAT1	up_ACOR_VSMC
GO:0002001	0.169	0.992	1	2	renin secretion into blood stream	BP	1	F2RL1	up_ACOR_VSMC
GO:0034627	0.169	0.992	1	2	'de novo' NAD biosynthetic process	BP	1	NMNAT1	up_ACOR_VSMC
GO:0034628	0.169	0.992	1	2	'de novo' NAD biosynthetic process from	BP	1	NMNAT1	up_ACOR_VSMC

GO:1900133	0.169	0.992	1	2	regulation of renin secretion into blood	BP	1	F2RL1	up_ACOR_VSMC
GO:0016055	0.169	0.986	1	134	Wnt signaling pathway	BP	1	TLR2	up_AFEM_VSMC
GO:0198738	0.169	0.986	1	134	cell-cell signaling by wnt	BP	1	TLR2	up_AFEM_VSMC
GO:0003231	0.169	0.986	1	48	cardiac ventricle development	BP	1	TBX5	up_APUL_EC
GO:0021543	0.169	0.986	1	49	pallium development	BP	1	NTRK2	up_APUL_EC
GO:0051224	0.169	0.986	1	47	negative regulation of protein transport	BP	1	NR1H4	up_APUL_EC
GO:0003279	0.169	0.986	1	48	cardiac septum development	BP	1	TBX5	up_APUL_EC
GO:0106106	0.169	0.986	1	48	cold-induced thermogenesis	BP	1	PLCL1	up_APUL_EC
GO:0120161	0.169	0.986	1	48	regulation of cold-induced thermogenesis	BP	1	PLCL1	up_APUL_EC
GO:1904950	0.169	0.986	1	47	negative regulation of establishment of protein localization	BP	1	NR1H4	up_APUL_EC
GO:0072554	0.169	0.992	1	2	blood vessel lumenization	BP	1	DLL4	up_VCAV_EC
GO:0071407	0.169	0.986	1	129	cellular response to organic cyclic compound	BP	1	CYP1A1	up_VCAV_VSMC
GO:0046785	0.169	0.986	1	23	microtubule polymerization	BP	1	MZT1	up_VPOR_EC
GO:1903578	0.169	0.986	1	22	regulation of ATP metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0061709	0.169	0.992	1	2	reticulophagy	BP	1	RETREG1	up_VSAP_EC
GO:0070091	0.169	0.992	1	2	glucagon secretion	BP	1	PASK	up_VSAP_EC
GO:0070092	0.169	0.992	1	2	regulation of glucagon secretion	BP	1	PASK	up_VSAP_EC
GO:0045216	0.169	0.986	1	44	cell-cell junction organization	BP	1	CAV1	up_VSAP_VSMC
GO:0048771	0.169	0.986	1	43	tissue remodeling	BP	1	CAV1	up_VSAP_VSMC
GO:0071346	0.169	0.986	1	41	cellular response to interferon-gamma	BP	1	TLR2	up_VSAP_VSMC
GO:0051171	0.169718017	0.86961	51	1697	regulation of nitrogen compound metabolic process	BP	1	NR1H4,GATA4,TRPS1,PLCL1,PKIB,SOX9,PKNOX2,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,IFI6,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,RARRES2,GMEB2,RIOX2,RNF114,NRP1,AZIN2,PRKCD,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0042554	0.169750089	0.98684	1	7	superoxide anion generation	BP	1	PRKCD	up_ACOR_EC
GO:0080090	0.169924794	0.86921	52	1734	regulation of primary metabolic process	BP	1	NR1H4,GATA4,TRPS1,PLCL1,PKIB,SOX9,PKNOX2,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,CCDC3,IFI6,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,RARRES2,GMEB2,RIOX2,RNF114,NRP1,AZIN2,PRKCD,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0051254	0.17	0.868	47	431	positive regulation of RNA metabolic process	BP	1	HOXA11,FZD1,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,ZBTB16,RARG,F2RL1,ICE1,ZFP36L1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,NUP98,NPAS2,CDK9,PRMT2,ZFP36L2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,TNRC6C,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:0016570	0.17	0.891	16	143	histone modification	BP	1	SREBF1,POLE3,PRMT1,CDK1,AURKB,EZH2,FBL,UHRF1,BRCA1,NOC2L,HASPIN,DMAP1,CCNA2,RBM14,BAP1,TADA2A	down_ACOR_VSMC
GO:0009952	0.17	0.912	8	66	anterior/posterior pattern specification	BP	1	HOXA3,HOXA7,HOXC10,HOXB7,HOXC6,HOXB5,HOXC4,HOXA9	down_ACOR_VSMC
GO:2000116	0.17	0.912	8	67	regulation of cysteine-type endopeptidase	BP	1	HMGB1,BIRC5,PDCD2,DHCR24,CYCS,ENSCAFG00000005299,AIFM1,DELE1	down_ACOR_VSMC
GO:0045665	0.17	0.913	8	55	negative regulation of neuron differentiation	BP	1	ITM2C,ZNF365,NRP1,ULK2,APP,PSEN1,ASAP1,B2M	up_ACOR_VSMC

GO:1901362	0.17	0.917	8	1293	organic cyclic compound biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0052547	0.17	0.916	7	82	regulation of peptidase activity	BP	1	PTGS2,CRYAB,LYN,FAM162A,REST,PAK2,SPINK2	down_VSAP_EC
GO:0045598	0.17	0.918	7	47	regulation of fat cell differentiation	BP	1	NAPEPLD,SAV1,ZBTB16,ZFP36L1,ZADH2,ZFP36L2,TAF8	up_VSAP_EC
GO:0007154	0.17	0.93	6	1622	cell communication	BP	1	DKK2,LNPEP,ERC1,TAOK1,CTNNAL1,GPR155	up_AORT_EC
GO:0045216	0.17	0.922	6	44	cell-cell junction organization	BP	1	PRKCH,OCLN,TJP1,CTNNA1,ENSCAFG00000002015,FSCN1	up_VCAV_EC
GO:0002062	0.17	0.928	5	48	chondrocyte differentiation	BP	1	SULF1,SERPINH1,CHSY1,CTNNB1,CREB3L2	down_VSAP_EC
GO:0002705	0.17	0.93	5	31	positive regulation of leukocyte mediated	BP	1	TP53BP1,F2RL1,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0042098	0.17	0.936	4	43	T cell proliferation	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0097696	0.17	0.936	4	43	STAT cascade	BP	1	DCN,BGN,ASPN,ARL2BP	down_VCAV_EC
GO:0007045	0.17	0.939	4	23	cell-substrate adherens junction assembly	BP	1	ACTN2,NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0048041	0.17	0.939	4	23	focal adhesion assembly	BP	1	ACTN2,NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0003401	0.17	0.951	3	15	axis elongation	BP	1	BMP4,FGFR2,ENSCAFG00000006238	up_ACOR_VSMC
GO:0010810	0.17	0.946	3	60	regulation of cell-substrate adhesion	BP	1	HOXA7,GREM1,KANK1	up_AFEM_EC
GO:0019438	0.17	0.957	3	1258	aromatic compound biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0051234	0.17	0.957	3	1283	establishment of localization	BP	1	SLC20A2,WNT7A,ARG2	up_AORT_VSMC
GO:0044087	0.17	0.948	3	339	regulation of cellular component biogenesis	BP	1	TRIM9,SIX1,CDC42EP5	up_VFEM_EC
GO:0090175	0.17	0.951	3	15	regulation of establishment of planar	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0006730	0.17	0.967	2	8	one-carbon metabolic process	BP	1	MAT2B,AHCYL1	up_ACOR_VSMC
GO:0045745	0.17	0.966	2	10	positive regulation of G protein-coupled receptor signaling pathway	BP	1	ACPP,CAV2	up_VCAV_EC
GO:0045822	0.17	0.967	2	8	negative regulation of heart contraction	BP	1	PDE4D,SPTBN4	up_VCAV_EC
GO:0097190	0.17	0.963	2	217	apoptotic signaling pathway	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0021522	0.17	0.968	2	8	spinal cord motor neuron differentiation	BP	1	HOXC10,GDPD5	up_VSAP_EC
GO:1904262	0.17	0.967	2	8	negative regulation of TORC1 signaling	BP	1	SESN1,CASTOR1	up_VSAP_EC
GO:0044703	0.17	0.963	2	172	multi-organism reproductive process	BP	1	HOXA11,HOXA9	up_VSAP_VSMC
GO:0010950	0.17	0.985	1	44	positive regulation of endopeptidase activity	BP	1	LYN	down_ACOR_EC
GO:1990823	0.17	0.985	1	39	response to leukemia inhibitory factor	BP	1	NRP2	down_ACOR_EC
GO:1990830	0.17	0.985	1	39	cellular response to leukemia inhibitory factor	BP	1	NRP2	down_ACOR_EC
GO:0033031	0.17	0.992	1	2	positive regulation of neutrophil apoptotic	BP	1	PIK3CD	down_ACOR_VSMC
GO:0035522	0.17	0.992	1	2	monoubiquitinated histone H2A	BP	1	BAP1	down_ACOR_VSMC
GO:0090205	0.17	0.992	1	2	positive regulation of cholesterol metabolic	BP	1	SREBF1	down_ACOR_VSMC
GO:0097167	0.17	0.992	1	2	circadian regulation of translation	BP	1	HNRNPD	down_ACOR_VSMC
GO:0106120	0.17	0.992	1	2	positive regulation of sterol biosynthetic	BP	1	SREBF1	down_ACOR_VSMC
GO:1902410	0.17	0.992	1	2	mitotic cytokinetic process	BP	1	NUP62	down_ACOR_VSMC
GO:0010792	0.17	0.992	1	2	DNA double-strand break processing involved in repair via single-strand	BP	1	RBBP8	down_ACOR_VSMC
GO:0035521	0.17	0.992	1	2	monoubiquitinated histone deubiquitination	BP	1	BAP1	down_ACOR_VSMC
GO:0045002	0.17	0.992	1	2	double-strand break repair via single-strand	BP	1	RBBP8	down_ACOR_VSMC
GO:0045542	0.17	0.992	1	2	positive regulation of cholesterol biosynthetic	BP	1	SREBF1	down_ACOR_VSMC
GO:0070494	0.17	0.992	1	2	regulation of thrombin-activated receptor	BP	1	STMN1	down_ACOR_VSMC

GO:0070495	0.17	0.992	1	2	negative regulation of thrombin-activated receptor signaling	BP	1	STMN1	down_ACOR_VSMC
GO:1900425	0.17	0.992	1	2	negative regulation of defense response to	BP	1	ARG2	down_ACOR_VSMC
GO:1905098	0.17	0.992	1	2	negative regulation of guanyl-nucleotide exchange factor activity	BP	1	STMN1	down_ACOR_VSMC
GO:2001045	0.17	0.992	1	2	negative regulation of integrin-mediated	BP	1	PHACTR4	down_ACOR_VSMC
GO:0031326	0.17	1	1	1176	regulation of cellular biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0060485	0.17	0.986	1	93	mesenchyme development	BP	1	CITED2	down_VPOR_EC
GO:0009890	0.17	0.99	1	420	negative regulation of biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0032364	0.17	0.99	1	3	oxygen homeostasis	BP	1	HIF1A	down_VSAP_EC
GO:1904468	0.17	0.99	1	3	negative regulation of tumor necrosis factor	BP	1	NR1H4	down_VSAP_EC
GO:0019249	0.17	0.992	1	2	lactate biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0032025	0.17	0.992	1	2	response to cobalt ion	BP	1	BNIP3	up_ACOR_VSMC
GO:0045764	0.17	0.992	1	2	positive regulation of cellular amino acid	BP	1	PARK7	up_ACOR_VSMC
GO:0045777	0.17	0.992	1	2	positive regulation of blood pressure	BP	1	ADRA1B	up_ACOR_VSMC
GO:0071279	0.17	0.992	1	2	cellular response to cobalt ion	BP	1	BNIP3	up_ACOR_VSMC
GO:1990442	0.17	0.992	1	2	intrinsic apoptotic signaling pathway in response to nitrosative	BP	1	PARK7	up_ACOR_VSMC
GO:2000823	0.17	0.992	1	2	regulation of androgen receptor activity	BP	1	PARK7	up_ACOR_VSMC
GO:2000825	0.17	0.992	1	2	positive regulation of androgen receptor	BP	1	PARK7	up_ACOR_VSMC
GO:0032878	0.17	0.986	1	8	regulation of establishment or	BP	1	KANK1	up_AFEM_EC
GO:0010608	0.17	0.986	1	154	posttranscriptional regulation of gene	BP	1	ESR1	up_AORT_VSMC
GO:0019953	0.17	0.987	1	152	sexual reproduction	BP	1	HOXA9	up_AORT_VSMC
GO:0045598	0.17	0.985	1	47	regulation of fat cell differentiation	BP	1	WIF1	up_APUL_EC
GO:0006910	0.17	0.992	1	2	phagocytosis, recognition	BP	1	PEAR1	up_VCAV_EC
GO:0043654	0.17	0.992	1	2	recognition of apoptotic cell	BP	1	PEAR1	up_VCAV_EC
GO:0032970	0.17	0.986	1	130	regulation of actin filament-based process	BP	1	LIMK1	up_VCAV_VSMC
GO:0009135	0.17	0.986	1	22	purine nucleoside diphosphate metabolic	BP	1	FBP1	up_VPOR_EC
GO:0009179	0.17	0.986	1	22	purine ribonucleoside diphosphate metabolic	BP	1	FBP1	up_VPOR_EC
GO:0046031	0.17	0.986	1	22	ADP metabolic process	BP	1	FBP1	up_VPOR_EC
GO:1902041	0.17	0.985	1	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	ARHGEF2	up_VPOR_EC
GO:2000027	0.17	0.986	1	72	regulation of animal organ morphogenesis	BP	1	ANKRD6	up_VPOR_VSMC
GO:0045637	0.17	0.986	1	73	regulation of myeloid cell differentiation	BP	1	HOXA9	up_VFEM_VSMC
GO:0045926	0.17	0.986	1	72	negative regulation of growth	BP	1	FBP1	up_VFEM_VSMC
GO:0035690	0.17	0.986	1	91	cellular response to drug	BP	1	SLIT2	up_VPUL_VSMC
GO:0090287	0.17	0.986	1	91	regulation of cellular response to growth factor	BP	1	SLIT2	up_VPUL_VSMC
GO:1902744	0.17	0.992	1	2	negative regulation of lamellipodium	BP	1	SLIT2	up_VSAP_EC
GO:0060401	0.17	0.985	1	42	cytosolic calcium ion transport	BP	1	CAV1	up_VSAP_VSMC
GO:0071695	0.17	0.985	1	45	anatomical structure maturation	BP	1	IRX5	up_VSAP_VSMC
GO:0015711	0.170474243	0.93505	4	81	organic anion transport	BP	1	CA4,CFI,SLC25A42,PRKCD	up_ACOR_EC
GO:0090322	0.170555125	0.98671	1	7	regulation of superoxide metabolic process	BP	1	PRKCD	up_ACOR_EC

GO:0042119	0.17059056	0.9867	1	7	neutrophil activation	BP	1	PRKCD	up_ACOR_EC
GO:2000778	0.170832463	0.98667	1	7	positive regulation of interleukin-6 secretion	BP	1	MAVS	up_ACOR_EC
GO:0043604	0.171	0.873	33	288	amide biosynthetic process	BP	1	PRR16,MRPL37,ACACB,ENSCAFG00000013986,CERS4,WARS2,ENSCAFG00000000071,PYM1,PDK2,ZFP36L1,EEF2,LARP6,RPL13,ANKHD1,FARS2,UBA52,RPUSD4,RPL15,ACSS2,EIF3G,SAMD4B,ZFP36L2,EIF3K,EIF3L,QARS,EIF3D,ASS1,TNRC6C,COA1,NCK1,MRPL4,LARS2,B3GALT4	up_VSAP_EC
GO:0001568	0.171	0.876	29	252	blood vessel development	BP	1	HOXA7,WNT11,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,WARS2,HPSE,CCBE1,RECK,PLPP3,DLX3,ZFP36L1,TBXA2R,SASH1,LOX,HPGD,ANPEP,ACVRL1,HMOX1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0051336	0.171	0.886	19	251	regulation of hydrolase activity	BP	1	NUAK1,PPP1R12A,PTGS2,DYNLL1,DNAJC10,CRYAB,ENSCAFG00000002015,LYN,FAM162A,GSK3B,TAX1BP3,HTT,REST,ABHD5,ARFGEF3,CALM1,PAK2,SPINK2,ARF4	down_VSAP_EC
GO:0043170	0.171	0.902	18	2980	macromolecule metabolic process	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,ASPN,NEDD4	down_ACOR_EC
GO:0019693	0.171	0.887	18	172	ribose phosphate metabolic process	BP	1	ACLY,HMGCR,RAN,CDK1,PFAS,RNASEH2B,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,PGD,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0044260	0.171	0.903	16	2593	cellular macromolecule metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ASPN,NEDD4	down_ACOR_EC
GO:0022604	0.171	0.892	15	122	regulation of cell morphogenesis	BP	1	WASF3,ENPP2,SLIT2,ABL1,CDC42EP5,PLXNA4,CDC42EP2,SHOX2,LRP4,DPYSL2,LIMD1,FBLN1,PQBP1,TTL,MAP2K2	up_VSAP_EC
GO:0051235	0.171	0.899	12	90	maintenance of location	BP	1	PLCG2,HTR2B,ITPR1,OS9,PRKCE,POLR2M,DAG1,CHD7,PLIN2,GAA,SUN1,PARK7	up_ACOR_VSMC
GO:0048232	0.171	0.901	11	95	male gamete generation	BP	1	NDC1,TRIP13,POC1A,HIST1H1A,HMGB2,SGPL1,ASPM,HOXA9,GLI1,H2AFX,TTLL1	down_ACOR_VSMC
GO:0030323	0.171	0.908	9	65	respiratory tube development	BP	1	THRB,WNT11,FGF7,SAV1,CCBE1,LOX,NFIB,MAP2K2,TGFBR2	up_VSAP_EC
GO:0031589	0.171	0.915	7	93	cell-substrate adhesion	BP	1	FBLN2,RHOD,THY1,EDIL3,GREM1,RAC2,ECM2	down_VCAV_EC
GO:0071559	0.171	0.915	7	75	response to transforming growth factor beta	BP	1	HSPA5,SNX25,TGFBR1,YES1,ADAM17,ENSCAFG00000002015,STRAP	down_VSAP_EC
GO:0002761	0.171	0.936	4	36	regulation of myeloid leukocyte differentiation	BP	1	PTPN2,EVI2B,CTNNB1,LYN	down_VSAP_EC
GO:0034765	0.171	0.935	4	91	regulation of ion transmembrane transport	BP	1	KCNC4,KCND1,FXYD1,CLIC4	up_AFEM_EC
GO:0072091	0.171	0.938	4	24	regulation of stem cell proliferation	BP	1	FERMT1,SOX18,CTNNA1,HIF1A	up_VCAV_EC
GO:0061008	0.171	0.938	4	23	hepaticobiliary system development	BP	1	HNF4A,LIMS2,SULF2,CITED2	up_VSAP_EC
GO:0032648	0.171	0.938	4	23	regulation of interferon-beta production	BP	1	NLRX1,RNF216,FLOT1,MAVS	up_VSAP_EC
GO:0009064	0.171	0.948	3	23	glutamine family amino acid metabolic process	BP	1	ASNS,NR1H4,ALDH18A1	down_VSAP_EC
GO:0010761	0.171	0.95	3	15	fibroblast migration	BP	1	PRKCE,DDR2,ARID5B	up_ACOR_VSMC
GO:0018130	0.171	0.957	3	1261	heterocycle biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0030030	0.171	0.948	3	377	cell projection organization	BP	1	ARHGEF26,SLITRK5,NTRK2	up_APUL_EC
GO:0055080	0.171	0.946	3	176	cation homeostasis	BP	1	C3AR1,HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0002832	0.171	0.95	3	15	negative regulation of response to biotic	BP	1	NLRX1,TKFC,MAPKBP1	up_VSAP_EC
GO:0010761	0.171	0.95	3	15	fibroblast migration	BP	1	DDR2,ZFAND5,BAG4	up_VSAP_EC
GO:0031952	0.171	0.95	3	15	regulation of protein autophosphorylation	BP	1	EEF2K,PDGFD,TNKS1BP1	up_VSAP_EC
GO:0001667	0.171	0.962	2	146	ameboidal-type cell migration	BP	1	ACVRL1,NRP2	down_ACOR_EC
GO:0072594	0.171	0.962	2	155	establishment of protein localization to organelle	BP	1	IPO7,NEDD4	down_ACOR_EC
GO:0044766	0.171	0.966	2	9	multi-organism transport	BP	1	CAV1,DDX39B	down_ACOR_VSMC
GO:1902579	0.171	0.966	2	9	multi-organism localization	BP	1	CAV1,DDX39B	down_ACOR_VSMC
GO:0031341	0.171	0.965	2	13	regulation of cell killing	BP	1	FAM49B,PVR	down_VSAP_EC

GO:0071300	0.171	0.965	2	12	cellular response to retinoic acid	BP	1	YES1,LYN	down_VSAP_EC
GO:2001273	0.171	0.965	2	12	regulation of glucose import in response to	BP	1	NR1H4,PTPN11	down_VSAP_EC
GO:1902600	0.171	0.962	2	31	proton transmembrane transport	BP	1	ATP6V1B2,ATP6V0B	up_AFEM_EC
GO:0030194	0.171	0.966	2	9	positive regulation of blood coagulation	BP	1	SELP,TLR4	up_VCAV_EC
GO:1900048	0.171	0.966	2	9	positive regulation of hemostasis	BP	1	SELP,TLR4	up_VCAV_EC
GO:0050769	0.171	0.962	2	95	positive regulation of neurogenesis	BP	1	ARHGEF2,SEMA3A	up_VPOR_EC
GO:0008217	0.171	0.985	1	38	regulation of blood pressure	BP	1	ACVRL1	down_ACOR_EC
GO:0031081	0.171	0.992	1	2	nuclear pore distribution	BP	1	NDC1	down_ACOR_VSMC
GO:0051664	0.171	0.992	1	2	nuclear pore localization	BP	1	NDC1	down_ACOR_VSMC
GO:0071635	0.171	0.992	1	2	negative regulation of transforming growth factor beta production	BP	1	SLC29A1	down_ACOR_VSMC
GO:0090129	0.171	0.992	1	2	positive regulation of synapse maturation	BP	1	CDC20	down_ACOR_VSMC
GO:1902725	0.171	0.992	1	2	negative regulation of satellite cell	BP	1	SIX4	down_ACOR_VSMC
GO:0035546	0.171	0.988	1	4	interferon-beta secretion	BP	1	MAVS	down_VCAV_EC
GO:0035547	0.171	0.988	1	4	regulation of interferon-beta secretion	BP	1	MAVS	down_VCAV_EC
GO:0035549	0.171	0.988	1	4	positive regulation of interferon-beta secretion	BP	1	MAVS	down_VCAV_EC
GO:0071214	0.171	0.986	1	93	cellular response to abiotic stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0104004	0.171	0.986	1	93	cellular response to environmental stimulus	BP	1	RAB11B	down_VPOR_EC
GO:0044265	0.171	0.989	1	423	cellular macromolecule catabolic process	BP	1	USP12	down_VFEM_EC
GO:0061684	0.171	0.989	1	3	chaperone-mediated autophagy	BP	1	PLK3	down_VSAP_EC
GO:0033240	0.171	0.989	1	3	positive regulation of cellular amine metabolic	BP	1	NR1H4	down_VSAP_EC
GO:0048514	0.171	0.987	1	214	blood vessel morphogenesis	BP	1	TGFBI	down_VSAP_VSMC
GO:0003294	0.171	0.992	1	2	atrial ventricular junction remodeling	BP	1	GJA1	up_ACOR_VSMC
GO:0035993	0.171	0.992	1	2	deltoid tuberosity development	BP	1	BMP4	up_ACOR_VSMC
GO:0060371	0.171	0.992	1	2	regulation of atrial cardiac muscle cell membrane	BP	1	GJA1	up_ACOR_VSMC
GO:0060373	0.171	0.992	1	2	regulation of ventricular cardiac muscle cell membrane depolarization	BP	1	GJA1	up_ACOR_VSMC
GO:0060577	0.171	0.992	1	2	pulmonary vein morphogenesis	BP	1	TBX20	up_ACOR_VSMC
GO:2001179	0.171	0.992	1	2	regulation of interleukin-10 secretion	BP	1	CD274	up_ACOR_VSMC
GO:2001181	0.171	0.992	1	2	positive regulation of interleukin-10 secretion	BP	1	CD274	up_ACOR_VSMC
GO:0060627	0.171	0.986	1	165	regulation of vesicle-mediated transport	BP	1	WNT7A	up_AORT_VSMC
GO:0030072	0.171	0.985	1	48	peptide hormone secretion	BP	1	NR1H4	up_APUL_EC
GO:0048534	0.171	0.987	1	262	hematopoietic or lymphoid organ	BP	1	HOXA3	up_APUL_VSMC
GO:0006772	0.171	0.989	1	3	thiamine metabolic process	BP	1	ACPP	up_VCAV_EC
GO:0042723	0.171	0.989	1	3	thiamine-containing compound metabolic	BP	1	ACPP	up_VCAV_EC
GO:0060907	0.171	0.992	1	2	positive regulation of macrophage cytokine	BP	1	TLR4	up_VCAV_EC
GO:0061081	0.171	0.992	1	2	positive regulation of myeloid leukocyte cytokine production	BP	1	TLR4	up_VCAV_EC
GO:0006865	0.171	0.985	1	23	amino acid transport	BP	1	SLC7A11	up_VPOR_EC
GO:0007045	0.171	0.985	1	23	cell-substrate adherens junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0048041	0.171	0.985	1	23	focal adhesion assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC

GO:2000779	0.171	0.985	1	25	regulation of double-strand break repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0051147	0.171	0.985	1	44	regulation of muscle cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0051056	0.171	0.985	1	87	regulation of small GTPase mediated signal	BP	1	FBP1	up_VFEM_VSMC
GO:0006429	0.171	0.992	1	2	leucyl-tRNA aminoacylation	BP	1	LARS2	up_VSAP_EC
GO:0044339	0.171	0.992	1	2	canonical Wnt signaling pathway involved in osteoblast differentiation	BP	1	FZD1	up_VSAP_EC
GO:1900425	0.171	0.992	1	2	negative regulation of defense response to	BP	1	MAPKBP1	up_VSAP_EC
GO:0050870	0.171	0.985	1	42	positive regulation of T cell activation	BP	1	CAV1	up_VSAP_VSMC
GO:2000377	0.171	0.985	1	41	regulation of reactive oxygen species metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0050707	0.171	0.985	1	44	regulation of cytokine secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0090288	0.171	0.985	1	44	negative regulation of cellular response to growth factor stimulus	BP	1	CAV1	up_VSAP_VSMC
GO:0002374	0.171105025	0.98662	1	7	cytokine secretion involved in immune	BP	1	NOD2	up_ACOR_EC
GO:0002685	0.171154524	0.94606	3	55	regulation of leukocyte migration	BP	1	MMP28,PTGER4,RARRES2	up_ACOR_EC
GO:0001710	0.171583435	0.98654	1	7	mesodermal cell fate commitment	BP	1	FOXC2	up_ACOR_EC
GO:0043409	0.171749473	0.94581	3	54	negative regulation of MAPK cascade	BP	1	NDRG2,DUSP26,PRKCD	up_ACOR_EC
GO:0048518	0.172	0.851	171	1676	positive regulation of biological process	BP	1	HOXA11,FZD1,PRR16,THRB,NAPEPLD,TWIST2,HOXA9,CDON,WNT11,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,PPARGC1B,PLEKHF1,MAB21L1,LIMS2,ACACB,DDHD1,IL6R,SLIT2,CRADD,CRIP2,ZHX3,HOXD3,CDH1,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,KLKB1,EMP2,CHRM1,DLL1,EPN2,OSR1,MAP3K5,CDC42EP5,IL17RC,TENT5C,FUZ,ADAMTSL4,PDGFD,SAV1,KLF15,C1QTNF2,HPSE,ANKRD54,CDC42EP2,ZBTB16,TOX,RARG,CCBE1,STAT5A,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,GLIS2,DDR2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,MYC,SSBP2,IRX3,ZEB1,FBXW4,TBXA2R,SULF2,SHOX2,ZC3H10,CIZ1,CFAP69,EEF2,SASH1,CDC25B,FBXO4,CREBRF,POLDIP2,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,GDPD5,ECM2,S100A4,TSPAN5,AZIN2,PHF1,CFD,NPAS2,PRKAB1,FBXO7,KCNB1,LIMD1,NLRX1,RNF166,RPUSD4,ENSCAFG00000011993,TKFC,PC,CDK9,CD83,PRMT2,KDM2B,PIP4K2B,OSBPL7,ZFP36L2,YPEL3,RAF1,PNP,TAF8,NFIB,ZNF580,ABHD14B,CYBA,ZNF205,CYB5D2,NCOA2,FXYD1,STX4,PQBP1,TTL,SMARCA2,EIF3D,ACVRL1,UBQLN2,UNC93B1,HTRA2,ASS1,FLOT1,TNRC6C,PP	up_VSAP_EC
GO:0048534	0.172	0.875	30	262	hematopoietic or lymphoid organ development	BP	1	HOXA7,HOXA9,PPARGC1B,CRIP2,ABL1,DLL1,ANKRD54,ZBTB16,TOX,RARG,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,ZEB1,EEF2,TFE3,FBXO7,CD83,ZFP36L2,RAF1,PNP,PPP3CB,MAP2K2,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0048514	0.172	0.879	25	214	blood vessel morphogenesis	BP	1	HOXA7,WNT11,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,WARS2,HPSE,CCBE1,ZFP36L1,TBXA2R,SASH1,LOX,HPGD,ANPEP,ACVRL1,HMOX1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0007420	0.172	0.883	21	169	brain development	BP	1	FGF13,BMP4,FGFR2,ATRX,SEC24B,ZNF365,TMEM108,NDRG2,ATRN,NRP1,SLITRK5,FZD3,FRS2,POMK,APP,PSEN1,SEMA6D,CHD7,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0006979	0.172	0.89	16	130	response to oxidative stress	BP	1	PRKAA2,PPARGC1A,TP53INP1,DAPK1,EGLN1,SESN3,FUT8,CHD6,APP,PSEN1,CLN8,SESN1,OXR1,CAT,PARK7,STC2	up_ACOR_VSMC
GO:0034976	0.172	0.894	14	112	response to endoplasmic reticulum stress	BP	1	TMX3,ITPR1,FAM129A,OS9,STT3B,SERINC3,SCAMP5,HERPUD1,TXNDC5,FAF2,WFS1,DZIP3,PARK7,STC2	up_ACOR_VSMC
GO:1990778	0.172	0.914	7	91	protein localization to cell periphery	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,CDH2,RAB31	down_VCAV_EC
GO:0017156	0.172	0.929	5	32	calcium ion regulated exocytosis	BP	1	FBXL20,STX11,PSEN1,SCAMP5,PREPL	up_ACOR_VSMC

GO:0010466	0.172	0.929	5	32	negative regulation of peptidase activity	BP	1	RECK,CST3,SH3RF1,SPINK2,PARK7	up_ACOR_VSMC
GO:0010951	0.172	0.929	5	32	negative regulation of endopeptidase activity	BP	1	RECK,CST3,SH3RF1,SPINK2,PARK7	up_ACOR_VSMC
GO:2001237	0.172	0.929	5	33	negative regulation of extrinsic apoptotic	BP	1	TNFAIP3,CTNNA1,RIPK1,ITGA6,ARHGEF2	up_VCAV_EC
GO:0022408	0.172	0.935	4	44	negative regulation of cell-cell adhesion	BP	1	PRNP,SDC4,GLI3,LOXL3	down_VCAV_EC
GO:0002690	0.172	0.947	3	26	positive regulation of leukocyte chemotaxis	BP	1	VEGFA,SERPINE1,ADAM17	down_VSAP_EC
GO:0045670	0.172	0.949	3	16	regulation of osteoclast differentiation	BP	1	PPARGC1B,PIK3R1,TFE3	up_VSAP_EC
GO:0034472	0.172	0.966	2	9	snRNA 3'-end processing	BP	1	INTS7,EXOSC5	down_ACOR_VSMC
GO:0010761	0.172	0.964	2	15	fibroblast migration	BP	1	SDC4,DDR2	down_VCAV_EC
GO:0043113	0.172	0.965	2	12	receptor clustering	BP	1	AGRN,APOE	down_VSAP_EC
GO:0002089	0.172	0.967	2	8	lens morphogenesis in camera-type eye	BP	1	BMP4,CITED2	up_ACOR_VSMC
GO:0060037	0.172	0.966	2	9	pharyngeal system development	BP	1	ADGRF5,GATA3	up_VCAV_EC
GO:0101023	0.172	0.967	2	8	vascular endothelial cell proliferation	BP	1	MEF2C,HMGB1	up_VCAV_EC
GO:1905562	0.172	0.967	2	8	regulation of vascular endothelial cell	BP	1	MEF2C,HMGB1	up_VCAV_EC
GO:0046034	0.172	0.961	2	88	ATP metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0036314	0.172	0.967	2	8	response to sterol	BP	1	OSBPL7,TGFBR2	up_VSAP_EC
GO:0051250	0.172	0.985	1	38	negative regulation of lymphocyte activation	BP	1	LYN	down_ACOR_EC
GO:0042476	0.172	0.985	1	36	odontogenesis	BP	1	ASPN	down_ACOR_EC
GO:0001787	0.172	0.992	1	2	natural killer cell proliferation	BP	1	ELF4	down_ACOR_VSMC
GO:0002154	0.172	0.992	1	2	thyroid hormone mediated signaling	BP	1	PRCP	down_ACOR_VSMC
GO:1900040	0.172	0.992	1	2	regulation of interleukin-2 secretion	BP	1	EZR	down_ACOR_VSMC
GO:0009889	0.172	1	1	1190	regulation of biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0021554	0.172	0.988	1	4	optic nerve development	BP	1	GLI3	down_VCAV_EC
GO:0031291	0.172	0.989	1	3	Ran protein signal transduction	BP	1	KPNB1	down_VSAP_EC
GO:0032351	0.172	0.989	1	3	negative regulation of hormone metabolic	BP	1	REST	down_VSAP_EC
GO:0032353	0.172	0.989	1	3	negative regulation of hormone biosynthetic	BP	1	REST	down_VSAP_EC
GO:0009134	0.172	0.989	1	3	nucleoside diphosphate catabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0060075	0.172	0.992	1	2	regulation of resting membrane potential	BP	1	PSEN1	up_ACOR_VSMC
GO:1902004	0.172	0.992	1	2	positive regulation of amyloid-beta formation	BP	1	APP	up_ACOR_VSMC
GO:1903995	0.172	0.992	1	2	regulation of non-membrane spanning protein tyrosine kinase	BP	1	DUSP22	up_ACOR_VSMC
GO:0045054	0.172	0.992	1	2	constitutive secretory pathway	BP	1	RAB11B	up_ACOR_VSMC
GO:0048733	0.172	0.992	1	2	sebaceous gland development	BP	1	ZDHHC21	up_ACOR_VSMC
GO:0060197	0.172	0.992	1	2	cloacal septation	BP	1	BMP4	up_ACOR_VSMC
GO:1903010	0.172	0.986	1	8	regulation of bone development	BP	1	GREM1	up_AFEM_EC
GO:0045087	0.172	0.986	1	161	innate immune response	BP	1	ESR1	up_AORT_VSMC
GO:0050866	0.172	0.985	1	48	negative regulation of cell activation	BP	1	BPI	up_APUL_EC
GO:0001944	0.172	0.987	1	263	vasculature development	BP	1	HOXA3	up_APUL_VSMC
GO:0030334	0.172	0.987	1	267	regulation of cell migration	BP	1	TBX5	up_APUL_VSMC
GO:0036123	0.172	0.992	1	2	histone H3-K9 dimethylation	BP	1	KDM3A	up_VCAV_EC
GO:0098722	0.172	0.992	1	2	asymmetric stem cell division	BP	1	ARHGEF2	up_VCAV_EC

GO:0032273	0.172	0.985	1	44	positive regulation of protein polymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0009108	0.172	0.985	1	68	coenzyme biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0051146	0.172	0.985	1	76	striated muscle cell differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0002685	0.172	0.985	1	55	regulation of leukocyte migration	BP	1	CCL24	up_VPUL_EC
GO:0002793	0.172	0.985	1	54	positive regulation of peptide secretion	BP	1	NR1H4	up_VPUL_EC
GO:0050714	0.172	0.985	1	54	positive regulation of protein secretion	BP	1	NR1H4	up_VPUL_EC
GO:0015721	0.172	0.992	1	2	bile acid and bile salt transport	BP	1	ABCB11	up_VSAP_EC
GO:0003018	0.172	0.985	1	42	vascular process in circulatory system	BP	1	CAV1	up_VSAP_VSMC
GO:0097696	0.172	0.985	1	43	STAT cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0090148	0.172220293	0.98644	1	7	membrane fission	BP	1	CHMP4B	up_ACOR_EC
GO:0051247	0.172367041	0.88737	17	502	positive regulation of protein metabolic process	BP	1	SOX9,ENSCAFG00000004331,EDEM2,FZD5,DUSP26,NOD2,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:1904294	0.172399633	0.98641	1	7	positive regulation of ERAD pathway	BP	1	EDEM2	up_ACOR_EC
GO:0033238	0.172532013	0.98639	1	7	regulation of cellular amine metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0060255	0.173	0.851	157	1782	regulation of macromolecule metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,IL7R,KIT,SELE,PPP2R5A,PRKCH,FLI1,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,TSPAN8,RELN,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,ODC1,CASP8,MTOR,TENT2,SAMD8,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,TUT7,SLK,SH3BP5,CNOT6,RSC1A1,ENC1,CCAR1,PPP1R2,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,APOD,NCK1,ESCO1,DPH5,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,PTGS2,MMD,TOP1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,PAN3,TAOK1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,PMAIP1,ZNF789,BLM,NUP133,SPTBN4,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,PDGFD,USP37,WTAP,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,IVNS1ABP,JCAD,PS	up_VCAV_EC
GO:0007017	0.173	0.882	21	273	microtubule-based process	BP	1	ARHGEF2,PLK3,MZT1,HOOK3,PPP1R12A,RPGR,KIF5B,HIF1A,DYNLL1,TRAK1,TUBB,TUBB2A,ZPR1,CTNNB1,KPNB1,GSK3B,CCSER2,HTT,DISC1,AP3S1,MID1	down_VSAP_EC
GO:0051248	0.173	0.883	20	316	negative regulation of protein metabolic process	BP	1	CST3,KIRREL1,DCN,PRNP,BGN,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,PRMT6,ASPN,THY1,PARK7,ZFP36L1,CLEC16A,SPRED1,A2M,GREM1,EIF4EBP1	down_VCAV_EC
GO:0050708	0.173	0.895	13	101	regulation of protein secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0006732	0.173	0.897	12	107	coenzyme metabolic process	BP	1	ACLY,HMGCR,NNT,MVD,ELOVL1,PDXP,GSTO1,ELOVL6,PDHA1,GGH,PGD,PDSS1	down_ACOR_VSMC
GO:0043269	0.173	0.899	11	135	regulation of ion transport	BP	1	REM1,WDR1,KIF5B,CTNNB1,APOE,LYN,NKAIN1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0008544	0.173	0.903	10	75	epidermis development	BP	1	HOXA7,FGF7,DLL1,SAV1,HPSE,ZFP36L1,LRP4,TRADD,KEAP1,LATS2	up_VSAP_EC
GO:0006898	0.173	0.911	8	57	receptor-mediated endocytosis	BP	1	DNAJC6,PLCG2,HTR2B,ATXN2,TMEM108,LRPAP1,B2M,AP2B1	up_ACOR_VSMC
GO:0072073	0.173	0.926	5	60	kidney epithelium development	BP	1	SMAD9,KANK2,CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0010822	0.173	0.928	5	31	positive regulation of mitochondrion	BP	1	DDHD1,MFN2,FBXO7,ZNF205,HTRA2	up_VSAP_EC
GO:0050810	0.173	0.949	3	17	regulation of steroid biosynthetic process	BP	1	SREBF1,SF1,INSIG1	down_ACOR_VSMC

GO:0040008	0.173	0.945	3	179	regulation of growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC
GO:0031016	0.173	0.95	3	15	pancreas development	BP	1	HNF4A,IL6R,DLL1	up_VSAP_EC
GO:0002053	0.173	0.949	3	15	positive regulation of mesenchymal cell	BP	1	FBXW4,SHOX2,TGFBR2	up_VSAP_EC
GO:0046326	0.173	0.95	3	15	positive regulation of glucose import	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0031960	0.173	0.963	2	15	response to corticosteroid	BP	1	NR3C1,ZFP36L1	down_VCAV_EC
GO:0051384	0.173	0.963	2	15	response to glucocorticoid	BP	1	NR3C1,ZFP36L1	down_VCAV_EC
GO:0032467	0.173	0.967	2	8	positive regulation of cytokinesis	BP	1	PKP4,PRKCE	up_ACOR_VSMC
GO:0086010	0.173	0.966	2	8	membrane depolarization during action potential	BP	1	TPC3,PTPN3	up_ACOR_VSMC
GO:0002828	0.173	0.966	2	9	regulation of type 2 immune response	BP	1	GATA3,ARG2	up_VCAV_EC
GO:0070885	0.173	0.966	2	9	negative regulation of calcineurin-NFAT signaling	BP	1	HOMER3,MTOR	up_VCAV_EC
GO:0106057	0.173	0.966	2	9	negative regulation of calcineurin-mediated	BP	1	HOMER3,MTOR	up_VCAV_EC
GO:0035518	0.173	0.966	2	8	histone H2A monoubiquitination	BP	1	DDB2,KDM2B	up_VSAP_EC
GO:0097065	0.173	0.992	1	2	anterior head development	BP	1	PFAS	down_ACOR_VSMC
GO:0007418	0.173	0.992	1	2	ventral midline development	BP	1	GLI1	down_ACOR_VSMC
GO:0021937	0.173	0.992	1	2	cerebellar Purkinje cell-granule cell precursor cell signaling involved in regulation of granule cell	BP	1	GLI1	down_ACOR_VSMC
GO:0021938	0.173	0.992	1	2	smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell	BP	1	GLI1	down_ACOR_VSMC
GO:0021940	0.173	0.992	1	2	positive regulation of cerebellar granule cell precursor proliferation	BP	1	GLI1	down_ACOR_VSMC
GO:0033280	0.173	0.988	1	4	response to vitamin D	BP	1	KANK2	down_VCAV_EC
GO:0010632	0.173	0.985	1	95	regulation of epithelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0002182	0.173	0.989	1	3	cytoplasmic translational elongation	BP	1	AARS	down_VSAP_EC
GO:1900247	0.173	0.989	1	3	regulation of cytoplasmic translational elongation	BP	1	AARS	down_VSAP_EC
GO:1903553	0.173	0.989	1	3	positive regulation of extracellular exosome	BP	1	SDC4	down_VSAP_EC
GO:0006678	0.173	0.989	1	3	glucosylceramide metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0015697	0.173	0.992	1	2	quaternary ammonium group transport	BP	1	SLC25A20	up_ACOR_VSMC
GO:0015838	0.173	0.992	1	2	amino-acid betaine transport	BP	1	SLC25A20	up_ACOR_VSMC
GO:0015879	0.173	0.992	1	2	carnitine transport	BP	1	SLC25A20	up_ACOR_VSMC
GO:0010460	0.173	0.992	1	2	positive regulation of heart rate	BP	1	EDN1	up_ACOR_VSMC
GO:0019276	0.173	0.992	1	2	UDP-N-acetylgalactosamine	BP	1	EXTL2	up_ACOR_VSMC
GO:0042483	0.173	0.992	1	2	negative regulation of odontogenesis	BP	1	TNFRSF11B	up_ACOR_VSMC
GO:0060920	0.173	0.992	1	2	cardiac pacemaker cell differentiation	BP	1	BVES	up_ACOR_VSMC
GO:0060926	0.173	0.992	1	2	cardiac pacemaker cell development	BP	1	BVES	up_ACOR_VSMC
GO:0070286	0.173	0.986	1	8	axonemal dynein complex assembly	BP	1	DNAL1	up_AFEM_EC
GO:0021561	0.173	0.986	1	8	facial nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0021610	0.173	0.986	1	8	facial nerve morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0035024	0.173	0.986	1	8	negative regulation of Rho protein signal	BP	1	KANK1	up_AFEM_EC
GO:0061430	0.173	0.986	1	8	bone trabecula morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:0101023	0.173	0.986	1	8	vascular endothelial cell proliferation	BP	1	ADAM17	up_AFEM_EC

GO:1905562	0.173	0.986	1	8	regulation of vascular endothelial cell	BP	1	ADAM17	up_AFEM_EC
GO:0002790	0.173	0.986	1	133	peptide secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0051090	0.173	0.986	1	134	regulation of DNA-binding transcription factor	BP	1	TLR2	up_AFEM_VSMC
GO:0060828	0.173	0.985	1	82	regulation of canonical Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:1905114	0.173	0.986	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	WNT7A	up_AORT_VSMC
GO:0040016	0.173	0.992	1	2	embryonic cleavage	BP	1	TOP1	up_VCAV_EC
GO:0046886	0.173	0.992	1	2	positive regulation of hormone biosynthetic	BP	1	HIF1A	up_VCAV_EC
GO:0071732	0.173	0.992	1	2	cellular response to nitric oxide	BP	1	GUCY1B1	up_VCAV_EC
GO:1903121	0.173	0.989	1	3	regulation of TRAIL-activated apoptotic	BP	1	ATF3	up_VCAV_EC
GO:0050878	0.173	0.985	1	75	regulation of body fluid levels	BP	1	CYP26B1	up_VPOR_VSMC
GO:0046661	0.173	0.985	1	45	male sex differentiation	BP	1	HOXA9	up_VFEM_EC
GO:0051258	0.173	0.985	1	94	protein polymerization	BP	1	SLIT2	up_VPUL_VSMC
GO:0043116	0.173	0.992	1	2	negative regulation of vascular permeability	BP	1	SLIT2	up_VSAP_EC
GO:0071676	0.173	0.992	1	2	negative regulation of mononuclear cell	BP	1	SLIT2	up_VSAP_EC
GO:0061476	0.173	0.992	1	2	response to anticoagulant	BP	1	SLIT2	up_VSAP_EC
GO:0071503	0.173	0.992	1	2	response to heparin	BP	1	SLIT2	up_VSAP_EC
GO:0071504	0.173	0.992	1	2	cellular response to heparin	BP	1	SLIT2	up_VSAP_EC
GO:0051147	0.173	0.985	1	44	regulation of muscle cell differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:1903729	0.173492168	0.98623	1	7	regulation of plasma membrane organization	BP	1	PRKCD	up_ACOR_EC
GO:0042981	0.173572392	0.88796	16	471	regulation of apoptotic process	BP	1	NR1H4,SOX9,AQP1,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0008038	0.173644115	0.98621	1	7	neuron recognition	BP	1	NRP1	up_ACOR_EC
GO:2000251	0.173680356	0.9862	1	7	positive regulation of actin cytoskeleton	BP	1	NRP1	up_ACOR_EC
GO:0033630	0.173699121	0.9862	1	7	positive regulation of cell adhesion mediated by	BP	1	FOXC2	up_ACOR_EC
GO:0051241	0.174	0.869	38	336	negative regulation of multicellular organismal process	BP	1	TMEM176B,TMEM176A,SMAD6,PLCL1,KCNE3,GATA5,CD83,PRDX4,ITM2C,FERMT1,BMP4,PDE5A,CD274,ZNF365,NDRG2,PLAC8B,LIMS2,F2RL1,NRP1,PTPN22,LRPAP1,ULK2,EVL,TBX5,FZD3,FRS2,RNLS,APP,PSEN1,SYNJ2BP,JUP,WWC2,ASAP1,B2M,TNFRSF11B,DOCK5,STC2,IL18R1	up_ACOR_VSMC
GO:2000146	0.174	0.897	12	92	negative regulation of cell motility	BP	1	TCAF1,RECK,TP53INP1,EVL,SPINT2,TBX5,DAG1,SEMA6D,SYNJ2BP,JUP,DUSP22,WASL	up_ACOR_VSMC
GO:2000241	0.174	0.92	6	40	regulation of reproductive process	BP	1	PRDX4,BMP4,FGFR2,PDE5A,CITED2,SPINK2	up_ACOR_VSMC
GO:0045595	0.174	0.919	6	469	regulation of cell differentiation	BP	1	HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,RNF6	up_VPOR_EC
GO:0045619	0.174	0.934	4	44	regulation of lymphocyte differentiation	BP	1	GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0055025	0.174	0.948	3	17	positive regulation of cardiac muscle tissue	BP	1	MEF2C,EDN1,CREB1	up_VCAV_EC
GO:0046326	0.174	0.963	2	15	positive regulation of glucose import	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0032350	0.174	0.964	2	12	regulation of hormone metabolic process	BP	1	HIF1A,REST	down_VSAP_EC
GO:0006357	0.174	0.965	2	547	regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0001816	0.174	0.961	2	194	cytokine production	BP	1	NR1H4,BPI	up_APUL_EC
GO:0010669	0.174	0.965	2	10	epithelial structure maintenance	BP	1	TLR4,LDB2	up_VCAV_EC
GO:0032239	0.174	0.967	2	7	regulation of nucleobase-containing compound	BP	1	IWS1,RIPK1	up_VCAV_EC
GO:1990774	0.174	0.965	2	9	tumor necrosis factor secretion	BP	1	ARG2,HMGB1	up_VCAV_EC

GO:0050767	0.174	0.961	2	184	regulation of neurogenesis	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0061061	0.174	0.961	2	179	muscle structure development	BP	1	SIX1,CYP26B1	up_VFEM_EC
GO:0051960	0.174	0.962	2	216	regulation of nervous system development	BP	1	FLRT3,ARHGEF2	up_VPUL_EC
GO:0000466	0.174	0.966	2	8	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	EXOSC7,RCL1	up_VSAP_EC
GO:0070570	0.174	0.966	2	8	regulation of neuron projection regeneration	BP	1	RTN4RL1,MAP2K2	up_VSAP_EC
GO:0050776	0.174	0.961	2	173	regulation of immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0035983	0.174	0.992	1	2	response to trichostatin A	BP	1	EZH2	down_ACOR_VSMC
GO:0035984	0.174	0.992	1	2	cellular response to trichostatin A	BP	1	EZH2	down_ACOR_VSMC
GO:0045475	0.174	0.988	1	4	locomotor rhythm	BP	1	NAGLU	down_VCAV_EC
GO:0022407	0.174	0.985	1	96	regulation of cell-cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0043010	0.174	0.985	1	96	camera-type eye development	BP	1	CITED2	down_VPOR_EC
GO:0051254	0.174	0.989	1	431	positive regulation of RNA metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0051649	0.174	0.992	1	630	establishment of localization in cell	BP	1	JUP	down_VFEM_VSMC
GO:0002675	0.174	0.989	1	3	positive regulation of acute inflammatory	BP	1	PTGS2	down_VSAP_EC
GO:0000820	0.174	0.989	1	3	regulation of glutamine family amino acid	BP	1	NR1H4	down_VSAP_EC
GO:0061325	0.174	0.989	1	3	cell proliferation involved in outflow tract	BP	1	CTNNB1	down_VSAP_EC
GO:0035922	0.174	0.992	1	2	foramen ovale closure	BP	1	TBX20	up_ACOR_VSMC
GO:0003193	0.174	0.992	1	2	pulmonary valve formation	BP	1	TBX20	up_ACOR_VSMC
GO:0035694	0.174	0.992	1	2	mitochondrial protein catabolic process	BP	1	BNIP3	up_ACOR_VSMC
GO:0042439	0.174	0.992	1	2	ethanolamine-containing compound metabolic	BP	1	MOXD1	up_ACOR_VSMC
GO:2000275	0.174	0.992	1	2	regulation of oxidative phosphorylation uncoupler activity	BP	1	PARK7	up_ACOR_VSMC
GO:0014044	0.174	0.986	1	8	Schwann cell development	BP	1	LGI4	up_AFEM_EC
GO:0021522	0.174	0.986	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	up_AFEM_EC
GO:0022011	0.174	0.986	1	8	myelination in peripheral nervous system	BP	1	LGI4	up_AFEM_EC
GO:0032292	0.174	0.986	1	8	peripheral nervous system axon	BP	1	LGI4	up_AFEM_EC
GO:0032506	0.174	0.986	1	8	cytokinetic process	BP	1	ANXA11	up_AFEM_EC
GO:0071711	0.174	0.986	1	8	basement membrane organization	BP	1	CTSS	up_AFEM_EC
GO:0072673	0.174	0.986	1	8	lamellipodium morphogenesis	BP	1	KANK1	up_AFEM_EC
GO:0030099	0.174	0.986	1	133	myeloid cell differentiation	BP	1	HOXA9	up_AFEM_VSMC
GO:0048839	0.174	0.985	1	50	inner ear development	BP	1	HOXA1	up_APUL_EC
GO:0061113	0.174	0.992	1	2	pancreas morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0033002	0.174	0.985	1	55	muscle cell proliferation	BP	1	TBX5	up_VPUL_EC
GO:0035265	0.174	0.985	1	54	organ growth	BP	1	TBX5	up_VPUL_EC
GO:0006425	0.174	0.992	1	2	glutaminyl-tRNA aminoacylation	BP	1	QARS	up_VSAP_EC
GO:1903039	0.174	0.985	1	43	positive regulation of leukocyte cell-cell	BP	1	CAV1	up_VSAP_VSMC
GO:0051046	0.174044998	0.91232	7	174	regulation of secretion	BP	1	NR1H4,AQP1,KCNB1,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0006517	0.174127154	0.98613	1	7	protein deglycosylation	BP	1	EDEM2	up_ACOR_EC
GO:0010712	0.174512412	0.98606	1	7	regulation of collagen metabolic process	BP	1	MFAP4	up_ACOR_EC
GO:0050792	0.174802298	0.94438	3	55	regulation of viral process	BP	1	TRIM8,MAVS,CHMP4B	up_ACOR_EC

GO:0061323	0.174824056	0.98601	1	7	cell proliferation involved in heart morphogenesis	BP	1	TBX5	up_ACOR_EC
GO:0001516	0.174986299	0.98598	1	7	prostaglandin biosynthetic process	BP	1	PTGDS	up_ACOR_EC
GO:0046457	0.174986299	0.98598	1	7	prostanoid biosynthetic process	BP	1	PTGDS	up_ACOR_EC
GO:0007154	0.175	0.867	44	1622	cell communication	BP	1	CMKLR1,LEP,KCNC4,LBH,CRY2,GAS1,ANGPT4,CD40,DLL1,F3,PLXNA4,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,HTR1D,FAM53B,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,RECK,PTHLH,TBXA2R,LGR6,RAB7A,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,KANK1,TNC	up_AFEM_EC
GO:0048878	0.175	0.88	21	283	chemical homeostasis	BP	1	SLC39A7,NR1H4,ERO1A,ENPP1,PTPN11,ATP2B1,PRCP,SMARCA4,SESN2,TMTC2,HIF1A,PTPN2,NEO1,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1,HOMER1	down_VSAP_EC
GO:0035148	0.175	0.905	9	66	tube formation	BP	1	FZD1,ABL1,OSR1,FUZ,RARG,IRX3,KDM2B,NFIB,CITED2	up_VSAP_EC
GO:0046328	0.175	0.909	8	61	regulation of JNK cascade	BP	1	EPHB1,MAP3K11,TLR4,EDN1,TLR3,TAOK1,HMGB1,RIPK1	up_VCAV_EC
GO:0070848	0.175	0.912	7	193	response to growth factor	BP	1	GAS1,DLL1,TMEM100,GREM1,GREM2,NR3C1,ADAM17	up_AFEM_EC
GO:0050921	0.175	0.926	5	39	positive regulation of chemotaxis	BP	1	CXCL8,PDGFB,PRKD2,SWAP70,HMGB1	up_VCAV_EC
GO:0044706	0.175	0.935	4	27	multi-multicellular organism process	BP	1	ACSL4,B4GALT1,PPARD,EMP2	down_ACOR_VSMC
GO:0010811	0.175	0.934	4	36	positive regulation of cell-substrate adhesion	BP	1	VEGFA,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:0060419	0.175	0.937	4	22	heart growth	BP	1	FGFR2,TBX20,TBX5,EDN1	up_ACOR_VSMC
GO:0031663	0.175	0.948	3	17	lipopolysaccharide-mediated signaling	BP	1	IRAK1,MTDH,CACTIN	down_ACOR_VSMC
GO:2000648	0.175	0.949	3	14	positive regulation of stem cell proliferation	BP	1	SMARCD3,FZD3,DISC1	up_ACOR_VSMC
GO:0043603	0.175	0.946	3	372	cellular amide metabolic process	BP	1	NR1H4,PCSK1N,ENSCAFG00000028814	up_APUL_EC
GO:0007610	0.175	0.961	2	146	behavior	BP	1	SPG11,HOXA1	down_ACOR_EC
GO:0007129	0.175	0.965	2	9	synapsis	BP	1	NDC1,TRIP13	down_ACOR_VSMC
GO:0045683	0.175	0.965	2	9	negative regulation of epidermis development	BP	1	EZH2,HOXA7	down_ACOR_VSMC
GO:0006084	0.175	0.963	2	15	acetyl-CoA metabolic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0040001	0.175	0.963	2	12	establishment of mitotic spindle localization	BP	1	KPNB1,HTT	down_VSAP_EC
GO:2000677	0.175	0.964	2	12	regulation of transcription regulatory region DNA	BP	1	CTNNB1,DDIT3	down_VSAP_EC
GO:0010717	0.175	0.961	2	32	regulation of epithelial to mesenchymal transition	BP	1	GREM1,AXIN2	up_AFEM_EC
GO:0038127	0.175	0.961	2	32	ERBB signaling pathway	BP	1	RAB7A,ADAM17	up_AFEM_EC
GO:1901222	0.175	0.961	2	32	regulation of NIK/NF-kappaB signaling	BP	1	GREM1,CYLD	up_AFEM_EC
GO:0009888	0.175	0.964	2	545	tissue development	BP	1	EYA1,BEND2	up_AFEM_VSMC
GO:0039528	0.175	0.965	2	9	cytoplasmic pattern recognition receptor signaling pathway in	BP	1	RIOK3,LSM14A	up_VCAV_EC
GO:0051258	0.175	0.96	2	94	protein polymerization	BP	1	MZT1,TWF1	up_VPOR_EC
GO:0031954	0.175	0.966	2	8	positive regulation of protein	BP	1	PDGFD,TNKS1BP1	up_VSAP_EC
GO:0060544	0.175	0.966	2	8	regulation of necroptotic process	BP	1	RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0060402	0.175	0.984	1	35	calcium ion transport into cytosol	BP	1	LYN	down_ACOR_EC
GO:1900409	0.175	0.988	1	4	positive regulation of cellular response to	BP	1	PARK7	down_VCAV_EC
GO:1902884	0.175	0.988	1	4	positive regulation of response to oxidative	BP	1	PARK7	down_VCAV_EC
GO:1903209	0.175	0.988	1	4	positive regulation of oxidative stress-induced	BP	1	PARK7	down_VCAV_EC
GO:0048280	0.175	0.988	1	4	vesicle fusion with Golgi apparatus	BP	1	USO1	down_VSAP_EC
GO:0034380	0.175	0.989	1	3	high-density lipoprotein particle assembly	BP	1	APOE	down_VSAP_EC

GO:0016198	0.175	0.992	1	2	axon choice point recognition	BP	1	APP	up_ACOR_VSMC
GO:0030185	0.175	0.992	1	2	nitric oxide transport	BP	1	EDN1	up_ACOR_VSMC
GO:0032713	0.175	0.992	1	2	negative regulation of interleukin-4 production	BP	1	CD83	up_ACOR_VSMC
GO:0035526	0.175	0.992	1	2	retrograde transport, plasma membrane to	BP	1	USP6NL	up_ACOR_VSMC
GO:0051709	0.175	0.992	1	2	regulation of killing of cells of other organism	BP	1	F2RL1	up_ACOR_VSMC
GO:0051712	0.175	0.992	1	2	positive regulation of killing of cells of other	BP	1	F2RL1	up_ACOR_VSMC
GO:0051818	0.175	0.992	1	2	disruption of cells of other organism involved in symbiotic interaction	BP	1	F2RL1	up_ACOR_VSMC
GO:0051883	0.175	0.992	1	2	killing of cells in other organism involved in	BP	1	F2RL1	up_ACOR_VSMC
GO:0055022	0.175	0.992	1	2	negative regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_VSMC
GO:0060044	0.175	0.992	1	2	negative regulation of cardiac muscle cell	BP	1	TBX5	up_ACOR_VSMC
GO:0061117	0.175	0.992	1	2	negative regulation of heart growth	BP	1	TBX5	up_ACOR_VSMC
GO:0002068	0.175	0.986	1	8	glandular epithelial cell development	BP	1	DLL1	up_AFEM_EC
GO:0002076	0.175	0.986	1	8	osteoblast development	BP	1	PTHLH	up_AFEM_EC
GO:0010658	0.175	0.986	1	8	striated muscle cell apoptotic process	BP	1	CAMK2A	up_AFEM_EC
GO:0010662	0.175	0.986	1	8	regulation of striated muscle cell apoptotic	BP	1	CAMK2A	up_AFEM_EC
GO:0031018	0.175	0.986	1	8	endocrine pancreas development	BP	1	DLL1	up_AFEM_EC
GO:0032369	0.175	0.986	1	8	negative regulation of lipid transport	BP	1	CRY2	up_AFEM_EC
GO:0045923	0.175	0.986	1	8	positive regulation of fatty acid metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0045933	0.175	0.986	1	8	positive regulation of muscle contraction	BP	1	TBXA2R	up_AFEM_EC
GO:0003044	0.175	0.986	1	8	regulation of systemic arterial blood pressure mediated by a chemical	BP	1	AVPR1A	up_AFEM_EC
GO:0060479	0.175	0.986	1	8	lung cell differentiation	BP	1	THRB	up_AFEM_EC
GO:1900117	0.175	0.986	1	8	regulation of execution phase of apoptosis	BP	1	FAP	up_AFEM_EC
GO:0032886	0.175	0.985	1	81	regulation of microtubule-based process	BP	1	TAOK1	up_AORT_EC
GO:0046883	0.175	0.985	1	49	regulation of hormone secretion	BP	1	NR1H4	up_APUL_EC
GO:0072358	0.175	0.987	1	268	cardiovascular system development	BP	1	HOXA3	up_APUL_VSMC
GO:1904776	0.175	0.992	1	2	regulation of protein localization to cell cortex	BP	1	EPB41	up_VCAV_EC
GO:1904778	0.175	0.992	1	2	positive regulation of protein localization to cell	BP	1	EPB41	up_VCAV_EC
GO:0030099	0.175	0.985	1	133	myeloid cell differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0006879	0.175	0.985	1	23	cellular iron ion homeostasis	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0021885	0.175	0.985	1	24	forebrain cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0021954	0.175	0.984	1	26	central nervous system neuron development	BP	1	SEMA3A	up_VPOR_EC
GO:0043588	0.175	0.985	1	74	skin development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0071559	0.175	0.985	1	75	response to transforming growth factor beta	BP	1	BAMBI	up_VPOR_VSMC
GO:0050680	0.175	0.985	1	44	negative regulation of epithelial cell proliferation	BP	1	MTSS1	up_VFEM_EC
GO:0007623	0.175	0.985	1	55	circadian rhythm	BP	1	HTR7	up_VPUL_EC
GO:0010632	0.175	0.985	1	95	regulation of epithelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0055074	0.175	0.985	1	95	calcium ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0023035	0.175	0.992	1	2	CD40 signaling pathway	BP	1	ENSCAFG00000011993	up_VSAP_EC
GO:0014846	0.175	0.992	1	2	esophagus smooth muscle contraction	BP	1	SULF2	up_VSAP_EC

GO:0001963	0.175189938	0.98595	1	7	synaptic transmission, dopaminergic	BP	1	CNTNAP4	up_ACOR_EC
GO:0019079	0.175212749	0.96085	2	29	viral genome replication	BP	1	ATG16L2,MAVS	up_ACOR_EC
GO:0031400	0.175326931	0.90696	8	205	negative regulation of protein modification	BP	1	PKIB,NDRG2,DUSP26,SMAD6,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0007420	0.175408054	0.91148	7	169	brain development	BP	1	NDRG2,AQP1,SEMA6D,DIXDC1,DCLK2,NRP1,PYGO2	up_ACOR_EC
GO:0060008	0.175578241	0.98588	1	7	Sertoli cell differentiation	BP	1	SOX9	up_ACOR_EC
GO:0007043	0.175592003	0.96078	2	28	cell-cell junction assembly	BP	1	NR1H4,FZD5	up_ACOR_EC
GO:1901881	0.17562983	0.98588	1	7	positive regulation of protein depolymerization	BP	1	ACTN2	up_ACOR_EC
GO:0006684	0.175866431	0.98584	1	7	sphingomyelin metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0030097	0.176	0.873	28	244	hemopoiesis	BP	1	HOXA7,HOXA9,PPARGC1B,CRIP2,ABL1,DLL1,ANKRD54,ZBTB16,TOX,RARG,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,ZEB1,EEF2,TFE3,FBXO7,CD83,ZFP36L2,PNP,PPP3CB,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0033993	0.176	0.879	22	186	response to lipid	BP	1	FAM107A,PTGFR,PPARGC1B,SLIT2,ABL1,GOT1,OSR1,RARG,ZFP36L1,TBXA2R,SASH1,CREBRF,MYD88,PRMT2,OSBPL7,ZFP36L2,NCOA2,HTRA2,BGLAP,TGFBR2,LBH,DDIT4	up_VSAP_EC
GO:0051961	0.176	0.904	9	73	negative regulation of nervous system	BP	1	EDNRB,ARHGEF15,IFRD1,PPP3CA,HOOK3,HMG20A,JAG1,RAPGEF2,CTNNA1	up_VCAV_EC
GO:0006417	0.176	0.907	8	109	regulation of translation	BP	1	LARP6,SAMD4B,EIF3K,EEF2,ZFP36L1,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0043534	0.176	0.909	8	57	blood vessel endothelial cell migration	BP	1	SLIT2,ABL1,HDAC7,EMP2,STAT5A,TBXA2R,ACVRL1,HMOX1	up_VSAP_EC
GO:0007507	0.176	0.911	7	194	heart development	BP	1	DLL1,TMEM100,GREM1,LUZP1,BVES,AXIN2,ACACB	up_AFEM_EC
GO:1903522	0.176	0.913	7	58	regulation of blood circulation	BP	1	DOCK4,PDE4D,STC1,EDN1,KCNJ2,GCH1,SPTBN4	up_VCAV_EC
GO:0034645	0.176	0.934	5	1546	cellular macromolecule biosynthetic process	BP	1	HDAC7,CITED2,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:0007599	0.176	0.925	5	48	hemostasis	BP	1	SERPINE1,APOE,LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0051480	0.176	0.925	5	50	regulation of cytosolic calcium ion concentration	BP	1	ERO1A,LYN,DDIT3,HTT,CALM1	down_VSAP_EC
GO:0009798	0.176	0.927	5	31	axis specification	BP	1	SMAD6,BMP4,CITED2,FRS2,PCSK6	up_ACOR_VSMC
GO:0045580	0.176	0.926	5	35	regulation of T cell differentiation	BP	1	IL7R,GATA3,ITPKB,HMGB1,ZEB1	up_VCAV_EC
GO:0000041	0.176	0.927	5	31	transition metal ion transport	BP	1	RAB11B,SLC25A28,SCARA5,STEAP3,FTL	up_VSAP_EC
GO:0071804	0.176	0.927	5	31	cellular potassium ion transport	BP	1	AMIGO1,KCNE3,KLHL24,KCNB1,KCNC4	up_VSAP_EC
GO:0071805	0.176	0.927	5	31	potassium ion transmembrane transport	BP	1	AMIGO1,KCNE3,KLHL24,KCNB1,KCNC4	up_VSAP_EC
GO:0032760	0.176	0.936	4	22	positive regulation of tumor necrosis factor	BP	1	TLR1,LEP,TLR3,NOD2	up_ACOR_VSMC
GO:0042278	0.176	0.935	4	25	purine nucleoside metabolic process	BP	1	ENPP4,PTGDR,ENSCAFG00000018611,NT5C2	up_ACOR_VSMC
GO:1903557	0.176	0.936	4	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	TLR1,LEP,TLR3,NOD2	up_ACOR_VSMC
GO:0023052	0.176	0.945	4	1602	signaling	BP	1	SLITRK5,LIMK1,GATA5,CA2	up_VCAV_VSMC
GO:0010628	0.176	0.934	4	527	positive regulation of gene expression	BP	1	EYA1,HOXA9,SIX1,CYP26B1	up_VFEM_EC
GO:0007565	0.176	0.936	4	23	female pregnancy	BP	1	EMP2,RECK,HPGD,CITED2	up_VSAP_EC
GO:0030042	0.176	0.947	3	17	actin filament depolymerization	BP	1	CAPG,LIMA1,PDXP	down_ACOR_VSMC
GO:0030834	0.176	0.947	3	17	regulation of actin filament depolymerization	BP	1	CAPG,LIMA1,PDXP	down_ACOR_VSMC
GO:0035065	0.176	0.947	3	17	regulation of histone acetylation	BP	1	BRCA1,NOC2L,TADA2A	down_ACOR_VSMC
GO:0048864	0.176	0.945	3	29	stem cell development	BP	1	BMPR1A,SEMA3C,RDH10	down_VCAV_EC
GO:0060675	0.176	0.945	3	29	ureteric bud morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0022029	0.176	0.946	3	23	telencephalon cell migration	BP	1	CTNNB1,DISC1,NRP1	down_VSAP_EC
GO:0042493	0.176	0.944	3	178	response to drug	BP	1	ARHGEF2,FBP1,SRP54	up_VPOR_EC
GO:0033013	0.176	0.948	3	15	tetrapyrrole metabolic process	BP	1	CLYBL,CPOX,HMOX1	up_VSAP_EC

GO:0097755	0.176	0.963	2	12	positive regulation of blood vessel diameter	BP	1	APOE,PLOD3	down_VSAP_EC
GO:0043536	0.176	0.96	2	32	positive regulation of blood vessel endothelial	BP	1	ANGPT4,ADAM17	up_AFEM_EC
GO:0045446	0.176	0.961	2	32	endothelial cell differentiation	BP	1	DLL1,TMEM100	up_AFEM_EC
GO:0042558	0.176	0.963	2	11	pteridine-containing compound metabolic	BP	1	PIPOX,GCH1	up_VCAV_EC
GO:0010837	0.176	0.965	2	8	regulation of keratinocyte proliferation	BP	1	FGF7,ZFP36L1	up_VSAP_EC
GO:0090308	0.176	0.992	1	2	regulation of methylation-dependent chromatin	BP	1	UHRF1	down_ACOR_VSMC
GO:0023061	0.176	0.985	1	95	signal release	BP	1	RAB11B	down_VPOR_EC
GO:0044093	0.176	0.989	1	437	positive regulation of molecular function	BP	1	PLCL1	down_VFEM_EC
GO:0032525	0.176	0.989	1	3	somite rostral/caudal axis specification	BP	1	TMED2	down_VSAP_EC
GO:1900118	0.176	0.989	1	3	negative regulation of execution phase of	BP	1	PAK2	down_VSAP_EC
GO:0061299	0.176	0.989	1	3	retina vasculature morphogenesis in camera-	BP	1	NRP1	down_VSAP_EC
GO:1900151	0.176	0.989	1	3	regulation of nuclear-transcribed mRNA catabolic process,	BP	1	CNOT7	down_VSAP_EC
GO:1900153	0.176	0.989	1	3	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	CNOT7	down_VSAP_EC
GO:0001775	0.176	0.986	1	219	cell activation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0072125	0.176	0.992	1	2	negative regulation of glomerular mesangial cell	BP	1	BMP4	up_ACOR_VSMC
GO:0090194	0.176	0.992	1	2	negative regulation of glomerulus development	BP	1	BMP4	up_ACOR_VSMC
GO:0110025	0.176	0.991	1	2	DNA strand resection involved in replication	BP	1	ZNF365	up_ACOR_VSMC
GO:0021548	0.176	0.991	1	2	pons development	BP	1	SEC24B	up_ACOR_VSMC
GO:0044062	0.176	0.991	1	2	regulation of excretion	BP	1	EDN1	up_ACOR_VSMC
GO:0072179	0.176	0.991	1	2	nephric duct formation	BP	1	BMP4	up_ACOR_VSMC
GO:0030851	0.176	0.985	1	8	granulocyte differentiation	BP	1	EVI2B	up_AFEM_EC
GO:0032331	0.176	0.986	1	8	negative regulation of chondrocyte	BP	1	GREM1	up_AFEM_EC
GO:0032462	0.176	0.985	1	8	regulation of protein homooligomerization	BP	1	CRYAB	up_AFEM_EC
GO:0043029	0.176	0.986	1	8	T cell homeostasis	BP	1	GPAM	up_AFEM_EC
GO:0045662	0.176	0.986	1	8	negative regulation of myoblast differentiation	BP	1	DLL1	up_AFEM_EC
GO:0050798	0.176	0.985	1	8	activated T cell proliferation	BP	1	GPAM	up_AFEM_EC
GO:0061037	0.176	0.986	1	8	negative regulation of cartilage development	BP	1	GREM1	up_AFEM_EC
GO:1990748	0.176	0.986	1	8	cellular detoxification	BP	1	SOD1	up_AFEM_EC
GO:0034764	0.176	0.984	1	50	positive regulation of transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0043491	0.176	0.984	1	50	protein kinase B signaling	BP	1	NTRK2	up_APUL_EC
GO:0017014	0.176	0.991	1	2	protein nitrosylation	BP	1	NOS2	up_VCAV_EC
GO:0031281	0.176	0.992	1	2	positive regulation of cyclase activity	BP	1	NOS2	up_VCAV_EC
GO:2001016	0.176	0.992	1	2	positive regulation of skeletal muscle cell	BP	1	MEF2C	up_VCAV_EC
GO:0009396	0.176	0.989	1	3	folic acid-containing compound biosynthetic	BP	1	GCH1	up_VCAV_EC
GO:0018119	0.176	0.991	1	2	peptidyl-cysteine S-nitrosylation	BP	1	NOS2	up_VCAV_EC
GO:0001701	0.176	0.985	1	134	in utero embryonic development	BP	1	C6	up_VCAV_VSMC
GO:0009185	0.176	0.984	1	23	ribonucleoside diphosphate metabolic	BP	1	FBP1	up_VPOR_EC
GO:0019359	0.176	0.984	1	23	nicotinamide nucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC

GO:0019363	0.176	0.984	1	23	pyridine nucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0030512	0.176	0.984	1	24	negative regulation of transforming growth factor beta receptor	BP	1	ASPN	up_VPOR_EC
GO:0031110	0.176	0.984	1	24	regulation of microtubule polymerization or depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0072665	0.176	0.984	1	25	protein localization to vacuole	BP	1	GCC2	up_VPOR_EC
GO:1903845	0.176	0.984	1	24	negative regulation of cellular response to transforming growth	BP	1	ASPN	up_VPOR_EC
GO:0050803	0.176	0.984	1	55	regulation of synapse structure or activity	BP	1	FLRT3	up_VPUL_EC
GO:0050807	0.176	0.984	1	55	regulation of synapse organization	BP	1	FLRT3	up_VPUL_EC
GO:0006971	0.176	0.992	1	2	hypotonic response	BP	1	SLC12A6	up_VSAP_EC
GO:0009448	0.176	0.992	1	2	gamma-aminobutyric acid metabolic process	BP	1	ABAT	up_VSAP_EC
GO:0043652	0.176	0.991	1	2	engulfment of apoptotic cell	BP	1	XKR8	up_VSAP_EC
GO:0071476	0.176	0.992	1	2	cellular hypotonic response	BP	1	SLC12A6	up_VSAP_EC
GO:1990051	0.176	0.992	1	2	activation of protein kinase C activity	BP	1	ABL1	up_VSAP_EC
GO:0055089	0.176034145	0.98581	1	7	fatty acid homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0030198	0.176520072	0.93186	4	81	extracellular matrix organization	BP	1	FMOD,ADAMTSL2,FOXC2,MFAP4	up_ACOR_EC
GO:2000136	0.176659136	0.9857	1	7	regulation of cell proliferation involved in	BP	1	TBX5	up_ACOR_EC
GO:0051179	0.17669529	0.8635	52	1747	localization	BP	1	SH3TC2,CA4,CDH3,NR1H4,CLIC3,BRSK1,CALY,SOX9,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,AGRN,SEMA6D,DIXDC1,NOD2,DYNC1I1,PLS1,ACTN2,ZMYND8,PAK3,CFI,MMP28,TRIM8,PTGER4,ARHGDIB,ELMO2,PREB,SLC25A42,DCLK2,MAPK8IP2,MAVS,FOXC2,LRRC15,TBX5,LRP4,LRRC4,SLC9A9,CHMP4B,TP53INP2,RARRES2,VPS16,ABCB9,NRP1,AZIN2,HM13,PRKCD,PM20D1,ENSCAFG00000010493,CCNYL1,ATP7B	up_ACOR_EC
GO:0048522	0.177	0.847	152	1484	positive regulation of cellular process	BP	1	HOXA11,FZD1,PRR16,THRB,NAPEPLD,TWIST2,HOXA9,CDON,WNT11,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,PPARGC1B,PLEKHF1,MAB21L1,LIMS2,DDHD1,IL6R,SLIT2,CRADD,CRIP2,ZHX3,HOXD3,CDH1,SLC6A4,FGF7,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,MAP3K5,CDC42EP5,IL17RC,FUZ,ADAMTSL4,PDGFD,SAV1,KLF15,C1QTNF2,HPSE,ANKRD54,CDC42EP2,ZBTB16,TOX,RARG,CCBE1,STAT5A,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,DDR2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,MYC,SSBP2,IRX3,ZEB1,FBXW4,SULF2,SHOX2,CIZ1,CFAP69,EEF2,SASH1,CDC25B,FBXO4,CREBRF,POLDIP2,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,GDPD5,S100A4,TSPAN5,PHF1,NPAS2,FBXO7,LIMD1,RNF166,RPUSD4,ENSCAFG00000011993,CDK9,CD83,PRMT2,KDM2B,PIP4K2B,OSBPL7,ZFP36L2,YPEL3,RAF1,PNP,TAF8,NFIB,ZNF580,ABHD14B,CYBA,ZNF205,CYB5D2,NCOA2,STX4,TTL,SMARCA2,EIF3D,ACVRL1,UBQLN2,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,LSM10,MAP2K2,TGFBR2,CITED2,BAG4,TRADD,JCHAIN,DEDD2,CXXC1,LBH,SOAT1,LATS2	up_VSAP_EC

GO:0051171	0.177	0.848	149	1697	regulation of nitrogen compound metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,KIT,PPP2R5A,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,CD34,PDE4D,IWS1,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RALB,APLNR,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,ODC1,CASP8,MTOR,TENT2,SAMD8,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,SLK,SH3BP5,CNOT6,RSC1A1,ENC1,CCAR1,PPP1R2,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,APOD,NCK1,ESCO1,DPH5,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,PTGS2,MMD,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,TAOK1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,NOS2,PMAIP1,ZNF789,BLM,NUP133,SPTBN4,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,PDGFD,USP37,WTAP,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,IVNS1ABP,JCAD,PSMB9,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0097190	0.177	0.874	25	217	apoptotic signaling pathway	BP	1	RHOT1,NACC2,ITM2C,BMP4,TLR3,TP53INP1,AR,ITPR1,DAPK1,BNIP3,CDKN1A,JMY,NRP1,UNC5B,SH3RF1,PSEN1,PERP,SIAH1,DDIT4,SERINC3,TNFRSF11B,HERPUD1,WFS1,PARK7,ZMAT3	up_ACOR_VSMC
GO:0051345	0.177	0.886	16	151	positive regulation of hydrolase activity	BP	1	SELE,MEF2C,RAPGEF1,CASP8,BMP2,PRKD2,RAPGEF2,BCL10,HMGB1,TBC1D1,PMAIP1,ITGA6,ALS2,ENSCAFG00000002015,RABGAP1,USP6NL	up_VCAV_EC
GO:0044270	0.177	0.893	12	147	cellular nitrogen compound catabolic	BP	1	ENPP1,PGK1,TPI1,PGAM1,ALDH1L2,HIF1A,ZPR1,ENTPD4,SMG7,CNOT7,ALDOC,SND1	down_VSAP_EC
GO:0048667	0.177	0.893	12	140	cell morphogenesis involved in neuron	BP	1	SIPA1L1,PTPN11,IFRD1,KIF5B,TNIK,NEO1,UST,CDH11,VLDLR,EXT1,NRP1,YWHAH	down_VSAP_EC
GO:0002253	0.177	0.895	12	92	activation of immune response	BP	1	ABL1,F2RL1,RBCK1,MYD88,CFD,NLRX1,TKFC,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0007162	0.177	0.904	9	66	negative regulation of cell adhesion	BP	1	HOXA7,FAM107A,CD274,CDH1,ABL1,PIK3R1,FBLN1,ACVRL1,ASS1	up_VSAP_EC
GO:0002253	0.177	0.911	7	92	activation of immune response	BP	1	CFD,PRNP,THY1,CYBA,MAVS,RAB7B,A2M	down_VCAV_EC
GO:0031109	0.177	0.925	5	36	microtubule polymerization or	BP	1	FBXO5,STMN1,RAC1,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0018023	0.177	0.935	4	23	peptidyl-lysine trimethylation	BP	1	IWS1,ARID4B,ATRX,TET2	up_VCAV_EC
GO:0090342	0.177	0.947	3	17	regulation of cell aging	BP	1	HMGA1,ARG2,RSL1D1	down_ACOR_VSMC
GO:1900744	0.177	0.948	3	15	regulation of p38MAPK cascade	BP	1	LEP,SASH1,PTPN22	up_ACOR_VSMC
GO:0010468	0.177	0.954	3	1270	regulation of gene expression	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:2000379	0.177	0.946	3	20	positive regulation of reactive oxygen species	BP	1	PDGFB,TLR4,RAB27A	up_VCAV_EC
GO:0046850	0.177	0.964	2	9	regulation of bone remodeling	BP	1	GREM1,TFRC	down_ACOR_VSMC
GO:0006826	0.177	0.962	2	15	iron ion transport	BP	1	SCARA5,ARHGAP1	down_VCAV_EC
GO:0031952	0.177	0.962	2	15	regulation of protein autophosphorylation	BP	1	EEF2K,GREM1	down_VCAV_EC
GO:0051094	0.177	0.962	2	388	positive regulation of developmental process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0040019	0.177	0.963	2	12	positive regulation of embryonic development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0071675	0.177	0.962	2	13	regulation of mononuclear cell	BP	1	SERPINE1,LYN	down_VSAP_EC
GO:0045933	0.177	0.965	2	8	positive regulation of muscle contraction	BP	1	ADRA1B,NPNT	up_ACOR_VSMC
GO:0051457	0.177	0.965	2	8	maintenance of protein location in nucleus	BP	1	SUN1,PARK7	up_ACOR_VSMC
GO:0006637	0.177	0.96	2	32	acyl-CoA metabolic process	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0010466	0.177	0.96	2	32	negative regulation of peptidase activity	BP	1	CRYAB,RECK	up_AFEM_EC
GO:0010951	0.177	0.96	2	32	negative regulation of endopeptidase activity	BP	1	CRYAB,RECK	up_AFEM_EC

GO:0017156	0.177	0.96	2	32	calcium ion regulated exocytosis	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0035383	0.177	0.96	2	32	thioester metabolic process	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0048869	0.177	0.97	2	1119	cellular developmental process	BP	1	TBX5,HOXB5	up_APUL_VSMC
GO:0048232	0.177	0.96	2	95	male gamete generation	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0006085	0.177	0.965	2	8	acetyl-CoA biosynthetic process	BP	1	PDK2,ACSS2	up_VSAP_EC
GO:0006730	0.177	0.965	2	8	one-carbon metabolic process	BP	1	ENSCAFG00000013986,AHCYL1	up_VSAP_EC
GO:0045103	0.177	0.965	2	8	intermediate filament-based process	BP	1	KLHL24,RAF1	up_VSAP_EC
GO:0045104	0.177	0.965	2	8	intermediate filament cytoskeleton organization	BP	1	KLHL24,RAF1	up_VSAP_EC
GO:0032101	0.177	0.96	2	173	regulation of response to external stimulus	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0010952	0.177	0.984	1	46	positive regulation of peptidase activity	BP	1	LYN	down_ACOR_EC
GO:0030073	0.177	0.984	1	42	insulin secretion	BP	1	STX4	down_ACOR_EC
GO:0035305	0.177	0.984	1	37	negative regulation of dephosphorylation	BP	1	MYO1D	down_ACOR_EC
GO:0050847	0.177	0.991	1	2	progesterone receptor signaling pathway	BP	1	NEDD4	down_ACOR_VSMC
GO:1904975	0.177	0.991	1	2	response to bleomycin	BP	1	TIMELESS	down_ACOR_VSMC
GO:1904976	0.177	0.991	1	2	cellular response to bleomycin	BP	1	TIMELESS	down_ACOR_VSMC
GO:1990778	0.177	0.985	1	91	protein localization to cell periphery	BP	1	GPSM2	down_AFEM_EC
GO:0002920	0.177	0.987	1	4	regulation of humoral immune response	BP	1	A2M	down_VCAV_EC
GO:0051138	0.177	0.987	1	4	positive regulation of NK T cell differentiation	BP	1	ZBTB16	down_VCAV_EC
GO:0070970	0.177	0.987	1	4	interleukin-2 secretion	BP	1	GPAM	down_VCAV_EC
GO:0006207	0.177	0.989	1	3	'de novo' pyrimidine nucleobase biosynthetic	BP	1	CMPK1	down_VSAP_EC
GO:0019856	0.177	0.989	1	3	pyrimidine nucleobase biosynthetic process	BP	1	CMPK1	down_VSAP_EC
GO:0035930	0.177	0.989	1	3	corticosteroid hormone secretion	BP	1	PTPN11	down_VSAP_EC
GO:0035933	0.177	0.989	1	3	glucocorticoid secretion	BP	1	PTPN11	down_VSAP_EC
GO:0060753	0.177	0.987	1	4	regulation of mast cell chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0072095	0.177	0.989	1	3	regulation of branch elongation involved in ureteric bud branching	BP	1	SIX4	down_VSAP_EC
GO:1902965	0.177	0.989	1	3	regulation of protein localization to early	BP	1	MSN	down_VSAP_EC
GO:1902966	0.177	0.989	1	3	positive regulation of protein localization to	BP	1	MSN	down_VSAP_EC
GO:1905666	0.177	0.989	1	3	regulation of protein localization to endosome	BP	1	MSN	down_VSAP_EC
GO:1905668	0.177	0.989	1	3	positive regulation of protein localization to	BP	1	MSN	down_VSAP_EC
GO:2000832	0.177	0.989	1	3	negative regulation of steroid hormone	BP	1	PTPN11	down_VSAP_EC
GO:2000846	0.177	0.989	1	3	regulation of corticosteroid hormone	BP	1	PTPN11	down_VSAP_EC
GO:2000847	0.177	0.989	1	3	negative regulation of corticosteroid hormone	BP	1	PTPN11	down_VSAP_EC
GO:2000849	0.177	0.989	1	3	regulation of glucocorticoid secretion	BP	1	PTPN11	down_VSAP_EC
GO:2000850	0.177	0.989	1	3	negative regulation of glucocorticoid secretion	BP	1	PTPN11	down_VSAP_EC
GO:2001054	0.177	0.989	1	3	negative regulation of mesenchymal cell apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:0018243	0.177	0.989	1	3	protein O-linked glycosylation via	BP	1	GALNT1	down_VSAP_EC
GO:0030953	0.177	0.989	1	3	astral microtubule organization	BP	1	KPNB1	down_VSAP_EC
GO:0071493	0.177	0.989	1	3	cellular response to UV-B	BP	1	CDKN1A	down_VSAP_EC
GO:0015889	0.177	0.991	1	2	cobalamin transport	BP	1	TCN2	up_ACOR_VSMC

GO:0034389	0.177	0.991	1	2	lipid droplet organization	BP	1	FAF2	up_ACOR_VSMC
GO:0003274	0.177	0.991	1	2	endocardial cushion fusion	BP	1	GATA5	up_ACOR_VSMC
GO:0072049	0.177	0.991	1	2	comma-shaped body morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0072050	0.177	0.991	1	2	S-shaped body morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0072205	0.177	0.991	1	2	metanephric collecting duct development	BP	1	BMP4	up_ACOR_VSMC
GO:0072278	0.177	0.991	1	2	metanephric comma-shaped body	BP	1	BMP4	up_ACOR_VSMC
GO:0072284	0.177	0.991	1	2	metanephric S-shaped body morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:1903800	0.177	0.991	1	2	positive regulation of production of miRNAs involved in gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:1904685	0.177	0.991	1	2	positive regulation of metalloendopeptidase	BP	1	MBP	up_ACOR_VSMC
GO:0006528	0.177	0.991	1	2	asparagine metabolic process	BP	1	NIT2	up_ACOR_VSMC
GO:0009597	0.177	0.991	1	2	detection of virus	BP	1	SERINC3	up_ACOR_VSMC
GO:0051006	0.177	0.991	1	2	positive regulation of lipoprotein lipase activity	BP	1	LMF1	up_ACOR_VSMC
GO:0061365	0.177	0.991	1	2	positive regulation of triglyceride lipase activity	BP	1	LMF1	up_ACOR_VSMC
GO:1901033	0.177	0.991	1	2	positive regulation of response to reactive	BP	1	PARK7	up_ACOR_VSMC
GO:0010758	0.177	0.985	1	8	regulation of macrophage chemotaxis	BP	1	CMKLR1	up_AFEM_EC
GO:0031954	0.177	0.985	1	8	positive regulation of protein	BP	1	GREM1	up_AFEM_EC
GO:0050829	0.177	0.985	1	8	defense response to Gram-negative bacterium	BP	1	BPI	up_AFEM_EC
GO:0051900	0.177	0.985	1	8	regulation of mitochondrial	BP	1	MLLT11	up_AFEM_EC
GO:0060628	0.177	0.985	1	8	regulation of ER to Golgi vesicle-mediated	BP	1	GAS1	up_AFEM_EC
GO:0009617	0.177	0.985	1	133	response to bacterium	BP	1	TLR2	up_AFEM_VSMC
GO:0016570	0.177	0.985	1	143	histone modification	BP	1	EYA1	up_AFEM_VSMC
GO:0032870	0.177	0.985	1	162	cellular response to hormone stimulus	BP	1	ESR1	up_AORT_VSMC
GO:0043254	0.177	0.985	1	164	regulation of protein complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0030326	0.177	0.984	1	51	embryonic limb morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0035113	0.177	0.984	1	51	embryonic appendage morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0043433	0.177	0.984	1	49	negative regulation of DNA-binding transcription factor activity	BP	1	NR1H4	up_APUL_EC
GO:0071219	0.177	0.984	1	50	cellular response to molecule of bacterial	BP	1	NR1H4	up_APUL_EC
GO:1990845	0.177	0.984	1	51	adaptive thermogenesis	BP	1	PLCL1	up_APUL_EC
GO:0046292	0.177	0.991	1	2	formaldehyde metabolic process	BP	1	KDM3A	up_VCAV_EC
GO:0033209	0.177	0.984	1	24	tumor necrosis factor-mediated signaling	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0045669	0.177	0.984	1	24	positive regulation of osteoblast differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0070972	0.177	0.984	1	23	protein localization to endoplasmic reticulum	BP	1	SRP54	up_VPOR_EC
GO:0008544	0.177	0.984	1	75	epidermis development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048762	0.177	0.984	1	77	mesenchymal cell differentiation	BP	1	BAMBI	up_VPOR_VSMC
GO:0008360	0.177	0.984	1	46	regulation of cell shape	BP	1	CDC42EP5	up_VFEM_EC
GO:0030595	0.177	0.984	1	57	leukocyte chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0043281	0.177	0.984	1	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	PTGER2	up_VPUL_EC
GO:0070838	0.177	0.985	1	96	divalent metal ion transport	BP	1	HOXA3	up_VPUL_VSMC

GO:0001827	0.177	0.991	1	2	inner cell mass cell fate commitment	BP	1	LATS2	up_VSAP_EC
GO:0001828	0.177	0.991	1	2	inner cell mass cellular morphogenesis	BP	1	LATS2	up_VSAP_EC
GO:0019072	0.177	0.991	1	2	viral genome packaging	BP	1	PC	up_VSAP_EC
GO:0019074	0.177	0.991	1	2	viral RNA genome packaging	BP	1	PC	up_VSAP_EC
GO:0048840	0.177	0.991	1	2	otolith development	BP	1	LRIG3	up_VSAP_EC
GO:0001662	0.177177017	0.98562	1	7	behavioral fear response	BP	1	MAPK8IP2	up_ACOR_EC
GO:0002209	0.177177017	0.98562	1	7	behavioral defense response	BP	1	MAPK8IP2	up_ACOR_EC
GO:0042596	0.177177017	0.98562	1	7	fear response	BP	1	MAPK8IP2	up_ACOR_EC
GO:2000112	0.178	0.851	102	1119	regulation of cellular macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,RSC1A1,ENC1,CCAR1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0051179	0.178	0.852	95	1747	localization	BP	1	GPAM,PDGFRB,SLC35F6,SNX18,LRP1,DCN,NDN,PRNP,SDC4,FOLR2,FBN1,GLIPR2,KANK2,TMEM230,BMPR1A,TLN2,NABP2,LMO4,RECK,FXYD1,TRPV2,CLIP3,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,DOCK10,MICALL2,LCAT,SNUPN,SSR2,SYDE1,HSD3B7,SCP2,SLC39A6,LAMA3,CACNB3,CSPG4,TRIM8,ANXA11,ATP5MC1,SCAMP4,SEMA3C,LRPAP1,THY1,CLTB,SSR3,WDR45,PEX5,MFSD3,ATP6V0C,MYO1B,SCAMP2,B4GALT1,OSBPL10,GLI3,PARK7,YIF1A,SLC17A9,SCARA5,ZFP36L1,SASH1,SLC2A10,TPC3,CYBA,ARL2BP,IFT57,MAVS,CDH2,TOM1,FUT8,ENSCAFG00000017708,SPRED1,MGARP,RAB7B,SPNS1,SEC61B,GLIS2,TWIST2,RAB31,HM13,ARHGAP1,DDR2,PCSK6,GREM1,EVI5L,LONP2,RAC2,CLIC4,FOXO3,SOAT1,PACSIN3,ANKRD54,SEC61A1,BRSK1	down_VCAV_EC
GO:0045935	0.178	0.861	48	491	positive regulation of nucleobase-containing compound metabolic process	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,HNRNPD,SREBF2,HINFP,U2AF2,SLC29A1,RFC2,INSIG1,CDK1,RFC5,RFC3,TIMELESS,THRAP3,FAM129B,AURKB,GREM1,RFC4,NEK2,SMARCC1,PCNA,DHX33,SF3B4,CKS2,BRCA1,E2F8,TFRC,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103	down_ACOR_VSMC
GO:0007610	0.178	0.882	18	146	behavior	BP	1	FGF13,LEP,HTR2B,FBXL20,HRH1,LRRN4,GLRB,CREBRF,SLITRK5,PRKCE,POMK,APP,PSEN1,CHD7,CLN8,OXR1,GAA,PARK7	up_ACOR_VSMC
GO:0016569	0.178	0.885	16	144	covalent chromatin modification	BP	1	SREBF1,POLE3,PRMT1,CDK1,AURKB,EZH2,FBL,UHRF1,BRCA1,NOC2L,HASPIN,DMAP1,CCNA2,RBM14,BAP1,TADA2A	down_ACOR_VSMC
GO:0010638	0.178	0.884	16	207	positive regulation of organelle organization	BP	1	FSCN1,WDR1,MSN,LMAN1,HIF1A,DYNLL1,ACTR3,CTNNB1,BNIP3,FAM162A,GSK3B,CDC37,SH3GLB1,SDC4,HTT,NRP1	down_VSAP_EC
GO:0072001	0.178	0.891	13	104	renal system development	BP	1	HOXA11,EMX2,WNT11,OSR2,SLIT2,DLL1,OSR1,KLF15,ZBTB16,GLIS2,IRX3,SULF2,LRP4	up_VSAP_EC
GO:0046700	0.178	0.893	12	147	heterocycle catabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,ALDH1L2,HIF1A,ZPR1,ENTPD4,SMG7,CNOT7,ALDOC,SND1	down_VSAP_EC
GO:0006164	0.178	0.899	10	86	purine nucleotide biosynthetic process	BP	1	ACLY,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,ATP5F1D	down_ACOR_VSMC
GO:0061448	0.178	0.906	8	89	connective tissue development	BP	1	SULF1,SERPINH1,NR1H4,CHSY1,HIF1A,ACTA2,CTNNB1,CREB3L2	down_VSAP_EC

GO:0009791	0.178	0.918	6	38	post-embryonic development	BP	1	BMP4,FGFR2,ATRX,ITPR1,PSEN1,ARID5B	up_ACOR_VSMC
GO:0021987	0.178	0.918	6	37	cerebral cortex development	BP	1	FGF13,NRP1,PSEN1,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0043524	0.178	0.918	6	39	negative regulation of neuron apoptotic process	BP	1	PPARGC1A,NRP1,UNC5B,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0050954	0.178	0.926	5	30	sensory perception of mechanical stimulus	BP	1	MBP,COCH,USP53,CHD7,WFS1	up_ACOR_VSMC
GO:0019217	0.178	0.934	4	27	regulation of fatty acid metabolic process	BP	1	SREBF1,INSIG1,CAV1,BRCA1	down_ACOR_VSMC
GO:1901879	0.178	0.934	4	26	regulation of protein depolymerization	BP	1	CAPG,LIMA1,PDXP,ARHGEF2	down_ACOR_VSMC
GO:0071901	0.178	0.932	4	37	negative regulation of protein serine/threonine	BP	1	APOE,LYN,CBLC,CDKN1A	down_VSAP_EC
GO:0031589	0.178	0.931	4	93	cell-substrate adhesion	BP	1	HOXA7,GREM1,BVES,KANK1	up_AFEM_EC
GO:0051093	0.178	0.932	4	273	negative regulation of developmental process	BP	1	HOOK3,SEMA3A,ASPN,RNF6	up_VPOR_EC
GO:0035116	0.178	0.947	3	15	embryonic hindlimb morphogenesis	BP	1	AFF3,BMP4,CHD7	up_ACOR_VSMC
GO:0035725	0.178	0.947	3	16	sodium ion transmembrane transport	BP	1	PTPN3,FXYD1,SLC8A1	up_ACOR_VSMC
GO:0048584	0.178	0.946	3	592	positive regulation of response to stimulus	BP	1	BAMBI,ANKRD6,C3AR1	up_VPOR_VSMC
GO:0006541	0.178	0.964	2	9	glutamine metabolic process	BP	1	PFAS,CTPS1	down_ACOR_VSMC
GO:0045806	0.178	0.962	2	15	negative regulation of endocytosis	BP	1	LRPAP1,PACSIN3	down_VCAV_EC
GO:0008209	0.178	0.965	2	8	androgen metabolic process	BP	1	HSD17B8,DHRS9	up_VSAP_EC
GO:0006892	0.178	0.984	1	39	post-Golgi vesicle-mediated transport	BP	1	ACSL3	down_ACOR_EC
GO:0030218	0.178	0.984	1	42	erythrocyte differentiation	BP	1	LYN	down_ACOR_EC
GO:0008630	0.178	0.984	1	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	USP28	down_ACOR_EC
GO:2000241	0.178	0.984	1	40	regulation of reproductive process	BP	1	SULF1	down_ACOR_EC
GO:0031936	0.178	0.991	1	2	negative regulation of chromatin silencing	BP	1	ATAD2	down_ACOR_VSMC
GO:0003365	0.178	0.991	1	2	establishment of cell polarity involved in ameboidal cell migration	BP	1	AMOTL1	down_ACOR_VSMC
GO:0006438	0.178	0.991	1	2	valyl-tRNA aminoacylation	BP	1	VARS	down_ACOR_VSMC
GO:0021564	0.178	0.991	1	2	vagus nerve development	BP	1	NAV2	down_ACOR_VSMC
GO:0044789	0.178	0.991	1	2	modulation by host of viral release from host cell	BP	1	SMC3	down_ACOR_VSMC
GO:0044791	0.178	0.991	1	2	positive regulation by host of viral release from	BP	1	SMC3	down_ACOR_VSMC
GO:0034654	0.178	1	1	1236	nucleobase-containing compound biosynthetic	BP	1	GATA5	down_AFEM_VSMC
GO:0007214	0.178	0.987	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	down_VCAV_EC
GO:0043031	0.178	0.987	1	4	negative regulation of macrophage activation	BP	1	BPI	down_VCAV_EC
GO:0043650	0.178	0.987	1	4	dicarboxylic acid biosynthetic process	BP	1	GLS2	down_VCAV_EC
GO:1904683	0.178	0.987	1	4	regulation of metalloendopeptidase	BP	1	RECK	down_VCAV_EC
GO:0022614	0.178	0.989	1	3	membrane to membrane docking	BP	1	MSN	down_VSAP_EC
GO:0036091	0.178	0.989	1	3	positive regulation of transcription from RNA polymerase II promoter in response to oxidative	BP	1	SESN2	down_VSAP_EC
GO:0089700	0.178	0.989	1	3	protein kinase D signaling	BP	1	VEGFA	down_VSAP_EC
GO:0002478	0.178	0.991	1	2	antigen processing and presentation of exogenous peptide	BP	1	B2M	up_ACOR_VSMC
GO:0045720	0.178	0.991	1	2	negative regulation of integrin biosynthetic	BP	1	AR	up_ACOR_VSMC
GO:0003130	0.178	0.991	1	2	BMP signaling pathway involved in heart	BP	1	BMP4	up_ACOR_VSMC
GO:0003133	0.178	0.991	1	2	endodermal-mesodermal cell signaling	BP	1	BMP4	up_ACOR_VSMC

GO:0003134	0.178	0.991	1	2	endodermal-mesodermal cell signaling involved in heart induction	BP	1	BMP4	up_ACOR_VSMC
GO:0007352	0.178	0.991	1	2	zygotic specification of dorsal/ventral axis	BP	1	SMAD6	up_ACOR_VSMC
GO:0010159	0.178	0.991	1	2	specification of animal organ position	BP	1	BMP4	up_ACOR_VSMC
GO:0019373	0.178	0.991	1	2	epoxygenase P450 pathway	BP	1	CYP2J2	up_ACOR_VSMC
GO:0072191	0.178	0.991	1	2	ureter smooth muscle development	BP	1	BMP4	up_ACOR_VSMC
GO:0072193	0.178	0.991	1	2	ureter smooth muscle cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0072198	0.178	0.991	1	2	mesenchymal cell proliferation involved in	BP	1	BMP4	up_ACOR_VSMC
GO:0072199	0.178	0.991	1	2	regulation of mesenchymal cell proliferation involved in	BP	1	BMP4	up_ACOR_VSMC
GO:0031272	0.178	0.985	1	8	regulation of pseudopodium assembly	BP	1	CDC42EP5	up_AFEM_EC
GO:0031274	0.178	0.985	1	8	positive regulation of pseudopodium assembly	BP	1	CDC42EP5	up_AFEM_EC
GO:0045116	0.178	0.985	1	8	protein neddylation	BP	1	DCUN1D3	up_AFEM_EC
GO:0016569	0.178	0.985	1	144	covalent chromatin modification	BP	1	EYA1	up_AFEM_VSMC
GO:0051052	0.178	0.985	1	145	regulation of DNA metabolic process	BP	1	EYA1	up_AFEM_VSMC
GO:0046649	0.178	0.985	1	162	lymphocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0003206	0.178	0.984	1	51	cardiac chamber morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0040007	0.178	0.986	1	276	growth	BP	1	TBX5	up_APUL_VSMC
GO:0051093	0.178	0.986	1	273	negative regulation of developmental process	BP	1	TBX5	up_APUL_VSMC
GO:2001045	0.178	0.991	1	2	negative regulation of integrin-mediated	BP	1	CTNNA1	up_VCAV_EC
GO:0006705	0.178	0.991	1	2	mineralocorticoid biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0031944	0.178	0.991	1	2	negative regulation of glucocorticoid metabolic	BP	1	BMP2	up_VCAV_EC
GO:0031947	0.178	0.991	1	2	negative regulation of glucocorticoid biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0032342	0.178	0.991	1	2	aldosterone biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0032345	0.178	0.991	1	2	negative regulation of aldosterone metabolic	BP	1	BMP2	up_VCAV_EC
GO:0032347	0.178	0.991	1	2	regulation of aldosterone biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0032348	0.178	0.991	1	2	negative regulation of aldosterone biosynthetic	BP	1	BMP2	up_VCAV_EC
GO:0035025	0.178	0.989	1	3	positive regulation of Rho protein signal	BP	1	GPR4	up_VCAV_EC
GO:0048875	0.178	0.991	1	2	chemical homeostasis within a tissue	BP	1	ADGRF5	up_VCAV_EC
GO:0090032	0.178	0.991	1	2	negative regulation of steroid hormone	BP	1	BMP2	up_VCAV_EC
GO:2000065	0.178	0.991	1	2	negative regulation of cortisol biosynthetic	BP	1	BMP2	up_VCAV_EC
GO:0043269	0.178	0.985	1	135	regulation of ion transport	BP	1	CA2	up_VCAV_VSMC
GO:0032755	0.178	0.984	1	24	positive regulation of interleukin-6 production	BP	1	ARHGEF2	up_VPOR_EC
GO:0022412	0.178	0.984	1	76	cellular process involved in reproduction in multicellular organism	BP	1	CYP26B1	up_VPOR_VSMC
GO:0031503	0.178	0.984	1	79	protein-containing complex localization	BP	1	NETO1	up_VFEM_VSMC
GO:0002322	0.178	0.991	1	2	B cell proliferation involved in immune	BP	1	ABL1	up_VSAP_EC
GO:0040016	0.178	0.991	1	2	embryonic cleavage	BP	1	TPRA1	up_VSAP_EC
GO:0043570	0.178	0.991	1	2	maintenance of DNA repeat elements	BP	1	AXIN2	up_VSAP_EC
GO:0034341	0.178	0.984	1	43	response to interferon-gamma	BP	1	TLR2	up_VSAP_VSMC
GO:0060675	0.178074054	0.95982	2	29	ureteric bud morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC

GO:0035304	0.178264408	0.95975	2	29	regulation of protein dephosphorylation	BP	1	DUSP26,PRKCD	up_ACOR_EC
GO:0051900	0.178325617	0.98514	1	8	regulation of mitochondrial	BP	1	IFI6	up_ACOR_EC
GO:1901293	0.179	0.901	9	106	nucleoside phosphate biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC,PAPSS1,AK5,CMPK1	down_VSAP_EC
GO:0030278	0.179	0.902	9	66	regulation of ossification	BP	1	SMAD6,RASSF2,BMP4,GJA1,ISG15,CLSTN1,NPNT,DDR2,SLC8A1	up_ACOR_VSMC
GO:0048583	0.179	0.91	8	1095	regulation of response to stimulus	BP	1	ACVRL1,LYN,IGF1R,PDPN,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0001838	0.179	0.907	8	56	embryonic epithelial tube formation	BP	1	SHROOM3,BMP4,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0051348	0.179	0.91	7	90	negative regulation of transferase activity	BP	1	DCN,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1	down_VCAV_EC
GO:0001816	0.179	0.909	7	194	cytokine production	BP	1	CMKLR1,LEP,DLL1,BPI,GPAM,ADAM17,AGPAT2	up_AFEM_EC
GO:0008016	0.179	0.917	6	48	regulation of heart contraction	BP	1	PDE4D,STC1,EDN1,KCNJ2,GCH1,SPTBN4	up_VCAV_EC
GO:0032231	0.179	0.925	5	32	regulation of actin filament bundle assembly	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,BAG4	up_VSAP_EC
GO:0042981	0.179	0.932	4	471	regulation of apoptotic process	BP	1	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0030501	0.179	0.946	3	16	positive regulation of bone mineralization	BP	1	BMP4,ISG15,SLC8A1	up_ACOR_VSMC
GO:1901362	0.179	0.953	3	1293	organic cyclic compound biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0098771	0.179	0.942	3	180	inorganic ion homeostasis	BP	1	C3AR1,HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0048646	0.179	0.944	3	349	anatomical structure formation involved in	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0060429	0.179	0.943	3	341	epithelium development	BP	1	HOXA11,SALL1,CAV1	up_VSAP_VSMC
GO:0006305	0.179	0.964	2	9	DNA alkylation	BP	1	EZH2,MIS18A	down_ACOR_VSMC
GO:0006306	0.179	0.964	2	9	DNA methylation	BP	1	EZH2,MIS18A	down_ACOR_VSMC
GO:0043931	0.179	0.964	2	9	ossification involved in bone maturation	BP	1	XYLT1,GREM1	down_ACOR_VSMC
GO:0070977	0.179	0.964	2	9	bone maturation	BP	1	XYLT1,GREM1	down_ACOR_VSMC
GO:2000279	0.179	0.964	2	9	negative regulation of DNA biosynthetic process	BP	1	FAM129B,TINF2	down_ACOR_VSMC
GO:0048333	0.179	0.962	2	12	mesodermal cell differentiation	BP	1	ITGA2,INHBA	down_VSAP_EC
GO:0048513	0.179	0.967	2	906	animal organ development	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0003299	0.179	0.965	2	8	muscle hypertrophy in response to stress	BP	1	MEF2C,PPP3CA	up_VCAV_EC
GO:0014887	0.179	0.965	2	8	cardiac muscle adaptation	BP	1	MEF2C,PPP3CA	up_VCAV_EC
GO:0014898	0.179	0.965	2	8	cardiac muscle hypertrophy in response	BP	1	MEF2C,PPP3CA	up_VCAV_EC
GO:0055074	0.179	0.959	2	95	calcium ion homeostasis	BP	1	C3AR1,HOXA3	up_VPOR_EC
GO:0009628	0.179	0.961	2	302	response to abiotic stimulus	BP	1	EYA1,NETO1	up_VFEM_VSMC
GO:0050798	0.179	0.965	2	8	activated T cell proliferation	BP	1	CD274,ABL1	up_VSAP_EC
GO:0042493	0.179	0.959	2	178	response to drug	BP	1	EMX2,CAV1	up_VSAP_VSMC
GO:0032092	0.179	0.984	1	38	positive regulation of protein binding	BP	1	HOXA3	down_ACOR_EC
GO:0031396	0.179	0.984	1	90	regulation of protein ubiquitination	BP	1	IVNS1ABP	down_AFEM_EC
GO:0044282	0.179	0.984	1	89	small molecule catabolic process	BP	1	ETFA	down_AFEM_EC
GO:0051235	0.179	0.984	1	90	maintenance of location	BP	1	GPSM2	down_AFEM_EC
GO:0048793	0.179	0.987	1	4	pronephros development	BP	1	SEC61A1	down_VCAV_EC
GO:1901565	0.179	0.988	1	442	organonitrogen compound catabolic	BP	1	USP12	down_VFEM_EC
GO:0034092	0.179	0.988	1	3	negative regulation of maintenance of sister chromatid cohesion	BP	1	NAA10	down_VSAP_EC
GO:0034183	0.179	0.988	1	3	negative regulation of maintenance of mitotic sister chromatid cohesion	BP	1	NAA10	down_VSAP_EC
GO:0045875	0.179	0.988	1	3	negative regulation of sister chromatid cohesion	BP	1	NAA10	down_VSAP_EC

GO:0060423	0.179	0.988	1	3	foregut regionalization	BP	1	CTNNB1	down_VSAP_EC
GO:0060492	0.179	0.988	1	3	lung induction	BP	1	CTNNB1	down_VSAP_EC
GO:1904796	0.179	0.988	1	3	regulation of core promoter binding	BP	1	CTNNB1	down_VSAP_EC
GO:0060424	0.179	0.988	1	3	lung field specification	BP	1	CTNNB1	down_VSAP_EC
GO:2000697	0.179	0.988	1	3	negative regulation of epithelial cell differentiation involved in	BP	1	CTNNB1	down_VSAP_EC
GO:0010561	0.179	0.991	1	2	negative regulation of glycoprotein biosynthetic	BP	1	ITM2C	up_ACOR_VSMC
GO:0002031	0.179	0.991	1	2	G protein-coupled receptor internalization	BP	1	HTR2B	up_ACOR_VSMC
GO:0003285	0.179	0.991	1	2	septum secundum development	BP	1	GATA4	up_ACOR_VSMC
GO:0150078	0.179	0.991	1	2	positive regulation of neuroinflammatory	BP	1	APP	up_ACOR_VSMC
GO:1903019	0.179	0.991	1	2	negative regulation of glycoprotein metabolic	BP	1	ITM2C	up_ACOR_VSMC
GO:1903980	0.179	0.991	1	2	positive regulation of microglial cell activation	BP	1	APP	up_ACOR_VSMC
GO:0007202	0.179	0.991	1	2	activation of phospholipase C activity	BP	1	HTR2B	up_ACOR_VSMC
GO:0030327	0.179	0.991	1	2	prenylated protein catabolic process	BP	1	PCYOX1	up_ACOR_VSMC
GO:0032379	0.179	0.991	1	2	positive regulation of intracellular lipid	BP	1	SCP2	up_ACOR_VSMC
GO:0032382	0.179	0.991	1	2	positive regulation of intracellular sterol	BP	1	SCP2	up_ACOR_VSMC
GO:0032385	0.179	0.991	1	2	positive regulation of intracellular cholesterol	BP	1	SCP2	up_ACOR_VSMC
GO:0046368	0.179	0.991	1	2	GDP-L-fucose metabolic process	BP	1	FUT8	up_ACOR_VSMC
GO:0051957	0.179	0.991	1	2	positive regulation of amino acid transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0060994	0.179	0.991	1	2	regulation of transcription from RNA polymerase II promoter involved in	BP	1	BMP4	up_ACOR_VSMC
GO:0061419	0.179	0.991	1	2	positive regulation of transcription from RNA polymerase II promoter in response to hypoxia	BP	1	HIF1A	up_VCAV_EC
GO:0006282	0.179	0.984	1	48	regulation of DNA repair	BP	1	EYA1	up_VFEM_EC
GO:0021953	0.179	0.984	1	49	central nervous system neuron differentiation	BP	1	HOXC10	up_VFEM_EC
GO:0072511	0.179	0.984	1	97	divalent inorganic cation transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0031666	0.179	0.991	1	2	positive regulation of lipopolysaccharide-mediated signaling	BP	1	SASH1	up_VSAP_EC
GO:0060397	0.179	0.991	1	2	JAK-STAT cascade involved in growth hormone signaling	BP	1	STAT5A	up_VSAP_EC
GO:0055002	0.179	0.984	1	45	striated muscle cell development	BP	1	SHOX2	up_VSAP_VSMC
GO:0071380	0.179857146	0.98516	1	7	cellular response to prostaglandin E stimulus	BP	1	PTGER4	up_ACOR_EC
GO:0071709	0.17985867	0.98487	1	8	membrane assembly	BP	1	LRP4	up_ACOR_EC
GO:0012501	0.18	0.882	17	561	programmed cell death	BP	1	GAS1,ANGPT4,CD40,DLL1,CRYAB,F3,GPAM,MLLT11,THRB,PLAGL2,GREM1,CAMK2A,CYLD,DCUN1D3,PPARGC1A,FAP,DMPK	up_AFEM_EC
GO:0016197	0.18	0.901	9	78	endosomal transport	BP	1	RAB6A,ANKRD50,ABCA1,SNX2,EHD4,GCC2,VPS54,ALS2,LMTK2	up_VCAV_EC
GO:0021915	0.18	0.906	8	58	neural tube development	BP	1	FZD1,ABL1,FUZ,RARG,AMBRA1,ZFP36L1,KDM2B,CITED2	up_VSAP_EC
GO:0050821	0.18	0.911	7	48	protein stabilization	BP	1	SAV1,PLPP3,MORC3,PIK3R1,HPS4,FLOT1,PEX6	up_VSAP_EC
GO:0051017	0.18	0.911	7	49	actin filament bundle assembly	BP	1	WNT11,FAM107A,ARHGEF5,ABL1,PIK3R1,MYO1B,BAG4	up_VSAP_EC
GO:0032944	0.18	0.916	6	48	regulation of mononuclear cell	BP	1	MEF2C,TLR4,PELI1,ARG2,NCK1,HMGB1	up_VCAV_EC
GO:0050670	0.18	0.916	6	48	regulation of lymphocyte proliferation	BP	1	MEF2C,TLR4,PELI1,ARG2,NCK1,HMGB1	up_VCAV_EC
GO:0071706	0.18	0.917	6	40	tumor necrosis factor superfamily cytokine	BP	1	CD274,C5AR2,PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC

GO:0032606	0.18	0.924	5	35	type I interferon production	BP	1	IRAK1,DHX33,CACTIN,HMGB2,POLR3F	down_ACOR_VSMC
GO:0019359	0.18	0.934	4	23	nicotinamide nucleotide biosynthetic process	BP	1	NADK,GALK1,PNP,DDIT4	up_VSAP_EC
GO:0019363	0.18	0.934	4	23	pyridine nucleotide biosynthetic process	BP	1	NADK,GALK1,PNP,DDIT4	up_VSAP_EC
GO:0032602	0.18	0.934	4	23	chemokine production	BP	1	IL6R,F2RL1,MYD88,MAVS	up_VSAP_EC
GO:1903902	0.18	0.945	3	18	positive regulation of viral life cycle	BP	1	SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0046824	0.18	0.943	3	30	positive regulation of nucleocytoplasmic	BP	1	ENSCAFG00000014978,GLI3,MAVS	down_VCAV_EC
GO:1903051	0.18	0.943	3	29	negative regulation of proteolysis involved in cellular protein catabolic	BP	1	PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:0060255	0.18	0.959	3	1782	regulation of macromolecule metabolic	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0045841	0.18	0.945	3	18	negative regulation of mitotic	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:1902100	0.18	0.945	3	18	negative regulation of metaphase/anaphase transition of cell cycle	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:1905819	0.18	0.945	3	18	negative regulation of chromosome separation	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:2000816	0.18	0.945	3	18	negative regulation of mitotic sister chromatid	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0009581	0.18	0.945	3	18	detection of external stimulus	BP	1	EPHB1,KIT,MMP24	up_VCAV_EC
GO:0009582	0.18	0.945	3	18	detection of abiotic stimulus	BP	1	EPHB1,KIT,MMP24	up_VCAV_EC
GO:0055013	0.18	0.946	3	17	cardiac muscle cell development	BP	1	EDN1,MTOR,PROX1	up_VCAV_EC
GO:1902743	0.18	0.946	3	16	regulation of lamellipodium	BP	1	MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0035329	0.18	0.946	3	16	hippo signaling	BP	1	SAV1,LIMD1,LATS2	up_VSAP_EC
GO:0018196	0.18	0.961	2	15	peptidyl-asparagine modification	BP	1	DDOST,FUT8	down_VCAV_EC
GO:0051926	0.18	0.961	2	14	negative regulation of calcium ion transport	BP	1	REM1,CALM1	down_VSAP_EC
GO:0032373	0.18	0.964	2	8	positive regulation of sterol transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0032376	0.18	0.964	2	8	positive regulation of cholesterol transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:1990126	0.18	0.964	2	8	retrograde transport, endosome to plasma	BP	1	RAB11B,VPS26A	up_ACOR_VSMC
GO:2000050	0.18	0.964	2	8	regulation of non-canonical Wnt signaling	BP	1	MLLT3,ZNRF3	up_ACOR_VSMC
GO:0050801	0.18	0.959	2	200	ion homeostasis	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0010586	0.18	0.964	2	8	miRNA metabolic process	BP	1	TENT2,TUT7	up_VCAV_EC
GO:0048745	0.18	0.964	2	8	smooth muscle tissue development	BP	1	OSR1,ZFAND5	up_VSAP_EC
GO:2001044	0.18	0.964	2	8	regulation of integrin-mediated signaling	BP	1	LIMS2,EMP2	up_VSAP_EC
GO:1901889	0.18	0.964	2	8	negative regulation of cell junction assembly	BP	1	FAM107A,ACVRL1	up_VSAP_EC
GO:1903307	0.18	0.964	2	8	positive regulation of regulated secretory	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0009743	0.18	0.984	1	40	response to carbohydrate	BP	1	STX4	down_ACOR_EC
GO:0030502	0.18	0.987	1	4	negative regulation of bone mineralization	BP	1	GREM1	down_VCAV_EC
GO:0034309	0.18	0.987	1	4	primary alcohol biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0006930	0.18	0.988	1	3	substrate-dependent cell migration, cell extension	BP	1	NRP1	down_VSAP_EC
GO:0038189	0.18	0.988	1	3	neuropilin signaling pathway	BP	1	NRP1	down_VSAP_EC
GO:0035740	0.18	0.991	1	2	CD8-positive, alpha-beta T cell proliferation	BP	1	PTPN22	up_ACOR_VSMC
GO:0003164	0.18	0.991	1	2	His-Purkinje system development	BP	1	TBX5	up_ACOR_VSMC
GO:0061000	0.18	0.991	1	2	negative regulation of dendritic spine	BP	1	ASAP1	up_ACOR_VSMC
GO:1903373	0.18	0.991	1	2	positive regulation of endoplasmic reticulum tubular network	BP	1	LNPK	up_ACOR_VSMC

GO:2000564	0.18	0.991	1	2	regulation of CD8-positive, alpha-beta T cell	BP	1	PTPN22	up_ACOR_VSMC
GO:0003166	0.18	0.991	1	2	bundle of His development	BP	1	TBX5	up_ACOR_VSMC
GO:0098884	0.18	0.991	1	2	postsynaptic neurotransmitter	BP	1	AP2B1	up_ACOR_VSMC
GO:0099590	0.18	0.991	1	2	neurotransmitter receptor internalization	BP	1	AP2B1	up_ACOR_VSMC
GO:0140239	0.18	0.991	1	2	postsynaptic endocytosis	BP	1	AP2B1	up_ACOR_VSMC
GO:1903377	0.18	0.991	1	2	negative regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:1903715	0.18	0.991	1	2	regulation of aerobic respiration	BP	1	BNIP3	up_ACOR_VSMC
GO:0050673	0.18	0.985	1	135	epithelial cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0030335	0.18	0.985	1	165	positive regulation of cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0048812	0.18	0.985	1	151	neuron projection morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0090066	0.18	0.985	1	162	regulation of anatomical structure size	BP	1	WNT7A	up_AORT_VSMC
GO:0120035	0.18	0.985	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	WNT7A	up_AORT_VSMC
GO:0046890	0.18	0.984	1	51	regulation of lipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:2000145	0.18	0.986	1	279	regulation of cell motility	BP	1	TBX5	up_APUL_VSMC
GO:1903898	0.18	0.988	1	3	negative regulation of PERK-mediated unfolded protein response	BP	1	NCK1	up_VCAV_EC
GO:0006094	0.18	0.984	1	24	gluconeogenesis	BP	1	FBP1	up_VPOR_EC
GO:0060326	0.18	0.984	1	84	cell chemotaxis	BP	1	C3AR1	up_VPOR_VSMC
GO:0031333	0.18	0.984	1	46	negative regulation of protein complex assembly	BP	1	TRIM9	up_VFEM_EC
GO:0042445	0.18	0.984	1	46	hormone metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0019318	0.18	0.984	1	75	hexose metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0032869	0.18	0.984	1	57	cellular response to insulin stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0070374	0.18	0.984	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	CCL24	up_VPUL_EC
GO:0060605	0.18	0.991	1	2	tube lumen cavitation	BP	1	NFIB	up_VSAP_EC
GO:0060662	0.18	0.991	1	2	salivary gland cavitation	BP	1	NFIB	up_VSAP_EC
GO:1904684	0.18	0.991	1	2	negative regulation of metalloendopeptidase	BP	1	RECK	up_VSAP_EC
GO:1905049	0.18	0.991	1	2	negative regulation of metallopeptidase activity	BP	1	RECK	up_VSAP_EC
GO:0001823	0.18	0.984	1	45	mesonephros development	BP	1	HOXA11	up_VSAP_VSMC
GO:0051701	0.18	0.984	1	45	interaction with host	BP	1	CAV1	up_VSAP_VSMC
GO:0021543	0.18	0.984	1	49	pallium development	BP	1	EMX2	up_VSAP_VSMC
GO:0050680	0.18	0.984	1	44	negative regulation of epithelial cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0008219	0.180496548	0.87725	20	611	cell death	BP	1	NR1H4,SOX9,AQP1,FZD5,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,USP53,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,CHMP4B,NRP1,PRKCD,PM20D1	up_ACOR_EC
GO:0051246	0.181	0.851	75	832	regulation of protein metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,IWS1,ATF3,TIPARP,RAPGEF1,TLR4,QKI,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,ODC1,CASP8,MTOR,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,SH3BP5,ENC1,PPP1R2,ITPKB,PROX1,SECISBP2L,MADD,PAK2,PRKD2,SWAP70,TLR3,APOD,NCK1,DPH5,OTUD4,NSD1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,CNOT7,HMGB1,PMAIP1,BLM,SPTBN4,RIPK1,PDGFD,CUL4A,UBE2D1,KDM5A,KDM3A,ATRX,IVNS1ABP,JCAD,PSMB9,ARHGEF2,CDON	up_VCAV_EC

GO:0000122	0.181	0.881	17	218	negative regulation of transcription by RNA polymerase II	BP	1	NR1H4,PLK3,ETV6,CBX5,FHL2,PTPN2,PEG3,MTDH,CNOT7,CTNNB1,WWC3,KLF5,STRAP,DDIT3,VLDLR,ZMYND8,HIF1AN	down_VSAP_EC
GO:0060485	0.181	0.892	12	93	mesenchyme development	BP	1	GATA5,GATA4,HTR2B,BMP4,FGFR2,CITED2,NRP1,TBX20,TBX5,DAG1,TGFBR1,EDN1	up_ACOR_VSMC
GO:0006874	0.181	0.904	8	91	cellular calcium ion homeostasis	BP	1	ERO1A,ATP2B1,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0006898	0.181	0.91	7	57	receptor-mediated endocytosis	BP	1	SELE,CXCL8,CALCRL,BMP2K,HIST1H1A,PLCG2,DNAJC13	up_VCAV_EC
GO:0033108	0.181	0.917	6	39	mitochondrial respiratory chain complex assembly	BP	1	NDUFS7,DMAC2,NDUFAF3,NDUFB10,SMIM20,COA1	up_VSAP_EC
GO:0006631	0.181	0.929	4	93	fatty acid metabolic process	BP	1	LEP,GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0044743	0.181	0.933	4	23	protein transmembrane import into intracellular	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0070664	0.181	0.945	3	18	negative regulation of leukocyte proliferation	BP	1	MNDA,GREM1,ARG2	down_ACOR_VSMC
GO:0010467	0.181	0.959	3	1787	gene expression	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0031323	0.181	0.958	3	1788	regulation of cellular metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0032501	0.181	0.958	3	1782	multicellular organismal process	BP	1	TGFBI,GATA5,TGFBR1	down_VSAP_VSMC
GO:0006897	0.181	0.959	2	158	endocytosis	BP	1	SPG11,NEDD4	down_ACOR_EC
GO:0001913	0.181	0.962	2	10	T cell mediated cytotoxicity	BP	1	FAM49B,EMP2	down_ACOR_VSMC
GO:1990774	0.181	0.963	2	9	tumor necrosis factor secretion	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0006629	0.181	0.961	2	382	lipid metabolic process	BP	1	HSD3B7,GBGT1	down_VPOR_EC
GO:0007063	0.181	0.962	2	12	regulation of sister chromatid cohesion	BP	1	NAA10,CTNNB1	down_VSAP_EC
GO:0009649	0.181	0.961	2	13	entrainment of circadian clock	BP	1	BHLHE40,GNAQ	down_VSAP_EC
GO:0007026	0.181	0.964	2	8	negative regulation of microtubule	BP	1	FGF13,MID1	up_ACOR_VSMC
GO:0015807	0.181	0.964	2	8	L-amino acid transport	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0034311	0.181	0.963	2	9	diol metabolic process	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0021515	0.181	0.963	2	9	cell differentiation in spinal cord	BP	1	DLL4,GDPD5	up_VCAV_EC
GO:0048468	0.181	0.962	2	553	cell development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0006805	0.181	0.964	2	8	xenobiotic metabolic process	BP	1	HNF4A,NCEH1	up_VSAP_EC
GO:0050766	0.181	0.964	2	8	positive regulation of phagocytosis	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0098801	0.181	0.964	2	8	regulation of renal system process	BP	1	EMP2,F2RL1	up_VSAP_EC
GO:0055080	0.181	0.959	2	176	cation homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0045040	0.181	0.988	1	3	protein import into mitochondrial outer	BP	1	SAMM50	down_ACOR_VSMC
GO:1903817	0.181	0.988	1	3	negative regulation of voltage-gated potassium	BP	1	CAV1	down_ACOR_VSMC
GO:0048731	0.181	1	1	1247	system development	BP	1	GATA5	down_AFEM_VSMC
GO:0051172	0.181	0.991	1	663	negative regulation of nitrogen compound	BP	1	CST3	down_AORT_EC
GO:0010421	0.181	0.987	1	4	hydrogen peroxide-mediated programmed	BP	1	PARK7	down_VCAV_EC
GO:0048478	0.181	0.987	1	4	replication fork protection	BP	1	FBH1	down_VCAV_EC
GO:0060633	0.181	0.987	1	4	negative regulation of transcription initiation from RNA polymerase II	BP	1	CLSTN1	down_VCAV_EC
GO:0097468	0.181	0.987	1	4	programmed cell death in response to reactive oxygen species	BP	1	PARK7	down_VCAV_EC
GO:2000143	0.181	0.987	1	4	negative regulation of DNA-templated	BP	1	CLSTN1	down_VCAV_EC
GO:0002070	0.181	0.988	1	3	epithelial cell maturation	BP	1	HIF1A	down_VSAP_EC
GO:0010757	0.181	0.988	1	3	negative regulation of plasminogen activation	BP	1	SERPINE1	down_VSAP_EC
GO:0060749	0.181	0.988	1	3	mammary gland alveolus development	BP	1	HIF1A	down_VSAP_EC

GO:0061377	0.181	0.988	1	3	mammary gland lobule development	BP	1	HIF1A	down_VSAP_EC
GO:0072578	0.181	0.988	1	3	neurotransmitter-gated ion channel clustering	BP	1	APOE	down_VSAP_EC
GO:0090166	0.181	0.988	1	3	Golgi disassembly	BP	1	PLK3	down_VSAP_EC
GO:1904948	0.181	0.988	1	3	midbrain dopaminergic neuron differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0021957	0.181	0.988	1	3	corticospinal tract morphogenesis	BP	1	CDH11	down_VSAP_EC
GO:0070208	0.181	0.988	1	3	protein heterotrimerization	BP	1	C1QTNF6	down_VSAP_EC
GO:0006477	0.181	0.991	1	2	protein sulfation	BP	1	TPST2	up_ACOR_VSMC
GO:0042415	0.181	0.991	1	2	norepinephrine metabolic process	BP	1	MOXD1	up_ACOR_VSMC
GO:0042421	0.181	0.991	1	2	norepinephrine biosynthetic process	BP	1	MOXD1	up_ACOR_VSMC
GO:0045915	0.181	0.991	1	2	positive regulation of catecholamine metabolic	BP	1	PARK7	up_ACOR_VSMC
GO:0045964	0.181	0.991	1	2	positive regulation of dopamine metabolic	BP	1	PARK7	up_ACOR_VSMC
GO:1903093	0.181	0.991	1	2	regulation of protein K48-linked deubiquitination	BP	1	PARK7	up_ACOR_VSMC
GO:1903179	0.181	0.991	1	2	regulation of dopamine biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903181	0.181	0.991	1	2	positive regulation of dopamine biosynthetic	BP	1	PARK7	up_ACOR_VSMC
GO:2001171	0.181	0.991	1	2	positive regulation of ATP biosynthetic process	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0031344	0.181	0.985	1	161	regulation of cell projection organization	BP	1	WNT7A	up_AORT_VSMC
GO:0002520	0.181	0.986	1	279	immune system development	BP	1	HOXA3	up_APUL_VSMC
GO:0048671	0.181	0.991	1	2	negative regulation of collateral sprouting	BP	1	IFRD1	up_VCAV_EC
GO:0048817	0.181	0.991	1	2	negative regulation of hair follicle maturation	BP	1	FERMT1	up_VCAV_EC
GO:0051054	0.181	0.984	1	81	positive regulation of DNA metabolic process	BP	1	EYA1	up_VFEM_VSMC
GO:0008654	0.181	0.984	1	58	phospholipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0110053	0.181	0.984	1	98	regulation of actin filament organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0060486	0.181	0.991	1	2	Clara cell differentiation	BP	1	NFIB	up_VSAP_EC
GO:0098722	0.181	0.991	1	2	asymmetric stem cell division	BP	1	ZBTB16	up_VSAP_EC
GO:1900040	0.181	0.991	1	2	regulation of interleukin-2 secretion	BP	1	ABL1	up_VSAP_EC
GO:1900452	0.181	0.991	1	2	regulation of long-term synaptic depression	BP	1	KCNB1	up_VSAP_EC
GO:0021953	0.181	0.983	1	49	central nervous system neuron differentiation	BP	1	HOXC10	up_VSAP_VSMC
GO:0009605	0.182	0.855	58	538	response to external stimulus	BP	1	NAPEPLD,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,C5AR2,ACKR2,ENPP2,PTGFR,SLC8B1,ACACB,SLIT2,CRADD,ABL1,KLKB1,CHRM1,SESN1,MAP3K5,IL17RC,HPSE,PLXNA4,SEMA5A,HSD3B7,F2RL1,PDK2,BATF2,PLA2G6,TBXA2R,RTN4RL1,SASH1,MYD88,DPYSL2,ACKR4,CASTOR1,WIPF1,CFD,NLRX1,TKFC,NR2F6,DENND5A,RNF216,RAF1,MAPKBP1,NFIB,ZNF580,CYBA,STX4,CA5B,PQBP1,NCK1,MAVS,BGLAP,MAP2K2,NPRL3,SAA1,JCHAIN,DDIT4	up_VSAP_EC
GO:0019220	0.182	0.866	31	525	regulation of phosphate metabolic process	BP	1	NOTCH2,PDGFRB,KIRREL1,DCN,PRNP,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,ASPN,THY1,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,SPRED1,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0051174	0.182	0.866	31	525	regulation of phosphorus metabolic process	BP	1	NOTCH2,PDGFRB,KIRREL1,DCN,PRNP,GLIPR2,BGN,BMPR1A,LMO4,CLIP3,ENSCAFG00000014978,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,ASPN,THY1,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,SPRED1,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC

GO:0007417	0.182	0.868	28	235	central nervous system development	BP	1	FGF13,LEP,MBP,BMP4,FGFR2,ATRX,SEC24B,WASF3,CITED2,ZNF365,LMO4,TMEM108,NDRG2,ATRN,NRP1,SLITRK5,TBX20,FZD3,FRS2,POMK,APP,PSEN1,SEMA6D,CHD7,CLN8,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0048589	0.182	0.873	23	188	developmental growth	BP	1	LGR6,LEP,BMP4,FGFR2,GJA1,ATRX,LATS2,TMEM108,ATRN,PLAC8B,ENSCAFG00000006238,NRP1,ULK2,TBX20,TBX5,APP,CHD7,DDR2,WWC2,EDN1,ARID5B,WDR48,STC2	up_ACOR_VSMC
GO:0044092	0.182	0.876	20	270	negative regulation of molecular function	BP	1	NR1H4,SOCS5,ERRFI1,TRIB3,BHLHE40,PTGS2,REM1,PTPN2,CRYAB,APOE,LYN,DDIT3,CBLC,GSK3B,ARFGEF3,CALM1,DISC1,PAK2,CDKN1A,SPINK2	down_VSAP_EC
GO:0005975	0.182	0.879	18	183	carbohydrate metabolic process	BP	1	PCDH12,PDGFB,ST6GAL1,ATF3,GK5,FAM3C,CHST7,PGM2,ST3GAL6,ENSCAFG00000010596,GALE,CHST1,ENSCAFG00000024323,APOD,PPP1CB,PMAIP1,IMPA1,HIF1A	up_VCAV_EC
GO:0006979	0.182	0.883	16	130	response to oxidative stress	BP	1	FZD1,PPARGC1B,ABL1,SESN1,MAP3K5,MGST1,NFE2L2,PDK2,FXN,NDUFS2,FBXO7,ZNF580,STX4,IDH1,HTRA2,HMOX1	up_VSAP_EC
GO:0001505	0.182	0.904	8	69	regulation of neurotransmitter levels	BP	1	CD34,MEF2C,TLR4,NOS3,SNCAIP,SNAP23,STX11,NOS2	up_VCAV_EC
GO:0009743	0.182	0.915	6	40	response to carbohydrate	BP	1	PRKAA2,LPL,SLC2A5,PRKCE,RAB11B,PFKL	up_ACOR_VSMC
GO:0009059	0.182	0.931	5	1563	macromolecule biosynthetic process	BP	1	HDAC7,CITED2,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:1905330	0.182	0.921	5	48	regulation of morphogenesis of an	BP	1	SULF1,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0032606	0.182	0.922	5	35	type I interferon production	BP	1	TMEM173,TLR4,RIOK3,TLR3,PLCG2	up_VCAV_EC
GO:0042742	0.182	0.922	5	39	defense response to bacterium	BP	1	LYZ,TLR4,IRF8,ARG2,NOS2	up_VCAV_EC
GO:0017148	0.182	0.931	4	36	negative regulation of translation	BP	1	SESN2,EIF4EBP1,CNOT7,EIF2S1	down_VSAP_EC
GO:0060415	0.182	0.932	4	27	muscle tissue morphogenesis	BP	1	CHD7,DLL4,BMP2,PROX1	up_VCAV_EC
GO:0007154	0.182	0.942	4	1622	cell communication	BP	1	SLITRK5,LIMK1,GATA5,CA2	up_VCAV_VSMC
GO:1901701	0.182	0.942	3	271	cellular response to oxygen-containing	BP	1	LYN,IGF1R,STX4	down_ACOR_EC
GO:0006022	0.182	0.942	3	29	aminoglycan metabolic process	BP	1	DCN,CHID1,ENSCAFG00000017708	down_VCAV_EC
GO:0060491	0.182	0.941	3	62	regulation of cell projection assembly	BP	1	CYLD,CDC42EP5,KANK1	up_AFEM_EC
GO:0120032	0.182	0.941	3	62	regulation of plasma membrane bounded cell	BP	1	CYLD,CDC42EP5,KANK1	up_AFEM_EC
GO:0007260	0.182	0.944	3	19	tyrosine phosphorylation of STAT protein	BP	1	HCLS1,KIT,CNOT7	up_VCAV_EC
GO:0090559	0.182	0.944	3	20	regulation of membrane permeability	BP	1	MTOR,SH3GLB1,PMAIP1	up_VCAV_EC
GO:0065008	0.182	0.949	3	1056	regulation of biological quality	BP	1	SLITRK5,LIMK1,CA2	up_VCAV_VSMC
GO:0045577	0.182	0.963	2	9	regulation of B cell differentiation	BP	1	MMP14,HMGB3	down_ACOR_VSMC
GO:0051253	0.182	0.96	2	359	negative regulation of RNA metabolic process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0045453	0.182	0.961	2	12	bone resorption	BP	1	CTNNB1,TFRC	down_VSAP_EC
GO:0031325	0.182	0.966	2	914	positive regulation of cellular metabolic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0035872	0.182	0.964	2	8	nucleotide-binding domain, leucine rich repeat containing	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0070423	0.182	0.964	2	8	nucleotide-binding oligomerization domain containing signaling	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0070431	0.182	0.964	2	8	nucleotide-binding oligomerization domain containing 2 signaling	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:1903959	0.182	0.963	2	8	regulation of anion transmembrane transport	BP	1	TCAF1,PSEN1	up_ACOR_VSMC
GO:2000026	0.182	0.962	2	560	regulation of multicellular organismal development	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0051094	0.182	0.96	2	388	positive regulation of developmental process	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0002115	0.182	0.964	2	8	store-operated calcium entry	BP	1	SLC8B1,CRACR2B	up_VSAP_EC
GO:0033617	0.182	0.963	2	8	mitochondrial respiratory chain complex IV	BP	1	SMIM20,COA1	up_VSAP_EC

GO:0050687	0.182	0.964	2	8	negative regulation of defense response to virus	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0048009	0.182	0.964	2	8	insulin-like growth factor receptor signaling	BP	1	PIK3R1,IGFBP6	up_VSAP_EC
GO:0050864	0.182	0.983	1	36	regulation of B cell activation	BP	1	LYN	down_ACOR_EC
GO:0097164	0.182	0.983	1	44	ammonium ion metabolic process	BP	1	ACSL3	down_ACOR_EC
GO:1903829	0.182	0.984	1	91	positive regulation of cellular protein	BP	1	GPSM2	down_AFEM_EC
GO:0018130	0.182	1	1	1261	heterocycle biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0019438	0.182	1	1	1258	aromatic compound biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0007617	0.182	0.987	1	4	mating behavior	BP	1	THRB	down_VCAV_EC
GO:0010715	0.182	0.987	1	4	regulation of extracellular matrix disassembly	BP	1	DDR2	down_VCAV_EC
GO:0034331	0.182	0.987	1	4	cell junction maintenance	BP	1	RASSF8	down_VCAV_EC
GO:0072538	0.182	0.987	1	4	T-helper 17 type immune response	BP	1	LOXL3	down_VCAV_EC
GO:0072539	0.182	0.987	1	4	T-helper 17 cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0030576	0.182	0.988	1	3	Cajal body organization	BP	1	ZPR1	down_VSAP_EC
GO:0033574	0.182	0.988	1	3	response to testosterone	BP	1	MSN	down_VSAP_EC
GO:0071394	0.182	0.988	1	3	cellular response to testosterone stimulus	BP	1	MSN	down_VSAP_EC
GO:1903025	0.182	0.988	1	3	regulation of RNA polymerase II regulatory region sequence-specific	BP	1	DDIT3	down_VSAP_EC
GO:0030252	0.182	0.988	1	3	growth hormone secretion	BP	1	PTPN11	down_VSAP_EC
GO:2000138	0.182	0.991	1	2	positive regulation of cell proliferation involved in heart morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0021679	0.182	0.991	1	2	cerebellar molecular layer development	BP	1	ZNF365	up_ACOR_VSMC
GO:0021687	0.182	0.991	1	2	cerebellar molecular layer morphogenesis	BP	1	ZNF365	up_ACOR_VSMC
GO:0039692	0.182	0.991	1	2	single stranded viral RNA replication via double stranded DNA	BP	1	INPP5K	up_ACOR_VSMC
GO:0045091	0.182	0.991	1	2	regulation of single stranded viral RNA replication via double	BP	1	INPP5K	up_ACOR_VSMC
GO:1904425	0.182	0.991	1	2	negative regulation of GTP binding	BP	1	ARHGAP28	up_ACOR_VSMC
GO:0045664	0.182	0.984	1	144	regulation of neuron differentiation	BP	1	EYA1	up_AFEM_VSMC
GO:0001525	0.182	0.984	1	173	angiogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0042157	0.182	0.983	1	51	lipoprotein metabolic process	BP	1	ZDHHC16	up_APUL_EC
GO:0031640	0.182	0.988	1	3	killing of cells of other organism	BP	1	LYZ	up_VCAV_EC
GO:0044364	0.182	0.988	1	3	disruption of cells of other organism	BP	1	LYZ	up_VCAV_EC
GO:0097048	0.182	0.991	1	2	dendritic cell apoptotic process	BP	1	RAPGEF2	up_VCAV_EC
GO:2000668	0.182	0.991	1	2	regulation of dendritic cell apoptotic process	BP	1	RAPGEF2	up_VCAV_EC
GO:2000670	0.182	0.991	1	2	positive regulation of dendritic cell apoptotic	BP	1	RAPGEF2	up_VCAV_EC
GO:0033143	0.182	0.983	1	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	RNF6	up_VPOR_EC
GO:0060348	0.182	0.984	1	78	bone development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001822	0.182	0.984	1	98	kidney development	BP	1	SLIT2	up_VPUL_VSMC
GO:0060192	0.182	0.991	1	2	negative regulation of lipase activity	BP	1	ABL1	up_VSAP_EC
GO:0060510	0.182	0.991	1	2	type II pneumocyte differentiation	BP	1	NFIB	up_VSAP_EC
GO:1904528	0.182	0.991	1	2	positive regulation of microtubule binding	BP	1	ABL1	up_VSAP_EC

GO:1905553	0.182	0.991	1	2	regulation of blood vessel branching	BP	1	ABL1	up_VSAP_EC
GO:1905555	0.182	0.991	1	2	positive regulation blood vessel branching	BP	1	ABL1	up_VSAP_EC
GO:0010976	0.182	0.983	1	47	positive regulation of neuron projection	BP	1	SHOX2	up_VSAP_VSMC
GO:0048864	0.182046146	0.95836	2	29	stem cell development	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0007160	0.182070611	0.94094	3	56	cell-matrix adhesion	BP	1	ARHGAP6,ACTN2,NRP1	up_ACOR_EC
GO:0009620	0.18274514	0.98436	1	8	response to fungus	BP	1	RARRES2	up_ACOR_EC
GO:0018200	0.182864446	0.98434	1	8	peptidyl-glutamic acid modification	BP	1	AGBL5	up_ACOR_EC
GO:1902532	0.182875989	0.90197	8	204	negative regulation of intracellular signal	BP	1	NR1H4,NDRG2,DUSP26,FIGNL1,LRRC15,LRRC4,CLU,PRKCD	up_ACOR_EC
GO:0034654	0.183	0.845	113	1236	nucleobase-containing compound biosynthetic process	BP	1	ELK3,PRPSAP1,HMGB1,SREBF1,ACLY,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,HNRNPD,SREBF2,HINFP,NEDD4,RRM1,MED17,SLC29A1,MTDH,HEY1,SRRT,POLE,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,ELOVL1,PPARD,POLH,YBX3,NCL,NUP62,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,RBM14,CYC1,POLR3F,HOXA10,ERF,TCERG1,ATP5F1A,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,NUDT1,HMGN1,CCT4,SIX4,CTPS1,MED16,ENSCAFG00000017103,ATP5F1D,POLR1C,NUDT3	down_ACOR_VSMC
GO:0030154	0.183	0.854	58	1040	cell differentiation	BP	1	NOTCH2,PDGFRB,LRP1,NAB2,NDN,ANGPT1,SDC4,VASN,FBN1,GLIPR2,BMPR1A,LMO4,TRPV2,ANPEP,COL6A1,CLIP3,NUMBL,NAGLU,AKT2,TFE3,LAMA3,CLSTN1,CSPG4,SEMA3C,THY1,PEX5,TLX2,B4GALT1,GLI3,ADAMTSL4,EEF2,ZFP36L1,NCDN,RBM38,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,A2M,IRX5,UST,GLIS2,TWIST2,PRKCSH,DDR2,RDH10,GREM1,NAPEPLD,FOXO3,SOAT1,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC
GO:0043933	0.183	0.857	47	698	protein-containing complex subunit organization	BP	1	ARHGEF2,VEGFA,CELF1,SERPINH1,C1QTNF6,VASP,P4HA1,SEC24D,PTPN11,FSCN1,MZT1,DPYSL3,FBLIM1,SMARCA4,ANKRA2,SRP54,WDR1,MSN,KIF5B,PRPF3,DDX39B,BRD2,CNOT7,ACTR3,CTNNB1,CRYAB,APOE,PLOD3,BNIP3,STRAP,DDIT3,TWF1,PLEKHG2,TLN1,GSK3B,GBP5,EIF2S1,PRMT1,P3H4,CLTC,CAPG,RSL24D1,COL12A1,TNFAIP1,SEC13,MYBPC2,MID1	down_VSAP_EC
GO:0006139	0.183	0.901	11	1909	nucleobase-containing compound metabolic	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0007166	0.183	0.904	8	686	cell surface receptor signaling pathway	BP	1	BARX1,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:0051146	0.183	0.908	7	76	striated muscle cell differentiation	BP	1	ACTN1,FHL2,WDR1,NEXN,SIX4,MYBPC2,HOMER1	down_VSAP_EC
GO:0032640	0.183	0.915	6	39	tumor necrosis factor production	BP	1	TLR1,LEP,TLR3,PTPN22,APP,NOD2	up_ACOR_VSMC
GO:0048585	0.183	0.914	6	475	negative regulation of response to stimulus	BP	1	BARX1,CXHXorf57,ARHGEF2,SEMA3A,ASPN,FBP1	up_VPOR_EC
GO:0032204	0.183	0.922	5	35	regulation of telomere maintenance	BP	1	HNRNPD,AURKB,NEK2,TINF2,CCT4	down_ACOR_VSMC
GO:0045445	0.183	0.931	4	27	myoblast differentiation	BP	1	HINFP,SDC1,GREM1,PPARD	down_ACOR_VSMC
GO:0060324	0.183	0.932	4	24	face development	BP	1	RARG,RAF1,ZFAND5,MAP2K2	up_VSAP_EC
GO:0000902	0.183	0.942	3	266	cell morphogenesis	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0042552	0.183	0.942	3	30	myelination	BP	1	NAB2,AKT2,ENSCAFG00000017708	down_VCAV_EC
GO:0050729	0.183	0.942	3	25	positive regulation of inflammatory response	BP	1	SERPINE1,PTGS2,GBP5	down_VSAP_EC

GO:0048661	0.183	0.944	3	17	positive regulation of smooth muscle cell	BP	1	CALCRL,PDGFB,EDN1	up_VCAV_EC
GO:0044091	0.183	0.962	2	10	membrane biogenesis	BP	1	CAV1,EMP2	down_ACOR_VSMC
GO:0035987	0.183	0.959	2	17	endodermal cell differentiation	BP	1	COL6A1,LAMA3	down_VCAV_EC
GO:0030865	0.183	0.96	2	13	cortical cytoskeleton organization	BP	1	WDR1,TLN1	down_VSAP_EC
GO:0010604	0.183	0.966	2	919	positive regulation of macromolecule metabolic	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0071225	0.183	0.963	2	8	cellular response to muramyl dipeptide	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0007040	0.183	0.958	2	33	lysosome organization	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0030534	0.183	0.958	2	33	adult behavior	BP	1	LEP,LGI4	up_AFEM_EC
GO:0080171	0.183	0.958	2	33	lytic vacuole organization	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0090263	0.183	0.958	2	33	positive regulation of canonical Wnt signaling	BP	1	FAM53B,KANK1	up_AFEM_EC
GO:0030900	0.183	0.957	2	101	forebrain development	BP	1	HOOK3,SEMA3A	up_VPOR_EC
GO:0045730	0.183	0.963	2	8	respiratory burst	BP	1	CYBA,JCHAIN	up_VSAP_EC
GO:0009620	0.183	0.963	2	8	response to fungus	BP	1	IL17RC,MYD88	up_VSAP_EC
GO:0016525	0.183	0.983	1	38	negative regulation of angiogenesis	BP	1	SULF1	down_ACOR_EC
GO:2000181	0.183	0.983	1	38	negative regulation of blood vessel	BP	1	SULF1	down_ACOR_EC
GO:0035690	0.183	0.983	1	91	cellular response to drug	BP	1	GABPA	down_AFEM_EC
GO:0021910	0.183	0.986	1	4	smoothened signaling pathway involved in ventral spinal cord	BP	1	GLI3	down_VCAV_EC
GO:0060592	0.183	0.986	1	4	mammary gland formation	BP	1	GLI3	down_VCAV_EC
GO:0007517	0.183	0.984	1	100	muscle organ development	BP	1	CITED2	down_VPOR_EC
GO:0010889	0.183	0.988	1	3	regulation of sequestering of triglyceride	BP	1	ABHD5	down_VSAP_EC
GO:0036480	0.183	0.988	1	3	neuron intrinsic apoptotic signaling pathway in response to oxidative	BP	1	HIF1A	down_VSAP_EC
GO:1903376	0.183	0.988	1	3	regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0061762	0.183	0.988	1	3	CAMKK-AMPK signaling cascade	BP	1	HTT	down_VSAP_EC
GO:0099004	0.183	0.988	1	3	calmodulin dependent kinase signaling pathway	BP	1	HTT	down_VSAP_EC
GO:1902713	0.183	0.988	1	3	regulation of interferon-gamma secretion	BP	1	NR1H4	down_VSAP_EC
GO:2000009	0.183	0.986	1	4	negative regulation of protein localization to cell	BP	1	TAX1BP3	down_VSAP_EC
GO:0042711	0.183	0.991	1	2	maternal behavior	BP	1	CREBRF	up_ACOR_VSMC
GO:0045349	0.183	0.991	1	2	interferon-alpha biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0045354	0.183	0.991	1	2	regulation of interferon-alpha biosynthetic	BP	1	TLR3	up_ACOR_VSMC
GO:0060746	0.183	0.991	1	2	parental behavior	BP	1	CREBRF	up_ACOR_VSMC
GO:1902308	0.183	0.991	1	2	regulation of peptidyl-serine dephosphorylation	BP	1	DUSP26	up_ACOR_VSMC
GO:2000147	0.183	0.984	1	169	positive regulation of cell motility	BP	1	WNT7A	up_AORT_VSMC
GO:0050663	0.183	0.983	1	52	cytokine secretion	BP	1	NR1H4	up_APUL_EC
GO:0090257	0.183	0.983	1	52	regulation of muscle system process	BP	1	NPNT	up_APUL_EC
GO:0038093	0.183	0.991	1	2	Fc receptor signaling pathway	BP	1	KIT	up_VCAV_EC
GO:0071417	0.183	0.984	1	142	cellular response to organonitrogen	BP	1	CA2	up_VCAV_VSMC
GO:0008202	0.183	0.983	1	80	steroid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:1902107	0.183	0.983	1	47	positive regulation of leukocyte differentiation	BP	1	TOX	up_VFEM_EC

GO:0007517	0.183	0.983	1	100	muscle organ development	BP	1	TBX5	up_VPUL_VSMC
GO:0019085	0.183	0.991	1	2	early viral transcription	BP	1	MON1B	up_VSAP_EC
GO:0019086	0.183	0.991	1	2	late viral transcription	BP	1	MON1B	up_VSAP_EC
GO:0043490	0.183	0.991	1	2	malate-aspartate shuttle	BP	1	SLC25A12	up_VSAP_EC
GO:0051775	0.183	0.991	1	2	response to redox state	BP	1	NPAS2	up_VSAP_EC
GO:0015846	0.183	0.991	1	2	polyamine transport	BP	1	AZIN2	up_VSAP_EC
GO:1902047	0.183	0.991	1	2	polyamine transmembrane transport	BP	1	AZIN2	up_VSAP_EC
GO:1902267	0.183	0.991	1	2	regulation of polyamine transmembrane transport	BP	1	AZIN2	up_VSAP_EC
GO:1902269	0.183	0.991	1	2	positive regulation of polyamine	BP	1	AZIN2	up_VSAP_EC
GO:2000650	0.183	0.991	1	2	negative regulation of sodium ion transmembrane	BP	1	OSR1	up_VSAP_EC
GO:0061351	0.183	0.983	1	50	neural precursor cell proliferation	BP	1	EMX2	up_VSAP_VSMC
GO:0051092	0.183	0.983	1	47	positive regulation of NF-kappaB transcription	BP	1	TLR2	up_VSAP_VSMC
GO:0031347	0.183230072	0.91211	6	144	regulation of defense response	BP	1	NR1H4,FNDC4,NOD2,IL33,PTGER4,MAVS	up_ACOR_EC
GO:0032269	0.183937567	0.89082	11	306	negative regulation of cellular protein metabolic	BP	1	PKIB,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,CST3,LRRC15,LRRC4,PRKCD,DBNDD2	up_ACOR_EC
GO:0010468	0.184	0.904	9	1270	regulation of gene expression	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,NEDD4	down_ACOR_EC
GO:0048754	0.184	0.903	8	57	branching morphogenesis of an epithelial tube	BP	1	BMP4,FGFR2,CLSTN1,NRP1,NPNT,TBX20,DAG1,EDN1	up_ACOR_VSMC
GO:0071383	0.184	0.903	8	58	cellular response to steroid hormone stimulus	BP	1	FAM107A,PPARGC1B,ZFP36L1,CREBRF,PRMT2,ZFP36L2,LBH,DDIT4	up_VSAP_EC
GO:0002706	0.184	0.921	5	35	regulation of lymphocyte mediated immunity	BP	1	IL7R,GATA3,NECTIN2,THOC1,HMGB1	up_VCAV_EC
GO:0010906	0.184	0.929	4	38	regulation of glucose metabolic process	BP	1	ENPP1,SESN2,SLC45A3,PTPN2	down_VSAP_EC
GO:2000145	0.184	0.928	4	279	regulation of cell motility	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0072132	0.184	0.931	4	23	mesenchyme morphogenesis	BP	1	WNT11,OSR1,ACVRL1,TGFBR2	up_VSAP_EC
GO:0040007	0.184	0.941	3	276	growth	BP	1	ACVRL1,SPG11,NRP2	down_ACOR_EC
GO:0071333	0.184	0.942	3	25	cellular response to glucose stimulus	BP	1	NR1H4,SMARCA4,HIF1A	down_VSAP_EC
GO:0007589	0.184	0.944	3	16	body fluid secretion	BP	1	GJA1,PRKCE,EDN1	up_ACOR_VSMC
GO:0060079	0.184	0.945	3	15	excitatory postsynaptic potential	BP	1	RELN,MEF2C,PPP3CA	up_VCAV_EC
GO:0002521	0.184	0.957	2	149	leukocyte differentiation	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0043277	0.184	0.962	2	9	apoptotic cell clearance	BP	1	HMGB1,JMJD6	down_ACOR_VSMC
GO:0045103	0.184	0.963	2	8	intermediate filament-based process	BP	1	DES,CLN8	up_ACOR_VSMC
GO:0045104	0.184	0.963	2	8	intermediate filament cytoskeleton organization	BP	1	DES,CLN8	up_ACOR_VSMC
GO:0072078	0.184	0.957	2	33	nephron tubule morphogenesis	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0007267	0.184	0.959	2	332	cell-cell signaling	BP	1	DKK2,LNPEP	up_AORT_EC
GO:0031175	0.184	0.958	2	224	neuron projection development	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0044854	0.184	0.988	1	3	plasma membrane raft assembly	BP	1	CAV1	down_ACOR_VSMC
GO:0044857	0.184	0.988	1	3	plasma membrane raft organization	BP	1	CAV1	down_ACOR_VSMC
GO:0006631	0.184	0.983	1	93	fatty acid metabolic process	BP	1	ETFA	down_AFEM_EC
GO:0010468	0.184	1	1	1270	regulation of gene expression	BP	1	GATA5	down_AFEM_VSMC
GO:0060033	0.184	0.986	1	4	anatomical structure regression	BP	1	BMPR1A	down_VCAV_EC
GO:0033578	0.184	0.986	1	4	protein glycosylation in Golgi	BP	1	FUT8	down_VCAV_EC
GO:1902176	0.184	0.986	1	4	negative regulation of oxidative stress-induced intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC

GO:0030202	0.184	0.988	1	3	heparin metabolic process	BP	1	ENSCAFG00000032470	down_VSAP_EC
GO:0006883	0.184	0.991	1	2	cellular sodium ion homeostasis	BP	1	SLC8A1	up_ACOR_VSMC
GO:0060684	0.184	0.991	1	2	epithelial-mesenchymal cell signaling	BP	1	BMP4	up_ACOR_VSMC
GO:0098735	0.184	0.991	1	2	positive regulation of the force of heart contraction	BP	1	SLC8A1	up_ACOR_VSMC
GO:1901301	0.184	0.991	1	2	regulation of cargo loading into COPII-coated	BP	1	SEC24B	up_ACOR_VSMC
GO:1905879	0.184	0.991	1	2	regulation of oogenesis	BP	1	PDE5A	up_ACOR_VSMC
GO:2000554	0.184	0.991	1	2	regulation of T-helper 1 cell cytokine production	BP	1	IL18R1	up_ACOR_VSMC
GO:2000556	0.184	0.991	1	2	positive regulation of T-helper 1 cell cytokine	BP	1	IL18R1	up_ACOR_VSMC
GO:0021814	0.184	0.991	1	2	cell motility involved in cerebral cortex radial glia	BP	1	SUN1	up_ACOR_VSMC
GO:0021815	0.184	0.991	1	2	modulation of microtubule cytoskeleton involved in cerebral	BP	1	SUN1	up_ACOR_VSMC
GO:0034165	0.184	0.991	1	2	positive regulation of toll-like receptor 9 signaling	BP	1	PTPN22	up_ACOR_VSMC
GO:0060281	0.184	0.991	1	2	regulation of oocyte development	BP	1	PDE5A	up_ACOR_VSMC
GO:0140074	0.184	0.991	1	2	cardiac endothelial to mesenchymal transition	BP	1	GATA5	up_ACOR_VSMC
GO:2000051	0.184	0.991	1	2	negative regulation of non-canonical Wnt signaling	BP	1	ZNRF3	up_ACOR_VSMC
GO:0050778	0.184	0.984	1	141	positive regulation of immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0051272	0.184	0.984	1	170	positive regulation of cellular component	BP	1	WNT7A	up_AORT_VSMC
GO:0002537	0.184	0.991	1	2	nitric oxide production involved in inflammatory	BP	1	TLR4	up_VCAV_EC
GO:0030213	0.184	0.988	1	3	hyaluronan biosynthetic process	BP	1	PDGFB	up_VCAV_EC
GO:0002138	0.184	0.988	1	3	retinoic acid biosynthetic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0072110	0.184	0.988	1	3	glomerular mesangial cell proliferation	BP	1	PDGFB	up_VCAV_EC
GO:0072124	0.184	0.988	1	3	regulation of glomerular mesangial cell	BP	1	PDGFB	up_VCAV_EC
GO:0090192	0.184	0.988	1	3	regulation of glomerulus development	BP	1	PDGFB	up_VCAV_EC
GO:0009756	0.184	0.991	1	2	carbohydrate mediated signaling	BP	1	SMARCA4	up_VCAV_EC
GO:0009757	0.184	0.991	1	2	hexose mediated signaling	BP	1	SMARCA4	up_VCAV_EC
GO:0010182	0.184	0.991	1	2	sugar mediated signaling pathway	BP	1	SMARCA4	up_VCAV_EC
GO:0010255	0.184	0.991	1	2	glucose mediated signaling pathway	BP	1	SMARCA4	up_VCAV_EC
GO:0016102	0.184	0.988	1	3	diterpenoid biosynthetic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0016114	0.184	0.988	1	3	terpenoid biosynthetic process	BP	1	ALDH1A3	up_VCAV_EC
GO:1902659	0.184	0.991	1	2	regulation of glucose mediated signaling	BP	1	SMARCA4	up_VCAV_EC
GO:1902661	0.184	0.991	1	2	positive regulation of glucose mediated	BP	1	SMARCA4	up_VCAV_EC
GO:1902725	0.184	0.991	1	2	negative regulation of satellite cell	BP	1	EPHB1	up_VCAV_EC
GO:0034333	0.184	0.983	1	25	adherens junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0072525	0.184	0.983	1	24	pyridine-containing compound biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0001837	0.184	0.983	1	48	epithelial to mesenchymal transition	BP	1	TIAM1	up_VFEM_EC
GO:0007219	0.184	0.983	1	59	Notch signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0048706	0.184	0.983	1	59	embryonic skeletal system development	BP	1	HOXA3	up_VPUL_EC
GO:0098542	0.184	0.983	1	100	defense response to other organism	BP	1	IL22RA1	up_VPUL_VSMC
GO:0001957	0.184	0.991	1	2	intramembranous ossification	BP	1	AXIN2	up_VSAP_EC
GO:0002246	0.184	0.991	1	2	wound healing involved in inflammatory response	BP	1	HMOX1	up_VSAP_EC

GO:0003383	0.184	0.991	1	2	apical constriction	BP	1	FRMD6	up_VSAP_EC
GO:0030174	0.184	0.991	1	2	regulation of DNA-dependent DNA	BP	1	CIZ1	up_VSAP_EC
GO:0032298	0.184	0.991	1	2	positive regulation of DNA-dependent DNA replication initiation	BP	1	CIZ1	up_VSAP_EC
GO:0032423	0.184	0.991	1	2	regulation of mismatch repair	BP	1	AXIN2	up_VSAP_EC
GO:0032571	0.184	0.991	1	2	response to vitamin K	BP	1	BGLAP	up_VSAP_EC
GO:0035771	0.184	0.991	1	2	interleukin-4-mediated signaling pathway	BP	1	STAT6	up_VSAP_EC
GO:0036072	0.184	0.991	1	2	direct ossification	BP	1	AXIN2	up_VSAP_EC
GO:0061181	0.184	0.991	1	2	regulation of chondrocyte development	BP	1	AXIN2	up_VSAP_EC
GO:0072162	0.184	0.991	1	2	metanephric mesenchymal cell	BP	1	OSR1	up_VSAP_EC
GO:0072183	0.184	0.991	1	2	negative regulation of nephron tubule epithelial cell differentiation	BP	1	OSR1	up_VSAP_EC
GO:0090269	0.184	0.991	1	2	fibroblast growth factor production	BP	1	WNT11	up_VSAP_EC
GO:0090270	0.184	0.991	1	2	regulation of fibroblast growth factor production	BP	1	WNT11	up_VSAP_EC
GO:0090272	0.184	0.991	1	2	negative regulation of fibroblast growth factor	BP	1	WNT11	up_VSAP_EC
GO:0090594	0.184	0.991	1	2	inflammatory response to wounding	BP	1	HMOX1	up_VSAP_EC
GO:0099093	0.184	0.991	1	2	calcium export from the mitochondrion	BP	1	SLC8B1	up_VSAP_EC
GO:1900063	0.184	0.991	1	2	regulation of peroxisome organization	BP	1	MAVS	up_VSAP_EC
GO:0034250	0.184	0.983	1	45	positive regulation of cellular amide metabolic	BP	1	PRR16	up_VSAP_VSMC
GO:0010605	0.185	0.849	70	745	negative regulation of macromolecule metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,HNRNPD,SREBF2,SMC1A,NEDD4,U2AF2,SLC29A1,MTDH,PPP1R15B,PARPBP,SRRT,NAB2,SLC35C2,RAN,BIRC5,CAV1,TIMELESS,THRAP3,FAM129B,NF2,EDC4,AURKB,CDKN2C,EZH2,GREM1,SMARCC1,RNASEH2B,PLK3,HOXA7,SMG9,UHRF1,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,PPARD,YWHAB,NCL,NUP62,SUV39H1,CACTIN,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,ENSCAFG00000015189,HAT1,HIST2H2AC,TINF2,H2AFX,EXOSC5,SIX4,ANXA7	down_ACOR_VSMC
GO:0032940	0.185	0.9	8	231	secretion by cell	BP	1	LEP,KCNC4,CRY2,GPAM,CHRM2,CAMK2A,RAB7A,CCL5	up_AFEM_EC
GO:0030595	0.185	0.903	8	57	leukocyte chemotaxis	BP	1	ARHGEF5,C5AR2,SLC8B1,SLIT2,IL17RC,HSD3B7,F2RL1,ZNF580	up_VSAP_EC
GO:0043412	0.185	0.912	7	1225	macromolecule modification	BP	1	NR1H4,MAPK10,PLCL1,GALNT17,ZDHHC16,NPNT,NTRK2	up_APUL_EC
GO:0030301	0.185	0.93	4	27	cholesterol transport	BP	1	SREBF2,LIMA1,LIPC,NUS1	down_ACOR_VSMC
GO:0015918	0.185	0.93	4	27	sterol transport	BP	1	SREBF2,LIMA1,LIPC,NUS1	down_ACOR_VSMC
GO:0051928	0.185	0.93	4	28	positive regulation of calcium ion transport	BP	1	PDGFB,STC1,APLNR,PLCG2	up_VCAV_EC
GO:0009628	0.185	0.941	3	302	response to abiotic stimulus	BP	1	USP28,HOXA1,NEDD4	down_ACOR_EC
GO:0032272	0.185	0.943	3	18	negative regulation of protein polymerization	BP	1	TMOD1,STMN1,TMOD3	up_VCAV_EC
GO:0008219	0.185	0.943	3	611	cell death	BP	1	CHL1,NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0048584	0.185	0.943	3	592	positive regulation of response to stimulus	BP	1	EYA1,NETO1,SHOX2	up_VFEM_VSMC
GO:0002682	0.185	0.941	3	343	regulation of immune system process	BP	1	HOXA9,TLR2,CAV1	up_VSAP_VSMC
GO:0043170	0.185	1	2	2980	macromolecule metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0099072	0.185	0.962	2	8	regulation of postsynaptic membrane neurotransmitter	BP	1	DAG1,AP2B1	up_ACOR_VSMC
GO:0001959	0.185	0.957	2	33	regulation of cytokine-mediated signaling	BP	1	CYLD,ADAM17	up_AFEM_EC
GO:0050796	0.185	0.957	2	33	regulation of insulin secretion	BP	1	LEP,CCL5	up_AFEM_EC

GO:0051592	0.185	0.957	2	33	response to calcium ion	BP	1	CPNE7,ANXA11	up_AFEM_EC
GO:0006952	0.185	0.958	2	319	defense response	BP	1	CYP26B1,C3AR1	up_VPOR_VSMC
GO:0046474	0.185	0.983	1	44	glycerophospholipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0002091	0.185	0.986	1	4	negative regulation of receptor internalization	BP	1	LRPAP1	down_VCAV_EC
GO:0046337	0.185	0.986	1	4	phosphatidylethanolamine metabolic process	BP	1	NAPEPLD	down_VCAV_EC
GO:0061158	0.185	0.986	1	4	3'-UTR-mediated mRNA destabilization	BP	1	ZFP36L1	down_VCAV_EC
GO:0006887	0.185	0.983	1	99	exocytosis	BP	1	RAB11B	down_VPOR_EC
GO:0005513	0.185	0.986	1	4	detection of calcium ion	BP	1	CALM1	down_VSAP_EC
GO:0032792	0.185	0.988	1	3	negative regulation of CREB transcription factor	BP	1	DDIT3	down_VSAP_EC
GO:0002836	0.185	0.986	1	4	positive regulation of response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:0002839	0.185	0.986	1	4	positive regulation of immune response to	BP	1	PVR	down_VSAP_EC
GO:0001957	0.185	0.991	1	2	intramembranous ossification	BP	1	FGF18	up_ACOR_VSMC
GO:0060523	0.185	0.991	1	2	prostate epithelial cord elongation	BP	1	FGFR2	up_ACOR_VSMC
GO:0060615	0.185	0.991	1	2	mammary gland bud formation	BP	1	FGFR2	up_ACOR_VSMC
GO:0060664	0.185	0.991	1	2	epithelial cell proliferation involved in salivary gland morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0060667	0.185	0.991	1	2	branch elongation involved in salivary gland	BP	1	FGFR2	up_ACOR_VSMC
GO:1904849	0.185	0.991	1	2	positive regulation of cell chemotaxis to fibroblast growth factor	BP	1	FGF18	up_ACOR_VSMC
GO:2000546	0.185	0.991	1	2	positive regulation of endothelial cell chemotaxis to fibroblast	BP	1	FGF18	up_ACOR_VSMC
GO:0036072	0.185	0.991	1	2	direct ossification	BP	1	FGF18	up_ACOR_VSMC
GO:0042045	0.185	0.991	1	2	epithelial fluid transport	BP	1	ITPR1	up_ACOR_VSMC
GO:0051595	0.185	0.991	1	2	response to methylglyoxal	BP	1	PARK7	up_ACOR_VSMC
GO:0060595	0.185	0.991	1	2	fibroblast growth factor receptor signaling pathway involved in	BP	1	FGFR2	up_ACOR_VSMC
GO:0060648	0.185	0.991	1	2	mammary gland bud morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0060915	0.185	0.991	1	2	mesenchymal cell differentiation involved in	BP	1	FGFR2	up_ACOR_VSMC
GO:0045017	0.185	0.983	1	52	glycerolipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0048592	0.185	0.983	1	53	eye morphogenesis	BP	1	NTRK2	up_APUL_EC
GO:0048022	0.185	0.991	1	2	negative regulation of melanin biosynthetic	BP	1	RAPGEF2	up_VCAV_EC
GO:1900377	0.185	0.991	1	2	negative regulation of secondary metabolite	BP	1	RAPGEF2	up_VCAV_EC
GO:0071605	0.185	0.988	1	3	monocyte chemotactic protein-1 production	BP	1	APOD	up_VCAV_EC
GO:0071637	0.185	0.988	1	3	regulation of monocyte chemotactic protein-1	BP	1	APOD	up_VCAV_EC
GO:0071638	0.185	0.988	1	3	negative regulation of monocyte chemotactic	BP	1	APOD	up_VCAV_EC
GO:0097114	0.185	0.991	1	2	NMDA glutamate receptor clustering	BP	1	RELN	up_VCAV_EC
GO:0050778	0.185	0.983	1	141	positive regulation of immune response	BP	1	C6	up_VCAV_VSMC
GO:0051289	0.185	0.983	1	25	protein homotetramerization	BP	1	FBP1	up_VPOR_EC
GO:0071229	0.185	0.983	1	51	cellular response to acid chemical	BP	1	CYP26B1	up_VFEM_EC
GO:0097191	0.185	0.983	1	79	extrinsic apoptotic signaling pathway	BP	1	EYA1	up_VFEM_VSMC
GO:0001558	0.185	0.983	1	101	regulation of cell growth	BP	1	SLIT2	up_VPUL_VSMC
GO:0008611	0.185	0.991	1	2	ether lipid biosynthetic process	BP	1	PEX7	up_VSAP_EC

GO:0010226	0.185	0.991	1	2	response to lithium ion	BP	1	CDH1	up_VSAP_EC
GO:0032825	0.185	0.991	1	2	positive regulation of natural killer cell	BP	1	TOX	up_VSAP_EC
GO:0034154	0.185	0.991	1	2	toll-like receptor 7 signaling pathway	BP	1	UNC93B1	up_VSAP_EC
GO:0034398	0.185	0.991	1	2	telomere tethering at nuclear periphery	BP	1	NUP98	up_VSAP_EC
GO:0034454	0.185	0.991	1	2	microtubule anchoring at centrosome	BP	1	CEP19	up_VSAP_EC
GO:0046504	0.185	0.991	1	2	glycerol ether biosynthetic process	BP	1	PEX7	up_VSAP_EC
GO:0060844	0.185	0.991	1	2	arterial endothelial cell fate commitment	BP	1	DLL1	up_VSAP_EC
GO:0060846	0.185	0.991	1	2	blood vessel endothelial cell fate commitment	BP	1	DLL1	up_VSAP_EC
GO:0060847	0.185	0.991	1	2	endothelial cell fate specification	BP	1	DLL1	up_VSAP_EC
GO:0071285	0.185	0.991	1	2	cellular response to lithium ion	BP	1	CDH1	up_VSAP_EC
GO:0097101	0.185	0.991	1	2	blood vessel endothelial cell fate specification	BP	1	DLL1	up_VSAP_EC
GO:0098779	0.185	0.991	1	2	positive regulation of mitophagy in response to mitochondrial	BP	1	MFN2	up_VSAP_EC
GO:0098885	0.185	0.991	1	2	modification of postsynaptic actin	BP	1	WASF3	up_VSAP_EC
GO:1901503	0.185	0.991	1	2	ether biosynthetic process	BP	1	PEX7	up_VSAP_EC
GO:1901526	0.185	0.991	1	2	positive regulation of mitophagy	BP	1	MFN2	up_VSAP_EC
GO:1905288	0.185	0.991	1	2	vascular associated smooth muscle cell	BP	1	MFN2	up_VSAP_EC
GO:1905459	0.185	0.991	1	2	regulation of vascular associated smooth muscle cell apoptotic process	BP	1	MFN2	up_VSAP_EC
GO:1905461	0.185	0.991	1	2	positive regulation of vascular associated smooth muscle cell	BP	1	MFN2	up_VSAP_EC
GO:0009411	0.185055117	0.93953	3	56	response to UV	BP	1	BRSK1,AQP1,MFAP4	up_ACOR_EC
GO:1901889	0.1851351	0.98393	1	8	negative regulation of cell junction assembly	BP	1	ARHGAP6	up_ACOR_EC
GO:0048009	0.185507446	0.98386	1	8	insulin-like growth factor receptor signaling	BP	1	CDH3	up_ACOR_EC
GO:0016043	0.185920323	0.85443	58	1973	cellular component organization	BP	1	CNTNAP4,SH3TC2,MYOZ2,FMOD,NR1H4,TMOD1,BRSK1,TRPS1,KCTD12,PKIB,CALY,SOX9,RHOU,ARHGAP6,PHF20,ATG16L2,AQP1,SYNPO2,KCNB1,FZD5,IFI6,DIXDC1,PDLIM3,RGMA,SMAD6,PLS1,ACTN2,ZMYND8,ARHGAP28,ESM1,PAK3,PTGER4,ARHGDIB,ELMO2,PREB,DCLK2,ADAMTSL2,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,LRRC4,CLU,CHMP4B,TP53INP2,VPS16,RIOX2,NRP1,AZIN2,ARHGEF26,PRKCD,PYGO2,DBNDD2,ENSCAFG00000010493,MFAP4,TUBB4A	up_ACOR_EC
GO:1901700	0.186	0.857	40	364	response to oxygen-containing compound	BP	1	HNF4A,PTGFR,PPARGC1B,SLIT2,CDH1,ABL1,GOT1,CHRM1,SESN1,OSR1,MAP3K5,PDGFD,KLF15,RARG,MGST1,STAT5A,RAB11B,LPL,PDK2,ZFP36L1,PIK3R1,ZEB1,TBXA2R,ABAT,SASH1,MYD88,CASTOR1,KCNB1,OSBPL7,RAF1,ZNF580,NCOA2,STX4,HTRA2,PPP3CB,NCK1,BGLAP,TGFBR2,DDIT4,RAB11FIP2	up_VSAP_EC
GO:0033993	0.186	0.871	22	186	response to lipid	BP	1	PLCG2,LBH,SKP2,PRKAA2,BMP4,ABCA1,MED14,AR,PTGIR,SASH1,FAM210B,ADCY6,ANKRD1,CREBRF,PTGDR,PRKCE,NR3C1,NOD2,FAM107A,DDIT4,TNFRSF11B,PARK7	up_ACOR_VSMC
GO:0030182	0.186	0.872	20	327	neuron differentiation	BP	1	NDN,SDC4,LMO4,TRPV2,NUMBL,NAGLU,SEMA3C,THY1,PEX5,TLX2,GLI3,NCDN,GSDME,ENSCAFG00000017708,IRX5,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0034762	0.186	0.885	13	122	regulation of transmembrane transport	BP	1	RELN,PDE4D,MEF2C,CHD7,EDN1,APLNR,CTTNBP2NL,YES1,RSC1A1,KCNJ3,KCNJ2,PLCG2,RIPK1	up_VCAV_EC
GO:0050804	0.186	0.894	10	87	modulation of chemical synaptic transmission	BP	1	EPHB1,PLK2,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,GRM8	up_VCAV_EC
GO:0099177	0.186	0.894	10	87	regulation of trans-synaptic signaling	BP	1	EPHB1,PLK2,RELN,MEF2C,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,GRM8	up_VCAV_EC
GO:0010721	0.186	0.898	9	73	negative regulation of cell development	BP	1	EDNRB,IFRD1,PPP3CA,HOOK3,HMG20A,JAG1,RAPGEF2,CTNNA1,TJP2	up_VCAV_EC

GO:0045931	0.186	0.912	6	49	positive regulation of mitotic cell cycle	BP	1	PDGFB,EDN1,RAB11A,SMC5,CUL4A,TMOD3	up_VCAV_EC
GO:0014020	0.186	0.913	6	41	primary neural tube formation	BP	1	FZD1,ABL1,FUZ,RARG,KDM2B,CITED2	up_VSAP_EC
GO:0050921	0.186	0.928	4	39	positive regulation of chemotaxis	BP	1	VEGFA,SERPINE1,ADAM17,NRP1	down_VSAP_EC
GO:0035282	0.186	0.94	3	30	segmentation	BP	1	BMPR1A,SEMA3C,PCSK6	down_VCAV_EC
GO:0009653	0.186	0.944	3	773	anatomical structure morphogenesis	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0001736	0.186	0.941	3	23	establishment of planar polarity	BP	1	PTK7,EXOC5,WDR1	down_VSAP_EC
GO:0007164	0.186	0.941	3	23	establishment of tissue polarity	BP	1	PTK7,EXOC5,WDR1	down_VSAP_EC
GO:0032228	0.186	0.962	2	8	regulation of synaptic transmission, GABAergic	BP	1	PLCL1,PRKCE	up_ACOR_VSMC
GO:0008593	0.186	0.957	2	33	regulation of Notch signaling pathway	BP	1	DLL1,POSTN	up_AFEM_EC
GO:0031114	0.186	0.961	2	9	regulation of microtubule depolymerization	BP	1	TAOK1,ARHGEF2	up_VCAV_EC
GO:0045063	0.186	0.961	2	9	T-helper 1 cell differentiation	BP	1	MTOR,HMGB1	up_VCAV_EC
GO:0045596	0.186	0.957	2	186	negative regulation of cell differentiation	BP	1	HOXA9,HOXA7	up_VFEM_EC
GO:0043436	0.186	0.958	2	303	oxoacid metabolic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0071346	0.186	0.983	1	41	cellular response to interferon-gamma	BP	1	STX4	down_ACOR_EC
GO:0017015	0.186	0.983	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	ASPN	down_ACOR_EC
GO:1903844	0.186	0.983	1	40	regulation of cellular response to transforming growth factor beta	BP	1	ASPN	down_ACOR_EC
GO:1990535	0.186	0.986	1	4	neuron projection maintenance	BP	1	PRNP	down_VCAV_EC
GO:0007351	0.186	0.986	1	4	tripartite regional subdivision	BP	1	PCSK6	down_VCAV_EC
GO:0008595	0.186	0.986	1	4	anterior/posterior axis specification, embryo	BP	1	PCSK6	down_VCAV_EC
GO:0046321	0.186	0.986	1	4	positive regulation of fatty acid oxidation	BP	1	AKT2	down_VCAV_EC
GO:0060340	0.186	0.986	1	4	positive regulation of type I interferon-mediated signaling pathway	BP	1	MAVS	down_VCAV_EC
GO:0042325	0.186	0.987	1	463	regulation of phosphorylation	BP	1	PLCL1	down_VFEM_EC
GO:0010457	0.186	0.987	1	3	centriole-centriole cohesion	BP	1	CTNNB1	down_VSAP_EC
GO:0045686	0.186	0.987	1	3	negative regulation of glial cell differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0097049	0.186	0.987	1	3	motor neuron apoptotic process	BP	1	ZPR1	down_VSAP_EC
GO:0042730	0.186	0.987	1	3	fibrinolysis	BP	1	SERPINE1	down_VSAP_EC
GO:0051917	0.186	0.987	1	3	regulation of fibrinolysis	BP	1	SERPINE1	down_VSAP_EC
GO:0060307	0.186	0.986	1	4	regulation of ventricular cardiac muscle cell membrane repolarization	BP	1	WDR1	down_VSAP_EC
GO:0072497	0.186	0.987	1	3	mesenchymal stem cell differentiation	BP	1	REST	down_VSAP_EC
GO:0099622	0.186	0.986	1	4	cardiac muscle cell membrane repolarization	BP	1	WDR1	down_VSAP_EC
GO:0099623	0.186	0.986	1	4	regulation of cardiac muscle cell membrane	BP	1	WDR1	down_VSAP_EC
GO:0099625	0.186	0.986	1	4	ventricular cardiac muscle cell membrane	BP	1	WDR1	down_VSAP_EC
GO:0055086	0.186	0.985	1	237	nucleobase-containing small molecule metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0006556	0.186	0.99	1	2	S-adenosylmethionine biosynthetic process	BP	1	MAT2B	up_ACOR_VSMC
GO:0001743	0.186	0.99	1	2	optic placode formation	BP	1	FRS2	up_ACOR_VSMC
GO:0061312	0.186	0.99	1	2	BMP signaling pathway involved in heart	BP	1	BMP4	up_ACOR_VSMC
GO:0014826	0.186	0.99	1	2	vein smooth muscle contraction	BP	1	EDN1	up_ACOR_VSMC
GO:0046619	0.186	0.99	1	2	optic placode formation involved in camera-type	BP	1	FRS2	up_ACOR_VSMC

GO:1905114	0.186	0.983	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	TLR2	up_AFEM_VSMC
GO:0043543	0.186	0.983	1	84	protein acylation	BP	1	TAOK1	up_AORT_EC
GO:0014070	0.186	0.984	1	172	response to organic cyclic compound	BP	1	ESR1	up_AORT_VSMC
GO:0010001	0.186	0.983	1	54	glial cell differentiation	BP	1	NTRK2	up_APUL_EC
GO:0051924	0.186	0.982	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_APUL_EC
GO:0060211	0.186	0.99	1	2	regulation of nuclear-transcribed mRNA poly(A)	BP	1	CNOT7	up_VCAV_EC
GO:0060213	0.186	0.99	1	2	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	BP	1	CNOT7	up_VCAV_EC
GO:0045664	0.186	0.983	1	144	regulation of neuron differentiation	BP	1	LIMK1	up_VCAV_VSMC
GO:0006641	0.186	0.982	1	25	triglyceride metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0007044	0.186	0.982	1	27	cell-substrate junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0034637	0.186	0.983	1	25	cellular carbohydrate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:1902105	0.186	0.983	1	80	regulation of leukocyte differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0140013	0.186	0.982	1	50	meiotic nuclear division	BP	1	CYP26B1	up_VFEM_EC
GO:0010959	0.186	0.983	1	79	regulation of metal ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0090596	0.186	0.983	1	84	sensory organ morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0030833	0.186	0.983	1	59	regulation of actin filament polymerization	BP	1	CCL24	up_VPUL_EC
GO:0060560	0.186	0.983	1	58	developmental growth involved in	BP	1	FLRT3	up_VPUL_EC
GO:2001236	0.186	0.983	1	59	regulation of extrinsic apoptotic signaling	BP	1	ARHGEF2	up_VPUL_EC
GO:0003186	0.186	0.99	1	2	tricuspid valve morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0021679	0.186	0.99	1	2	cerebellar molecular layer development	BP	1	DLL1	up_VSAP_EC
GO:0021687	0.186	0.99	1	2	cerebellar molecular layer morphogenesis	BP	1	DLL1	up_VSAP_EC
GO:0021692	0.186	0.99	1	2	cerebellar Purkinje cell layer morphogenesis	BP	1	DLL1	up_VSAP_EC
GO:0042711	0.186	0.99	1	2	maternal behavior	BP	1	CREBRF	up_VSAP_EC
GO:0045607	0.186	0.99	1	2	regulation of inner ear auditory receptor cell	BP	1	DLL1	up_VSAP_EC
GO:0045631	0.186	0.99	1	2	regulation of mechanoreceptor	BP	1	DLL1	up_VSAP_EC
GO:0060746	0.186	0.99	1	2	parental behavior	BP	1	CREBRF	up_VSAP_EC
GO:2000980	0.186	0.99	1	2	regulation of inner ear receptor cell	BP	1	DLL1	up_VSAP_EC
GO:2001179	0.186	0.99	1	2	regulation of interleukin-10 secretion	BP	1	CD274	up_VSAP_EC
GO:2001181	0.186	0.99	1	2	positive regulation of interleukin-10 secretion	BP	1	CD274	up_VSAP_EC
GO:0072014	0.186	0.99	1	2	proximal tubule development	BP	1	DLL1	up_VSAP_EC
GO:0008361	0.186	0.982	1	50	regulation of cell size	BP	1	PRR16	up_VSAP_VSMC
GO:0055001	0.186	0.982	1	47	muscle cell development	BP	1	SHOX2	up_VSAP_VSMC
GO:0034613	0.186169763	0.87406	19	576	cellular protein localization	BP	1	SH3TC2,KCNB1,EDEM2,AGRN,PLS1,ACTN2,TRIM8,PREB,DCLK2,MAVS,LRRC15,LRP4,LRRC4,CHMP4B,TP53INP2,VPS16,NRP1,HM13,PRKCD	up_ACOR_EC
GO:0050803	0.186236989	0.93899	3	55	regulation of synapse structure or activity	BP	1	CNTNAP4,LRP4,LRRC4	up_ACOR_EC
GO:0050807	0.186236989	0.93899	3	55	regulation of synapse organization	BP	1	CNTNAP4,LRP4,LRRC4	up_ACOR_EC
GO:1903670	0.186371282	0.95668	2	30	regulation of sprouting angiogenesis	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0072171	0.1864265	0.95666	2	30	mesonephric tubule morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0090596	0.186582105	0.9264	4	84	sensory organ morphogenesis	BP	1	SOX9,AQP1,FZD5,EFEMP1	up_ACOR_EC

GO:0048638	0.186838479	0.9263	4	82	regulation of developmental growth	BP	1	PLS1,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0008284	0.187	0.865	27	238	positive regulation of cell proliferation	BP	1	VEGFD,LEP,LBH,CDC7,HTR2B,BMP4,FGFR2,MARCKSL1,AR,FGF18,PLAC8B,CDKN1A,PTPN22,SMARCD3,TBX20,TBX5,FZD3,CCPG1,TGFBR1,DDR2,FOSL2,EDN1,DISC1,RPRD1B,WDR48,RREB1,CRKL	up_ACOR_VSMC
GO:0010243	0.187	0.866	25	238	response to organonitrogen compound	BP	1	TNFAIP3,PPARG,P2RX7,BAIAP2L1,SELL,PDE4D,MEF2C,RAPGEF1,TLR4,MTOR,ABCA1,MAPK13,NCK1,TIMELESS,JAG1,RAPGEF2,CREB1,CTNNA1,BLM,USP13,PDGFD,NR4A1,P2RX2,ZEB1,ARHGEF2	up_VCAV_EC
GO:1902532	0.187	0.871	21	204	negative regulation of intracellular signal transduction	BP	1	TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,APLNR,ARAP3,HOMER3,FIGNL1,CASP8,MTOR,PREX2,RIOK3,STMN1,PTGS2,RIPK1,HIF1A,TNFAIP1,IVNS1ABP,ARHGEF2	up_VCAV_EC
GO:0016192	0.187	0.881	14	452	vesicle-mediated transport	BP	1	TRAPPC3L,LEP,RAB20,GAS1,DLL1,CHRM2,MYO1D,GREM1,CAMK2A,ICAM5,BVES,RAB7A,KXD1,ANXA11	up_AFEM_EC
GO:0009987	0.187	0.941	13	5086	cellular process	BP	1	ETFA,GPSM2,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15,FSCN1	down_AFEM_EC
GO:0051345	0.187	0.886	12	151	positive regulation of hydrolase activity	BP	1	PPP1R12A,DYNLL1,DNAJC10,ENSCAFG00000002015,LYN,FAM162A,GSK3B,TAX1BP3,REST,ABHD5,CALM1,ARF4	down_VSAP_EC
GO:0006260	0.187	0.887	12	98	DNA replication	BP	1	BAZ1A,THOC1,ESCO1,TOP1,ETAA1,BLM,RAD17,USP37,ATRX,TOPBP1,RBBP6,GINS4	up_VCAV_EC
GO:0031056	0.187	0.907	7	50	regulation of histone modification	BP	1	IWS1,GATA3,PRKD2,NSD1,KDM5A,KDM3A,ATRX	up_VCAV_EC
GO:0009566	0.187	0.93	4	24	fertilization	BP	1	GLRB,DKKL1,SPINK2,WDR48	up_ACOR_VSMC
GO:0014033	0.187	0.94	3	30	neural crest cell differentiation	BP	1	BMPR1A,SEMA3C,RDH10	down_VCAV_EC
GO:0021885	0.187	0.94	3	24	forebrain cell migration	BP	1	CTNNB1,DISC1,NRP1	down_VSAP_EC
GO:0009967	0.187	0.941	3	435	positive regulation of signal transduction	BP	1	NR1H4,CCL24,NEO1	up_VPUL_EC
GO:0021602	0.187	0.943	3	16	cranial nerve morphogenesis	BP	1	HOXD3,PLXNA4,CITED2	up_VSAP_EC
GO:1903530	0.187	0.956	2	165	regulation of secretion by cell	BP	1	LYN,STX4	down_ACOR_EC
GO:0009954	0.187	0.958	2	16	proximal/distal pattern formation	BP	1	GLI3,GREM1	down_VCAV_EC
GO:0008089	0.187	0.959	2	14	anterograde axonal transport	BP	1	TRAK1,AP3S1	down_VSAP_EC
GO:0051196	0.187	0.959	2	13	regulation of coenzyme metabolic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0002026	0.187	0.962	2	8	regulation of the force of heart contraction	BP	1	GAA,SLC8A1	up_ACOR_VSMC
GO:0046621	0.187	0.962	2	8	negative regulation of organ growth	BP	1	TBX5,WWC2	up_ACOR_VSMC
GO:0097530	0.187	0.956	2	33	granulocyte migration	BP	1	CMKLR1,CCL5	up_AFEM_EC
GO:0050918	0.187	0.96	2	10	positive chemotaxis	BP	1	CXCL8,ANGPT2	up_VCAV_EC
GO:0098771	0.187	0.956	2	180	inorganic ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0006909	0.187	0.982	1	42	phagocytosis	BP	1	SPG11	down_ACOR_EC
GO:0051262	0.187	0.982	1	40	protein tetramerization	BP	1	IGF1R	down_ACOR_EC
GO:0009205	0.187	0.983	1	98	purine ribonucleoside triphosphate metabolic	BP	1	NDUFA10	down_AFEM_EC
GO:1901362	0.187	1	1	1293	organic cyclic compound biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0071702	0.187	0.99	1	687	organic substance transport	BP	1	SCAMP4	down_AORT_EC
GO:0003256	0.187	0.986	1	4	regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	down_VCAV_EC
GO:0006521	0.187	0.986	1	4	regulation of cellular amino acid metabolic	BP	1	PARK7	down_VCAV_EC
GO:0034505	0.187	0.986	1	4	tooth mineralization	BP	1	ASPN	down_VCAV_EC
GO:0043691	0.187	0.986	1	4	reverse cholesterol transport	BP	1	LCAT	down_VCAV_EC
GO:0046548	0.187	0.986	1	4	retinal rod cell development	BP	1	NAGLU	down_VCAV_EC

GO:0048563	0.187	0.986	1	4	post-embryonic animal organ morphogenesis	BP	1	FBN1	down_VCAV_EC
GO:0048703	0.187	0.986	1	4	embryonic viscerocranium morphogenesis	BP	1	RDH10	down_VCAV_EC
GO:0098810	0.187	0.986	1	4	neurotransmitter reuptake	BP	1	PARK7	down_VCAV_EC
GO:2001225	0.187	0.986	1	4	regulation of chloride transport	BP	1	PRNP	down_VCAV_EC
GO:0006435	0.187	0.987	1	3	threonyl-tRNA aminoacylation	BP	1	TARS	down_VSAP_EC
GO:0030449	0.187	0.987	1	3	regulation of complement activation	BP	1	A2M	down_VSAP_EC
GO:0042640	0.187	0.987	1	3	anagen	BP	1	CTNNB1	down_VSAP_EC
GO:0051884	0.187	0.987	1	3	regulation of timing of anagen	BP	1	CTNNB1	down_VSAP_EC
GO:2000257	0.187	0.987	1	3	regulation of protein activation cascade	BP	1	A2M	down_VSAP_EC
GO:0140059	0.187	0.987	1	3	dendrite arborization	BP	1	NRP1	down_VSAP_EC
GO:0042226	0.187	0.99	1	2	interleukin-6 biosynthetic process	BP	1	TLR1	up_ACOR_VSMC
GO:0045408	0.187	0.99	1	2	regulation of interleukin-6 biosynthetic process	BP	1	TLR1	up_ACOR_VSMC
GO:0098885	0.187	0.99	1	2	modification of postsynaptic actin	BP	1	WASF3	up_ACOR_VSMC
GO:0009314	0.187	0.983	1	143	response to radiation	BP	1	EYA1	up_AFEM_VSMC
GO:0120039	0.187	0.984	1	158	plasma membrane bounded cell projection	BP	1	WNT7A	up_AORT_VSMC
GO:0048878	0.187	0.985	1	283	chemical homeostasis	BP	1	HOXA3	up_APUL_VSMC
GO:0001977	0.187	0.987	1	3	renal system process involved in regulation of	BP	1	PDGFB	up_VCAV_EC
GO:0002420	0.187	0.987	1	3	natural killer cell mediated cytotoxicity directed against tumor	BP	1	NECTIN2	up_VCAV_EC
GO:0002423	0.187	0.987	1	3	natural killer cell mediated immune	BP	1	NECTIN2	up_VCAV_EC
GO:0002855	0.187	0.987	1	3	regulation of natural killer cell mediated immune response to tumor cell	BP	1	NECTIN2	up_VCAV_EC
GO:0002857	0.187	0.987	1	3	positive regulation of natural killer cell mediated immune	BP	1	NECTIN2	up_VCAV_EC
GO:0002858	0.187	0.987	1	3	regulation of natural killer cell mediated cytotoxicity directed against tumor	BP	1	NECTIN2	up_VCAV_EC
GO:0002860	0.187	0.987	1	3	positive regulation of natural killer cell mediated cytotoxicity	BP	1	NECTIN2	up_VCAV_EC
GO:0003093	0.187	0.987	1	3	regulation of glomerular filtration	BP	1	PDGFB	up_VCAV_EC
GO:0032056	0.187	0.987	1	3	positive regulation of translation in response to	BP	1	NCK1	up_VCAV_EC
GO:0035739	0.187	0.987	1	3	CD4-positive, alpha-beta T cell proliferation	BP	1	ARG2	up_VCAV_EC
GO:2000561	0.187	0.987	1	3	regulation of CD4-positive, alpha-beta T cell	BP	1	ARG2	up_VCAV_EC
GO:0007015	0.187	0.983	1	144	actin filament organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0072676	0.187	0.982	1	25	lymphocyte migration	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:1901214	0.187	0.983	1	81	regulation of neuron death	BP	1	CHL1	up_VPOR_VSMC
GO:0015711	0.187	0.983	1	81	organic anion transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0016042	0.187	0.982	1	80	lipid catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0031334	0.187	0.982	1	84	positive regulation of protein complex assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0009152	0.187	0.983	1	80	purine ribonucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0042391	0.187	0.983	1	81	regulation of membrane potential	BP	1	NETO1	up_VFEM_VSMC
GO:1901617	0.187	0.982	1	60	organic hydroxy compound biosynthetic	BP	1	NR1H4	up_VPUL_EC
GO:0030900	0.187	0.983	1	101	forebrain development	BP	1	SLIT2	up_VPUL_VSMC

GO:0001911	0.187	0.99	1	2	negative regulation of leukocyte mediated	BP	1	PPP3CB	up_VSAP_EC
GO:0001915	0.187	0.99	1	2	negative regulation of T cell mediated cytotoxicity	BP	1	PPP3CB	up_VSAP_EC
GO:0002031	0.187	0.99	1	2	G protein-coupled receptor internalization	BP	1	UBQLN2	up_VSAP_EC
GO:0002517	0.187	0.99	1	2	T cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0002664	0.187	0.99	1	2	regulation of T cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0002666	0.187	0.99	1	2	positive regulation of T cell tolerance induction	BP	1	TGFBR2	up_VSAP_EC
GO:0003274	0.187	0.99	1	2	endocardial cushion fusion	BP	1	TGFBR2	up_VSAP_EC
GO:0006106	0.187	0.99	1	2	fumarate metabolic process	BP	1	GOT1	up_VSAP_EC
GO:0006436	0.187	0.99	1	2	tryptophanyl-tRNA aminoacylation	BP	1	WARS2	up_VSAP_EC
GO:0006533	0.187	0.99	1	2	aspartate catabolic process	BP	1	GOT1	up_VSAP_EC
GO:0009403	0.187	0.99	1	2	toxin biosynthetic process	BP	1	MPST	up_VSAP_EC
GO:0014067	0.187	0.99	1	2	negative regulation of phosphatidylinositol 3-kinase signaling	BP	1	PIK3IP1	up_VSAP_EC
GO:0018282	0.187	0.99	1	2	metal incorporation into metallo-sulfur cluster	BP	1	FXN	up_VSAP_EC
GO:0018283	0.187	0.99	1	2	iron incorporation into metallo-sulfur cluster	BP	1	FXN	up_VSAP_EC
GO:0031342	0.187	0.99	1	2	negative regulation of cell killing	BP	1	PPP3CB	up_VSAP_EC
GO:0032226	0.187	0.99	1	2	positive regulation of synaptic transmission,	BP	1	FLOT1	up_VSAP_EC
GO:0042439	0.187	0.99	1	2	ethanolamine-containing compound metabolic	BP	1	NAPEPLD	up_VSAP_EC
GO:0002513	0.187	0.99	1	2	tolerance induction to self antigen	BP	1	TGFBR2	up_VSAP_EC
GO:0048382	0.187	0.99	1	2	mesendoderm development	BP	1	ZFP36L1	up_VSAP_EC
GO:0051006	0.187	0.99	1	2	positive regulation of lipoprotein lipase activity	BP	1	LMF1	up_VSAP_EC
GO:0051194	0.187	0.99	1	2	positive regulation of cofactor metabolic	BP	1	ZNF205	up_VSAP_EC
GO:0060434	0.187	0.99	1	2	bronchus morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0060994	0.187	0.99	1	2	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GLIS2	up_VSAP_EC
GO:0061365	0.187	0.99	1	2	positive regulation of triglyceride lipase activity	BP	1	LMF1	up_VSAP_EC
GO:0070814	0.187	0.99	1	2	hydrogen sulfide biosynthetic process	BP	1	MPST	up_VSAP_EC
GO:0071435	0.187	0.99	1	2	potassium ion export	BP	1	KCNE3	up_VSAP_EC
GO:0086036	0.187	0.99	1	2	regulation of cardiac muscle cell membrane	BP	1	FXYD1	up_VSAP_EC
GO:0097623	0.187	0.99	1	2	potassium ion export across plasma membrane	BP	1	KCNE3	up_VSAP_EC
GO:1903215	0.187	0.99	1	2	negative regulation of protein targeting to	BP	1	BAG4	up_VSAP_EC
GO:1903677	0.187	0.99	1	2	regulation of cap-independent translational	BP	1	NCK1	up_VSAP_EC
GO:1903679	0.187	0.99	1	2	positive regulation of cap-independent translational initiation	BP	1	NCK1	up_VSAP_EC
GO:1903748	0.187	0.99	1	2	negative regulation of establishment of protein localization to	BP	1	BAG4	up_VSAP_EC
GO:1904688	0.187	0.99	1	2	regulation of cytoplasmic translational initiation	BP	1	NCK1	up_VSAP_EC
GO:1904690	0.187	0.99	1	2	positive regulation of cytoplasmic translational	BP	1	NCK1	up_VSAP_EC
GO:2000172	0.187	0.99	1	2	regulation of branching morphogenesis of a nerve	BP	1	SHOX2	up_VSAP_EC
GO:0007204	0.187	0.982	1	46	positive regulation of cytosolic calcium ion	BP	1	CAV1	up_VSAP_VSMC
GO:0032689	0.1872724	0.98354	1	8	negative regulation of interferon-gamma	BP	1	NR1H4	up_ACOR_EC
GO:0050829	0.187697744	0.98347	1	8	defense response to Gram-negative bacterium	BP	1	RARRES2	up_ACOR_EC

GO:0031468	0.187736945	0.98346	1	8	nuclear envelope reassembly	BP	1	CHMP4B	up_ACOR_EC
GO:0071071	0.187815531	0.98344	1	8	regulation of phospholipid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:0048518	0.188	0.841	109	1676	positive regulation of biological process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,SPARC,JCAD,CASP3,FAM49B,BCAR3,PTPN11,FSCN1,DPYSL3,TRIB3,TMED2,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,WDR1,MYO1C,PIK3C2A,CHSY1,MSN,HOXB7,KIF5B,LMAN1,HIF1A,DYNLL1,SLC45A3,ACTG2,TNIK,ZPR1,PTPN2,EIF2B1,EVI2B,PVR,YES1,NEO1,PEG3,MTDH,ESM1,DDX39B,ADAM17,ACTA2,EIF4EBP1,SKAP2,CNOT7,ACTR3,MAGED1,CTNNB1,ANLN,ENSCAFG00000002015,TFRC,APOE,PTP4A1,KLF5,LYN,BNIP3,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,GBP5,SH3GLB1,SDC4,HTT,REST,ABHD5,EIF2S1,PRMT1,CALM1,DISC1,RAD23A,PAK2,LRRTM2,A2M,INHBA,NR4A1,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,ARF4,YWHAH,MADD,MARCKSL1,SEC13,KDM3A,MID1,HOMER1	down_VSAP_EC
GO:0006796	0.188	0.848	63	938	phosphate-containing compound metabolic process	BP	1	ARHGEF2,VEGFA,NR1H4,SOCS5,SGK1,ENPP1,ERRFI1,JCAD,SNX25,PGK1,BCAR3,NUAK1,PTPN11,TPI1,TRIB3,PGAM1,ILK,PPP1R12A,SESN2,PTGS2,HIF1A,DYNLL1,NMNAT2,DNAJC10,TNIK,PTPN2,ENTPD4,YES1,PLCL1,ADAM17,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,CDK8,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,GSK3B,VLDLR,AK5,GTF2H1,SH3GLB1,HTT,MAPK10,EIF2S1,ARFGEF3,CALM1,PAK2,INHBA,CAMK2D,BTK,CDKN1A,NRP1,SH3RF3,MADD,MID1,CMPK1	down_VSAP_EC
GO:0019220	0.188	0.85	57	525	regulation of phosphate metabolic process	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,AR,SASH1,LMO4,FGF18,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,MARF1,FRS2,DAG1,PPP1R26,PARP9,APP,PSEN1,SYNJ2BP,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,LRRC4,PRKAG3,DDIT4,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,GPATCH2,ZFYVE1,CRKL	up_ACOR_VSMC
GO:0051174	0.188	0.85	57	525	regulation of phosphorus metabolic process	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,BMP4,FGFR2,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,AR,SASH1,LMO4,FGF18,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,MARF1,FRS2,DAG1,PPP1R26,PARP9,APP,PSEN1,SYNJ2BP,CCL5,DDR2,DUSP22,EDN1,AKTIP,DUSP26,NOD2,LRRC4,PRKAG3,DDIT4,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,GPATCH2,ZFYVE1,CRKL	up_ACOR_VSMC
GO:0009790	0.188	0.859	33	335	embryo development	BP	1	HOXB7,PCDH12,ADGRF5,KIT,CXCL8,TIE1,AMOT,PDGFB,MEF2C,CHD7,DLL4,GATA3,EDN1,HOXB8,SOX18,BMP2,HHEX,PROX1,MDFI,HOXB5,TOP1,BCL10,NUP133,SKIL,CUL4A,HIF1A,ALDH1A3,LUZP1,RBBP6,VASH1,ZEB1,CDON,GINS4	up_VCAV_EC
GO:0035303	0.188	0.897	9	65	regulation of dephosphorylation	BP	1	SH3RF2,NPNT,SMPD1,MARF1,PPP1R26,DUSP26,INPP5K,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0009607	0.188	0.898	8	232	response to biotic stimulus	BP	1	CD40,BPI,GPAM,CHRM2,SLC17A5,TBXA2R,CCL5,ADAM17	up_AFEM_EC
GO:0006637	0.188	0.92	5	32	acyl-CoA metabolic process	BP	1	ACSM3,ACACB,PDK2,ACSS2,MVK	up_VSAP_EC
GO:0035383	0.188	0.92	5	32	thioester metabolic process	BP	1	ACSM3,ACACB,PDK2,ACSS2,MVK	up_VSAP_EC
GO:0003158	0.188	0.927	4	38	endothelium development	BP	1	MSN,CTNNB1,STARD13,PLOD3	down_VSAP_EC
GO:0031325	0.188	0.931	4	914	positive regulation of cellular metabolic process	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0042255	0.188	0.939	3	29	ribosome assembly	BP	1	RPS10,MRPS11,RPS27	down_VCAV_EC
GO:0070252	0.188	0.942	3	17	actin-mediated cell contraction	BP	1	TNNT2,KCNE3,JUP	up_ACOR_VSMC
GO:2000179	0.188	0.943	3	14	positive regulation of neural precursor cell	BP	1	SMARCD3,FZD3,DISC1	up_ACOR_VSMC

GO:0006195	0.188	0.96	2	10	purine nucleotide catabolic process	BP	1	NUDT1,NUDT3	down_ACOR_VSMC
GO:0019222	0.188	0.979	2	1934	regulation of metabolic process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:1901021	0.188	0.958	2	13	positive regulation of calcium ion transmembrane	BP	1	HTT,CALM1	down_VSAP_EC
GO:0030970	0.188	0.958	2	14	retrograde protein transport, ER to cytosol	BP	1	HM13,SEL1L	down_VSAP_EC
GO:1903513	0.188	0.958	2	14	endoplasmic reticulum to cytosol transport	BP	1	HM13,SEL1L	down_VSAP_EC
GO:0014044	0.188	0.962	2	8	Schwann cell development	BP	1	SH3TC2,DAG1	up_ACOR_VSMC
GO:0022011	0.188	0.962	2	8	myelination in peripheral nervous system	BP	1	SH3TC2,DAG1	up_ACOR_VSMC
GO:0032292	0.188	0.962	2	8	peripheral nervous system axon	BP	1	SH3TC2,DAG1	up_ACOR_VSMC
GO:0048729	0.188	0.956	2	209	tissue morphogenesis	BP	1	TBX5,NPNT	up_APUL_EC
GO:1903115	0.188	0.959	2	12	regulation of actin filament-based movement	BP	1	PDE4D,STC1	up_VCAV_EC
GO:0007399	0.188	0.96	2	564	nervous system development	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0006082	0.188	0.957	2	305	organic acid metabolic process	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0006384	0.188	0.986	1	4	transcription initiation from RNA polymerase III	BP	1	CRCP	down_VCAV_EC
GO:0042069	0.188	0.986	1	4	regulation of catecholamine metabolic	BP	1	PARK7	down_VCAV_EC
GO:0035630	0.188	0.986	1	4	bone mineralization involved in bone	BP	1	GREM1	down_VCAV_EC
GO:0035754	0.188	0.986	1	4	B cell chemotaxis	BP	1	HSD3B7	down_VCAV_EC
GO:0042053	0.188	0.986	1	4	regulation of dopamine metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0048263	0.188	0.986	1	4	determination of dorsal identity	BP	1	GREM1	down_VCAV_EC
GO:0051923	0.188	0.986	1	4	sulfation	BP	1	HS3ST3B1	down_VCAV_EC
GO:0071280	0.188	0.986	1	4	cellular response to copper ion	BP	1	PRNP	down_VCAV_EC
GO:0090073	0.188	0.986	1	4	positive regulation of protein homodimerization	BP	1	PARK7	down_VCAV_EC
GO:0090336	0.188	0.986	1	4	positive regulation of brown fat cell	BP	1	NAPEPLD	down_VCAV_EC
GO:1902950	0.188	0.986	1	4	regulation of dendritic spine maintenance	BP	1	PRNP	down_VCAV_EC
GO:2001135	0.188	0.986	1	4	regulation of endocytic recycling	BP	1	ARHGAP1	down_VCAV_EC
GO:0010817	0.188	0.983	1	102	regulation of hormone levels	BP	1	RAB11B	down_VPOR_EC
GO:0006450	0.188	0.986	1	4	regulation of translational fidelity	BP	1	AARS	down_VSAP_EC
GO:0031652	0.188	0.987	1	3	positive regulation of heat generation	BP	1	PTGS2	down_VSAP_EC
GO:0046628	0.188	0.987	1	3	positive regulation of insulin receptor signaling	BP	1	NR1H4	down_VSAP_EC
GO:0060385	0.188	0.987	1	3	axonogenesis involved in innervation	BP	1	NRP1	down_VSAP_EC
GO:0008284	0.188	0.984	1	238	positive regulation of cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0036515	0.188	0.99	1	2	serotonergic neuron axon guidance	BP	1	FZD3	up_ACOR_VSMC
GO:1904938	0.188	0.99	1	2	planar cell polarity pathway involved in axon	BP	1	FZD3	up_ACOR_VSMC
GO:0018242	0.188	0.99	1	2	protein O-linked glycosylation via serine	BP	1	GALNT3	up_ACOR_VSMC
GO:0034154	0.188	0.99	1	2	toll-like receptor 7 signaling pathway	BP	1	PTPN22	up_ACOR_VSMC
GO:0035235	0.188	0.99	1	2	ionotropic glutamate receptor signaling	BP	1	APP	up_ACOR_VSMC
GO:0036514	0.188	0.99	1	2	dopaminergic neuron axon guidance	BP	1	FZD3	up_ACOR_VSMC
GO:1902177	0.188	0.99	1	2	positive regulation of oxidative stress-induced intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:2000282	0.188	0.99	1	2	regulation of cellular amino acid biosynthetic	BP	1	PARK7	up_ACOR_VSMC
GO:0031347	0.188	0.983	1	144	regulation of defense response	BP	1	TLR2	up_AFEM_VSMC

GO:0048858	0.188	0.983	1	159	cell projection morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0001659	0.188	0.982	1	54	temperature homeostasis	BP	1	PLCL1	up_APUL_EC
GO:0003025	0.188	0.99	1	2	regulation of systemic arterial blood pressure by baroreceptor feedback	BP	1	NAV2	up_VCAV_EC
GO:0070433	0.188	0.99	1	2	negative regulation of nucleotide-binding oligomerization domain	BP	1	TNFAIP3	up_VCAV_EC
GO:0098962	0.188	0.987	1	3	regulation of postsynaptic neurotransmitter	BP	1	HOMER3	up_VCAV_EC
GO:0021978	0.188	0.987	1	3	telencephalon regionalization	BP	1	BMP2	up_VCAV_EC
GO:0060754	0.188	0.987	1	3	positive regulation of mast cell chemotaxis	BP	1	SWAP70	up_VCAV_EC
GO:0070425	0.188	0.99	1	2	negative regulation of nucleotide-binding oligomerization domain	BP	1	TNFAIP3	up_VCAV_EC
GO:0032872	0.188	0.982	1	77	regulation of stress-activated MAPK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0015711	0.188	0.982	1	81	organic anion transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:0000050	0.188	0.99	1	2	urea cycle	BP	1	ASS1	up_VSAP_EC
GO:0000480	0.188	0.99	1	2	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-	BP	1	RCL1	up_VSAP_EC
GO:0001574	0.188	0.99	1	2	ganglioside biosynthetic process	BP	1	B3GALT4	up_VSAP_EC
GO:0001999	0.188	0.99	1	2	renal response to blood flow involved in circulatory renin-angiotensin regulation of	BP	1	F2RL1	up_VSAP_EC
GO:0003342	0.188	0.99	1	2	proepicardium development	BP	1	ZFP36L1	up_VSAP_EC
GO:0003343	0.188	0.99	1	2	septum transversum development	BP	1	ZFP36L1	up_VSAP_EC
GO:0003402	0.188	0.99	1	2	planar cell polarity pathway involved in axis	BP	1	WNT11	up_VSAP_EC
GO:0006059	0.188	0.99	1	2	hexitol metabolic process	BP	1	GALK1	up_VSAP_EC
GO:0006404	0.188	0.99	1	2	RNA import into nucleus	BP	1	SNUPN	up_VSAP_EC
GO:0006568	0.188	0.99	1	2	tryptophan metabolic process	BP	1	IDO2	up_VSAP_EC
GO:0006569	0.188	0.99	1	2	tryptophan catabolic process	BP	1	IDO2	up_VSAP_EC
GO:0006586	0.188	0.99	1	2	indolalkylamine metabolic process	BP	1	IDO2	up_VSAP_EC
GO:0006703	0.188	0.99	1	2	estrogen biosynthetic process	BP	1	HSD17B8	up_VSAP_EC
GO:0006741	0.188	0.99	1	2	NADP biosynthetic process	BP	1	NADK	up_VSAP_EC
GO:0006788	0.188	0.99	1	2	heme oxidation	BP	1	HMOX1	up_VSAP_EC
GO:0007197	0.188	0.99	1	2	adenylate cyclase-inhibiting G protein-coupled acetylcholine	BP	1	CHRM1	up_VSAP_EC
GO:0007207	0.188	0.99	1	2	phospholipase C-activating G protein-coupled acetylcholine	BP	1	CHRM1	up_VSAP_EC
GO:0007567	0.188	0.99	1	2	parturition	BP	1	HPGD	up_VSAP_EC
GO:0016338	0.188	0.99	1	2	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion	BP	1	CLDN1	up_VSAP_EC
GO:0019230	0.188	0.99	1	2	proprioception	BP	1	FXN	up_VSAP_EC
GO:0019433	0.188	0.99	1	2	triglyceride catabolic process	BP	1	LIPC	up_VSAP_EC
GO:0019441	0.188	0.99	1	2	tryptophan catabolic process to kynurenine	BP	1	IDO2	up_VSAP_EC
GO:0030656	0.188	0.99	1	2	regulation of vitamin metabolic process	BP	1	CLYBL	up_VSAP_EC
GO:0002001	0.188	0.99	1	2	renin secretion into blood stream	BP	1	F2RL1	up_VSAP_EC
GO:0032713	0.188	0.99	1	2	negative regulation of interleukin-4 production	BP	1	CD83	up_VSAP_EC

GO:0032915	0.188	0.99	1	2	positive regulation of transforming growth factor beta2 production	BP	1	WNT11	up_VSAP_EC
GO:0034418	0.188	0.99	1	2	urate biosynthetic process	BP	1	PNP	up_VSAP_EC
GO:0034473	0.188	0.99	1	2	U1 snRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0034476	0.188	0.99	1	2	U5 snRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0035726	0.188	0.99	1	2	common myeloid progenitor cell	BP	1	FBXO4	up_VSAP_EC
GO:0035999	0.188	0.99	1	2	tetrahydrofolate interconversion	BP	1	ENSCAFG00000013986	up_VSAP_EC
GO:0036493	0.188	0.99	1	2	positive regulation of translation in response to endoplasmic reticulum	BP	1	NCK1	up_VSAP_EC
GO:0038107	0.188	0.99	1	2	nodal signaling pathway involved in determination of left/right asymmetry	BP	1	CITED2	up_VSAP_EC
GO:0042436	0.188	0.99	1	2	indole-containing compound catabolic	BP	1	IDO2	up_VSAP_EC
GO:0042670	0.188	0.99	1	2	retinal cone cell differentiation	BP	1	THRB	up_VSAP_EC
GO:0042816	0.188	0.99	1	2	vitamin B6 metabolic process	BP	1	PNPO	up_VSAP_EC
GO:0042822	0.188	0.99	1	2	pyridoxal phosphate metabolic process	BP	1	PNPO	up_VSAP_EC
GO:0044110	0.188	0.99	1	2	growth involved in symbiotic interaction	BP	1	MYD88	up_VSAP_EC
GO:0044116	0.188	0.99	1	2	growth of symbiont involved in interaction	BP	1	MYD88	up_VSAP_EC
GO:0044117	0.188	0.99	1	2	growth of symbiont in host	BP	1	MYD88	up_VSAP_EC
GO:0044126	0.188	0.99	1	2	regulation of growth of symbiont in host	BP	1	MYD88	up_VSAP_EC
GO:0044130	0.188	0.99	1	2	negative regulation of growth of symbiont in	BP	1	MYD88	up_VSAP_EC
GO:0044144	0.188	0.99	1	2	modulation of growth of symbiont involved in interaction with host	BP	1	MYD88	up_VSAP_EC
GO:0044146	0.188	0.99	1	2	negative regulation of growth of symbiont involved in interaction	BP	1	MYD88	up_VSAP_EC
GO:0045054	0.188	0.99	1	2	constitutive secretory pathway	BP	1	RAB11B	up_VSAP_EC
GO:0045777	0.188	0.99	1	2	positive regulation of blood pressure	BP	1	TBXA2R	up_VSAP_EC
GO:0046102	0.188	0.99	1	2	inosine metabolic process	BP	1	PNP	up_VSAP_EC
GO:0046218	0.188	0.99	1	2	indolalkylamine catabolic process	BP	1	IDO2	up_VSAP_EC
GO:0046415	0.188	0.99	1	2	urate metabolic process	BP	1	PNP	up_VSAP_EC
GO:0046549	0.188	0.99	1	2	retinal cone cell development	BP	1	THRB	up_VSAP_EC
GO:0046642	0.188	0.99	1	2	negative regulation of alpha-beta T cell	BP	1	CD274	up_VSAP_EC
GO:0048148	0.188	0.99	1	2	behavioral response to cocaine	BP	1	ABAT	up_VSAP_EC
GO:0048389	0.188	0.99	1	2	intermediate mesoderm development	BP	1	OSR1	up_VSAP_EC
GO:0048742	0.188	0.99	1	2	regulation of skeletal muscle fiber development	BP	1	SHOX2	up_VSAP_EC
GO:0051030	0.188	0.99	1	2	snRNA transport	BP	1	SNUPN	up_VSAP_EC
GO:0051709	0.188	0.99	1	2	regulation of killing of cells of other organism	BP	1	F2RL1	up_VSAP_EC
GO:0051712	0.188	0.99	1	2	positive regulation of killing of cells of other	BP	1	F2RL1	up_VSAP_EC
GO:0051818	0.188	0.99	1	2	disruption of cells of other organism involved in symbiotic interaction	BP	1	F2RL1	up_VSAP_EC
GO:0051883	0.188	0.99	1	2	killing of cells in other organism involved in	BP	1	F2RL1	up_VSAP_EC
GO:0051953	0.188	0.99	1	2	negative regulation of amine transport	BP	1	OSR1	up_VSAP_EC
GO:0060031	0.188	0.99	1	2	mediolateral intercalation	BP	1	WNT11	up_VSAP_EC
GO:0060197	0.188	0.99	1	2	cloacal septation	BP	1	WNT11	up_VSAP_EC

GO:0060267	0.188	0.99	1	2	positive regulation of respiratory burst	BP	1	JCHAIN	up_VSAP_EC
GO:0060353	0.188	0.99	1	2	regulation of cell adhesion molecule production	BP	1	FLOT1	up_VSAP_EC
GO:0060355	0.188	0.99	1	2	positive regulation of cell adhesion molecule	BP	1	FLOT1	up_VSAP_EC
GO:0060708	0.188	0.99	1	2	spongiotrophoblast differentiation	BP	1	GJB5	up_VSAP_EC
GO:0060775	0.188	0.99	1	2	planar cell polarity pathway involved in gastrula mediolateral	BP	1	WNT11	up_VSAP_EC
GO:0060971	0.188	0.99	1	2	embryonic heart tube left/right pattern	BP	1	CITED2	up_VSAP_EC
GO:0061015	0.188	0.99	1	2	snRNA import into nucleus	BP	1	SNUPN	up_VSAP_EC
GO:0061033	0.188	0.99	1	2	secretion by lung epithelial cell involved in	BP	1	FGF7	up_VSAP_EC
GO:0061227	0.188	0.99	1	2	pattern specification involved in mesonephros	BP	1	OSR1	up_VSAP_EC
GO:0070189	0.188	0.99	1	2	kynurenine metabolic process	BP	1	IDO2	up_VSAP_EC
GO:0071042	0.188	0.99	1	2	nuclear polyadenylation-dependent mRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0071047	0.188	0.99	1	2	polyadenylation-dependent mRNA	BP	1	EXOSC7	up_VSAP_EC
GO:0071281	0.188	0.99	1	2	cellular response to iron ion	BP	1	HMOX1	up_VSAP_EC
GO:0071798	0.188	0.99	1	2	response to prostaglandin D	BP	1	PTGFR	up_VSAP_EC
GO:0071799	0.188	0.99	1	2	cellular response to prostaglandin D stimulus	BP	1	PTGFR	up_VSAP_EC
GO:0072086	0.188	0.99	1	2	specification of loop of Henle identity	BP	1	IRX3	up_VSAP_EC
GO:0072098	0.188	0.99	1	2	anterior/posterior pattern specification involved in kidney development	BP	1	OSR1	up_VSAP_EC
GO:0072131	0.188	0.99	1	2	kidney mesenchyme morphogenesis	BP	1	OSR1	up_VSAP_EC
GO:0072133	0.188	0.99	1	2	metanephric mesenchyme	BP	1	OSR1	up_VSAP_EC
GO:0072180	0.188	0.99	1	2	mesonephric duct morphogenesis	BP	1	OSR1	up_VSAP_EC
GO:0072190	0.188	0.99	1	2	ureter urothelium development	BP	1	OSR1	up_VSAP_EC
GO:0072268	0.188	0.99	1	2	pattern specification involved in metanephros	BP	1	OSR1	up_VSAP_EC
GO:0086011	0.188	0.99	1	2	membrane repolarization during action potential	BP	1	KCNE3	up_VSAP_EC
GO:0090155	0.188	0.99	1	2	negative regulation of sphingolipid biosynthetic	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:0090156	0.188	0.99	1	2	cellular sphingolipid homeostasis	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:0098706	0.188	0.99	1	2	ferric iron import across cell outer membrane	BP	1	STEAP3	up_VSAP_EC
GO:0098903	0.188	0.99	1	2	regulation of membrane repolarization during action potential	BP	1	KCNE3	up_VSAP_EC
GO:1900060	0.188	0.99	1	2	negative regulation of ceramide biosynthetic	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:1900094	0.188	0.99	1	2	regulation of transcription from RNA polymerase II promoter involved in determination of	BP	1	CITED2	up_VSAP_EC
GO:1900133	0.188	0.99	1	2	regulation of renin secretion into blood	BP	1	F2RL1	up_VSAP_EC
GO:1900164	0.188	0.99	1	2	nodal signaling pathway involved in determination of lateral mesoderm	BP	1	CITED2	up_VSAP_EC
GO:1901072	0.188	0.99	1	2	glucosamine-containing compound catabolic	BP	1	GNPDA1	up_VSAP_EC
GO:1901490	0.188	0.99	1	2	regulation of lymphangiogenesis	BP	1	CCBE1	up_VSAP_EC
GO:1902260	0.188	0.99	1	2	negative regulation of delayed rectifier potassium channel	BP	1	KCNE3	up_VSAP_EC
GO:1903445	0.188	0.99	1	2	protein transport from ciliary membrane to	BP	1	RILPL2	up_VSAP_EC
GO:1903789	0.188	0.99	1	2	regulation of amino acid transmembrane transport	BP	1	OSR1	up_VSAP_EC

GO:1905397	0.188	0.99	1	2	activated CD8-positive, alpha-beta T cell	BP	1	CD274	up_VSAP_EC
GO:1905402	0.188	0.99	1	2	regulation of activated CD8-positive, alpha-beta T cell apoptotic process	BP	1	CD274	up_VSAP_EC
GO:1990009	0.188	0.99	1	2	retinal cell apoptotic process	BP	1	THRB	up_VSAP_EC
GO:2000312	0.188	0.99	1	2	regulation of kainate selective glutamate	BP	1	KLHL24	up_VSAP_EC
GO:2000341	0.188	0.99	1	2	regulation of chemokine (C-X-C motif) ligand 2	BP	1	MYD88	up_VSAP_EC
GO:2000562	0.188	0.99	1	2	negative regulation of CD4-positive, alpha-beta T cell proliferation	BP	1	CD274	up_VSAP_EC
GO:0009074	0.188	0.99	1	2	aromatic amino acid family catabolic process	BP	1	IDO2	up_VSAP_EC
GO:0019373	0.188	0.99	1	2	epoxygenase P450 pathway	BP	1	ENSCAFG00000023820	up_VSAP_EC
GO:0048681	0.188	0.99	1	2	negative regulation of axon regeneration	BP	1	RTN4RL1	up_VSAP_EC
GO:0055022	0.188	0.99	1	2	negative regulation of cardiac muscle tissue	BP	1	SAV1	up_VSAP_EC
GO:0060044	0.188	0.99	1	2	negative regulation of cardiac muscle cell	BP	1	SAV1	up_VSAP_EC
GO:0061117	0.188	0.99	1	2	negative regulation of heart growth	BP	1	SAV1	up_VSAP_EC
GO:2001257	0.188842052	0.95575	2	30	regulation of cation channel activity	BP	1	ACTN2,MAPK8IP2	up_ACOR_EC
GO:0009719	0.189	0.855	39	395	response to endogenous stimulus	BP	1	HCLS1,KIT,PRCP,CXCL8,PPARG,BAIAP2L1,PDE4D,MEF2C,FERMT1,DLL4,RAPGEF1,TLR4,GATA3,SMAD1,TFPI,YES1,MTOR,BMP2,ABCA1,MAPK13,ENSCAFG00000010596,PRKD2,SMARCA4,NCK1,TIMELESS,RAPGEF2,CTDSPL2,CREB1,CTNNA1,ADIPOR2,BLM,SKIL,PDGFD,UFSP2,KDM3A,NR4A1,ENSCAFG00000002015,ZEB1,ARHGEF2	up_VCAV_EC
GO:0001655	0.189	0.891	10	116	urogenital system development	BP	1	SULF1,ENSCAFG00000032470,ILK,HOXB7,ACTA2,MAGED1,CTNNB1,MYO1E,SIX4,NRP1	down_VSAP_EC
GO:0071824	0.189	0.892	10	92	protein-DNA complex subunit organization	BP	1	PSME4,NASP,SMARCA4,CENPC,HIST1H1A,SENP6,ASF1A,HMGB1,ATRX,HP1BP3	up_VCAV_EC
GO:0052548	0.189	0.895	9	80	regulation of endopeptidase activity	BP	1	HMGB1,PRELID1,BIRC5,PDCD2,DHCR24,CYCS,ENSCAFG00000005299,AIFM1,DELE1	down_ACOR_VSMC
GO:0043547	0.189	0.9	8	61	positive regulation of GTPase activity	BP	1	RAPGEF1,RAPGEF2,TBC1D1,ITGA6,ALS2,ENSCAFG00000002015,RABGAP1,USP6NL	up_VCAV_EC
GO:0022412	0.189	0.904	7	76	cellular process involved in reproduction in multicellular organism	BP	1	CELF1,ETV6,CTNNB1,CDYL,INHBA,SPINK2,KDM3A	down_VSAP_EC
GO:1905330	0.189	0.905	7	48	regulation of morphogenesis of an	BP	1	MLLT3,BMP4,FGFR2,SEC24B,ZNRF3,FZD3,RREB1	up_ACOR_VSMC
GO:0051092	0.189	0.911	6	47	positive regulation of NF-kappaB transcription	BP	1	PRKCH,PRKD2,TLR3,BCL10,RIPK1,ARHGEF2	up_VCAV_EC
GO:0019751	0.189	0.919	5	33	polyol metabolic process	BP	1	PLCG2,PCBD1,PPIP5K1,INPP5K,PTS	up_ACOR_VSMC
GO:0110020	0.189	0.919	5	31	regulation of actomyosin structure organization	BP	1	ARHGAP28,NRP1,EVL,EDN1,INPP5K	up_ACOR_VSMC
GO:0007569	0.189	0.919	5	36	cell aging	BP	1	PLK2,ARG2,MAP3K3,SMC5,VASH1	up_VCAV_EC
GO:0043067	0.189	0.927	4	479	regulation of programmed cell death	BP	1	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0010604	0.189	0.931	4	919	positive regulation of macromolecule metabolic	BP	1	EYA1,HOXA9,HOXA11,SHOX2	up_VFEM_VSMC
GO:0030316	0.189	0.939	3	31	osteoclast differentiation	BP	1	NOTCH2,FBN1,TFE3	down_VCAV_EC
GO:0072171	0.189	0.939	3	30	mesonephric tubule morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0070661	0.189	0.937	3	63	leukocyte proliferation	BP	1	LEP,GPAM,GREM1	up_AFEM_EC
GO:0045596	0.189	0.937	3	186	negative regulation of cell differentiation	BP	1	HOOK3,SEMA3A,RNF6	up_VPOR_EC
GO:0010324	0.189	0.942	3	16	membrane invagination	BP	1	F2RL1,XKR8,ARHGAP12	up_VSAP_EC
GO:2001057	0.189	0.942	3	16	reactive nitrogen species metabolic process	BP	1	SUOX,MARC1,ASS1	up_VSAP_EC
GO:0007423	0.189	0.956	2	155	sensory organ development	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0032528	0.189	0.96	2	9	microvillus organization	BP	1	FSCN1,EZR	down_ACOR_VSMC
GO:0007585	0.189	0.957	2	16	respiratory gaseous exchange	BP	1	NDN,FUT8	down_VCAV_EC

GO:0001912	0.189	0.96	2	9	positive regulation of leukocyte mediated	BP	1	F2RL1,B2M	up_ACOR_VSMC
GO:0009719	0.189	0.958	2	395	response to endogenous stimulus	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:1901228	0.189	0.985	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GREM1	down_VCAV_EC
GO:0032700	0.189	0.985	1	4	negative regulation of interleukin-17 production	BP	1	PRNP	down_VCAV_EC
GO:0033147	0.189	0.985	1	4	negative regulation of intracellular estrogen receptor signaling	BP	1	KANK2	down_VCAV_EC
GO:0034447	0.189	0.985	1	4	very-low-density lipoprotein particle	BP	1	LRPAP1	down_VCAV_EC
GO:1903147	0.189	0.985	1	4	negative regulation of autophagy of	BP	1	CLEC16A	down_VCAV_EC
GO:0071702	0.189	0.99	1	687	organic substance transport	BP	1	JUP	down_VFEM_VSMC
GO:0070102	0.189	0.987	1	3	interleukin-6-mediated signaling pathway	BP	1	PTPN2	down_VSAP_EC
GO:1902003	0.189	0.985	1	4	regulation of amyloid-beta formation	BP	1	APOE	down_VSAP_EC
GO:0034433	0.189	0.985	1	4	steroid esterification	BP	1	APOE	down_VSAP_EC
GO:0034434	0.189	0.985	1	4	sterol esterification	BP	1	APOE	down_VSAP_EC
GO:0034435	0.189	0.985	1	4	cholesterol esterification	BP	1	APOE	down_VSAP_EC
GO:0048843	0.189	0.987	1	3	negative regulation of axon extension involved in axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0006958	0.189	0.99	1	2	complement activation, classical pathway	BP	1	C1S	up_ACOR_VSMC
GO:0034398	0.189	0.99	1	2	telomere tethering at nuclear periphery	BP	1	SUN1	up_ACOR_VSMC
GO:0051403	0.189	0.982	1	89	stress-activated MAPK cascade	BP	1	TAOK1	up_AORT_EC
GO:0001817	0.189	0.983	1	182	regulation of cytokine production	BP	1	ARG2	up_AORT_VSMC
GO:0051640	0.189	0.983	1	174	organelle localization	BP	1	WNT7A	up_AORT_VSMC
GO:0006575	0.189	0.982	1	53	cellular modified amino acid metabolic process	BP	1	ENSCAFG00000028814	up_APUL_EC
GO:0007611	0.189	0.982	1	54	learning or memory	BP	1	NTRK2	up_APUL_EC
GO:0035265	0.189	0.982	1	54	organ growth	BP	1	TBX5	up_APUL_EC
GO:0014012	0.189	0.99	1	2	peripheral nervous system axon regeneration	BP	1	APOD	up_VCAV_EC
GO:0061820	0.189	0.99	1	2	telomeric D-loop disassembly	BP	1	BLM	up_VCAV_EC
GO:0090657	0.189	0.99	1	2	telomeric loop disassembly	BP	1	BLM	up_VCAV_EC
GO:0031620	0.189	0.99	1	2	regulation of fever generation	BP	1	PTGS2	up_VCAV_EC
GO:0031622	0.189	0.99	1	2	positive regulation of fever generation	BP	1	PTGS2	up_VCAV_EC
GO:0061101	0.189	0.987	1	3	neuroendocrine cell differentiation	BP	1	BMP2	up_VCAV_EC
GO:0007610	0.189	0.983	1	146	behavior	BP	1	SLITRK5	up_VCAV_VSMC
GO:0031347	0.189	0.983	1	144	regulation of defense response	BP	1	C6	up_VCAV_VSMC
GO:0030500	0.189	0.982	1	25	regulation of bone mineralization	BP	1	ACVR2A	up_VPOR_EC
GO:0090307	0.189	0.982	1	26	mitotic spindle assembly	BP	1	MZT1	up_VPOR_EC
GO:0015672	0.189	0.982	1	89	monovalent inorganic cation transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:0035107	0.189	0.982	1	60	appendage morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0035108	0.189	0.982	1	60	limb morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0072507	0.189	0.982	1	103	divalent inorganic cation homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0051302	0.189	0.982	1	47	regulation of cell division	BP	1	FGF5	up_VSAP_VSMC
GO:0071453	0.189	0.982	1	46	cellular response to oxygen levels	BP	1	CAV1	up_VSAP_VSMC

GO:0060628	0.189440048	0.98314	1	8	regulation of ER to Golgi vesicle-mediated	BP	1	PREB	up_ACOR_EC
GO:1902188	0.189870204	0.98306	1	8	positive regulation of viral release from host cell	BP	1	CHMP4B	up_ACOR_EC
GO:0044703	0.19	0.872	18	172	multi-organism reproductive process	BP	1	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,ARID4B,HIST1H1A,PTGS2,SPTBN4,AFF4,ARHGDIB,KDM3A,ATRX,SPATA6,FBXO5	up_VCAV_EC
GO:0007389	0.19	0.88	14	137	pattern specification process	BP	1	HOXB7,RELN,MEF2C,DLL4,STC1,EDN1,HOXB8,BMP2,HHEX,MFNG,HOXB5,HIF1A,ZEB1,CDON	up_VCAV_EC
GO:1903827	0.19	0.887	11	164	regulation of cellular protein localization	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,TRIM8,GLI3,PARK7,MAVS,CDH2,GLIS2	down_VCAV_EC
GO:0072657	0.19	0.89	10	144	protein localization to membrane	BP	1	LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,SSR2,SSR3,CDH2,SEC61B,RAB31	down_VCAV_EC
GO:0035148	0.19	0.895	9	66	tube formation	BP	1	SHROOM3,BMP4,FGFR2,SEC24B,CITED2,SPINT1,LMO4,SPINT2,FZD3	up_ACOR_VSMC
GO:0050817	0.19	0.905	7	50	coagulation	BP	1	HNF4A,KLKB1,PDGFD,HPSE,F2RL1,HPS4,FBLN1	up_VSAP_EC
GO:0043393	0.19	0.908	6	77	regulation of protein binding	BP	1	LRP1,CLSTN1,PLCL1,LRPAP1,PARK7,MAPRE3	down_VCAV_EC
GO:0032409	0.19	0.917	5	52	regulation of transporter activity	BP	1	REM1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0071426	0.19	0.918	5	35	ribonucleoprotein complex export from	BP	1	IWS1,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0120034	0.19	0.927	4	28	positive regulation of plasma membrane bounded cell projection	BP	1	FSCN1,ANLN,RAC1,CDC42EP4	down_ACOR_VSMC
GO:0042742	0.19	0.926	4	39	defense response to bacterium	BP	1	NR1H4,SERPINE1,ADAM17,DEFB124	down_VSAP_EC
GO:0042592	0.19	0.927	4	522	homeostatic process	BP	1	GATM,HOXC10,STIM1,CAV1	up_VSAP_VSMC
GO:1900407	0.19	0.939	3	24	regulation of cellular response to oxidative	BP	1	P4HB,HIF1A,CTNNB1	down_VSAP_EC
GO:0055010	0.19	0.942	3	15	ventricular cardiac muscle tissue morphogenesis	BP	1	TNNT2,FGFR2,CHD7	up_ACOR_VSMC
GO:0061337	0.19	0.941	3	16	cardiac conduction	BP	1	KCNE3,GJA1,JUP	up_ACOR_VSMC
GO:0034612	0.19	0.937	3	63	response to tumor necrosis factor	BP	1	CYLD,CCL5,ADAM17	up_AFEM_EC
GO:0046879	0.19	0.937	3	63	hormone secretion	BP	1	LEP,CRY2,CCL5	up_AFEM_EC
GO:0009719	0.19	0.939	3	395	response to endogenous stimulus	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0044093	0.19	0.939	3	437	positive regulation of molecular function	BP	1	HOXA3,CCL24,ARHGEF2	up_VPUL_EC
GO:1901135	0.19	0.958	2	390	carbohydrate derivative metabolic process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0043370	0.19	0.959	2	10	regulation of CD4-positive, alpha-beta T cell	BP	1	GATA3,HMGB1	up_VCAV_EC
GO:0045428	0.19	0.959	2	10	regulation of nitric oxide biosynthetic process	BP	1	CD34,TLR4	up_VCAV_EC
GO:0030855	0.19	0.955	2	183	epithelial cell differentiation	BP	1	SALL1,CAV1	up_VSAP_VSMC
GO:0099173	0.19	0.982	1	40	postsynapse organization	BP	1	NRP2	down_ACOR_EC
GO:0009126	0.19	0.982	1	100	purine nucleoside monophosphate metabolic process	BP	1	NDUFA10	down_AFEM_EC
GO:0009167	0.19	0.982	1	100	purine ribonucleoside monophosphate metabolic process	BP	1	NDUFA10	down_AFEM_EC
GO:0098703	0.19	0.985	1	4	calcium ion import across plasma membrane	BP	1	PRNP	down_VCAV_EC
GO:1902656	0.19	0.985	1	4	calcium ion import into cytosol	BP	1	PRNP	down_VCAV_EC
GO:0034135	0.19	0.985	1	4	regulation of toll-like receptor 2 signaling	BP	1	CYBA	down_VCAV_EC
GO:0035584	0.19	0.985	1	4	calcium-mediated signaling using	BP	1	PRNP	down_VCAV_EC
GO:1902307	0.19	0.985	1	4	positive regulation of sodium ion	BP	1	FXYD1	down_VCAV_EC
GO:0045765	0.19	0.982	1	105	regulation of angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0045785	0.19	0.982	1	107	positive regulation of cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0009057	0.19	0.987	1	473	macromolecule catabolic process	BP	1	USP12	down_VFEM_EC
GO:0007166	0.19	0.99	1	686	cell surface receptor signaling pathway	BP	1	GATA5	down_VFEM_VSMC

GO:0001842	0.19	0.987	1	3	neural fold formation	BP	1	HIF1A	down_VSAP_EC
GO:0060316	0.19	0.985	1	4	positive regulation of ryanodine-sensitive calcium-release channel	BP	1	CALM1	down_VSAP_EC
GO:0014831	0.19	0.987	1	3	gastro-intestinal system smooth muscle	BP	1	SULF1	down_VSAP_EC
GO:0001955	0.19	0.987	1	3	blood vessel maturation	BP	1	DDIT3	down_VSAP_EC
GO:0072103	0.19	0.99	1	2	glomerulus vasculature morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0072104	0.19	0.99	1	2	glomerular capillary formation	BP	1	BMP4	up_ACOR_VSMC
GO:0051235	0.19	0.982	1	90	maintenance of location	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0002218	0.19	0.982	1	53	activation of innate immune response	BP	1	NR1H4	up_APUL_EC
GO:0051270	0.19	0.984	1	296	regulation of cellular component movement	BP	1	TBX5	up_APUL_VSMC
GO:0019388	0.19	0.987	1	3	galactose catabolic process	BP	1	GALE	up_VCAV_EC
GO:0060017	0.19	0.987	1	3	parathyroid gland development	BP	1	GATA3	up_VCAV_EC
GO:1900425	0.19	0.99	1	2	negative regulation of defense response to	BP	1	ARG2	up_VCAV_EC
GO:0071347	0.19	0.982	1	25	cellular response to interleukin-1	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:1901879	0.19	0.982	1	26	regulation of protein depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0050900	0.19	0.982	1	89	leukocyte migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0070302	0.19	0.982	1	78	regulation of stress-activated protein kinase	BP	1	ANKRD6	up_VPOR_VSMC
GO:0042180	0.19	0.982	1	61	cellular ketone metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0010975	0.19	0.982	1	103	regulation of neuron projection development	BP	1	SLIT2	up_VPUL_VSMC
GO:1903707	0.19	0.982	1	48	negative regulation of hemopoiesis	BP	1	HOXA9	up_VSAP_VSMC
GO:0003281	0.190217099	0.95523	2	30	ventricular septum development	BP	1	SMAD6,TBX5	up_ACOR_EC
GO:0043534	0.190269338	0.93699	3	57	blood vessel endothelial cell migration	BP	1	ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC
GO:0015672	0.190469938	0.92419	4	89	monovalent inorganic cation transport	BP	1	KCNB1,ACTN2,SLC9A9,PM20D1	up_ACOR_EC
GO:0031323	0.190697916	0.85138	53	1788	regulation of cellular metabolic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,PLCL1,PKIB,SOX9,PKNOX2,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,IFI6,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,RIOX2,RNF114,NRP1,PRKCD,PPP1R26,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0051716	0.191	0.852	53	2001	cellular response to stimulus	BP	1	CMKLR1,MT2A,LEP,LBH,CRY2,ENSCAFG00000009113,RAB20,GAS1,ANGPT4,CD40,DLL1,CRYAB,CPNE7,F3,PLXNA4,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,MFAP4,HCK,TMEM100,PLAGL2,GREM1,HTR1D,NFE2L1,FAM53B,AVPR1A,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,RECK,NR3C1,PTHLH,TBXA2R,LGR6,RAB7A,AXIN2,PPARGC1A,CCL5,CDC42EP5,DMPK,ADAM17,KANK1,TNC,SOD1	up_AFEM_EC
GO:0044237	0.191	0.889	20	3491	cellular metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,MYO1D,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0034728	0.191	0.904	7	56	nucleosome organization	BP	1	PSME4,NASP,SMARCA4,HIST1H1A,ASF1A,ATRX,HP1BP3	up_VCAV_EC
GO:0035050	0.191	0.927	4	28	embryonic heart tube development	BP	1	MEF2C,SOX18,HHEX,HIF1A	up_VCAV_EC
GO:0032608	0.191	0.928	4	24	interferon-beta production	BP	1	NLRX1,RNF216,FLOT1,MAVS	up_VSAP_EC
GO:0072350	0.191	0.94	3	18	tricarboxylic acid metabolic process	BP	1	ACLY,SUCLG1,PDHA1	down_ACOR_VSMC
GO:0045185	0.191	0.939	3	25	maintenance of protein location	BP	1	HSPA5,TLN1,KDELR2	down_VSAP_EC

GO:1902116	0.191	0.941	3	16	negative regulation of organelle assembly	BP	1	FEZ1,EVI5L,FEZ2	up_ACOR_VSMC
GO:0010812	0.191	0.94	3	19	negative regulation of cell-substrate adhesion	BP	1	ANGPT2,APOD,JAG1	up_VCAV_EC
GO:0043551	0.191	0.94	3	17	regulation of phosphatidylinositol 3-	BP	1	TEK,PDGFB,SH3GLB1	up_VCAV_EC
GO:0039694	0.191	0.959	2	9	viral RNA genome replication	BP	1	ATG16L2,INPP5K	up_ACOR_VSMC
GO:0061900	0.191	0.961	2	8	glial cell activation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0150076	0.191	0.961	2	8	neuroinflammatory response	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0034101	0.191	0.981	1	45	erythrocyte homeostasis	BP	1	LYN	down_ACOR_EC
GO:0034341	0.191	0.981	1	43	response to interferon-gamma	BP	1	STX4	down_ACOR_EC
GO:0031295	0.191	0.987	1	3	T cell costimulation	BP	1	CAV1	down_ACOR_VSMC
GO:0009199	0.191	0.982	1	100	ribonucleoside triphosphate metabolic	BP	1	NDUFA10	down_AFEM_EC
GO:0003253	0.191	0.985	1	4	cardiac neural crest cell migration involved in outflow tract	BP	1	SEMA3C	down_VCAV_EC
GO:0032287	0.191	0.985	1	4	peripheral nervous system myelin	BP	1	AKT2	down_VCAV_EC
GO:0001660	0.191	0.987	1	3	fever generation	BP	1	PTGS2	down_VSAP_EC
GO:0045955	0.191	0.987	1	3	negative regulation of calcium ion-dependent	BP	1	REST	down_VSAP_EC
GO:0051205	0.191	0.985	1	4	protein insertion into membrane	BP	1	SH3GLB1	down_VSAP_EC
GO:0050855	0.191	0.985	1	4	regulation of B cell receptor signaling	BP	1	LYN	down_VSAP_EC
GO:0050861	0.191	0.985	1	4	positive regulation of B cell receptor signaling	BP	1	LYN	down_VSAP_EC
GO:0051409	0.191	0.985	1	4	response to nitrosative stress	BP	1	DDIT3	down_VSAP_EC
GO:0051388	0.191	0.99	1	2	positive regulation of neurotrophin TRK receptor signaling	BP	1	TMEM108	up_ACOR_VSMC
GO:1990416	0.191	0.99	1	2	cellular response to brain-derived neurotrophic	BP	1	TMEM108	up_ACOR_VSMC
GO:0015846	0.191	0.99	1	2	polyamine transport	BP	1	AZIN2	up_ACOR_VSMC
GO:0032472	0.191	0.99	1	2	Golgi calcium ion transport	BP	1	ATP2C1	up_ACOR_VSMC
GO:0051643	0.191	0.99	1	2	endoplasmic reticulum localization	BP	1	POLR2M	up_ACOR_VSMC
GO:0060298	0.191	0.99	1	2	positive regulation of sarcomere organization	BP	1	EDN1	up_ACOR_VSMC
GO:1902047	0.191	0.99	1	2	polyamine transmembrane transport	BP	1	AZIN2	up_ACOR_VSMC
GO:1902267	0.191	0.99	1	2	regulation of polyamine transmembrane transport	BP	1	AZIN2	up_ACOR_VSMC
GO:1902269	0.191	0.99	1	2	positive regulation of polyamine	BP	1	AZIN2	up_ACOR_VSMC
GO:1903526	0.191	0.99	1	2	negative regulation of membrane tubulation	BP	1	WASL	up_ACOR_VSMC
GO:0008045	0.191	0.983	1	9	motor neuron axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:0002793	0.191	0.981	1	54	positive regulation of peptide secretion	BP	1	NR1H4	up_APUL_EC
GO:0001649	0.191	0.981	1	54	osteoblast differentiation	BP	1	NPNT	up_APUL_EC
GO:0050714	0.191	0.981	1	54	positive regulation of protein secretion	BP	1	NR1H4	up_APUL_EC
GO:0001787	0.191	0.99	1	2	natural killer cell proliferation	BP	1	ELF4	up_VCAV_EC
GO:0031081	0.191	0.99	1	2	nuclear pore distribution	BP	1	NUP133	up_VCAV_EC
GO:0045342	0.191	0.99	1	2	MHC class II biosynthetic process	BP	1	TLR4	up_VCAV_EC
GO:0045346	0.191	0.99	1	2	regulation of MHC class II biosynthetic process	BP	1	TLR4	up_VCAV_EC
GO:0051664	0.191	0.99	1	2	nuclear pore localization	BP	1	NUP133	up_VCAV_EC
GO:0052646	0.191	0.987	1	3	alditol phosphate metabolic process	BP	1	GK5	up_VCAV_EC
GO:0070494	0.191	0.99	1	2	regulation of thrombin-activated receptor	BP	1	STMN1	up_VCAV_EC

GO:0070495	0.191	0.99	1	2	negative regulation of thrombin-activated receptor signaling	BP	1	STMN1	up_VCAV_EC
GO:1905098	0.191	0.99	1	2	negative regulation of guanyl-nucleotide exchange factor activity	BP	1	STMN1	up_VCAV_EC
GO:0045348	0.191	0.99	1	2	positive regulation of MHC class II biosynthetic	BP	1	TLR4	up_VCAV_EC
GO:0009132	0.191	0.982	1	25	nucleoside diphosphate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0046596	0.19125202	0.98281	1	8	regulation of viral entry into host cell	BP	1	TRIM8	up_ACOR_EC
GO:0070570	0.191340838	0.98279	1	8	regulation of neuron projection regeneration	BP	1	RGMA	up_ACOR_EC
GO:0032770	0.191487174	0.98276	1	8	positive regulation of monooxygenase activity	BP	1	CDH3	up_ACOR_EC
GO:0032462	0.191665123	0.98273	1	8	regulation of protein homooligomerization	BP	1	CLU	up_ACOR_EC
GO:0043067	0.191785464	0.87414	16	479	regulation of programmed cell death	BP	1	NR1H4,SOX9,AQP1,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0048522	0.192	0.839	97	1484	positive regulation of cellular process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,SPARC,JCAD,CASP3,FAM49B,BCAR3,PTPN11,FSCN1,DPYSL3,TRIB3,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,WDR1,MYO1C,PIK3C2A,CHSY1,MSN,KIF5B,LMAN1,HIF1A,DYNLL1,SLC45A3,TNIK,ZPR1,PTPN2,EVI2B,YES1,NEO1,PEG3,MTDH,ESM1,DDX39B,ADAM17,EIF4EBP1,CNOT7,ACTR3,MAGED1,CTNNB1,ANLN,ENSCAFG00000002015,TFRC,APOE,PTP4A1,KLF5,LYN,BNIP3,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,GBP5,SH3GLB1,SDC4,HTT,REST,ABHD5,EIF2S1,PRMT1,CALM1,DISC1,RAD23A,PAK2,LRRTM2,INHBA,NR4A1,HIF1AN,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,ARF4,YWHAH,MADD,MARCKSL1,SEC13,KDM3A,MID1	down_VSAP_EC
GO:1901615	0.192	0.879	14	128	organic hydroxy compound metabolic process	BP	1	SQLE,LSS,SREBF1,HMGCR,INSIG1,ENSCAFG00000018572,DHCR24,MVD,PDXP,FDFT1,LIPC,NUS1,GK5,NUDT3	down_ACOR_VSMC
GO:0010256	0.192	0.878	14	129	endomembrane system organization	BP	1	BAIAP2L1,RAB11A,RAB27A,MTSS1,NECTIN2,HOOK3,CAV2,ABCA1,CREB1,GCC2,DNAJC13,ZW10,ALS2,USP6NL	up_VCAV_EC
GO:0050767	0.192	0.882	12	184	regulation of neurogenesis	BP	1	BMPR1A,TRPV2,NUMBL,THY1,TLX2,GLI3,CDH2,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0001667	0.192	0.888	10	146	ameboidal-type cell migration	BP	1	DCN,SDC4,GLIPR2,KANK2,SYDE1,SEMA3C,SASH1,SPRED1,DDR2,GREM1	down_VCAV_EC
GO:0046822	0.192	0.903	7	53	regulation of nucleocytoplasmic	BP	1	HCLS1,MX2,TMEM173,IWS1,FERMT1,APOD,CTDSPL2	up_VCAV_EC
GO:0071229	0.192	0.903	7	51	cellular response to acid chemical	BP	1	PTGFR,OSR1,PDGFD,RARG,ZEB1,CASTOR1,HTRA2	up_VSAP_EC
GO:0001763	0.192	0.908	6	78	morphogenesis of a branching structure	BP	1	CLSTN1,SEMA3C,B4GALT1,GLI3,RDH10,GREM1	down_VCAV_EC
GO:0034249	0.192	0.909	6	41	negative regulation of cellular amide metabolic	BP	1	ENSCAFG00000000071,ZFP36L1,ANKHD1,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0006672	0.192	0.917	5	33	ceramide metabolic process	BP	1	UGCG,ORMDL3,SMPD1,CLN8,NEU3	up_ACOR_VSMC
GO:0007585	0.192	0.941	3	16	respiratory gaseous exchange	BP	1	FUT8,EDN1,GAA	up_ACOR_VSMC
GO:0001755	0.192	0.94	3	16	neural crest cell migration	BP	1	HTR2B,BMP4,NRP1	up_ACOR_VSMC
GO:1901998	0.192	0.941	3	16	toxin transport	BP	1	CD274,BNIP3,NRP1	up_ACOR_VSMC
GO:0042113	0.192	0.936	3	64	B cell activation	BP	1	CD40,DLL1,CYLD	up_AFEM_EC
GO:0035019	0.192	0.94	3	16	somatic stem cell population maintenance	BP	1	ZFP36L2,RAF1,LBH	up_VSAP_EC
GO:0048667	0.192	0.954	2	140	cell morphogenesis involved in neuron	BP	1	SPG11,NRP2	down_ACOR_EC
GO:1904031	0.192	0.959	2	10	positive regulation of cyclin-dependent protein	BP	1	SLC29A1,CKS2	down_ACOR_VSMC
GO:0001836	0.192	0.956	2	18	release of cytochrome c from mitochondria	BP	1	BNIP3,FAM162A	down_VSAP_EC
GO:0038061	0.192	0.954	2	34	NIK/NF-kappaB signaling	BP	1	GREM1,CYLD	up_AFEM_EC
GO:0006366	0.192	0.959	2	583	transcription by RNA polymerase II	BP	1	EYA1,HOXA9	up_AFEM_VSMC

GO:0045321	0.192	0.954	2	191	leukocyte activation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0006047	0.192	0.985	1	4	UDP-N-acetylglucosamine metabolic process	BP	1	GFPT2	down_VCAV_EC
GO:0006573	0.192	0.985	1	4	valine metabolic process	BP	1	ENSCAFG00000002977	down_VCAV_EC
GO:0008298	0.192	0.985	1	4	intracellular mRNA localization	BP	1	ZFP36L1	down_VCAV_EC
GO:1902003	0.192	0.985	1	4	regulation of amyloid-beta formation	BP	1	PRNP	down_VCAV_EC
GO:0006704	0.192	0.987	1	3	glucocorticoid biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0031946	0.192	0.987	1	3	regulation of glucocorticoid	BP	1	REST	down_VSAP_EC
GO:0034650	0.192	0.987	1	3	cortisol metabolic process	BP	1	REST	down_VSAP_EC
GO:0034651	0.192	0.987	1	3	cortisol biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0090030	0.192	0.987	1	3	regulation of steroid hormone biosynthetic	BP	1	REST	down_VSAP_EC
GO:1902645	0.192	0.987	1	3	tertiary alcohol biosynthetic process	BP	1	REST	down_VSAP_EC
GO:2000064	0.192	0.987	1	3	regulation of cortisol biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0008356	0.192	0.987	1	3	asymmetric cell division	BP	1	ARHGEF2	down_VSAP_EC
GO:0045198	0.192	0.985	1	4	establishment of epithelial cell apical/basal	BP	1	MSN	down_VSAP_EC
GO:0061438	0.192	0.987	1	3	renal system vasculature morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0061439	0.192	0.987	1	3	kidney vasculature morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0001964	0.192	0.99	1	2	startle response	BP	1	GLRB	up_ACOR_VSMC
GO:0017014	0.192	0.99	1	2	protein nitrosylation	BP	1	OXR1	up_ACOR_VSMC
GO:0018119	0.192	0.99	1	2	peptidyl-cysteine S-nitrosylation	BP	1	OXR1	up_ACOR_VSMC
GO:1901963	0.192	0.99	1	2	regulation of cell proliferation involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:0021783	0.192	0.982	1	9	preganglionic parasympathetic fiber	BP	1	PLXNA4	up_AFEM_EC
GO:0048485	0.192	0.982	1	9	sympathetic nervous system development	BP	1	PLXNA4	up_AFEM_EC
GO:0098815	0.192	0.982	1	9	modulation of excitatory postsynaptic potential	BP	1	DMPK	up_AFEM_EC
GO:0035239	0.192	0.984	1	299	tube morphogenesis	BP	1	HOXA3	up_APUL_VSMC
GO:0033089	0.192	0.987	1	3	positive regulation of T cell differentiation in	BP	1	IL7R	up_VCAV_EC
GO:0050746	0.192	0.987	1	3	regulation of lipoprotein metabolic process	BP	1	APOD	up_VCAV_EC
GO:0072378	0.192	0.99	1	2	blood coagulation, fibrin clot formation	BP	1	KLKB1	up_VCAV_EC
GO:0002460	0.192	0.981	1	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	IL18BP	up_VPUL_EC
GO:0034329	0.192	0.981	1	60	cell junction assembly	BP	1	NR1H4	up_VPUL_EC
GO:0072001	0.192	0.982	1	104	renal system development	BP	1	SLIT2	up_VPUL_VSMC
GO:0002440	0.192	0.981	1	51	production of molecular mediator of immune	BP	1	TLR2	up_VSAP_VSMC
GO:0070727	0.192071246	0.86944	19	579	cellular macromolecule localization	BP	1	SH3TC2,KCNB1,EDEM2,AGRN,PLS1,ACTN2,TRIM8,PREB,DCLK2,MAVS,LRRC15,LRP4,LRRC4,CHMP4B,TP53INP2,VPS16,NRP1,HM13,PRKCD	up_ACOR_EC
GO:0045662	0.192100286	0.98265	1	8	negative regulation of myoblast differentiation	BP	1	SOX9	up_ACOR_EC
GO:1902916	0.192116792	0.98264	1	8	positive regulation of protein polyubiquitination	BP	1	NOD2	up_ACOR_EC
GO:0044804	0.192514374	0.98257	1	8	autophagy of nucleus	BP	1	ENSCAFG00000010493	up_ACOR_EC
GO:0032069	0.192761006	0.98252	1	8	regulation of nuclease activity	BP	1	PRKCD	up_ACOR_EC
GO:0071225	0.192866997	0.9825	1	8	cellular response to muramyl dipeptide	BP	1	NOD2	up_ACOR_EC

GO:0048519	0.193	0.834	140	1554	negative regulation of biological process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,IRAK1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,TFPI,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,WDR76,U2AF2,ZW10,INTS7,MNDA,CAPG,SLC29A1,MTDH,HOXA3,PPM1G,TRIP13,SLC25A5,PPP1R15B,PARPBP,SRRT,FBXO5,HSPA9,NAB2,SLC35C2,RAN,PRELID1,BIRC5,INSIG1,PRMT1,CAV1,CDK1,CASP2,FANCI,TIMELESS,THRAP3,LIMA1,FAM129B,NF2,EDC4,AURKB,MMP14,CDKN2C,TOPBP1,ABHD5,EZH2,STMN1,SLC30A1,GREM1,MAP3K20,NEK2,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,HMGB3,HOXA7,SMG9,ARG2,ANXA5,UHRF1,HOXC10,RNF152,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,E2F8,B4GALT1,PPARD,NDC80,RAP2C,YWHAB,NCL,RAC1,NUP62,DTL,PRR11,IQGAP1,SUV39H1,CACTIN,HMGB2,GSTO1,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,ENSCAFG00000005299,EZR,CLSPN,BUB1,RBM14,CORO1A,BEND6,PHACTR4,TTK,ERF,ASPM,TCERG1,ENSCAFG00000010224,TXNDC12,REM1,CTH,NCOA5,ARHGEF2,KNL1,ENSCAFG00000015189,TWIST2,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,H2AFX,CDC5L,ATRIP,EXOSC5,CDKN3,SIX4,MTBP,ZWINT,GEN1,AMER1,ANXA7	down_ACOR_VSMC
GO:0031323	0.193	0.836	116	1788	regulation of cellular metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,MEIS2,ENPP1,ERRFI1,JCAD,SNX25,CBX5,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PGAM1,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,MSN,HIF1A,DYNLL1,SLC45A3,IWS1,DNAJC10,TNIK,NXN,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,SH3GLB1,HTT,REST,ABHD5,ZMYND8,EIF2S1,PRMT1,ARFGEF3,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,LRRTM2,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0044093	0.193	0.857	31	437	positive regulation of molecular function	BP	1	ARHGEF2,VEGFA,PTPN11,TRIB3,PPP1R12A,SMARCA4,DYNLL1,DNAJC10,TNIK,PLCL1,MTDH,ADAM17,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,LYN,DDIT3,FAM162A,MMD,GSK3B,VLDLR,SH3GLB1,TAX1BP3,HTT,REST,ABHD5,CALM1,PAK2,ARF4,MADD	down_VSAP_EC
GO:0048729	0.193	0.865	22	209	tissue morphogenesis	BP	1	HOXB7,PODXL,MEF2C,CHD7,DLL4,STC1,GATA3,EDN1,NTN4,MTSS1,MTOR,BMP2,HHEX,PROX1,BTBD7,EXOC5,TIMELESS,JAG1,BCL10,HIF1A,ALDH1A3,LUZP1	up_VCAV_EC
GO:0008150	0.193	0.957	14	5646	biological_process	BP	1	ANKRD50,ETFA,GPSM2,IVNS1ABP,EXTL2,DARS,SUCLG2,EIF3M,SRSF6,USP33,GABPA,NDUFA10,TSEN15,FSCN1	down_AFEM_EC
GO:0048522	0.193	0.895	10	1484	positive regulation of cellular process	BP	1	ACVRL1,LYN,HOXA3,IGF1R,PDPN,SULF1,HOXA1,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0051607	0.193	0.897	8	58	defense response to virus	BP	1	MAP3K14,F2RL1,NLRX1,TKFC,RNF216,PQBP1,MAVS,DDIT4	up_VSAP_EC
GO:0010646	0.193	0.905	7	945	regulation of cell communication	BP	1	ACVRL1,LYN,IGF1R,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0009108	0.193	0.907	6	68	coenzyme biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0050817	0.193	0.915	5	50	coagulation	BP	1	SERPINE1,APOE,LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0008643	0.193	0.924	4	45	carbohydrate transport	BP	1	CLIP3,ENSCAFG00000014978,AKT2,SLC2A10	down_VCAV_EC
GO:0030433	0.193	0.924	4	38	ubiquitin-dependent ERAD pathway	BP	1	HSP90B1,DNAJC10,DNAJB9,USP14	down_VSAP_EC
GO:0006022	0.193	0.926	4	29	aminoglycan metabolic process	BP	1	PDGFB,LYVE1,CHST7,CHST1	up_VCAV_EC
GO:0010604	0.193	0.929	4	919	positive regulation of macromolecule metabolic	BP	1	NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC

GO:0000184	0.193	0.939	3	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	RNPS1,EIF4A3,SMG9	down_ACOR_VSMC
GO:0070887	0.193	0.941	3	775	cellular response to chemical stimulus	BP	1	CITED2,RAB11B,HSD3B7	down_VPOR_EC
GO:0046427	0.193	0.94	3	16	positive regulation of JAK-STAT cascade	BP	1	LEP,CRLF3,PARP9	up_ACOR_VSMC
GO:0048738	0.193	0.935	3	64	cardiac muscle tissue development	BP	1	DLL1,GREM1,BVES	up_AFEM_EC
GO:2000107	0.193	0.956	2	16	negative regulation of leukocyte apoptotic	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0032413	0.193	0.956	2	15	negative regulation of ion transmembrane transporter activity	BP	1	REM1,CALM1	down_VSAP_EC
GO:0044381	0.193	0.957	2	13	glucose import in response to insulin	BP	1	NR1H4,PTPN11	down_VSAP_EC
GO:0045913	0.193	0.956	2	15	positive regulation of carbohydrate metabolic	BP	1	SLC45A3,PTPN2	down_VSAP_EC
GO:0006956	0.193	0.96	2	8	complement activation	BP	1	C1S,C7	up_ACOR_VSMC
GO:0032924	0.193	0.959	2	9	activin receptor signaling pathway	BP	1	CITED2,TGFBR1	up_ACOR_VSMC
GO:0098754	0.193	0.959	2	9	detoxification	BP	1	SESN1,PARK7	up_ACOR_VSMC
GO:0009953	0.193	0.954	2	34	dorsal/ventral pattern formation	BP	1	GREM1,GREM2	up_AFEM_EC
GO:0030879	0.193	0.954	2	34	mammary gland development	BP	1	HOXA9,LBH	up_AFEM_EC
GO:0042752	0.193	0.954	2	34	regulation of circadian rhythm	BP	1	CRY2,PPARGC1A	up_AFEM_EC
GO:0072329	0.193	0.954	2	34	monocarboxylic acid catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0010165	0.193	0.959	2	9	response to X-ray	BP	1	GATA3,BLM	up_VCAV_EC
GO:0007507	0.193	0.954	2	194	heart development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0045596	0.193	0.954	2	186	negative regulation of cell differentiation	BP	1	HOXA9,CAV1	up_VSAP_VSMC
GO:0002700	0.193	0.981	1	40	regulation of production of molecular mediator of immune response	BP	1	STX4	down_ACOR_EC
GO:0099504	0.193	0.981	1	42	synaptic vesicle cycle	BP	1	STX4	down_ACOR_EC
GO:0003174	0.193	0.985	1	4	mitral valve development	BP	1	BMPR1A	down_VCAV_EC
GO:0070200	0.193	0.985	1	4	establishment of protein localization to telomere	BP	1	NABP2	down_VCAV_EC
GO:1901857	0.193	0.985	1	4	positive regulation of cellular respiration	BP	1	PARK7	down_VCAV_EC
GO:0033234	0.193	0.985	1	4	negative regulation of protein sumoylation	BP	1	PARK7	down_VCAV_EC
GO:0090520	0.193	0.985	1	4	sphingolipid mediated signaling pathway	BP	1	SPNS1	down_VCAV_EC
GO:1902187	0.193	0.985	1	4	negative regulation of viral release from host cell	BP	1	TRIM8	down_VCAV_EC
GO:2001046	0.193	0.985	1	4	positive regulation of integrin-mediated	BP	1	LOXL3	down_VCAV_EC
GO:0006610	0.193	0.986	1	3	ribosomal protein import into nucleus	BP	1	KPNB1	down_VSAP_EC
GO:0030002	0.193	0.986	1	3	cellular anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0051415	0.193	0.986	1	3	microtubule nucleation by interphase microtubule organizing center	BP	1	MZT1	down_VSAP_EC
GO:0051418	0.193	0.986	1	3	microtubule nucleation by microtubule organizing	BP	1	MZT1	down_VSAP_EC
GO:1902855	0.193	0.985	1	4	regulation of non-motile cilium assembly	BP	1	DYNLL1	down_VSAP_EC
GO:1902857	0.193	0.985	1	4	positive regulation of non-motile cilium assembly	BP	1	DYNLL1	down_VSAP_EC
GO:0030320	0.193	0.986	1	3	cellular monovalent inorganic anion	BP	1	ENPP1	down_VSAP_EC
GO:1901660	0.193	0.986	1	3	calcium ion export	BP	1	ATP2B1	down_VSAP_EC
GO:0009214	0.193	0.99	1	2	cyclic nucleotide catabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:1903891	0.193	0.99	1	2	regulation of ATF6-mediated unfolded	BP	1	WFS1	up_ACOR_VSMC
GO:1990966	0.193	0.99	1	2	ATP generation from poly-ADP-D-ribose	BP	1	NMNAT1	up_ACOR_VSMC

GO:2000721	0.193	0.99	1	2	positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation	BP	1	NPNT	up_ACOR_VSMC
GO:0015012	0.193	0.982	1	9	heparan sulfate proteoglycan biosynthetic	BP	1	XYLT1	up_AFEM_EC
GO:0043368	0.193	0.982	1	9	positive T cell selection	BP	1	CYLD	up_AFEM_EC
GO:0006954	0.193	0.982	1	147	inflammatory response	BP	1	TLR2	up_AFEM_VSMC
GO:0019953	0.193	0.982	1	152	sexual reproduction	BP	1	HOXA9	up_AFEM_VSMC
GO:0032504	0.193	0.982	1	152	multicellular organism reproduction	BP	1	HOXA9	up_AFEM_VSMC
GO:0048609	0.193	0.982	1	152	multicellular organismal reproductive process	BP	1	HOXA9	up_AFEM_VSMC
GO:0007160	0.193	0.981	1	56	cell-matrix adhesion	BP	1	NPNT	up_APUL_EC
GO:0022603	0.193	0.984	1	301	regulation of anatomical structure morphogenesis	BP	1	TBX5	up_APUL_VSMC
GO:0002154	0.193	0.99	1	2	thyroid hormone mediated signaling	BP	1	PRCP	up_VCAV_EC
GO:0018202	0.193	0.986	1	3	peptidyl-histidine modification	BP	1	DPH5	up_VCAV_EC
GO:0002521	0.193	0.982	1	149	leukocyte differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0006954	0.193	0.982	1	147	inflammatory response	BP	1	C6	up_VCAV_VSMC
GO:0007568	0.193	0.981	1	50	aging	BP	1	MME	up_VFEM_EC
GO:0009260	0.193	0.981	1	83	ribonucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046390	0.193	0.981	1	83	ribose phosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:2001020	0.193	0.981	1	88	regulation of response to DNA damage stimulus	BP	1	EYA1	up_VFEM_VSMC
GO:0031032	0.193	0.981	1	61	actomyosin structure organization	BP	1	MYBPC2	up_VPUL_EC
GO:0050679	0.193	0.981	1	62	positive regulation of epithelial cell proliferation	BP	1	CCL24	up_VPUL_EC
GO:0042692	0.193	0.982	1	105	muscle cell differentiation	BP	1	TBX5	up_VPUL_VSMC
GO:0071219	0.193	0.981	1	50	cellular response to molecule of bacterial	BP	1	TLR2	up_VSAP_VSMC
GO:0045822	0.193318174	0.98242	1	8	negative regulation of heart contraction	BP	1	RNLS	up_ACOR_EC
GO:2001233	0.193797447	0.90546	6	149	regulation of apoptotic signaling pathway	BP	1	IFI6,MAPK8IP2,FIGNL1,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0048844	0.19380155	0.95385	2	30	artery morphogenesis	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0048518	0.194	0.832	150	1676	positive regulation of biological process	BP	1	ACSL3,FSCN1,HMGB1,RNPS1,SREBF1,IRAK1,ANLN,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,NEDD4,U2AF2,MNDA,SLC29A1,MTDH,HOXA3,COLGALT1,SLC25A5,SRRT,SDC1,CTDNEP1,FBXO5,SLC35C2,RAN,PRELID1,CDCA7L,RFC2,BIRC5,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,CASP2,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,NF2,AURKB,MMP14,ABHD5,EZH2,STMN1,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,FEN1,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,PCNA,DHX33,BID,ARG2,SF3B4,CKS2,PDCD2,RNF152,HOXB7,POC1A,BRCA1,MVD,FASTKD3,EIF5A,E2F8,B4GALT1,TFRC,NRAS,PPARD,CDC6,NDC80,RAP2C,HIST1H1A,CYCS,FAM49B,NCL,RAC1,NUP62,EMP2,DTL,PDXP,FOSL1,PLK4,IQGAP2,CACTIN,HMGB2,GSTO1,DMAP1,CDC42EP4,SMC3,CDK2,FGF5,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,SMC6,TOX,ELOVL6,RBM14,MIOS,RAD23A,CORO1A,BEND6,POLR3F,CDC20,ASPM,MELK,ARPC1B,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,CDC25A,SUPT16H,TWIST2,TADA2A,HOXA9,GLI1,JMJD6,PPIH,UBE2C,NUS1,CCT4,AMOTL1,SIX4,MTBP,DEPDC1B,TPBG,ENSCAFG00000017103,GEN1,AMER1,DCUN1D5,PIK3CD	down_ACOR_VSMC

GO:0040011	0.194	0.845	55	505	locomotion	BP	1	FGF13,VEGFD,SEMA5A,LGR6,HTR2B,TCAF1,ZRANB1,RECK,FEZ1,FERMT1,BMP4,GJA1,HRH1,SH3RF2,TP53INP1,SASH1,LMO4,FGF18,F2RL1,NRP1,PTPN22,GPM6A,UNC5B,EVL,SPINT2,TBX20,TBX5,PRKCE,FZD3,DAG1,FUT8,POMK,APP,LAMA3,PSEN1,SEMA6D,SYNJ2BP,JUP,CCL5,DDR2,DUSP22,EDN1,ARID5B,FAM107A,JAM3,DISC1,FEZ2,SUN1,WASL,DOCK5,ENSCAFG00000029553,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0000902	0.194	0.856	31	266	cell morphogenesis	BP	1	CDC7,EPYC,ZRANB1,SHROOM3,FEZ1,FGFR2,SEC24B,WASF3,LATS2,ZNF365,TMEM108,ARHGEF26,ZMYM2,NRP1,GPM6A,ULK2,UNC5B,SPINT2,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL,DOCK5,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0030036	0.194	0.86	26	223	actin cytoskeleton organization	BP	1	SYNPO2L,PDLIM3,EPB41L4A,ARHGAP28,ACTN2,SYNPO2,XIRP1,WASF3,NEBL,F2RL1,JMY,NRP1,EVL,PRKCE,MYO1B,TTC17,RND1,SIPA1L1,SSH3,EDN1,FAM107A,JAM3,INPP5K,WASL,ATP2C1,MYOZ2	up_ACOR_VSMC
GO:0071407	0.194	0.873	16	129	cellular response to organic cyclic compound	BP	1	LBH,SKP2,BMP4,MED14,AR,FAM210B,ADCY6,AKAP6,CREBRF,APLP1,JUP,NR3C1,FAM107A,DDIT4,INPP5K,PARK7	up_ACOR_VSMC
GO:0098771	0.194	0.876	14	180	inorganic ion homeostasis	BP	1	SLC39A7,ERO1A,ENPP1,ATP2B1,TMTC2,HIF1A,NEO1,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0019439	0.194	0.881	12	150	aromatic compound catabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,ALDH1L2,HIF1A,ZPR1,ENTPD4,SMG7,CNOT7,ALDOC,SND1	down_VSAP_EC
GO:0030335	0.194	0.883	11	165	positive regulation of cell migration	BP	1	PDGFRB,GLIPR2,RHOD,AKT2,SYDE1,SEMA3C,THY1,SASH1,TWIST2,DDR2,RAC2	down_VCAV_EC
GO:0034655	0.194	0.884	11	135	nucleobase-containing compound catabolic	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ZPR1,ENTPD4,SMG7,CNOT7,ALDOC,SND1	down_VSAP_EC
GO:0006469	0.194	0.888	10	78	negative regulation of protein kinase activity	BP	1	BMP4,LATS2,CDKN1A,SMPD1,PSEN1,DUSP22,DUSP26,LRRC4,INPP5K,PARK7	up_ACOR_VSMC
GO:0061572	0.194	0.902	7	50	actin filament bundle organization	BP	1	WNT11,FAM107A,ARHGEF5,ABL1,PIK3R1,MYO1B,BAG4	up_VSAP_EC
GO:0001890	0.194	0.907	6	51	placenta development	BP	1	PCDH12,PDGFB,MDFI,PTGS2,HIF1A,VASH1	up_VCAV_EC
GO:0050796	0.194	0.916	5	33	regulation of insulin secretion	BP	1	LEP,TM7SF3,PRKCE,CCL5,PFKL	up_ACOR_VSMC
GO:1904029	0.194	0.925	4	28	regulation of cyclin-dependent protein kinase	BP	1	SLC29A1,CDKN2C,CKS2,CCNB3	down_ACOR_VSMC
GO:0007164	0.194	0.927	4	23	establishment of tissue polarity	BP	1	MLLT3,SEC24B,ZNRF3,FZD3	up_ACOR_VSMC
GO:0001736	0.194	0.927	4	23	establishment of planar polarity	BP	1	MLLT3,SEC24B,ZNRF3,FZD3	up_ACOR_VSMC
GO:0042307	0.194	0.926	4	23	positive regulation of protein import into	BP	1	LEP,PTPN22,PSEN1,JUP	up_ACOR_VSMC
GO:0006357	0.194	0.925	4	547	regulation of transcription by RNA polymerase II	BP	1	EYA1,HOXA9,HOXA7,SIX1	up_VFEM_EC
GO:0034767	0.194	0.936	3	31	positive regulation of ion transmembrane transport	BP	1	FXYD1,THY1,PARK7	down_VCAV_EC
GO:0019218	0.194	0.937	3	25	regulation of steroid metabolic process	BP	1	NR1H4,APOE,REST	down_VSAP_EC
GO:0002090	0.194	0.956	2	14	regulation of receptor internalization	BP	1	VEGFA,LRRTM2	down_VSAP_EC
GO:0051646	0.194	0.957	2	12	mitochondrion localization	BP	1	HIF1A,TRAK1	down_VSAP_EC
GO:0003009	0.194	0.959	2	9	skeletal muscle contraction	BP	1	DMPK,GAA	up_ACOR_VSMC
GO:0001952	0.194	0.954	2	34	regulation of cell-matrix adhesion	BP	1	HOXA7,GREM1	up_AFEM_EC
GO:0010975	0.194	0.953	2	103	regulation of neuron projection development	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0008045	0.194	0.959	2	9	motor neuron axon guidance	BP	1	SLIT2,PLXNA4	up_VSAP_EC
GO:0006836	0.194	0.981	1	47	neurotransmitter transport	BP	1	STX4	down_ACOR_EC
GO:0007178	0.194	0.981	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:0006508	0.194	0.986	1	483	proteolysis	BP	1	USP12	down_VFEM_EC
GO:0032341	0.194	0.986	1	3	aldosterone metabolic process	BP	1	REST	down_VSAP_EC
GO:0032344	0.194	0.986	1	3	regulation of aldosterone metabolic process	BP	1	REST	down_VSAP_EC
GO:0035112	0.194	0.986	1	3	genitalia morphogenesis	BP	1	CTNNB1	down_VSAP_EC

GO:0036462	0.194	0.985	1	4	TRAIL-activated apoptotic signaling pathway	BP	1	ATF3	down_VSAP_EC
GO:0051343	0.194	0.985	1	4	positive regulation of cyclic-nucleotide phosphodiesterase	BP	1	CALM1	down_VSAP_EC
GO:0060766	0.194	0.986	1	3	negative regulation of androgen receptor	BP	1	SMARCA4	down_VSAP_EC
GO:2001015	0.194	0.986	1	3	negative regulation of skeletal muscle cell	BP	1	SIX4	down_VSAP_EC
GO:0008212	0.194	0.986	1	3	mineralocorticoid metabolic process	BP	1	REST	down_VSAP_EC
GO:0051342	0.194	0.985	1	4	regulation of cyclic-nucleotide	BP	1	CALM1	down_VSAP_EC
GO:0002578	0.194	0.99	1	2	negative regulation of antigen processing and	BP	1	TAPBPL	up_ACOR_VSMC
GO:0014072	0.194	0.99	1	2	response to isoquinoline alkaloid	BP	1	PRKCE	up_ACOR_VSMC
GO:0043278	0.194	0.99	1	2	response to morphine	BP	1	PRKCE	up_ACOR_VSMC
GO:0043490	0.194	0.99	1	2	malate-aspartate shuttle	BP	1	SLC25A12	up_ACOR_VSMC
GO:0048817	0.194	0.99	1	2	negative regulation of hair follicle maturation	BP	1	FERMT1	up_ACOR_VSMC
GO:1901858	0.194	0.99	1	2	regulation of mitochondrial DNA	BP	1	PPARGC1A	up_ACOR_VSMC
GO:1904684	0.194	0.99	1	2	negative regulation of metalloendopeptidase	BP	1	RECK	up_ACOR_VSMC
GO:1905049	0.194	0.99	1	2	negative regulation of metallopeptidase activity	BP	1	RECK	up_ACOR_VSMC
GO:0000002	0.194	0.982	1	9	mitochondrial genome maintenance	BP	1	PPARGC1A	up_AFEM_EC
GO:0010224	0.194	0.982	1	9	response to UV-B	BP	1	MFAP4	up_AFEM_EC
GO:0021515	0.194	0.982	1	9	cell differentiation in spinal cord	BP	1	HOXC10	up_AFEM_EC
GO:0031103	0.194	0.982	1	9	axon regeneration	BP	1	TNC	up_AFEM_EC
GO:0042462	0.194	0.982	1	9	eye photoreceptor cell development	BP	1	THRB	up_AFEM_EC
GO:0045577	0.194	0.982	1	9	regulation of B cell differentiation	BP	1	CYLD	up_AFEM_EC
GO:0046189	0.194	0.982	1	9	phenol-containing compound biosynthetic	BP	1	MOXD1	up_AFEM_EC
GO:0070233	0.194	0.982	1	9	negative regulation of T cell apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0070986	0.194	0.982	1	9	left/right axis specification	BP	1	DLL1	up_AFEM_EC
GO:2001233	0.194	0.982	1	149	regulation of apoptotic signaling pathway	BP	1	EYA1	up_AFEM_VSMC
GO:0032990	0.194	0.982	1	167	cell part morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0033002	0.194	0.981	1	55	muscle cell proliferation	BP	1	TBX5	up_APUL_EC
GO:0040012	0.194	0.984	1	303	regulation of locomotion	BP	1	TBX5	up_APUL_VSMC
GO:0045059	0.194	0.986	1	3	positive thymic T cell selection	BP	1	ITPKB	up_VCAV_EC
GO:0019319	0.194	0.981	1	26	hexose biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0044282	0.194	0.981	1	89	small molecule catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0030041	0.194	0.981	1	62	actin filament polymerization	BP	1	CCL24	up_VPUL_EC
GO:0043122	0.194	0.981	1	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	up_VPUL_EC
GO:0045927	0.194	0.981	1	61	positive regulation of growth	BP	1	TBX5	up_VPUL_EC
GO:0007224	0.194	0.981	1	50	smoothened signaling pathway	BP	1	SHOX2	up_VSAP_VSMC
GO:0051693	0.194102479	0.98227	1	8	actin filament capping	BP	1	TMOD1	up_ACOR_EC
GO:0032703	0.194367992	0.98222	1	8	negative regulation of interleukin-2 production	BP	1	NR1H4	up_ACOR_EC
GO:0010837	0.194380873	0.98222	1	8	regulation of keratinocyte proliferation	BP	1	CDH3	up_ACOR_EC
GO:0002726	0.194557005	0.98218	1	8	positive regulation of T cell cytokine production	BP	1	FZD5	up_ACOR_EC
GO:0002076	0.194609204	0.98217	1	8	osteoblast development	BP	1	PTH1R	up_ACOR_EC

GO:0060255	0.195	0.835	116	1782	regulation of macromolecule metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,MEIS2,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,CBX5,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PGAM1,TMED2,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,MSN,HIF1A,IWS1,DNAJC10,ACTG2,TNIK,NXN,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,STRAP,DDIT3,FAM162A,BACH1,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,HTT,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,SPOP,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,LRRTM2,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0045666	0.195	0.891	9	68	positive regulation of neuron differentiation	BP	1	CDON,HOXD3,IRX3,ZEB1,SHOX2,GDPD5,CYB5D2,NCK1,MAP2K2	up_VSAP_EC
GO:0030705	0.195	0.896	8	56	cytoskeleton-dependent intracellular transport	BP	1	RHOT1,TMEM108,IFT43,APP,DYNC1I2,SUN1,DYNC1I1,ENSCAFG00000013536	up_ACOR_VSMC
GO:0006631	0.195	0.899	7	93	fatty acid metabolic process	BP	1	GPAM,AKT2,ACAA1,THNSL2,PEX5,LONP2,ACAT1	down_VCAV_EC
GO:0034764	0.195	0.901	7	50	positive regulation of transmembrane transport	BP	1	AMIGO1,ABL1,KLF15,C1QTNF2,PIK3R1,AZIN2,FXYD1	up_VSAP_EC
GO:0046165	0.195	0.908	6	42	alcohol biosynthetic process	BP	1	PLCG2,PCBD1,PPIP5K1,MOXD1,PTS,PARK7	up_ACOR_VSMC
GO:0006119	0.195	0.908	6	40	oxidative phosphorylation	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,NDUFS2,NDUFV1	up_VSAP_EC
GO:0006487	0.195	0.915	5	34	protein N-linked glycosylation	BP	1	ST3GAL5,CCDC126,MAGT1,STT3B,FUT8	up_ACOR_VSMC
GO:0048015	0.195	0.923	4	48	phosphatidylinositol-mediated signaling	BP	1	PDGFRB,DCN,ZFP36L1,MYDGF	down_VCAV_EC
GO:0048017	0.195	0.923	4	48	inositol lipid-mediated signaling	BP	1	PDGFRB,DCN,ZFP36L1,MYDGF	down_VCAV_EC
GO:0060048	0.195	0.924	4	30	cardiac muscle contraction	BP	1	PDE4D,STC1,MTOR,KCNJ2	up_VCAV_EC
GO:0045844	0.195	0.926	4	24	positive regulation of striated muscle tissue	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0048636	0.195	0.926	4	24	positive regulation of muscle organ	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0000387	0.195	0.938	3	19	spliceosomal snRNP assembly	BP	1	USP4,PRMT5,GEMIN7	down_ACOR_VSMC
GO:1901654	0.195	0.936	3	31	response to ketone	BP	1	ADCY6,NR3C1,PARK7	down_VCAV_EC
GO:0032879	0.195	0.94	3	767	regulation of localization	BP	1	HOXA3,TBX5,SLIT2	up_VPUL_VSMC
GO:0007585	0.195	0.939	3	16	respiratory gaseous exchange	BP	1	CCBE1,PASK,ZFAND5	up_VSAP_EC
GO:1902108	0.195	0.956	2	14	regulation of mitochondrial membrane permeability involved in	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0014829	0.195	0.959	2	8	vascular smooth muscle contraction	BP	1	EDN1,DOCK5	up_ACOR_VSMC
GO:0033158	0.195	0.959	2	8	regulation of protein import into nucleus,	BP	1	CDKN1A,PSEN1	up_ACOR_VSMC
GO:0061548	0.195	0.959	2	8	ganglion development	BP	1	NRP1,FZD3	up_ACOR_VSMC
GO:0001938	0.195	0.953	2	34	positive regulation of endothelial cell	BP	1	F3,ADAM17	up_AFEM_EC
GO:0061213	0.195	0.957	2	11	positive regulation of mesonephros	BP	1	HOXB7,GATA3	up_VCAV_EC
GO:1901522	0.195	0.958	2	9	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical	BP	1	BMP2,HIF1A	up_VCAV_EC
GO:0009127	0.195	0.98	1	47	purine nucleoside monophosphate biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0009168	0.195	0.98	1	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0009144	0.195	0.981	1	103	purine nucleoside triphosphate metabolic	BP	1	NDUFA10	down_AFEM_EC

GO:0006790	0.195	0.981	1	99	sulfur compound metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0006171	0.195	0.983	1	5	cAMP biosynthetic process	BP	1	ADCY6	down_VCAV_EC
GO:0042135	0.195	0.985	1	4	neurotransmitter catabolic process	BP	1	MAOA	down_VCAV_EC
GO:0046058	0.195	0.983	1	5	cAMP metabolic process	BP	1	ADCY6	down_VCAV_EC
GO:0006482	0.195	0.984	1	5	protein demethylation	BP	1	HR	down_VCAV_EC
GO:0008214	0.195	0.984	1	5	protein dealkylation	BP	1	HR	down_VCAV_EC
GO:0010155	0.195	0.984	1	4	regulation of proton transport	BP	1	PARK7	down_VCAV_EC
GO:0016577	0.195	0.984	1	5	histone demethylation	BP	1	HR	down_VCAV_EC
GO:0060712	0.195	0.985	1	4	spongiotrophoblast layer development	BP	1	ZFP36L1	down_VCAV_EC
GO:0060753	0.195	0.984	1	4	regulation of mast cell chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0070076	0.195	0.984	1	5	histone lysine demethylation	BP	1	HR	down_VCAV_EC
GO:0070257	0.195	0.984	1	4	positive regulation of mucus secretion	BP	1	CYBA	down_VCAV_EC
GO:0071941	0.195	0.984	1	4	nitrogen cycle metabolic process	BP	1	SUOX	down_VCAV_EC
GO:0001503	0.195	0.981	1	109	ossification	BP	1	HDAC7	down_VPOR_EC
GO:0001833	0.195	0.984	1	4	inner cell mass cell proliferation	BP	1	ZPR1	down_VSAP_EC
GO:0010560	0.195	0.986	1	3	positive regulation of glycoprotein biosynthetic	BP	1	CTNNB1	down_VSAP_EC
GO:1903020	0.195	0.986	1	3	positive regulation of glycoprotein metabolic	BP	1	CTNNB1	down_VSAP_EC
GO:0021769	0.195	0.989	1	2	orbitofrontal cortex development	BP	1	FGFR2	up_ACOR_VSMC
GO:0035607	0.195	0.989	1	2	fibroblast growth factor receptor signaling pathway involved in	BP	1	FGFR2	up_ACOR_VSMC
GO:0072318	0.195	0.989	1	2	clathrin coat disassembly	BP	1	DNAJC6	up_ACOR_VSMC
GO:0072319	0.195	0.989	1	2	vesicle uncoating	BP	1	DNAJC6	up_ACOR_VSMC
GO:0010870	0.195	0.989	1	2	positive regulation of receptor biosynthetic	BP	1	EDN1	up_ACOR_VSMC
GO:0021847	0.195	0.989	1	2	ventricular zone neuroblast division	BP	1	FGFR2	up_ACOR_VSMC
GO:0031666	0.195	0.989	1	2	positive regulation of lipopolysaccharide-mediated signaling	BP	1	SASH1	up_ACOR_VSMC
GO:0032095	0.195	0.989	1	2	regulation of response to food	BP	1	LEP	up_ACOR_VSMC
GO:0032096	0.195	0.989	1	2	negative regulation of response to food	BP	1	LEP	up_ACOR_VSMC
GO:0032098	0.195	0.989	1	2	regulation of appetite	BP	1	LEP	up_ACOR_VSMC
GO:0032099	0.195	0.989	1	2	negative regulation of appetite	BP	1	LEP	up_ACOR_VSMC
GO:0038108	0.195	0.989	1	2	negative regulation of appetite by leptin-mediated signaling	BP	1	LEP	up_ACOR_VSMC
GO:0048671	0.195	0.989	1	2	negative regulation of collateral sprouting	BP	1	ULK2	up_ACOR_VSMC
GO:0051767	0.195	0.989	1	2	nitric-oxide synthase biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0051769	0.195	0.989	1	2	regulation of nitric-oxide synthase biosynthetic	BP	1	EDN1	up_ACOR_VSMC
GO:0010002	0.195	0.982	1	9	cardioblast differentiation	BP	1	GREM1	up_AFEM_EC
GO:0030206	0.195	0.982	1	9	chondroitin sulfate biosynthetic process	BP	1	XYLT1	up_AFEM_EC
GO:0032309	0.195	0.982	1	9	icosanoid secretion	BP	1	LEP	up_AFEM_EC
GO:0042417	0.195	0.982	1	9	dopamine metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0044458	0.195	0.982	1	9	motile cilium assembly	BP	1	SPATA6	up_AFEM_EC
GO:0045920	0.195	0.982	1	9	negative regulation of exocytosis	BP	1	RAB7A	up_AFEM_EC

GO:0050999	0.195	0.982	1	9	regulation of nitric-oxide synthase activity	BP	1	LEP	up_AFEM_EC
GO:1900745	0.195	0.982	1	9	positive regulation of p38MAPK cascade	BP	1	LEP	up_AFEM_EC
GO:1905331	0.195	0.982	1	9	negative regulation of morphogenesis of an	BP	1	GREM1	up_AFEM_EC
GO:1905476	0.195	0.982	1	9	negative regulation of protein localization to	BP	1	LRRC15	up_AFEM_EC
GO:0000075	0.195	0.981	1	91	cell cycle checkpoint	BP	1	TAOK1	up_AORT_EC
GO:0007420	0.195	0.982	1	169	brain development	BP	1	WNT7A	up_AORT_VSMC
GO:0030155	0.195	0.982	1	180	regulation of cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0040017	0.195	0.982	1	180	positive regulation of locomotion	BP	1	WNT7A	up_AORT_VSMC
GO:0002329	0.195	0.989	1	2	pre-B cell differentiation	BP	1	ATP11C	up_VCAV_EC
GO:0035983	0.195	0.989	1	2	response to trichostatin A	BP	1	MEF2C	up_VCAV_EC
GO:0035984	0.195	0.989	1	2	cellular response to trichostatin A	BP	1	MEF2C	up_VCAV_EC
GO:2000111	0.195	0.989	1	2	positive regulation of macrophage apoptotic	BP	1	MEF2C	up_VCAV_EC
GO:0006729	0.195	0.984	1	4	tetrahydrobiopterin biosynthetic process	BP	1	GCH1	up_VCAV_EC
GO:0046146	0.195	0.984	1	4	tetrahydrobiopterin metabolic process	BP	1	GCH1	up_VCAV_EC
GO:0006090	0.195	0.981	1	26	pyruvate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0001738	0.195	0.981	1	27	morphogenesis of a polarized epithelium	BP	1	PTK7	up_VPOR_EC
GO:1900542	0.195	0.981	1	26	regulation of purine nucleotide metabolic	BP	1	FBP1	up_VPOR_EC
GO:0090596	0.195	0.981	1	84	sensory organ morphogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0043547	0.195	0.981	1	61	positive regulation of GTPase activity	BP	1	CCL24	up_VPUL_EC
GO:0046879	0.195	0.981	1	63	hormone secretion	BP	1	NR1H4	up_VPUL_EC
GO:0003206	0.195	0.981	1	51	cardiac chamber morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0048512	0.195062632	0.98208	1	8	circadian behavior	BP	1	PTGDS	up_ACOR_EC
GO:1901215	0.195148847	0.93461	3	57	negative regulation of neuron death	BP	1	CHMP4B,NRP1,PM20D1	up_ACOR_EC
GO:0006677	0.195362737	0.98203	1	8	glycosylceramide metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0061298	0.195402832	0.98202	1	8	retina vasculature development in camera-	BP	1	NRP1	up_ACOR_EC
GO:0048340	0.1954805	0.982	1	8	paraxial mesoderm morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0007183	0.195515781	0.982	1	8	SMAD protein complex assembly	BP	1	SMAD6	up_ACOR_EC
GO:0008406	0.195527706	0.93443	3	57	gonad development	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:0045137	0.195527706	0.93443	3	57	development of primary sexual characteristics	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:0008285	0.196	0.865	20	201	negative regulation of cell proliferation	BP	1	EPHB1,TNFAIP3,MEF2C,FERMT1,DLL4,RAPGEF1,GATA3,PELI1,MTSS1,ARG2,BMP2,CAV2,PROX1,MCC,APOD,RAPGEF2,CTNNA1,CNOT7,VASH1,ZEB1	up_VCAV_EC
GO:0010639	0.196	0.875	14	128	negative regulation of organelle organization	BP	1	ARHGAP28,TMOD1,STMN1,SWAP70,TAOK1,RAD21,ZW10,KDM5A,KDM3A,ATRX,DCP2,TMOD3,ARHGEF2,FBXO5	up_VCAV_EC
GO:2001234	0.196	0.89	9	75	negative regulation of apoptotic signaling	BP	1	TNFAIP3,FIGNL1,PTGS2,CTNNA1,RIPK1,ITGA6,HIF1A,IVNS1ABP,ARHGEF2	up_VCAV_EC
GO:0043433	0.196	0.906	6	49	negative regulation of DNA-binding transcription factor activity	BP	1	TNFAIP3,NLRC5,PELI1,PROX1,ENSCAFG00000010596,CD200	up_VCAV_EC
GO:0031325	0.196	0.909	6	914	positive regulation of cellular metabolic process	BP	1	HOXA11,HOXA9,SALL1,PRR16,CAV1,SHOX2	up_VSAP_VSMC
GO:0032989	0.196	0.922	4	292	cellular component morphogenesis	BP	1	ARHGEF2,ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0034394	0.196	0.937	3	19	protein localization to cell surface	BP	1	USP4,SLC29A1,EMP2	down_ACOR_VSMC
GO:0009914	0.196	0.934	3	64	hormone transport	BP	1	LEP,CRY2,CCL5	up_AFEM_EC
GO:0071363	0.196	0.934	3	188	cellular response to growth factor stimulus	BP	1	ENSCAFG00000002015,ASPN,ACVR2A	up_VPOR_EC

GO:0019682	0.196	0.957	2	10	glyceraldehyde-3-phosphate metabolic	BP	1	TKT,PGD	down_ACOR_VSMC
GO:0015991	0.196	0.955	2	16	ATP hydrolysis coupled proton transport	BP	1	ATP5MC1,ATP6V0C	down_VCAV_EC
GO:0050854	0.196	0.955	2	16	regulation of antigen receptor-mediated	BP	1	PRNP,THY1	down_VCAV_EC
GO:0090662	0.196	0.955	2	16	ATP hydrolysis coupled transmembrane transport	BP	1	ATP5MC1,ATP6V0C	down_VCAV_EC
GO:0099131	0.196	0.955	2	16	ATP hydrolysis coupled ion transmembrane	BP	1	ATP5MC1,ATP6V0C	down_VCAV_EC
GO:0045995	0.196	0.98	1	40	regulation of embryonic development	BP	1	SULF1	down_ACOR_EC
GO:0051701	0.196	0.98	1	45	interaction with host	BP	1	NEDD4	down_ACOR_EC
GO:0009161	0.196	0.981	1	103	ribonucleoside monophosphate	BP	1	NDUFA10	down_AFEM_EC
GO:0006689	0.196	0.984	1	4	ganglioside catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0032383	0.196	0.984	1	4	regulation of intracellular cholesterol transport	BP	1	SCP2	down_VCAV_EC
GO:0072321	0.196	0.984	1	4	chaperone-mediated protein transport	BP	1	CLIP3	down_VCAV_EC
GO:0032377	0.196	0.984	1	4	regulation of intracellular lipid transport	BP	1	SCP2	down_VCAV_EC
GO:0032380	0.196	0.984	1	4	regulation of intracellular sterol transport	BP	1	SCP2	down_VCAV_EC
GO:0034116	0.196	0.984	1	4	positive regulation of heterotypic cell-cell	BP	1	THY1	down_VCAV_EC
GO:0036462	0.196	0.984	1	4	TRAIL-activated apoptotic signaling pathway	BP	1	PARK7	down_VCAV_EC
GO:0042573	0.196	0.984	1	4	retinoic acid metabolic process	BP	1	RDH10	down_VCAV_EC
GO:0046533	0.196	0.984	1	4	negative regulation of photoreceptor cell	BP	1	THRB	down_VCAV_EC
GO:0061218	0.196	0.984	1	4	negative regulation of mesonephros	BP	1	GREM1	down_VCAV_EC
GO:0006820	0.196	0.981	1	109	anion transport	BP	1	RAB11B	down_VPOR_EC
GO:0001654	0.196	0.981	1	110	eye development	BP	1	CITED2	down_VPOR_EC
GO:0048880	0.196	0.981	1	110	sensory system development	BP	1	CITED2	down_VPOR_EC
GO:0150063	0.196	0.981	1	110	visual system development	BP	1	CITED2	down_VPOR_EC
GO:0045935	0.196	0.986	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0045719	0.196	0.986	1	3	negative regulation of glycogen biosynthetic	BP	1	ENPP1	down_VSAP_EC
GO:0070874	0.196	0.986	1	3	negative regulation of glycogen metabolic	BP	1	ENPP1	down_VSAP_EC
GO:0002281	0.196	0.989	1	2	macrophage activation involved in immune	BP	1	PRKCE	up_ACOR_VSMC
GO:0002092	0.196	0.982	1	9	positive regulation of receptor internalization	BP	1	GREM1	up_AFEM_EC
GO:0002228	0.196	0.982	1	9	natural killer cell mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0003009	0.196	0.982	1	9	skeletal muscle contraction	BP	1	DMPK	up_AFEM_EC
GO:0042267	0.196	0.982	1	9	natural killer cell mediated cytotoxicity	BP	1	LEP	up_AFEM_EC
GO:0044060	0.196	0.982	1	9	regulation of endocrine process	BP	1	CRY2	up_AFEM_EC
GO:0045616	0.196	0.982	1	9	regulation of keratinocyte differentiation	BP	1	HOXA7	up_AFEM_EC
GO:0045655	0.196	0.982	1	9	regulation of monocyte differentiation	BP	1	HOXA7	up_AFEM_EC
GO:0046329	0.196	0.982	1	9	negative regulation of JNK cascade	BP	1	CYLD	up_AFEM_EC
GO:0048246	0.196	0.982	1	9	macrophage chemotaxis	BP	1	CMKLR1	up_AFEM_EC
GO:0050857	0.196	0.982	1	9	positive regulation of antigen receptor-mediated signaling	BP	1	CYLD	up_AFEM_EC
GO:0098754	0.196	0.982	1	9	detoxification	BP	1	SOD1	up_AFEM_EC
GO:1905521	0.196	0.982	1	9	regulation of macrophage migration	BP	1	CMKLR1	up_AFEM_EC
GO:0051223	0.196	0.982	1	181	regulation of protein transport	BP	1	ARG2	up_AORT_VSMC

GO:0051930	0.196	0.986	1	3	regulation of sensory perception of pain	BP	1	ACPP	up_VCAV_EC
GO:0051931	0.196	0.986	1	3	regulation of sensory perception	BP	1	ACPP	up_VCAV_EC
GO:0071609	0.196	0.986	1	3	chemokine (C-C motif) ligand 5 production	BP	1	ARG2	up_VCAV_EC
GO:0071649	0.196	0.986	1	3	regulation of chemokine (C-C motif) ligand 5	BP	1	ARG2	up_VCAV_EC
GO:0021761	0.196	0.981	1	27	limbic system development	BP	1	SEMA3A	up_VPOR_EC
GO:0050804	0.196	0.981	1	87	modulation of chemical synaptic transmission	BP	1	NETO1	up_VFEM_VSMC
GO:0099177	0.196	0.981	1	87	regulation of trans-synaptic signaling	BP	1	NETO1	up_VFEM_VSMC
GO:0045766	0.196	0.981	1	63	positive regulation of angiogenesis	BP	1	CCL24	up_VPUL_EC
GO:0030178	0.196	0.98	1	52	negative regulation of Wnt signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0060055	0.196167548	0.98187	1	8	angiogenesis involved in wound healing	BP	1	FOXC2	up_ACOR_EC
GO:0006915	0.196403331	0.86743	18	550	apoptotic process	BP	1	NR1H4,SOX9,AQP1,FZD5,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,USP53,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0061061	0.196969682	0.89743	7	179	muscle structure development	BP	1	MYOZ2,TMOD1,SOX9,ACTN2,FOXC2,TBX5,RBM38	up_ACOR_EC
GO:0031401	0.197	0.857	26	358	positive regulation of protein modification process	BP	1	ARHGEF2,PRICKLE1,VEGFA,HSPA5,JCAD,BCAR3,PTPN11,TRIB3,ILK,PPP1R12A,PTGS2,TNIK,YES1,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,CALM1,PAK2,INHBA,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0008152	0.197	0.885	21	3714	metabolic process	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,MYO1D,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0043436	0.197	0.865	19	303	oxoacid metabolic process	BP	1	GPAM,DCN,AKT2,ACAA1,ME3,UROS,THNSL2,SUOX,PEX5,PARK7,ENSCAFG00000002977,HPDL,ACSS2,RDH10,CRTAP,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0043900	0.197	0.883	11	104	regulation of multi-organism process	BP	1	CXCL8,TNFAIP3,TMEM173,IRF8,ARG2,NECTIN2,RIOK3,PROX1,SMARCA4,CNOT7,ARHGDIB	up_VCAV_EC
GO:0008544	0.197	0.887	10	75	epidermis development	BP	1	EXPH5,FERMT1,BMP4,FGFR2,SEC24B,LATS2,FZD3,FOSL2,ATP2C1,ZDHHC21	up_ACOR_VSMC
GO:0042692	0.197	0.889	9	105	muscle cell differentiation	BP	1	ACTN1,IFRD1,FHL2,WDR1,CTNNB1,NEXN,SIX4,MYBPC2,HOMER1	down_VSAP_EC
GO:0048519	0.197	0.896	9	1554	negative regulation of biological process	BP	1	HOXC10,EYA1,HOXA9,MAP2K6,TRIM9,HOXA7,SIX1,CYP26B1,MTSS1	up_VFEM_EC
GO:0051053	0.197	0.906	6	45	negative regulation of DNA metabolic process	BP	1	SMC1A,PARPBP,FAM129B,GMNN,SMC3,TINF2	down_ACOR_VSMC
GO:0006650	0.197	0.904	6	78	glycerophospholipid metabolic process	BP	1	GPAM,PDGFRB,ENSCAFG00000014978,LCAT,PIGS,NAPEPLD	down_VCAV_EC
GO:0045995	0.197	0.906	6	40	regulation of embryonic development	BP	1	MBP,BMP4,SEC24B,FZD3,DAG1,LAMA3	up_ACOR_VSMC
GO:0070663	0.197	0.906	6	50	regulation of leukocyte proliferation	BP	1	MEF2C,TLR4,PELI1,ARG2,NCK1,HMGB1	up_VCAV_EC
GO:0030534	0.197	0.914	5	33	adult behavior	BP	1	SEZ6L,FXN,CTNS,ABAT,HTRA2	up_VSAP_EC
GO:0050864	0.197	0.923	4	36	regulation of B cell activation	BP	1	TFRC,LYN,BTK,CDKN1A	down_VSAP_EC
GO:0009132	0.197	0.924	4	25	nucleoside diphosphate metabolic process	BP	1	ENSCAFG00000018611,ALDOC,ENTPD3,DDIT4	up_ACOR_VSMC
GO:0071322	0.197	0.923	4	29	cellular response to carbohydrate stimulus	BP	1	CALCRL,MAPK13,SMARCA4,HIF1A	up_VCAV_EC
GO:0007272	0.197	0.935	3	31	ensheathment of neurons	BP	1	NAB2,AKT2,ENSCAFG00000017708	down_VCAV_EC
GO:0008366	0.197	0.935	3	31	axon ensheathment	BP	1	NAB2,AKT2,ENSCAFG00000017708	down_VCAV_EC
GO:0051651	0.197	0.935	3	31	maintenance of location in cell	BP	1	TLN2,PARK7,ARL2BP	down_VCAV_EC
GO:1902106	0.197	0.935	3	31	negative regulation of leukocyte differentiation	BP	1	FBN1,GLI3,LOXL3	down_VCAV_EC
GO:0070373	0.197	0.936	3	26	negative regulation of ERK1 and ERK2 cascade	BP	1	PTPN2,LYN,ATF3	down_VSAP_EC
GO:0050701	0.197	0.938	3	16	interleukin-1 secretion	BP	1	ABCA1,F2RL1,NOD2	up_ACOR_VSMC
GO:0045670	0.197	0.938	3	16	regulation of osteoclast differentiation	BP	1	MTOR,CREB1,TJP2	up_VCAV_EC
GO:0048699	0.197	0.935	3	371	generation of neurons	BP	1	HOXC10,EYA1,SIX1	up_VFEM_EC

GO:0007010	0.197	0.936	3	441	cytoskeleton organization	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0043330	0.197	0.938	3	16	response to exogenous dsRNA	BP	1	PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0043551	0.197	0.954	2	17	regulation of phosphatidylinositol 3-	BP	1	PDGFRB,ENSCAFG00000014978	down_VCAV_EC
GO:0002711	0.197	0.955	2	14	positive regulation of T cell mediated immunity	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0072595	0.197	0.955	2	14	maintenance of protein localization in organelle	BP	1	HSPA5,KDELR2	down_VSAP_EC
GO:0071345	0.197	0.953	2	210	cellular response to cytokine stimulus	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0046636	0.197	0.957	2	10	negative regulation of alpha-beta T cell	BP	1	ARG2,HMGB1	up_VCAV_EC
GO:0071715	0.197	0.957	2	10	icosanoid transport	BP	1	SLCO3A1,NOS2	up_VCAV_EC
GO:1901571	0.197	0.957	2	10	fatty acid derivative transport	BP	1	SLCO3A1,NOS2	up_VCAV_EC
GO:1903671	0.197	0.957	2	10	negative regulation of sprouting angiogenesis	BP	1	ADAMTS9,DLL4	up_VCAV_EC
GO:0006605	0.197	0.952	2	99	protein targeting	BP	1	GCC2,SRP54	up_VPOR_EC
GO:0002695	0.197	0.98	1	44	negative regulation of leukocyte activation	BP	1	LYN	down_ACOR_EC
GO:0002221	0.197	0.98	1	46	pattern recognition receptor signaling	BP	1	LYN	down_ACOR_EC
GO:0002758	0.197	0.98	1	46	innate immune response-activating signal	BP	1	LYN	down_ACOR_EC
GO:0009071	0.197	0.984	1	4	serine family amino acid catabolic process	BP	1	THNSL2	down_VCAV_EC
GO:0009072	0.197	0.984	1	4	aromatic amino acid family metabolic process	BP	1	HPDL	down_VCAV_EC
GO:0021516	0.197	0.984	1	4	dorsal spinal cord development	BP	1	LMO4	down_VCAV_EC
GO:0042574	0.197	0.984	1	4	retinal metabolic process	BP	1	RDH10	down_VCAV_EC
GO:0051409	0.197	0.984	1	4	response to nitrosative stress	BP	1	PARK7	down_VCAV_EC
GO:0060710	0.197	0.984	1	4	chorio-allantoic fusion	BP	1	ZFP36L1	down_VCAV_EC
GO:0071294	0.197	0.984	1	4	cellular response to zinc ion	BP	1	MT2A	down_VCAV_EC
GO:0010557	0.197	0.986	1	492	positive regulation of macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0014816	0.197	0.986	1	3	skeletal muscle satellite cell differentiation	BP	1	SIX4	down_VSAP_EC
GO:0060600	0.197	0.986	1	3	dichotomous subdivision of an epithelial terminal	BP	1	NRP1	down_VSAP_EC
GO:0060666	0.197	0.986	1	3	dichotomous subdivision of terminal units involved in salivary gland	BP	1	NRP1	down_VSAP_EC
GO:0032493	0.197	0.989	1	2	response to bacterial lipoprotein	BP	1	TLR1	up_ACOR_VSMC
GO:0061888	0.197	0.989	1	2	regulation of astrocyte activation	BP	1	APP	up_ACOR_VSMC
GO:0071220	0.197	0.989	1	2	cellular response to bacterial lipoprotein	BP	1	TLR1	up_ACOR_VSMC
GO:0071221	0.197	0.989	1	2	cellular response to bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC
GO:0071725	0.197	0.989	1	2	response to triacyl bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC
GO:0071727	0.197	0.989	1	2	cellular response to triacyl bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC
GO:0097050	0.197	0.989	1	2	type B pancreatic cell apoptotic process	BP	1	WFS1	up_ACOR_VSMC
GO:1901407	0.197	0.989	1	2	regulation of phosphorylation of RNA polymerase II C-terminal	BP	1	CCNT1	up_ACOR_VSMC
GO:1901409	0.197	0.989	1	2	positive regulation of phosphorylation of RNA polymerase II C-terminal	BP	1	CCNT1	up_ACOR_VSMC
GO:2000674	0.197	0.989	1	2	regulation of type B pancreatic cell apoptotic	BP	1	WFS1	up_ACOR_VSMC
GO:2000675	0.197	0.989	1	2	negative regulation of type B pancreatic cell	BP	1	WFS1	up_ACOR_VSMC
GO:0042494	0.197	0.989	1	2	detection of bacterial lipoprotein	BP	1	TLR1	up_ACOR_VSMC
GO:0042495	0.197	0.989	1	2	detection of triacyl bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC

GO:0070339	0.197	0.989	1	2	response to bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC
GO:0070340	0.197	0.989	1	2	detection of bacterial lipopeptide	BP	1	TLR1	up_ACOR_VSMC
GO:0070425	0.197	0.989	1	2	negative regulation of nucleotide-binding oligomerization domain	BP	1	PTPN22	up_ACOR_VSMC
GO:0070433	0.197	0.989	1	2	negative regulation of nucleotide-binding oligomerization domain	BP	1	PTPN22	up_ACOR_VSMC
GO:0051882	0.197	0.982	1	9	mitochondrial depolarization	BP	1	MLLT11	up_AFEM_EC
GO:0015849	0.197	0.98	1	56	organic acid transport	BP	1	NTRK2	up_APUL_EC
GO:0046942	0.197	0.98	1	56	carboxylic acid transport	BP	1	NTRK2	up_APUL_EC
GO:1900034	0.197	0.986	1	3	regulation of cellular response to heat	BP	1	CD34	up_VCAV_EC
GO:0019627	0.197	0.986	1	3	urea metabolic process	BP	1	ARG2	up_VCAV_EC
GO:0030510	0.197	0.98	1	27	regulation of BMP signaling pathway	BP	1	ACVR2A	up_VPOR_EC
GO:0034764	0.197	0.98	1	50	positive regulation of transmembrane transport	BP	1	STIM1	up_VSAP_VSMC
GO:0014912	0.197189725	0.98167	1	8	negative regulation of smooth muscle cell	BP	1	SEMA6D	up_ACOR_EC
GO:0042542	0.197277853	0.95243	2	31	response to hydrogen peroxide	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:0061024	0.197353723	0.89214	8	215	membrane organization	BP	1	SH3TC2,PREB,LRP4,LRRC4,CHMP4B,VPS16,AZIN2,PRKCD	up_ACOR_EC
GO:0040011	0.198	0.841	54	505	locomotion	BP	1	EMX2,HOXA7,PEX7,TWIST2,WNT11,FAM107A,ACKR3,ARHGEF5,C5AR2,ACKR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,CHRM1,IL17RC,FUZ,PDGFD,PLXNA4,SEMA5A,HSD3B7,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,DPYSL2,ACKR4,FBXO7,LIMD1,PC,FBLN1,NFIB,ZNF580,STX4,ZFAND5,ACVRL1,PPP3CB,NCK1,HMOX1,MAP2K2,TGFBR2,SAA1,BAG4	up_VSAP_EC
GO:0042325	0.198	0.843	50	463	regulation of phosphorylation	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,DDR2,TRAF7,PIK3R1,MYC,PIK3IP1,RTN4RL1,SASH1,MYD88,LRP4,FBXO7,CDK9,FBLN1,RAF1,QARS,ACVRL1,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0045596	0.198	0.864	19	186	negative regulation of cell differentiation	BP	1	EPHB1,EDNRB,IFRD1,PDGFB,GATA3,HOXB8,PPP3CA,HOOK3,BMP2,HMG20A,ITPKB,JAG1,RAPGEF2,CTNNA1,HMGB1,SKIL,CUL4A,ZEB1,TJP2	up_VCAV_EC
GO:0009987	0.198	0.958	9	5086	cellular process	BP	1	SLITRK5,CYP1A1,LIMK1,GATA5,CA2,LRRC17,C6,TGFBI,ENSCAFG00000028814	up_VCAV_VSMC
GO:1903829	0.198	0.893	8	91	positive regulation of cellular protein	BP	1	PLK3,SESN2,MYO1C,MSN,KIF5B,ZPR1,GSK3B,SH3GLB1	down_VSAP_EC
GO:2000146	0.198	0.892	8	92	negative regulation of cell motility	BP	1	SULF1,SERPINE1,DPYSL3,STARD13,APOE,MMP28,STRAP,ZMYND8	down_VSAP_EC
GO:0048522	0.198	0.9	8	1484	positive regulation of cellular process	BP	1	NR1H4,TBX5,HOXA3,SLITRK5,WIF1,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0050801	0.198	0.896	7	200	ion homeostasis	BP	1	RAB20,GPAM,MLLT11,CNNM4,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0007569	0.198	0.913	5	36	cell aging	BP	1	HMGA1,ARG2,NUP62,RSL1D1,SMC6	down_ACOR_VSMC
GO:0009116	0.198	0.913	5	39	nucleoside metabolic process	BP	1	PRPSAP1,RAN,TK1,PRPS1,CTPS1	down_ACOR_VSMC
GO:0048513	0.198	0.916	5	906	animal organ development	BP	1	TBX5,HOXA3,NR1H4,EVI2B,FLRT3	up_VPUL_EC
GO:0050806	0.198	0.935	3	25	positive regulation of synaptic transmission	BP	1	KIF5B,APOE,LRRTM2	down_VSAP_EC
GO:0006690	0.198	0.938	3	16	icosanoid metabolic process	BP	1	CYP2J2,EDN1,HPGD	up_ACOR_VSMC
GO:0022008	0.198	0.935	3	406	neurogenesis	BP	1	MAPK10,SLITRK5,NTRK2	up_APUL_EC
GO:0046637	0.198	0.937	3	18	regulation of alpha-beta T cell differentiation	BP	1	GATA3,ITPKB,HMGB1	up_VCAV_EC
GO:0010033	0.198	0.939	3	772	response to organic substance	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC

GO:0010828	0.198	0.938	3	16	positive regulation of glucose transmembrane	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0007019	0.198	0.955	2	13	microtubule depolymerization	BP	1	ARHGEF2,MID1	down_VSAP_EC
GO:2001259	0.198	0.955	2	13	positive regulation of cation channel activity	BP	1	HTT,CALM1	down_VSAP_EC
GO:0051960	0.198	0.952	2	216	regulation of nervous system development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0032958	0.198	0.957	2	9	inositol phosphate biosynthetic process	BP	1	ITPKB,PLCG2	up_VCAV_EC
GO:0045932	0.198	0.958	2	8	negative regulation of muscle contraction	BP	1	DOCK4,GUCY1A1	up_VCAV_EC
GO:0048821	0.198	0.956	2	10	erythrocyte development	BP	1	ADGRF5,TMOD3	up_VCAV_EC
GO:0071363	0.198	0.952	2	188	cellular response to growth factor stimulus	BP	1	CAV1,FGF5	up_VSAP_VSMC
GO:1901343	0.198	0.98	1	42	negative regulation of vasculature development	BP	1	SULF1	down_ACOR_EC
GO:0043535	0.198	0.98	1	45	regulation of blood vessel endothelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0050707	0.198	0.98	1	44	regulation of cytokine secretion	BP	1	LYN	down_ACOR_EC
GO:0009123	0.198	0.981	1	104	nucleoside monophosphate	BP	1	NDUFA10	down_AFEM_EC
GO:0043062	0.198	0.98	1	99	extracellular structure organization	BP	1	FSCN1	down_AFEM_EC
GO:0007275	0.198	1	1	1370	multicellular organism development	BP	1	GATA5	down_AFEM_VSMC
GO:0060916	0.198	0.986	1	3	mesenchymal cell proliferation involved in	BP	1	CTNNB1	down_VSAP_EC
GO:0001787	0.198	0.989	1	2	natural killer cell proliferation	BP	1	LEP	up_ACOR_VSMC
GO:0086042	0.198	0.989	1	2	cardiac muscle cell-cardiac muscle cell	BP	1	JUP	up_ACOR_VSMC
GO:0086073	0.198	0.989	1	2	bundle of His cell-Purkinje myocyte adhesion involved in cell	BP	1	JUP	up_ACOR_VSMC
GO:0002159	0.198	0.989	1	2	desmosome assembly	BP	1	JUP	up_ACOR_VSMC
GO:0031268	0.198	0.981	1	9	pseudopodium organization	BP	1	CDC42EP5	up_AFEM_EC
GO:0031269	0.198	0.981	1	9	pseudopodium assembly	BP	1	CDC42EP5	up_AFEM_EC
GO:0007283	0.198	0.98	1	91	spermatogenesis	BP	1	HOXA9	up_AORT_EC
GO:0033993	0.198	0.982	1	186	response to lipid	BP	1	ESR1	up_AORT_VSMC
GO:0071363	0.198	0.982	1	188	cellular response to growth factor stimulus	BP	1	WNT7A	up_AORT_VSMC
GO:0048754	0.198	0.98	1	57	branching morphogenesis of an epithelial tube	BP	1	NPNT	up_APUL_EC
GO:0010668	0.198	0.989	1	2	ectodermal cell differentiation	BP	1	ITGA6	up_VCAV_EC
GO:0010739	0.198	0.989	1	2	positive regulation of protein kinase A signaling	BP	1	AKAP12	up_VCAV_EC
GO:0039533	0.198	0.986	1	3	regulation of MDA-5 signaling pathway	BP	1	RIOK3	up_VCAV_EC
GO:0039534	0.198	0.986	1	3	negative regulation of MDA-5 signaling pathway	BP	1	RIOK3	up_VCAV_EC
GO:0061450	0.198	0.986	1	3	trophoblast cell migration	BP	1	ARHGDIB	up_VCAV_EC
GO:1901163	0.198	0.986	1	3	regulation of trophoblast cell migration	BP	1	ARHGDIB	up_VCAV_EC
GO:0006446	0.198	0.98	1	27	regulation of translational initiation	BP	1	EIF5	up_VPOR_EC
GO:0035690	0.198	0.98	1	91	cellular response to drug	BP	1	FBP1	up_VFEM_VSMC
GO:0009914	0.198	0.98	1	64	hormone transport	BP	1	NR1H4	up_VPUL_EC
GO:0050663	0.198	0.98	1	52	cytokine secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0046456	0.198005235	0.98152	1	8	icosanoid biosynthetic process	BP	1	PTGDS	up_ACOR_EC
GO:0071379	0.198014191	0.98151	1	8	cellular response to prostaglandin stimulus	BP	1	PTGER4	up_ACOR_EC
GO:0090103	0.198290425	0.98146	1	8	cochlea morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0035872	0.198309528	0.98146	1	8	nucleotide-binding domain, leucine rich repeat containing	BP	1	NOD2	up_ACOR_EC

GO:0070423	0.198309528	0.98146	1	8	nucleotide-binding oligomerization domain containing signaling	BP	1	NOD2	up_ACOR_EC
GO:0070431	0.198309528	0.98146	1	8	nucleotide-binding oligomerization domain containing 2 signaling	BP	1	NOD2	up_ACOR_EC
GO:0002009	0.1984611	0.89645	7	177	morphogenesis of an epithelium	BP	1	BRSK1,SOX9,FZD5,FOXC2,TBX5,CLSTN1,NRP1	up_ACOR_EC
GO:0007610	0.198537527	0.90249	6	146	behavior	BP	1	CNTNAP4,TMOD1,BRSK1,GNAO1,PTGDS,MAPK8IP2	up_ACOR_EC
GO:0051966	0.198726291	0.98138	1	8	regulation of synaptic transmission,	BP	1	MAPK8IP2	up_ACOR_EC
GO:0071840	0.199	0.83	132	2059	cellular component organization or biogenesis	BP	1	ARHGEF2,VEGFA,SIPA1L1,SULF1,CELF1,SERPINH1,MYH9,NR1H4,FMNL3,PLK3,C1QTNF6,SERPINE1,ACTN1,ETV6,SPARC,VASP,SGK1,ERO1A,ENPP1,P4HA1,SEC24D,TPM4,AKAP2,PTPN11,EXOC5,CORO1C,FSCN1,FLNB,SEC23A,MZT1,DPYSL3,LRRC8A,HOOK3,IFRD1,ENSCAFG00000007260,FBLIM1,ILK,PPP1R12A,SMARCA4,ANKRA2,SESN2,SRP54,WDR1,MYO1C,MSN,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TUBB,MRPL1,IWS1,TNIK,NAA10,UBA6,ZPR1,MORF4L2,TMSB10,NEO1,SMG7,USO1,ESM1,PRPF3,DDX39B,ADAM17,BRD2,UST,CNOT7,CDH11,ACTR3,PALLD,CTNNB1,KPNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,PLOD3,PDCD11,IGFBP7,KLF5,LYN,BNIP3,STRAP,DDIT3,TWF1,PDS5B,FAM162A,PLEKHG2,TLN1,CLCN3,PLS3,GSK3B,VLDLR,NEXN,CDC37,DAAM1,GBP5,CCSER2,SH3GLB1,MYO1E,SDC4,HTT,REST,ENSCAFG00000017326,ZMYND8,EIF2S1,PRMT1,P3H4,EXT1,DISC1,PAK2,CLTC,LRRTM2,CAPG,INHBA,SIX4,CDKN1A,RSL24D1,SLC25A46,NRP1,ARF4,YWHAH,COL12A1,ENSCAFG00000030508,BLZF1,TNFAIP1,SEC13,KDM3A,MYBPC2,MID1	down_VSAP_EC
GO:0010468	0.199	0.831	114	1270	regulation of gene expression	BP	1	EDNRB,HCLS1,IL7R,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,TSPAN8,RELN,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,TENT2,ELF4,BMP2,CDYL,HMG20A,HHEX,CREM,TUT7,CNOT6,RSC1A1,ENC1,CCAR1,MAPK13,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,TOP1,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,PAN3,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,ZNF789,BLM,NUP133,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,WTAP,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0097659	0.199	0.832	97	1072	nucleic acid-templated transcription	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0042493	0.199	0.873	14	178	response to drug	BP	1	ARHGEF2,PTPN11,PPP1R12A,SRP54,AGRN,GNAQ,CTNNB1,SRP72,CRYAB,TFRC,KPNA4,REST,INHBA,HOMER1	down_VSAP_EC

GO:0030335	0.199	0.875	13	165	positive regulation of cell migration	BP	1	ARHGEF2,VEGFA,HSPA5,SERPINE1,SPARC,JCAD,MYO1C,PIK3C2A,HIF1A,ADAM17,PTP4A1,LYN,NRP1	down_VSAP_EC
GO:2001234	0.199	0.885	10	75	negative regulation of apoptotic signaling	BP	1	BMP4,AR,DAPK1,NRP1,UNC5B,SH3RF1,PSEN1,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0050896	0.199	0.909	8	2346	response to stimulus	BP	1	CHL1,FGF5,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0023051	0.199	0.901	7	954	regulation of signaling	BP	1	ACVRL1,LYN,IGF1R,SULF1,STX4,ASPN,NEDD4	down_ACOR_EC
GO:0006939	0.199	0.914	5	32	smooth muscle contraction	BP	1	ADRA1B,HTR2B,NPNT,EDN1,DOCK5	up_ACOR_VSMC
GO:1903321	0.199	0.913	5	33	negative regulation of protein modification by small protein conjugation	BP	1	SH3RF2,ISG15,PRKCE,PSEN1,PARK7	up_ACOR_VSMC
GO:0032479	0.199	0.913	5	33	regulation of type I interferon production	BP	1	NLRX1,RNF216,PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0008652	0.199	0.924	4	24	cellular amino acid biosynthetic process	BP	1	GOT1,GLUL,ENSCAFG00000016140,ASS1	up_VSAP_EC
GO:0045185	0.199	0.923	4	25	maintenance of protein location	BP	1	MORC3,CIZ1,TAF8,KEAP1	up_VSAP_EC
GO:1901607	0.199	0.924	4	24	alpha-amino acid biosynthetic process	BP	1	GOT1,GLUL,ENSCAFG00000016140,ASS1	up_VSAP_EC
GO:0071326	0.199	0.934	3	26	cellular response to monosaccharide stimulus	BP	1	NR1H4,SMARCA4,HIF1A	down_VSAP_EC
GO:0071331	0.199	0.934	3	26	cellular response to hexose stimulus	BP	1	NR1H4,SMARCA4,HIF1A	down_VSAP_EC
GO:0072091	0.199	0.935	3	24	regulation of stem cell proliferation	BP	1	HIF1A,CTNNB1,DISC1	down_VSAP_EC
GO:0009948	0.199	0.937	3	16	anterior/posterior axis specification	BP	1	BMP4,FRS2,PCSK6	up_ACOR_VSMC
GO:0070887	0.199	0.938	3	775	cellular response to chemical stimulus	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0051253	0.199	0.934	3	359	negative regulation of RNA metabolic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0034123	0.199	0.956	2	10	positive regulation of toll-like receptor signaling	BP	1	HMGB1,CAV1	down_ACOR_VSMC
GO:1903053	0.199	0.956	2	10	regulation of extracellular matrix organization	BP	1	FSCN1,COLGALT1	down_ACOR_VSMC
GO:0050794	0.199	1	2	3075	regulation of cellular process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048260	0.199	0.954	2	15	positive regulation of receptor-mediated	BP	1	VEGFA,SERPINE1	down_VSAP_EC
GO:1902742	0.199	0.954	2	14	apoptotic process involved in development	BP	1	ZPR1,CRYAB	down_VSAP_EC
GO:0060502	0.199	0.957	2	9	epithelial cell proliferation involved in lung	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0002682	0.199	0.953	2	343	regulation of immune system process	BP	1	HOXA9,BPI	up_AORT_EC
GO:0007566	0.199	0.956	2	10	embryo implantation	BP	1	PTGS2,ARHGDIB	up_VCAV_EC
GO:0050820	0.199	0.956	2	10	positive regulation of coagulation	BP	1	SELP,TLR4	up_VCAV_EC
GO:0070527	0.199	0.956	2	10	platelet aggregation	BP	1	ITGB3,PEAR1	up_VCAV_EC
GO:0007021	0.199	0.985	1	3	tubulin complex assembly	BP	1	TBCC	down_ACOR_VSMC
GO:0022417	0.199	0.984	1	4	protein maturation by protein folding	BP	1	ERO1A	down_VSAP_EC
GO:0031392	0.199	0.985	1	3	regulation of prostaglandin	BP	1	PTGS2	down_VSAP_EC
GO:0090336	0.199	0.984	1	4	positive regulation of brown fat cell	BP	1	PTGS2	down_VSAP_EC
GO:0001568	0.199	0.982	1	252	blood vessel development	BP	1	TGFBI	down_VSAP_VSMC
GO:0003129	0.199	0.986	1	3	heart induction	BP	1	BMP2	up_VCAV_EC
GO:0042487	0.199	0.986	1	3	regulation of odontogenesis of dentin-	BP	1	BMP2	up_VCAV_EC
GO:0090129	0.199	0.989	1	2	positive regulation of synapse maturation	BP	1	RELN	up_VCAV_EC
GO:1903429	0.199	0.985	1	3	regulation of cell maturation	BP	1	EDNRB	up_VCAV_EC
GO:1904753	0.199	0.989	1	2	negative regulation of vascular associated smooth muscle cell	BP	1	MEF2C	up_VCAV_EC
GO:0035234	0.199	0.985	1	3	ectopic germ cell programmed cell death	BP	1	KIT	up_VCAV_EC
GO:0006164	0.199	0.98	1	86	purine nucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC

GO:0031330	0.199	0.98	1	85	negative regulation of cellular catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0030324	0.199	0.98	1	64	lung development	BP	1	TBX5	up_VPUL_EC
GO:0033500	0.199	0.98	1	64	carbohydrate homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0042593	0.199	0.98	1	64	glucose homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0014044	0.199212434	0.98128	1	8	Schwann cell development	BP	1	SH3TC2	up_ACOR_EC
GO:0022011	0.199212434	0.98128	1	8	myelination in peripheral nervous system	BP	1	SH3TC2	up_ACOR_EC
GO:0032292	0.199212434	0.98128	1	8	peripheral nervous system axon	BP	1	SH3TC2	up_ACOR_EC
GO:0046824	0.199385689	0.95167	2	30	positive regulation of nucleocytoplasmic	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:1901654	0.199413802	0.95159	2	31	response to ketone	BP	1	AQP1,PTGER4	up_ACOR_EC
GO:0046621	0.199630868	0.9812	1	8	negative regulation of organ growth	BP	1	TBX5	up_ACOR_EC
GO:0097530	0.199704712	0.95136	2	33	granulocyte migration	BP	1	PTGER4,RARRES2	up_ACOR_EC
GO:0051607	0.199708324	0.93233	3	58	defense response to virus	BP	1	MAVS,IFIT2,AGBL5	up_ACOR_EC
GO:0071478	0.199714223	0.93233	3	58	cellular response to radiation	BP	1	AQP1,FIGNL1,MFAP4	up_ACOR_EC
GO:0046620	0.199805073	0.95151	2	30	regulation of organ growth	BP	1	FOXC2,TBX5	up_ACOR_EC
GO:0007167	0.2	0.851	31	274	enzyme linked receptor protein signaling pathway	BP	1	SH3TC2,VEGFD,SMAD6,EFNB2,ANGPT1,RASSF2,FERMT1,BMP4,FGFR2,CITED2,PTGIR,TMEM108,FGF18,CDKN2B,NCEH1,NRP1,NPNT,TBX20,SESN3,FRS2,FUT8,APP,PSEN1,TGFBR1,SIPA1L1,DUSP22,HPGD,ARID5B,ENSCAFG00000018360,INPP5K,PAG1	up_ACOR_VSMC
GO:0006952	0.2	0.857	23	319	defense response	BP	1	ARHGEF2,NR1H4,SERPINE1,SOCS5,FLNB,COTL1,PRCP,PTGS2,MYO1C,KIF5B,HIF1A,PTPN2,PVR,ADAM17,CNOT7,APOE,LYN,BNIP3,CDC37,GBP5,A2M,BTK,DEFB124	down_VSAP_EC
GO:0071900	0.2	0.869	16	131	regulation of protein serine/threonine kinase activity	BP	1	HTR2B,BMP4,LATS2,PDE5A,SASH1,FGF18,CDKN2B,CDKN1A,SMPD1,CCNT1,FRS2,PSEN1,EDN1,PRKAG3,MAP3K7,INPP5K	up_ACOR_VSMC
GO:1901615	0.2	0.887	9	128	organic hydroxy compound metabolic	BP	1	MAOA,LCAT,ACAA1,CYB5R3,CYP1B1,RETSAT,PARK7,NAPEPLD,SOAT1	down_VCAV_EC
GO:0060840	0.2	0.904	6	42	artery development	BP	1	WNT11,LOX,HPGD,ACVRL1,NPRL3,CITED2	up_VSAP_EC
GO:0042445	0.2	0.92	4	46	hormone metabolic process	BP	1	CYP1B1,RETSAT,RDH10,PCSK6	down_VCAV_EC
GO:0045930	0.2	0.919	4	97	negative regulation of mitotic cell cycle	BP	1	GAS1,OVOL1,DCUN1D3,FAP	up_AFEM_EC
GO:0006952	0.2	0.933	3	319	defense response	BP	1	LYN,IPO7,STX4	down_ACOR_EC
GO:0042306	0.2	0.933	3	31	regulation of protein import into nucleus	BP	1	ENSCAFG00000014978,GLI3,MAVS	down_VCAV_EC
GO:0006695	0.2	0.937	3	16	cholesterol biosynthetic process	BP	1	INSIG2,MVK,CYB5R3	up_VSAP_EC
GO:0003197	0.2	0.937	3	16	endocardial cushion development	BP	1	ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:1902653	0.2	0.937	3	16	secondary alcohol biosynthetic process	BP	1	INSIG2,MVK,CYB5R3	up_VSAP_EC
GO:0035725	0.2	0.937	3	16	sodium ion transmembrane transport	BP	1	OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0048661	0.2	0.953	2	17	positive regulation of smooth muscle cell	BP	1	PDGFRB,BMPR1A	down_VCAV_EC
GO:0032366	0.2	0.958	2	8	intracellular sterol transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0032367	0.2	0.958	2	8	intracellular cholesterol transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0071800	0.2	0.958	2	8	podosome assembly	BP	1	ASAP1,KIF9	up_ACOR_VSMC
GO:0001656	0.2	0.951	2	35	metanephros development	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0036124	0.2	0.957	2	8	histone H3-K9 trimethylation	BP	1	ARID4B,ATRX	up_VCAV_EC
GO:0050764	0.2	0.954	2	13	regulation of phagocytosis	BP	1	RAB27A,HMGB1	up_VCAV_EC
GO:1901099	0.2	0.956	2	10	negative regulation of signal transduction in	BP	1	CTNNA1,RIPK1	up_VCAV_EC
GO:2001240	0.2	0.956	2	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	CTNNA1,RIPK1	up_VCAV_EC

GO:0031103	0.2	0.956	2	9	axon regeneration	BP	1	RTN4RL1,MAP2K2	up_VSAP_EC
GO:0055082	0.2	0.951	2	189	cellular chemical homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0072331	0.2	0.98	1	49	signal transduction by p53 class mediator	BP	1	USP28	down_ACOR_EC
GO:0098656	0.2	0.98	1	42	anion transmembrane transport	BP	1	PDPN	down_ACOR_EC
GO:0031324	0.2	0.989	1	735	negative regulation of cellular metabolic process	BP	1	CST3	down_AORT_EC
GO:0065009	0.2	0.989	1	735	regulation of molecular function	BP	1	CST3	down_AORT_EC
GO:0014706	0.2	0.98	1	112	striated muscle tissue development	BP	1	CITED2	down_VPOR_EC
GO:0001922	0.2	0.985	1	3	B-1 B cell homeostasis	BP	1	HIF1A	down_VSAP_EC
GO:0050930	0.2	0.984	1	4	induction of positive chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0061469	0.2	0.984	1	4	regulation of type B pancreatic cell	BP	1	NR4A1	down_VSAP_EC
GO:0070831	0.2	0.985	1	3	basement membrane assembly	BP	1	PLOD3	down_VSAP_EC
GO:0072008	0.2	0.984	1	4	glomerular mesangial cell differentiation	BP	1	ACTA2	down_VSAP_EC
GO:0072144	0.2	0.984	1	4	glomerular mesangial cell development	BP	1	ACTA2	down_VSAP_EC
GO:0045597	0.2	0.982	1	253	positive regulation of cell differentiation	BP	1	GATA5	down_VSAP_VSMC
GO:0001827	0.2	0.989	1	2	inner cell mass cell fate commitment	BP	1	LATS2	up_ACOR_VSMC
GO:0001828	0.2	0.989	1	2	inner cell mass cellular morphogenesis	BP	1	LATS2	up_ACOR_VSMC
GO:0150018	0.2	0.989	1	2	basal dendrite development	BP	1	NRP1	up_ACOR_VSMC
GO:0150019	0.2	0.989	1	2	basal dendrite morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0150020	0.2	0.989	1	2	basal dendrite arborization	BP	1	NRP1	up_ACOR_VSMC
GO:0001816	0.2	0.981	1	194	cytokine production	BP	1	ARG2	up_AORT_VSMC
GO:0007179	0.2	0.98	1	57	transforming growth factor beta receptor	BP	1	NPNT	up_APUL_EC
GO:0016358	0.2	0.979	1	58	dendrite development	BP	1	SLITRK5	up_APUL_EC
GO:0032869	0.2	0.98	1	57	cellular response to insulin stimulus	BP	1	NR1H4	up_APUL_EC
GO:0070374	0.2	0.98	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	NPNT	up_APUL_EC
GO:0014866	0.2	0.985	1	3	skeletal myofibril assembly	BP	1	PROX1	up_VCAV_EC
GO:0030240	0.2	0.985	1	3	skeletal muscle thin filament assembly	BP	1	PROX1	up_VCAV_EC
GO:0035635	0.2	0.985	1	3	entry of bacterium into host cell	BP	1	CXCL8	up_VCAV_EC
GO:1903588	0.2	0.989	1	2	negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	DLL4	up_VCAV_EC
GO:2000535	0.2	0.985	1	3	regulation of entry of bacterium into host cell	BP	1	CXCL8	up_VCAV_EC
GO:0001765	0.2	0.984	1	4	membrane raft assembly	BP	1	CAV2	up_VCAV_EC
GO:0043523	0.2	0.98	1	52	regulation of neuron apoptotic process	BP	1	SIX1	up_VFEM_EC
GO:0006302	0.2	0.98	1	97	double-strand break repair	BP	1	EYA1	up_VFEM_VSMC
GO:0051188	0.2	0.98	1	81	cofactor biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0044057	0.2	0.98	1	110	regulation of system process	BP	1	GATA5	up_VPUL_VSMC
GO:0021561	0.200010734	0.98112	1	8	facial nerve development	BP	1	NRP1	up_ACOR_EC
GO:0021610	0.200010734	0.98112	1	8	facial nerve morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0003177	0.200302992	0.98107	1	8	pulmonary valve development	BP	1	SMAD6	up_ACOR_EC
GO:0045655	0.200397135	0.98077	1	9	regulation of monocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0006956	0.200537269	0.98102	1	8	complement activation	BP	1	C7	up_ACOR_EC

GO:0051882	0.200590112	0.98073	1	9	mitochondrial depolarization	BP	1	IFI6	up_ACOR_EC
GO:0031532	0.200966018	0.95098	2	31	actin cytoskeleton reorganization	BP	1	ARHGDIB,NRP1	up_ACOR_EC
GO:0032774	0.201	0.83	97	1073	RNA biosynthetic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0032504	0.201	0.867	16	152	multicellular organism reproduction	BP	1	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,ARID4B,HIST1H1A,PTGS2,AFF4,KDM3A,ATRX,SPATA6,FBXO5	up_VCAV_EC
GO:0048609	0.201	0.867	16	152	multicellular organismal reproductive process	BP	1	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,ARID4B,HIST1H1A,PTGS2,AFF4,KDM3A,ATRX,SPATA6,FBXO5	up_VCAV_EC
GO:0043405	0.201	0.88	11	85	regulation of MAP kinase activity	BP	1	HTR2B,BMP4,PDE5A,SASH1,FGF18,SMPD1,FRS2,PSEN1,EDN1,MAP3K7,INPP5K	up_ACOR_VSMC
GO:0043542	0.201	0.88	11	86	endothelial cell migration	BP	1	SLIT2,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:0021537	0.201	0.884	10	73	telencephalon development	BP	1	FGF13,BMP4,TMEM108,NRP1,SLITRK5,PSEN1,CHD7,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0030218	0.201	0.904	6	42	erythrocyte differentiation	BP	1	BMP4,CITED2,ISG15,FAM210B,P4HTM,B2M	up_ACOR_VSMC
GO:0006464	0.201	0.908	6	1162	cellular protein modification process	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0036211	0.201	0.908	6	1162	protein modification process	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0060411	0.201	0.912	5	33	cardiac septum morphogenesis	BP	1	FZD1,WNT11,SAV1,TGFBR2,CITED2	up_VSAP_EC
GO:0006357	0.201	0.921	4	547	regulation of transcription by RNA polymerase II	BP	1	HOXA9,SALL1,CAV1,SHOX2	up_VSAP_VSMC
GO:0032527	0.201	0.935	3	19	protein exit from endoplasmic reticulum	BP	1	HM13,INSIG1,PREB	down_ACOR_VSMC
GO:0035850	0.201	0.934	3	25	epithelial cell differentiation involved in	BP	1	ACTA2,CTNNB1,MYO1E	down_VSAP_EC
GO:1903037	0.201	0.932	3	65	regulation of leukocyte cell-cell adhesion	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0072359	0.201	0.933	3	368	circulatory system development	BP	1	EYA1,HOXA7,SIX1	up_VFEM_EC
GO:0042127	0.201	0.934	3	452	regulation of cell proliferation	BP	1	TBX5,HOXA3,CCL24	up_VPUL_EC
GO:2000785	0.201	0.936	3	16	regulation of autophagosome assembly	BP	1	PIP4K2B,UBQLN2,NPRL3	up_VSAP_EC
GO:0050776	0.201	0.951	2	173	regulation of immune response	BP	1	LYN,STX4	down_ACOR_EC
GO:0046685	0.201	0.955	2	10	response to arsenic-containing substance	BP	1	GSTO1,RBM14	down_ACOR_VSMC
GO:0071157	0.201	0.955	2	10	negative regulation of cell cycle arrest	BP	1	SLC29A1,CDK4	down_ACOR_VSMC
GO:0016477	0.201	0.953	2	426	cell migration	BP	1	HDAC7,HSD3B7	down_VPOR_EC
GO:0018279	0.201	0.953	2	14	protein N-linked glycosylation via	BP	1	STT3A,RPN1	down_VSAP_EC
GO:0045581	0.201	0.954	2	13	negative regulation of T cell differentiation	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:0072583	0.201	0.954	2	13	clathrin-dependent endocytosis	BP	1	CANX,GPR107	down_VSAP_EC
GO:1904705	0.201	0.954	2	14	regulation of vascular smooth muscle cell	BP	1	ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:1990874	0.201	0.954	2	14	vascular smooth muscle cell proliferation	BP	1	ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:0090141	0.201	0.956	2	9	positive regulation of mitochondrial fission	BP	1	MARCH5,BNIP3	up_ACOR_VSMC
GO:0061333	0.201	0.951	2	35	renal tubule morphogenesis	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0043277	0.201	0.956	2	9	apoptotic cell clearance	BP	1	HMGB1,PEAR1	up_VCAV_EC

GO:0010243	0.201	0.951	2	238	response to organonitrogen	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0045837	0.201	0.985	1	3	negative regulation of membrane potential	BP	1	PRELID1	down_ACOR_VSMC
GO:1903320	0.201	0.98	1	102	regulation of protein modification by small protein conjugation or	BP	1	IVNS1ABP	down_AFEM_EC
GO:0010629	0.201	0.985	1	502	negative regulation of gene expression	BP	1	MOSPD1	down_VFEM_EC
GO:0065009	0.201	0.989	1	735	regulation of molecular function	BP	1	JUP	down_VFEM_VSMC
GO:0032483	0.201	0.985	1	3	regulation of Rab protein signal transduction	BP	1	MADD	down_VSAP_EC
GO:0033483	0.201	0.983	1	4	gas homeostasis	BP	1	HIF1A	down_VSAP_EC
GO:0010996	0.201	0.985	1	3	response to auditory stimulus	BP	1	HTT	down_VSAP_EC
GO:0021824	0.201	0.985	1	3	cerebral cortex tangential migration using cell-axon interactions	BP	1	NRP1	down_VSAP_EC
GO:0021828	0.201	0.985	1	3	gonadotrophin-releasing hormone neuronal migration to the	BP	1	NRP1	down_VSAP_EC
GO:0021856	0.201	0.985	1	3	hypothalamic tangential migration using cell-axon interactions	BP	1	NRP1	down_VSAP_EC
GO:0021886	0.201	0.985	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	down_VSAP_EC
GO:0021888	0.201	0.985	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	down_VSAP_EC
GO:0021979	0.201	0.985	1	3	hypothalamus cell differentiation	BP	1	NRP1	down_VSAP_EC
GO:0035290	0.201	0.985	1	3	trunk segmentation	BP	1	NRP1	down_VSAP_EC
GO:0036484	0.201	0.985	1	3	trunk neural crest cell migration	BP	1	NRP1	down_VSAP_EC
GO:0036486	0.201	0.985	1	3	ventral trunk neural crest cell migration	BP	1	NRP1	down_VSAP_EC
GO:0097490	0.201	0.985	1	3	sympathetic neuron projection extension	BP	1	NRP1	down_VSAP_EC
GO:0097491	0.201	0.985	1	3	sympathetic neuron projection guidance	BP	1	NRP1	down_VSAP_EC
GO:1901166	0.201	0.985	1	3	neural crest cell migration involved in autonomic nervous system	BP	1	NRP1	down_VSAP_EC
GO:1903375	0.201	0.985	1	3	facioacoustic ganglion development	BP	1	NRP1	down_VSAP_EC
GO:0009794	0.201	0.989	1	2	regulation of mitotic cell cycle, embryonic	BP	1	FZD3	up_ACOR_VSMC
GO:0045359	0.201	0.989	1	2	positive regulation of interferon-beta	BP	1	TLR3	up_ACOR_VSMC
GO:0045448	0.201	0.989	1	2	mitotic cell cycle, embryonic	BP	1	FZD3	up_ACOR_VSMC
GO:0002730	0.201	0.989	1	2	regulation of dendritic cell cytokine production	BP	1	TLR3	up_ACOR_VSMC
GO:0045976	0.201	0.989	1	2	negative regulation of mitotic cell cycle,	BP	1	FZD3	up_ACOR_VSMC
GO:0070201	0.201	0.981	1	187	regulation of establishment of protein	BP	1	ARG2	up_AORT_VSMC
GO:0090087	0.201	0.981	1	185	regulation of peptide transport	BP	1	ARG2	up_AORT_VSMC
GO:0034163	0.201	0.985	1	3	regulation of toll-like receptor 9 signaling	BP	1	HMGB1	up_VCAV_EC
GO:0090308	0.201	0.989	1	2	regulation of methylation-dependent chromatin	BP	1	UHRF2	up_VCAV_EC
GO:0090481	0.201	0.985	1	3	pyrimidine nucleotide-sugar transmembrane	BP	1	SLC35A3	up_VCAV_EC
GO:0038033	0.201	0.985	1	3	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular	BP	1	PRKD2	up_VCAV_EC
GO:0014031	0.201	0.979	1	27	mesenchymal cell development	BP	1	SEMA3A	up_VPOR_EC
GO:0014032	0.201	0.979	1	27	neural crest cell development	BP	1	SEMA3A	up_VPOR_EC
GO:0002690	0.201	0.979	1	26	positive regulation of leukocyte chemotaxis	BP	1	C3AR1	up_VPOR_EC

GO:0046364	0.201	0.979	1	27	monosaccharide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0061448	0.201	0.98	1	89	connective tissue development	BP	1	HOXA3	up_VPOR_VSMC
GO:0001818	0.201	0.98	1	65	negative regulation of cytokine production	BP	1	NR1H4	up_VPUL_EC
GO:0048738	0.201	0.979	1	64	cardiac muscle tissue development	BP	1	TBX5	up_VPUL_EC
GO:0007266	0.201	0.979	1	64	Rho protein signal transduction	BP	1	ARHGEF2	up_VPUL_EC
GO:0007409	0.201	0.98	1	109	axonogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0051480	0.201	0.979	1	50	regulation of cytosolic calcium ion concentration	BP	1	CAV1	up_VSAP_VSMC
GO:0048592	0.201	0.979	1	53	eye morphogenesis	BP	1	IRX5	up_VSAP_VSMC
GO:0061318	0.20107912	0.98091	1	8	renal filtration cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0072010	0.20107912	0.98091	1	8	glomerular epithelium development	BP	1	FOXC2	up_ACOR_EC
GO:0072112	0.20107912	0.98091	1	8	glomerular visceral epithelial cell	BP	1	FOXC2	up_ACOR_EC
GO:0072311	0.20107912	0.98091	1	8	glomerular epithelial cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0001502	0.20163391	0.9808	1	8	cartilage condensation	BP	1	SOX9	up_ACOR_EC
GO:0098743	0.20163391	0.9808	1	8	cell aggregation	BP	1	SOX9	up_ACOR_EC
GO:0055007	0.201642339	0.95071	2	31	cardiac muscle cell differentiation	BP	1	ACTN2,TBX5	up_ACOR_EC
GO:0033158	0.201772382	0.98077	1	8	regulation of protein import into nucleus,	BP	1	MAVS	up_ACOR_EC
GO:0007263	0.201864327	0.98076	1	8	nitric oxide mediated signal transduction	BP	1	GUCY1B1	up_ACOR_EC
GO:0042306	0.201885365	0.95062	2	31	regulation of protein import into nucleus	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0048856	0.202	0.833	83	1533	anatomical structure development	BP	1	ADAMTS2,NOTCH2,HSPB6,PDGFRB,SMAD9,LRP1,DCN,NAB2,NDN,ANGPT1,SDC4,VASN,FBN1,GLIPR2,KANK2,THBS3,BMPR1A,LOX,LMO4,RECK,TRPV2,ANPEP,COL6A1,NUMBL,NAGLU,CHRDL1,TBX15,AKT2,TFE3,ENSCAFG00000018277,SYDE1,HOXC4,LAMA3,CLSTN1,CSPG4,PKD1,ENSCAFG00000013404,SEMA3C,ASPN,POLDIP2,CRISPLD2,THY1,TEAD1,HAPLN3,PEX5,TLX2,VCAN,B4GALT1,GLI3,ADAMTSL4,EEF2,ZFP36L1,MYDGF,SASH1,NCDN,RBM38,IFT57,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,IRX5,TSC22D3,UST,GLIS2,PRKCSH,DDR2,SHC1,RDH10,PCSK6,OMD,GREM1,CLIC4,FOXO3,THRB,ZBTB16,ANKRD54,RGMA,SEC61A1,BRSK1	down_VCAV_EC
GO:0045892	0.202	0.855	24	328	negative regulation of transcription, DNA-templated	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,CBX5,FHL2,SMARCA4,PTPN2,MORF4L2,PEG3,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,HIF1AN,SIX4	down_VSAP_EC
GO:0007409	0.202	0.871	14	109	axonogenesis	BP	1	EPYC,FEZ1,FGFR2,NRP1,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2	up_ACOR_VSMC
GO:0016070	0.202	0.889	10	1479	RNA metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,WDR12,NEDD4	down_ACOR_EC
GO:0022407	0.202	0.895	7	96	regulation of cell-cell adhesion	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0043010	0.202	0.894	7	96	camera-type eye development	BP	1	PDGFRB,FBN1,THY1,GLI3,IRX5,RDH10,THRB	down_VCAV_EC
GO:0048705	0.202	0.894	7	95	skeletal system morphogenesis	BP	1	NAB2,THBS3,TBX15,GLI3,IRX5,RDH10,GREM1	down_VCAV_EC
GO:0045055	0.202	0.897	7	52	regulated exocytosis	BP	1	FBXL20,STX11,F2RL1,PSEN1,RAB11B,SCAMP5,PREPL	up_ACOR_VSMC
GO:0008344	0.202	0.921	4	25	adult locomotory behavior	BP	1	SEZ6L,FXN,CTNS,HTRA2	up_VSAP_EC
GO:0031623	0.202	0.932	3	31	receptor internalization	BP	1	LRPAP1,RAB31,GREM1	down_VCAV_EC
GO:0043502	0.202	0.936	3	16	regulation of muscle adaptation	BP	1	GATA5,PDE5A,EDN1	up_ACOR_VSMC
GO:0001818	0.202	0.931	3	65	negative regulation of cytokine production	BP	1	CMKLR1,DLL1,BPI	up_AFEM_EC
GO:0007566	0.202	0.955	2	10	embryo implantation	BP	1	PPARD,EMP2	down_ACOR_VSMC

GO:1903825	0.202	0.952	2	17	organic acid transmembrane transport	BP	1	FOLR2,AKT2	down_VCAV_EC
GO:1905039	0.202	0.952	2	17	carboxylic acid transmembrane transport	BP	1	FOLR2,AKT2	down_VCAV_EC
GO:0015914	0.202	0.955	2	10	phospholipid transport	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0055094	0.202	0.956	2	9	response to lipoprotein particle	BP	1	TLR4,ABCA1	up_VCAV_EC
GO:0009205	0.202	0.95	2	98	purine ribonucleoside triphosphate metabolic	BP	1	AK5,FBP1	up_VPOR_EC
GO:0072507	0.202	0.95	2	103	divalent inorganic cation homeostasis	BP	1	C3AR1,HOXA3	up_VPOR_EC
GO:0007507	0.202	0.951	2	194	heart development	BP	1	SALL1,SHOX2	up_VSAP_VSMC
GO:0042274	0.202	0.979	1	47	ribosomal small subunit biogenesis	BP	1	RPSA	down_ACOR_EC
GO:0060401	0.202	0.979	1	42	cytosolic calcium ion transport	BP	1	LYN	down_ACOR_EC
GO:0042060	0.202	0.98	1	103	wound healing	BP	1	SRSF6	down_AFEM_EC
GO:0010605	0.202	0.989	1	745	negative regulation of macromolecule metabolic	BP	1	CST3	down_AORT_EC
GO:0044501	0.202	0.983	1	4	modulation of signal transduction in other	BP	1	CALM1	down_VSAP_EC
GO:0052250	0.202	0.983	1	4	modulation of signal transduction in other organism involved in	BP	1	CALM1	down_VSAP_EC
GO:0021559	0.202	0.985	1	3	trigeminal nerve development	BP	1	NRP1	down_VSAP_EC
GO:0021636	0.202	0.985	1	3	trigeminal nerve morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0021637	0.202	0.985	1	3	trigeminal nerve structural organization	BP	1	NRP1	down_VSAP_EC
GO:0021785	0.202	0.985	1	3	branchiomotor neuron axon guidance	BP	1	NRP1	down_VSAP_EC
GO:1902287	0.202	0.985	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0043583	0.202	0.979	1	59	ear development	BP	1	HOXA1	up_APUL_EC
GO:0072006	0.202	0.979	1	59	nephron development	BP	1	NPNT	up_APUL_EC
GO:0002322	0.202	0.989	1	2	B cell proliferation involved in immune	BP	1	TLR4	up_VCAV_EC
GO:0032627	0.202	0.985	1	3	interleukin-23 production	BP	1	TLR4	up_VCAV_EC
GO:0032667	0.202	0.985	1	3	regulation of interleukin-23 production	BP	1	TLR4	up_VCAV_EC
GO:2001280	0.202	0.989	1	2	positive regulation of unsaturated fatty acid	BP	1	PTGS2	up_VCAV_EC
GO:0044706	0.202	0.979	1	27	multi-multicellular organism process	BP	1	ACVR2A	up_VPOR_EC
GO:0003012	0.202	0.979	1	90	muscle system process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007283	0.202	0.979	1	91	spermatogenesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:1903046	0.202	0.979	1	55	meiotic cell cycle process	BP	1	CYP26B1	up_VFEM_EC
GO:0030323	0.202	0.979	1	65	respiratory tube development	BP	1	TBX5	up_VPUL_EC
GO:1903708	0.202	0.979	1	65	positive regulation of hemopoiesis	BP	1	EVI2B	up_VPUL_EC
GO:0051051	0.202	0.98	1	112	negative regulation of transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0001936	0.202	0.979	1	49	regulation of endothelial cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0061548	0.202032585	0.98072	1	8	ganglion development	BP	1	NRP1	up_ACOR_EC
GO:0034695	0.202946357	0.98054	1	8	response to prostaglandin E	BP	1	PTGER4	up_ACOR_EC

GO:0007166	0.203	0.833	73	686	cell surface receptor signaling pathway	BP	1	SH3TC2,VEGFD,SMAD6,LGR6,PLCG2,IFNGR1,LEP,GATA5,ADGRD1,EFNB2,ANGPT1,RASSF2,ZRANB1,RECK,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,ELF1,TLR3,LATS2,CITED2,ZNRF3,CD274,AR,PTGIR,SASH1,TMEM108,FGF18,CDKN2B,LIMS2,F2RL1,ADGRL1,PSEN2,DAPK1,NCEH1,CLSTN1,CREBRF,NRP1,PTPN22,DMPK,NPNT,UNC5B,TBX20,SESN3,SH3RF1,CCDC3,PRKCE,FZD3,FRS2,FUT8,PARP9,APP,PSEN1,TGFBR1,SYNJ2BP,SIPA1L1,CCL5,PERP,DUSP22,EDN1,HPGD,LRRC4,ARID5B,INSYN1,ENSCAFG00000018360,DISC1,GNAQ,CELSR2,INPP5K,PARK7,PAG1	up_ACOR_VSMC
GO:0007167	0.203	0.851	27	274	enzyme linked receptor protein signaling pathway	BP	1	TEK,NPR1,KIT,PDGFB,BAIAP2L1,KDR,FERMT1,TIPARP,RAPGEF1,GATA3,SMAD1,BMP2,HHEX,ANGPT2,STMN1,PRKD2,APOD,NCK1,FES,RAPGEF2,CTDSPL2,SKIL,PDGFD,BMX,HIF1A,JCAD,ZEB1	up_VCAV_EC
GO:0071417	0.203	0.866	16	142	cellular response to organonitrogen compound	BP	1	PPARG,BAIAP2L1,PDE4D,MEF2C,RAPGEF1,MTOR,MAPK13,NCK1,TIMELESS,RAPGEF2,CTNNA1,BLM,PDGFD,NR4A1,ZEB1,ARHGEF2	up_VCAV_EC
GO:0030099	0.203	0.866	16	133	myeloid cell differentiation	BP	1	HOXA7,HOXA9,PPARGC1B,DLL1,ANKRD54,ZBTB16,RARG,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,TFE3,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0001655	0.203	0.871	14	116	urogenital system development	BP	1	HOXA11,EMX2,WNT11,OSR2,SLIT2,DLL1,OSR1,KLF15,ZBTB16,RARG,GLIS2,IRX3,SULF2,LRP4	up_VSAP_EC
GO:0007167	0.203	0.884	9	274	enzyme linked receptor protein signaling pathway	BP	1	DLL1,F3,HCK,TMEM100,GREM1,GREM2,RAB7A,ADAM17,KANK1	up_AFEM_EC
GO:0022412	0.203	0.885	9	76	cellular process involved in reproduction in multicellular organism	BP	1	KIT,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,AFF4,KDM3A,FBXO5	up_VCAV_EC
GO:0031589	0.203	0.889	8	93	cell-substrate adhesion	BP	1	VEGFA,SERPINE1,ACTN1,ILK,CTNNB1,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:0042773	0.203	0.911	5	32	ATP synthesis coupled electron transport	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,NDUFS2,NDUFV1	up_VSAP_EC
GO:0046425	0.203	0.919	4	39	regulation of JAK-STAT cascade	BP	1	SOCS5,PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0106027	0.203	0.921	4	24	neuron projection organization	BP	1	ZNF365,APP,PSEN1,WASL	up_ACOR_VSMC
GO:0045646	0.203	0.934	3	19	regulation of erythrocyte differentiation	BP	1	HSPA9,PRMT1,HMGB2	down_ACOR_VSMC
GO:0060079	0.203	0.936	3	15	excitatory postsynaptic potential	BP	1	TMEM108,DMPK,APP	up_ACOR_VSMC
GO:0051279	0.203	0.934	3	19	regulation of release of sequestered calcium ion into cytosol	BP	1	PDE4D,CHD7,APLNR	up_VCAV_EC
GO:1905898	0.203	0.935	3	16	positive regulation of response to endoplasmic	BP	1	PIK3R1,UBQLN2,NCK1	up_VSAP_EC
GO:0090407	0.203	0.95	2	177	organophosphate biosynthetic process	BP	1	ACSL3,TNRC6B	down_ACOR_EC
GO:0031063	0.203	0.955	2	10	regulation of histone deacetylation	BP	1	SREBF1,TADA2A	down_ACOR_VSMC
GO:0055025	0.203	0.952	2	17	positive regulation of cardiac muscle tissue	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0006220	0.203	0.953	2	14	pyrimidine nucleotide metabolic process	BP	1	ENTPD4,CMPK1	down_VSAP_EC
GO:0051293	0.203	0.953	2	13	establishment of spindle localization	BP	1	KPNB1,HTT	down_VSAP_EC
GO:1903035	0.203	0.953	2	14	negative regulation of response to wounding	BP	1	SERPINE1,APOE	down_VSAP_EC
GO:2000401	0.203	0.953	2	13	regulation of lymphocyte migration	BP	1	MSN,ADAM17	down_VSAP_EC
GO:0042129	0.203	0.95	2	35	regulation of T cell proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0044272	0.203	0.95	2	35	sulfur compound biosynthetic process	BP	1	XYLT1,ACACB	up_AFEM_EC
GO:0045807	0.203	0.95	2	35	positive regulation of endocytosis	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0048584	0.203	0.955	2	592	positive regulation of response to stimulus	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0080135	0.203	0.951	2	240	regulation of cellular response to stress	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0014065	0.203	0.979	1	39	phosphatidylinositol 3-kinase signaling	BP	1	NEDD4	down_ACOR_EC
GO:0032372	0.203	0.985	1	3	negative regulation of sterol transport	BP	1	SREBF2	down_ACOR_VSMC
GO:0032375	0.203	0.985	1	3	negative regulation of cholesterol transport	BP	1	SREBF2	down_ACOR_VSMC

GO:0045743	0.203	0.985	1	3	positive regulation of fibroblast growth factor receptor signaling	BP	1	CTNNB1	down_VSAP_EC
GO:0021649	0.203	0.988	1	2	vestibulocochlear nerve structural organization	BP	1	NRP1	up_ACOR_VSMC
GO:0061552	0.203	0.988	1	2	ganglion morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0097374	0.203	0.988	1	2	sensory neuron axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1904835	0.203	0.988	1	2	dorsal root ganglion morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0009725	0.203	0.981	1	188	response to hormone	BP	1	ESR1	up_AORT_VSMC
GO:0098609	0.203	0.981	1	181	cell-cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0034329	0.203	0.979	1	60	cell junction assembly	BP	1	NR1H4	up_APUL_EC
GO:0002318	0.203	0.985	1	3	myeloid progenitor cell differentiation	BP	1	KIT	up_VCAV_EC
GO:0042095	0.203	0.985	1	3	interferon-gamma biosynthetic process	BP	1	TLR3	up_VCAV_EC
GO:0042416	0.203	0.985	1	3	dopamine biosynthetic process	BP	1	GCH1	up_VCAV_EC
GO:0045078	0.203	0.985	1	3	positive regulation of interferon-gamma	BP	1	TLR3	up_VCAV_EC
GO:0045072	0.203	0.985	1	3	regulation of interferon-gamma biosynthetic	BP	1	TLR3	up_VCAV_EC
GO:0071294	0.203	0.983	1	4	cellular response to zinc ion	BP	1	CREB1	up_VCAV_EC
GO:0030003	0.203	0.98	1	157	cellular cation homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0048638	0.203	0.979	1	82	regulation of developmental growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0005996	0.203	0.979	1	85	monosaccharide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0045165	0.203	0.979	1	65	cell fate commitment	BP	1	ARHGEF2	up_VPUL_EC
GO:0009952	0.203	0.979	1	66	anterior/posterior pattern specification	BP	1	HOXA3	up_VPUL_EC
GO:0016358	0.203512312	0.93043	3	58	dendrite development	BP	1	PAK3,MAPK8IP2,NRP1	up_ACOR_EC
GO:0048469	0.203706273	0.94989	2	31	cell maturation	BP	1	PTH1R,FZD5	up_ACOR_EC
GO:2000479	0.203953956	0.98034	1	8	regulation of cAMP-dependent protein kinase	BP	1	PKIB	up_ACOR_EC
GO:0009259	0.204	0.864	17	166	ribonucleotide metabolic process	BP	1	ACLY,HMGCR,RAN,CDK1,PFAS,RNASEH2B,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0006520	0.204	0.87	14	114	cellular amino acid metabolic process	BP	1	ENOSF1,PRDX4,ENSCAFG00000002977,TARSL2,NIT2,ERO1B,EGLN1,P4HA1,SARDH,SGSM2,PCYOX1,AZIN2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0010647	0.204	0.868	14	460	positive regulation of cell communication	BP	1	LEP,DLL1,F3,MLLT11,LMCD1,PLAGL2,GREM1,FAM53B,CLEC16A,CYLD,LGR6,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0046483	0.204	0.887	11	1948	heterocycle metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0001505	0.204	0.885	9	69	regulation of neurotransmitter levels	BP	1	FBXL20,MAOA,STX11,MOXD1,PSEN1,CLN8,KCNC4,PREPL,PARK7	up_ACOR_VSMC
GO:0017038	0.204	0.894	7	96	protein import	BP	1	ENSCAFG00000014978,SNUPN,PEX5,GLI3,MAVS,SEC61B,LONP2	down_VCAV_EC
GO:0001763	0.204	0.894	7	78	morphogenesis of a branching structure	BP	1	SULF1,ILK,HOXB7,MAGED1,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0016070	0.204	0.918	5	1479	RNA metabolic process	BP	1	IVNS1ABP,DARS,SRSF6,GABPA,TSEN15	down_AFEM_EC
GO:0097553	0.204	0.91	5	32	calcium ion transmembrane import	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0051250	0.204	0.909	5	38	negative regulation of lymphocyte activation	BP	1	TNFAIP3,PELI1,ARG2,THOC1,HMGB1	up_VCAV_EC
GO:0071166	0.204	0.909	5	36	ribonucleoprotein complex localization	BP	1	IWS1,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0009719	0.204	0.908	5	395	response to endogenous stimulus	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,RNF6	up_VPOR_EC
GO:0060425	0.204	0.92	4	25	lung morphogenesis	BP	1	BMP4,FGFR2,SEC24B,DAG1	up_ACOR_VSMC
GO:0010646	0.204	0.923	4	945	regulation of cell communication	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0000041	0.204	0.931	3	31	transition metal ion transport	BP	1	SLC39A6,SCARA5,ARHGAP1	down_VCAV_EC

GO:2000117	0.204	0.932	3	27	negative regulation of cysteine-type	BP	1	PTGS2,CRYAB,PAK2	down_VSAP_EC
GO:0060575	0.204	0.955	2	9	intestinal epithelial cell differentiation	BP	1	GATA5,GATA4	up_ACOR_VSMC
GO:0030182	0.204	0.951	2	327	neuron differentiation	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0010470	0.204	0.955	2	9	regulation of gastrulation	BP	1	HNF4A,OSR1	up_VSAP_EC
GO:0048532	0.204	0.955	2	9	anatomical structure arrangement	BP	1	DLL1,PLXNA4	up_VSAP_EC
GO:0099054	0.204	0.955	2	9	presynapse assembly	BP	1	FZD1,LRP4	up_VSAP_EC
GO:0001977	0.204	0.985	1	3	renal system process involved in regulation of	BP	1	EMP2	down_ACOR_VSMC
GO:0003093	0.204	0.985	1	3	regulation of glomerular filtration	BP	1	EMP2	down_ACOR_VSMC
GO:1900044	0.204	0.982	1	5	regulation of protein K63-linked ubiquitination	BP	1	SASH1	down_VCAV_EC
GO:0031328	0.204	0.985	1	512	positive regulation of cellular biosynthetic	BP	1	MOSPD1	down_VFEM_EC
GO:0010452	0.204	0.985	1	3	histone H3-K36 methylation	BP	1	IWS1	down_VSAP_EC
GO:0045794	0.204	0.985	1	3	negative regulation of cell volume	BP	1	CLCN3	down_VSAP_EC
GO:0021648	0.204	0.985	1	3	vestibulocochlear nerve morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0034135	0.204	0.983	1	4	regulation of toll-like receptor 2 signaling	BP	1	LYN	down_VSAP_EC
GO:0061029	0.204	0.983	1	4	eyelid development in camera-type eye	BP	1	INHBA	down_VSAP_EC
GO:0090521	0.204	0.985	1	3	glomerular visceral epithelial cell migration	BP	1	ANLN	down_VSAP_EC
GO:0048232	0.204	0.979	1	95	male gamete generation	BP	1	HOXA9	up_AORT_EC
GO:1901990	0.204	0.979	1	94	regulation of mitotic cell cycle phase transition	BP	1	TAOK1	up_AORT_EC
GO:1903912	0.204	0.985	1	3	negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation	BP	1	NCK1	up_VCAV_EC
GO:0044262	0.204	0.979	1	89	cellular carbohydrate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0014706	0.204	0.979	1	112	striated muscle tissue development	BP	1	TBX5	up_VPUL_VSMC
GO:0071360	0.204767881	0.97988	1	9	cellular response to exogenous dsRNA	BP	1	MAVS	up_ACOR_EC
GO:1903050	0.204829035	0.9162	4	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0046755	0.20492838	0.97985	1	9	viral budding	BP	1	CHMP4B	up_ACOR_EC
GO:0007165	0.205	0.83	81	1496	signal transduction	BP	1	NOTCH2,PDGFRB,SLC35F6,SMAD9,ITGB5,DCN,NDN,ANGPT1,PRNP,VASN,FBN1,ADCY6,GLIPR2,BGN,KANK2,SH3BP1,BMPR1A,EVC,RECK,IGFBP6,NUMBL,ARHGEF25,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,AKT2,DOCK10,SYDE1,CLSTN1,PLCL1,CSPG4,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,SEMA3C,ASPN,GNAZ,THY1,TEAD1,ARHGAP10,ATP6V0C,GLI3,PARK7,ZMAT3,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ENSCAFG00000018194,ARL2BP,IFT57,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,RAB7B,SPNS1,GLIS2,ARHGAP1,SHC1,CRCP,FBH1,GREM1,NPHP4,RAC2,FOXO3,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:0008150	0.205	0.883	49	5646	biological_process	BP	1	C3AR1,BARX1,HTR7,OSTC,CXHXorf57,PTK7,OGA,MZT1,HOOK3,XPOT,HOXA3,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,OAS3,SLC7A11,SEMA3A,ENSCAFG00000005494,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,GOLT1B,GCC2,SV2C,RPL10L,ABHD5,TWF1,SLC25A16,SEMA3D,PDE1C,FAM135A,RRP15,SRP54,KLHL28,PUM3,TMEM87B,TMEM68,EIF5,CCAR1,STK17B,HOXA2,USP33,ENSCAFG00000032731,NAALADL2,GNPNAT1,RNF6	up_VPOR_EC

GO:1901565	0.205	0.846	31	442	organonitrogen compound catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,TRIB3,ALDH1L2,CEMIP2,MSN,SEL1L,USP12,DNAJC10,UBA6,ENTPD4,UCHL5,SPOPL,DNAJB9,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CUL2,SPOP,DISC1,RAD23A,TMTC3,USP14,TNFAIP1	down_VSAP_EC
GO:2000113	0.205	0.849	28	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,ENPP1,CBX5,FHL2,SMARCA4,SESN2,PTPN2,MORF4L2,PEG3,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,EIF2S1,HIF1AN,SIX4	down_VSAP_EC
GO:0006082	0.205	0.858	19	305	organic acid metabolic process	BP	1	GPAM,DCN,AKT2,ACAA1,ME3,UROS,THNSL2,SUOX,PEX5,PARK7,ENSCAFG00000002977,HPDL,ACSS2,RDH10,CRTAP,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0072594	0.205	0.873	12	155	establishment of protein localization to organelle	BP	1	PRICKLE1,TRAM1,SRP54,ZPR1,SRPRA,KPNB1,SRP72,KPNA4,DDIT3,SH3GLB1,KPNA1,CDKN1A	down_VSAP_EC
GO:0030336	0.205	0.877	11	86	negative regulation of cell migration	BP	1	TCAF1,RECK,TP53INP1,EVL,TBX5,DAG1,SEMA6D,SYNJ2BP,JUP,DUSP22,WASL	up_ACOR_VSMC
GO:0002757	0.205	0.881	10	78	immune response-activating signal	BP	1	TLR1,PLCG2,ELF1,TLR3,F2RL1,PTPN22,PRKCE,PSEN1,DUSP22,NOD2	up_ACOR_VSMC
GO:0051092	0.205	0.901	6	47	positive regulation of NF-kappaB transcription	BP	1	IRAK1,MTDH,GREM1,DHX33,CTH,ARHGEF2	down_ACOR_VSMC
GO:0009855	0.205	0.902	6	42	determination of bilateral symmetry	BP	1	GJA1,CITED2,TBX20,PSEN1,PCSK6,PSKH1	up_ACOR_VSMC
GO:0033135	0.205	0.902	6	40	regulation of peptidyl-serine phosphorylation	BP	1	PLCL1,RASSF2,APP,INPP5K,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0043487	0.205	0.91	5	33	regulation of RNA stability	BP	1	AXIN2,TENT5C,ZFP36L1,SAMD4B,ZFP36L2	up_VSAP_EC
GO:1903008	0.205	0.917	4	47	organelle disassembly	BP	1	GABARAP,WDR45,CLEC16A,RETREG1	down_VCAV_EC
GO:0051784	0.205	0.919	4	28	negative regulation of nuclear division	BP	1	RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0061462	0.205	0.935	3	15	protein localization to lysosome	BP	1	SCARB2,LAMP2,SH3BP4	up_ACOR_VSMC
GO:0032868	0.205	0.929	3	66	response to insulin	BP	1	LEP,CRY2,KANK1	up_AFEM_EC
GO:0070848	0.205	0.93	3	193	response to growth factor	BP	1	ENSCAFG00000002015,ASPN,ACVR2A	up_VPOR_EC
GO:0048103	0.205	0.954	2	10	somatic stem cell division	BP	1	ASPM,ARHGEF2	down_ACOR_VSMC
GO:2000757	0.205	0.954	2	10	negative regulation of peptidyl-lysine acetylation	BP	1	BRCA1,NOC2L	down_ACOR_VSMC
GO:1902229	0.205	0.951	2	17	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	TMEM161A,FBH1	down_VCAV_EC
GO:0050999	0.205	0.955	2	9	regulation of nitric-oxide synthase activity	BP	1	LEP,HTR2B	up_ACOR_VSMC
GO:0008637	0.205	0.949	2	35	apoptotic mitochondrial changes	BP	1	MLLT11,CAMK2A	up_AFEM_EC
GO:0032459	0.205	0.953	2	12	regulation of protein oligomerization	BP	1	RIOK3,PMAIP1	up_VCAV_EC
GO:0003008	0.205	0.951	2	336	system process	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0051241	0.205	0.951	2	336	negative regulation of multicellular organismal	BP	1	HOXC10,HOXA9	up_VFEM_VSMC
GO:0010831	0.205	0.955	2	9	positive regulation of myotube differentiation	BP	1	SHOX2,FLOT1	up_VSAP_EC
GO:0070848	0.205	0.949	2	193	response to growth factor	BP	1	CAV1,FGF5	up_VSAP_VSMC
GO:0009156	0.205	0.978	1	50	ribonucleoside monophosphate	BP	1	TNRC6B	down_ACOR_EC
GO:1903044	0.205	0.985	1	3	protein localization to membrane raft	BP	1	CAV1	down_ACOR_VSMC
GO:1901342	0.205	0.979	1	114	regulation of vasculature development	BP	1	HDAC7	down_VPOR_EC
GO:0010605	0.205	0.988	1	745	negative regulation of macromolecule metabolic	BP	1	GATA5	down_VFEM_VSMC
GO:0010039	0.205	0.983	1	4	response to iron ion	BP	1	HIF1A	down_VSAP_EC
GO:0042574	0.205	0.983	1	4	retinal metabolic process	BP	1	RDH11	down_VSAP_EC
GO:0044090	0.205	0.983	1	4	positive regulation of vacuole organization	BP	1	SH3GLB1	down_VSAP_EC
GO:0050832	0.205	0.983	1	4	defense response to fungus	BP	1	COTL1	down_VSAP_EC
GO:0060982	0.205	0.985	1	3	coronary artery morphogenesis	BP	1	NRP1	down_VSAP_EC

GO:2000786	0.205	0.983	1	4	positive regulation of autophagosome assembly	BP	1	SH3GLB1	down_VSAP_EC
GO:0035989	0.205	0.988	1	2	tendon development	BP	1	BMP4	up_ACOR_VSMC
GO:0001867	0.205	0.988	1	2	complement activation, lectin pathway	BP	1	C1S	up_ACOR_VSMC
GO:1990051	0.205	0.988	1	2	activation of protein kinase C activity	BP	1	LEP	up_ACOR_VSMC
GO:0045087	0.205	0.98	1	161	innate immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0045321	0.205	0.98	1	191	leukocyte activation	BP	1	ARG2	up_AORT_VSMC
GO:0007219	0.205	0.979	1	59	Notch signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0008654	0.205	0.979	1	58	phospholipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0035107	0.205	0.978	1	60	appendage morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0035108	0.205	0.978	1	60	limb morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0023035	0.205	0.988	1	2	CD40 signaling pathway	BP	1	TNFAIP3	up_VCAV_EC
GO:0120035	0.205	0.98	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0010770	0.205	0.979	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0050803	0.205	0.978	1	55	regulation of synapse structure or activity	BP	1	SIX1	up_VFEM_EC
GO:0050807	0.205	0.978	1	55	regulation of synapse organization	BP	1	SIX1	up_VFEM_EC
GO:0009416	0.205	0.979	1	88	response to light stimulus	BP	1	NETO1	up_VFEM_VSMC
GO:0050769	0.205	0.979	1	95	positive regulation of neurogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0050730	0.205	0.979	1	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	ARHGEF2	up_VPUL_EC
GO:2000116	0.205	0.979	1	67	regulation of cysteine-type endopeptidase	BP	1	PTGER2	up_VPUL_EC
GO:0031398	0.205	0.978	1	51	positive regulation of protein ubiquitination	BP	1	CAV1	up_VSAP_VSMC
GO:0002793	0.205	0.979	1	54	positive regulation of peptide secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0050714	0.205	0.979	1	54	positive regulation of protein secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0009190	0.205021763	0.98012	1	8	cyclic nucleotide biosynthetic process	BP	1	GUCY1B1	up_ACOR_EC
GO:0052652	0.205021763	0.98012	1	8	cyclic purine nucleotide metabolic process	BP	1	GUCY1B1	up_ACOR_EC
GO:0032434	0.205996119	0.92915	3	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	PIAS1,CLU,RNF114	up_ACOR_EC
GO:0009887	0.206	0.853	23	314	animal organ morphogenesis	BP	1	SULF1,SERPINH1,SERPINE1,ERRFI1,BCAR3,ENSCAFG00000032470,TMED2,ILK,FHL2,TGFBR1,CHSY1,MSN,HOXB7,HIF1A,ACTG2,UCHL5,ACTA2,MAGED1,CTNNB1,PLOD3,INHBA,SIX4,NRP1	down_VSAP_EC
GO:0071396	0.206	0.864	16	134	cellular response to lipid	BP	1	FAM107A,PTGFR,PPARGC1B,ABL1,OSR1,RARG,ZFP36L1,SASH1,CREBRF,MYD88,PRMT2,OSBPL7,ZFP36L2,HTRA2,LBH,DDIT4	up_VSAP_EC
GO:1901137	0.206	0.865	15	232	carbohydrate derivative biosynthetic process	BP	1	ADCY6,KRTCAP2,DDOST,ATP5MC1,GFPT2,PIGS,NECAB3,ADK,B4GALT1,AMPD2,FUT8,ACSS2,RPN2,SOAT1,ACAT1	down_VCAV_EC
GO:0045765	0.206	0.871	13	105	regulation of angiogenesis	BP	1	ENPP2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,CCBE1,TBXA2R,SASH1,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0009416	0.206	0.879	10	88	response to light stimulus	BP	1	USP1,HMGCR,NEDD4,AURKB,PCNA,NOC2L,POLH,DTL,CDC25A,HMGN1	down_ACOR_VSMC
GO:1902275	0.206	0.889	8	60	regulation of chromatin organization	BP	1	IWS1,GATA3,UHRF2,PRKD2,NSD1,KDM5A,KDM3A,ATRX	up_VCAV_EC
GO:0051896	0.206	0.908	5	39	regulation of protein kinase B signaling	BP	1	TEK,HCLS1,RAPGEF1,GATA3,MTOR	up_VCAV_EC
GO:0046660	0.206	0.919	4	28	female sex differentiation	BP	1	KIT,CHD7,TIPARP,EIF2B2	up_VCAV_EC
GO:0001906	0.206	0.932	3	20	cell killing	BP	1	FAM49B,EMP2,CORO1A	down_ACOR_VSMC
GO:0019217	0.206	0.931	3	27	regulation of fatty acid metabolic process	BP	1	TRIB3,PTGS2,SLC45A3	down_VSAP_EC

GO:0007162	0.206	0.929	3	66	negative regulation of cell adhesion	BP	1	HOXA7,CYLD,KANK1	up_AFEM_EC
GO:0016331	0.206	0.929	3	66	morphogenesis of embryonic epithelium	BP	1	IRX3,GREM1,LUZP1	up_AFEM_EC
GO:0035148	0.206	0.929	3	66	tube formation	BP	1	IRX3,GREM1,LUZP1	up_AFEM_EC
GO:0003300	0.206	0.933	3	18	cardiac muscle hypertrophy	BP	1	MEF2C,EDN1,PPP3CA	up_VCAV_EC
GO:0014896	0.206	0.933	3	18	muscle hypertrophy	BP	1	MEF2C,EDN1,PPP3CA	up_VCAV_EC
GO:0014897	0.206	0.933	3	18	striated muscle hypertrophy	BP	1	MEF2C,EDN1,PPP3CA	up_VCAV_EC
GO:0046503	0.206	0.953	2	10	glycerolipid catabolic process	BP	1	ABHD5,LIPC	down_ACOR_VSMC
GO:0046636	0.206	0.953	2	10	negative regulation of alpha-beta T cell	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0055081	0.206	0.951	2	17	anion homeostasis	BP	1	GPAM,ENSCAFG00000018277	down_VCAV_EC
GO:0035767	0.206	0.951	2	14	endothelial cell chemotaxis	BP	1	VEGFA,NRP1	down_VSAP_EC
GO:0060191	0.206	0.952	2	14	regulation of lipase activity	BP	1	ABHD5,ARF4	down_VSAP_EC
GO:0002021	0.206	0.954	2	9	response to dietary excess	BP	1	LEP,PPARGC1A	up_ACOR_VSMC
GO:0010762	0.206	0.954	2	9	regulation of fibroblast migration	BP	1	PRKCE,DDR2	up_ACOR_VSMC
GO:2000738	0.206	0.954	2	9	positive regulation of stem cell differentiation	BP	1	BMP4,TBX5	up_ACOR_VSMC
GO:0043207	0.206	0.949	2	216	response to external biotic stimulus	BP	1	NR1H4,BPI	up_APUL_EC
GO:0051707	0.206	0.949	2	216	response to other organism	BP	1	NR1H4,BPI	up_APUL_EC
GO:0048584	0.206	0.954	2	592	positive regulation of response to stimulus	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0007409	0.206	0.948	2	109	axonogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0021515	0.206	0.954	2	9	cell differentiation in spinal cord	BP	1	HOXC10,GDPD5	up_VSAP_EC
GO:0048193	0.206	0.979	1	116	Golgi vesicle transport	BP	1	ERGIC1	down_VPOR_EC
GO:0048732	0.206	0.979	1	116	gland development	BP	1	CITED2	down_VPOR_EC
GO:0007016	0.206	0.984	1	3	cytoskeletal anchoring at plasma membrane	BP	1	TLN1	down_VSAP_EC
GO:0033169	0.206	0.984	1	3	histone H3-K9 demethylation	BP	1	KDM3A	down_VSAP_EC
GO:0010739	0.206	0.988	1	2	positive regulation of protein kinase A signaling	BP	1	ENSCAFG00000029553	up_ACOR_VSMC
GO:0070848	0.206	0.98	1	193	response to growth factor	BP	1	WNT7A	up_AORT_VSMC
GO:0072073	0.206	0.978	1	60	kidney epithelium development	BP	1	NPNT	up_APUL_EC
GO:0072138	0.206	0.984	1	3	mesenchymal cell proliferation involved in ureteric bud development	BP	1	BMP2	up_VCAV_EC
GO:2000347	0.206	0.988	1	2	positive regulation of hepatocyte proliferation	BP	1	TNFAIP3	up_VCAV_EC
GO:0006873	0.206	0.979	1	160	cellular ion homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0031344	0.206	0.979	1	161	regulation of cell projection organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0000018	0.206	0.978	1	31	regulation of DNA recombination	BP	1	CXHXorf57	up_VPOR_EC
GO:0030098	0.206	0.979	1	87	lymphocyte differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0032868	0.206	0.978	1	66	response to insulin	BP	1	NR1H4	up_VPUL_EC
GO:1901605	0.206	0.978	1	67	alpha-amino acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0001935	0.206	0.978	1	50	endothelial cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0090257	0.206	0.978	1	52	regulation of muscle system process	BP	1	CAV1	up_VSAP_VSMC
GO:0030833	0.206532314	0.92888	3	59	regulation of actin filament polymerization	BP	1	TMOD1,PAK3,PRKCD	up_ACOR_EC
GO:1901016	0.206938196	0.97943	1	9	regulation of potassium ion transmembrane transporter activity	BP	1	ACTN2	up_ACOR_EC
GO:1903076	0.206979598	0.94851	2	32	regulation of protein localization to plasma	BP	1	PLS1,LRRC15	up_ACOR_EC

GO:0080090	0.207	0.82	151	1734	regulation of primary metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,ADGRF5,KIT,PPP2R5A,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,TMEM173,RELN,PDE4D,IWS1,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,RALB,APLNR,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,FAM3C,ODC1,CASP8,MTOR,TENT2,SAMD8,ELF4,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,SLK,SH3BP5,CNOT6,RSC1A1,ENC1,CCAR1,PPP1R2,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,PAK2,PRKD2,THOC1,SH3GLB1,SWAP70,SMARCA4,TLR3,APOD,NCK1,ESCO1,DPH5,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,PTGS2,MMD,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,TAOK1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,NOS2,PMAIP1,ZNF789,BLM,NUP133,SPTBN4,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,PDGFD,USP37,WTAP,MTA2,CUL4A,NR1D2,UBE2D1,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,IVNS1ABP,JCAD,PSMB9,ZEB1,TET2,ARHGEF2,CDON,ELK3,ZNF609	up_VCAV_EC
GO:0009056	0.207	0.835	51	755	catabolic process	BP	1	PRICKLE1,PLK3,HSPA5,SOCS5,HM13,HSP90B1,ENPP1,SNX25,PGK1,TPI1,TRIB3,PGAM1,ALDH1L2,SESN2,CEMIP2,MSN,SEL1L,HIF1A,USP12,DNAJC10,UBA6,ZPR1,ENTPD4,UCHL5,SPOPL,PLCL1,SMG7,MTDH,CNOT7,DNAJB9,ALDOC,SND1,APOE,USP48,BNIP3,DDIT3,CBLC,GSK3B,CDC37,CUL2,SH3GLB1,GALE,HTT,ABHD5,SPOP,DISC1,RAD23A,TMTC3,USP14,YWHAH,TNFAIP1	down_VSAP_EC
GO:0009890	0.207	0.845	30	420	negative regulation of biosynthetic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,ENPP1,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTPN2,MORF4L2,PEG3,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,EIF2S1,HIF1AN,SIX4	down_VSAP_EC
GO:1902679	0.207	0.851	24	329	negative regulation of RNA biosynthetic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,CBX5,FHL2,SMARCA4,PTPN2,MORF4L2,PEG3,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,HIF1AN,SIX4	down_VSAP_EC
GO:1903507	0.207	0.851	24	329	negative regulation of nucleic acid-templated transcription	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,CBX5,FHL2,SMARCA4,PTPN2,MORF4L2,PEG3,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,HIF1AN,SIX4	down_VSAP_EC
GO:0045321	0.207	0.854	22	191	leukocyte activation	BP	1	CD274,TBC1D10C,ABL1,DLL1,ZBTB16,TOX,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,STX4,PPP3CB,NCK1,TGFBR2	up_VSAP_EC
GO:0060627	0.207	0.874	11	165	regulation of vesicle-mediated transport	BP	1	LRP1,SDC4,CLIP3,AKT2,LRPAP1,CYBA,ARHGAP1,GREM1,EVI5L,RAC2,PACSIN3	down_VCAV_EC
GO:0007269	0.207	0.908	5	34	neurotransmitter secretion	BP	1	FBXL20,STX11,PSEN1,KCNC4,PREPL	up_ACOR_VSMC
GO:0099643	0.207	0.908	5	34	signal release from synapse	BP	1	FBXL20,STX11,PSEN1,KCNC4,PREPL	up_ACOR_VSMC
GO:0010508	0.207	0.907	5	38	positive regulation of autophagy	BP	1	PLK2,RALB,SPTLC2,SH3GLB1,HIF1A	up_VCAV_EC
GO:0048704	0.207	0.916	4	46	embryonic skeletal system morphogenesis	BP	1	TBX15,GLI3,IRX5,RDH10	down_VCAV_EC
GO:0051668	0.207	0.917	4	39	localization within membrane	BP	1	SEC24D,AGRN,APOE,SEC13	down_VSAP_EC
GO:0050729	0.207	0.919	4	25	positive regulation of inflammatory response	BP	1	TLR3,APP,NOD2,PARK7	up_ACOR_VSMC
GO:1904591	0.207	0.919	4	25	positive regulation of protein import	BP	1	ARHGEF5,CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0042102	0.207	0.932	3	19	positive regulation of T cell proliferation	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0034763	0.207	0.93	3	27	negative regulation of transmembrane transport	BP	1	ENPP1,REM1,CALM1	down_VSAP_EC
GO:0030278	0.207	0.929	3	66	regulation of ossification	BP	1	TWIST2,GREM1,AXIN2	up_AFEM_EC
GO:0001756	0.207	0.95	2	17	somitogenesis	BP	1	BMPR1A,SEMA3C	down_VCAV_EC

GO:1903204	0.207	0.954	2	9	negative regulation of oxidative stress-induced	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0031175	0.207	0.949	2	224	neuron projection development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0051984	0.207	0.953	2	10	positive regulation of chromosome segregation	BP	1	SMC5,RAD21	up_VCAV_EC
GO:0032743	0.207	0.953	2	10	positive regulation of interleukin-2 production	BP	1	PDE4D,PRKD2	up_VCAV_EC
GO:1900449	0.207	0.954	2	9	regulation of glutamate receptor signaling	BP	1	RELN,MEF2C	up_VCAV_EC
GO:0009126	0.207	0.948	2	100	purine nucleoside monophosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0009167	0.207	0.948	2	100	purine ribonucleoside monophosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0032944	0.207	0.978	1	48	regulation of mononuclear cell	BP	1	LYN	down_ACOR_EC
GO:0050670	0.207	0.978	1	48	regulation of lymphocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0060041	0.207	0.978	1	41	retina development in camera-type eye	BP	1	ACVRL1	down_ACOR_EC
GO:0071222	0.207	0.978	1	46	cellular response to lipopolysaccharide	BP	1	LYN	down_ACOR_EC
GO:0097529	0.207	0.978	1	52	myeloid leukocyte migration	BP	1	LYN	down_ACOR_EC
GO:0008104	0.207	0.988	1	763	protein localization	BP	1	SCAMP4	down_AORT_EC
GO:0009891	0.207	0.984	1	521	positive regulation of biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0001944	0.207	0.981	1	263	vasculature development	BP	1	TGFBI	down_VSAP_VSMC
GO:0010948	0.207	0.978	1	96	negative regulation of cell cycle process	BP	1	TAOK1	up_AORT_EC
GO:0010810	0.207	0.978	1	60	regulation of cell-substrate adhesion	BP	1	NPNT	up_APUL_EC
GO:0007635	0.207	0.988	1	2	chemosensory behavior	BP	1	CHD7	up_VCAV_EC
GO:0010612	0.207	0.988	1	2	regulation of cardiac muscle adaptation	BP	1	PPP3CA	up_VCAV_EC
GO:0042048	0.207	0.988	1	2	olfactory behavior	BP	1	CHD7	up_VCAV_EC
GO:0044557	0.207	0.988	1	2	relaxation of smooth muscle	BP	1	GUCY1A1	up_VCAV_EC
GO:0060087	0.207	0.988	1	2	relaxation of vascular smooth muscle	BP	1	GUCY1A1	up_VCAV_EC
GO:1903242	0.207	0.988	1	2	regulation of cardiac muscle hypertrophy in	BP	1	PPP3CA	up_VCAV_EC
GO:0010633	0.207	0.978	1	28	negative regulation of epithelial cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0003012	0.207	0.978	1	90	muscle system process	BP	1	GATM	up_VFEM_VSMC
GO:0032102	0.207	0.978	1	67	negative regulation of response to external	BP	1	NR1H4	up_VPUL_EC
GO:0048736	0.207	0.978	1	66	appendage development	BP	1	TBX5	up_VPUL_EC
GO:0060173	0.207	0.978	1	66	limb development	BP	1	TBX5	up_VPUL_EC
GO:0043536	0.207552125	0.94827	2	32	positive regulation of blood vessel endothelial	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0060429	0.208	0.84	38	341	epithelium development	BP	1	EXPH5,SMAD6,LBH,GATA5,GATA4,SHROOM3,MLLT3,FERMT1,BMP4,FGFR2,GJA1,ATRX,SEC24B,LATS2,CITED2,SPINT1,ZNRF3,LMO4,ARHGEF26,F2RL1,CTSB,ENSCAFG00000006238,CLSTN1,NRP1,NPNT,SPINT2,TBX20,TBX5,FZD3,FRS2,DAG1,PSEN1,CHD7,FOSL2,EDN1,SERPINB5,RREB1,ZDHHC21	up_ACOR_VSMC
GO:0022414	0.208	0.843	33	294	reproductive process	BP	1	LEP,GATA4,PRDX4,RECK,BMP4,FGFR2,ATRX,PDE5A,CITED2,SPINT1,GLRB,CTSB,EGLN1,ENSCAFG00000006238,CREBRF,SPINT2,PTGDR,MARF1,AFF4,DKKL1,FRS2,APP,CHD7,SPINK2,HPGD,ARID5B,DMC1,SERPINB5,JAM3,SUN1,HERPUD2,LHX9,WDR48	up_ACOR_VSMC
GO:0001822	0.208	0.872	12	98	kidney development	BP	1	HOXA11,WNT11,OSR2,SLIT2,DLL1,OSR1,KLF15,ZBTB16,GLIS2,IRX3,SULF2,LRP4	up_VSAP_EC
GO:0006954	0.208	0.877	10	147	inflammatory response	BP	1	LRP1,CHID1,CLSTN1,ENSCAFG00000013404,B4GALT1,PARK7,CYBA,LOXL3,A2M,NAPEPLD	down_VCAV_EC
GO:0001933	0.208	0.877	10	146	negative regulation of protein phosphorylation	BP	1	KIRREL1,DCN,PRNP,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1,GREM1	down_VCAV_EC

GO:0051251	0.208	0.882	9	69	positive regulation of lymphocyte activation	BP	1	CD274,ZBTB16,TOX,STAT6,MYD88,CD83,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0072593	0.208	0.897	6	68	reactive oxygen species metabolic process	BP	1	PRCP,SESN2,HIF1A,BNIP3,CDKN1A,ARF4	down_VSAP_EC
GO:1905897	0.208	0.907	5	34	regulation of response to endoplasmic reticulum	BP	1	OS9,SERINC3,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:1902107	0.208	0.916	4	47	positive regulation of leukocyte differentiation	BP	1	CLSTN1,GLI3,ZFP36L1,ZBTB16	down_VCAV_EC
GO:0016064	0.208	0.918	4	26	immunoglobulin mediated immune	BP	1	NECTIN2,THOC1,SWAP70,BCL10	up_VCAV_EC
GO:0019724	0.208	0.918	4	26	B cell mediated immunity	BP	1	NECTIN2,THOC1,SWAP70,BCL10	up_VCAV_EC
GO:0071466	0.208	0.933	3	17	cellular response to xenobiotic stimulus	BP	1	NCEH1,NR3C1,DDIT4	up_ACOR_VSMC
GO:0120035	0.208	0.948	2	160	regulation of plasma membrane bounded cell projection organization	BP	1	LYN,PDPN	down_ACOR_EC
GO:0048599	0.208	0.953	2	10	oocyte development	BP	1	TRIP13,FBXO5	down_ACOR_VSMC
GO:0032945	0.208	0.95	2	17	negative regulation of mononuclear cell	BP	1	PRNP,SDC4	down_VCAV_EC
GO:0050672	0.208	0.95	2	17	negative regulation of lymphocyte proliferation	BP	1	PRNP,SDC4	down_VCAV_EC
GO:0010955	0.208	0.951	2	14	negative regulation of protein processing	BP	1	SERPINE1,A2M	down_VSAP_EC
GO:0034142	0.208	0.951	2	14	toll-like receptor 4 signaling pathway	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0042446	0.208	0.951	2	14	hormone biosynthetic process	BP	1	HIF1A,REST	down_VSAP_EC
GO:0042982	0.208	0.95	2	15	amyloid precursor protein metabolic process	BP	1	APOE,LYN	down_VSAP_EC
GO:1903318	0.208	0.951	2	14	negative regulation of protein maturation	BP	1	SERPINE1,A2M	down_VSAP_EC
GO:0009893	0.208	0.958	2	995	positive regulation of metabolic process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0002230	0.208	0.954	2	9	positive regulation of defense response to virus	BP	1	PTPN22,PARP9	up_ACOR_VSMC
GO:1900745	0.208	0.954	2	9	positive regulation of p38MAPK cascade	BP	1	LEP,SASH1	up_ACOR_VSMC
GO:0036003	0.208	0.953	2	10	positive regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	ATF3,HIF1A	up_VCAV_EC
GO:0045601	0.208	0.953	2	10	regulation of endothelial cell differentiation	BP	1	JAG1,ZEB1	up_VCAV_EC
GO:0071320	0.208	0.953	2	9	cellular response to cAMP	BP	1	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:0009199	0.208	0.947	2	100	ribonucleoside triphosphate metabolic	BP	1	AK5,FBP1	up_VPOR_EC
GO:0006811	0.208	0.95	2	330	ion transport	BP	1	NETO1,SLC16A12	up_VFEM_VSMC
GO:0070986	0.208	0.954	2	9	left/right axis specification	BP	1	DLL1,CITED2	up_VSAP_EC
GO:0030518	0.208	0.978	1	42	intracellular steroid hormone receptor	BP	1	NEDD4	down_ACOR_EC
GO:0009124	0.208	0.978	1	51	nucleoside monophosphate	BP	1	TNRC6B	down_ACOR_EC
GO:1905446	0.208	0.984	1	3	regulation of mitochondrial ATP synthesis coupled	BP	1	CDK1	down_ACOR_VSMC
GO:0006732	0.208	0.978	1	107	coenzyme metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0009141	0.208	0.978	1	110	nucleoside triphosphate metabolic process	BP	1	NDUFA10	down_AFEM_EC
GO:0010631	0.208	0.978	1	118	epithelial cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0045787	0.208	0.978	1	117	positive regulation of cell cycle	BP	1	CITED2	down_VPOR_EC
GO:0060537	0.208	0.978	1	117	muscle tissue development	BP	1	CITED2	down_VPOR_EC
GO:0090132	0.208	0.978	1	118	epithelium migration	BP	1	HDAC7	down_VPOR_EC
GO:0042592	0.208	0.984	1	522	homeostatic process	BP	1	PLCL1	down_VFEM_EC
GO:0030502	0.208	0.982	1	4	negative regulation of bone mineralization	BP	1	HIF1A	down_VSAP_EC
GO:0042532	0.208	0.982	1	4	negative regulation of tyrosine phosphorylation	BP	1	PTPN2	down_VSAP_EC
GO:0010544	0.208	0.982	1	4	negative regulation of platelet activation	BP	1	APOE	down_VSAP_EC

GO:1900272	0.208	0.982	1	4	negative regulation of long-term synaptic	BP	1	APOE	down_VSAP_EC
GO:0060978	0.208	0.988	1	2	angiogenesis involved in coronary vascular	BP	1	NRP1	up_ACOR_VSMC
GO:0008285	0.208	0.979	1	201	negative regulation of cell proliferation	BP	1	ARG2	up_AORT_VSMC
GO:0045927	0.208	0.978	1	61	positive regulation of growth	BP	1	TBX5	up_APUL_EC
GO:0031115	0.208	0.984	1	3	negative regulation of microtubule	BP	1	STMN1	up_VCAV_EC
GO:0090066	0.208	0.979	1	162	regulation of anatomical structure size	BP	1	LIMK1	up_VCAV_VSMC
GO:0070936	0.208	0.978	1	28	protein K48-linked ubiquitination	BP	1	RNF6	up_VPOR_EC
GO:2001021	0.208	0.978	1	30	negative regulation of response to DNA damage	BP	1	CXHXorf57	up_VPOR_EC
GO:0051100	0.208	0.978	1	53	negative regulation of binding	BP	1	CAV1	up_VSAP_VSMC
GO:0034644	0.208476138	0.9479	2	32	cellular response to UV	BP	1	AQP1,MFAP4	up_ACOR_EC
GO:0039694	0.208570955	0.97909	1	9	viral RNA genome replication	BP	1	ATG16L2	up_ACOR_EC
GO:0006725	0.209	0.884	11	1956	cellular aromatic compound metabolic	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:1902115	0.209	0.882	9	77	regulation of organelle assembly	BP	1	FSCN1,SMC1A,SDC1,NUP62,PLK4,SMC3,STAG1,EZR,RBM14	down_ACOR_VSMC
GO:1901652	0.209	0.88	9	105	response to peptide	BP	1	ARHGEF2,NR1H4,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,PTPN2,NR4A1	down_VSAP_EC
GO:2001236	0.209	0.887	8	59	regulation of extrinsic apoptotic signaling	BP	1	ITM2C,BMP4,AR,DAPK1,NRP1,UNC5B,SH3RF1,PARK7	up_ACOR_VSMC
GO:0042063	0.209	0.886	8	67	gliogenesis	BP	1	PRKCH,RELN,TLR4,EIF2B2,MTOR,BMP2,ENSCAFG00000010224,MMP24	up_VCAV_EC
GO:0072175	0.209	0.886	8	60	epithelial tube formation	BP	1	FZD1,ABL1,OSR1,FUZ,RARG,IRX3,KDM2B,CITED2	up_VSAP_EC
GO:0021700	0.209	0.904	5	65	developmental maturation	BP	1	THBS3,RECK,IRX5,GREM1,FOXO3	down_VCAV_EC
GO:0008361	0.209	0.905	5	50	regulation of cell size	BP	1	LRRC8A,IFRD1,MSN,CLCN3,NRP1	down_VSAP_EC
GO:0030099	0.209	0.903	5	133	myeloid cell differentiation	BP	1	HOXA9,HOXA7,DLL1,NFE2L1,EVI2B	up_AFEM_EC
GO:0033045	0.209	0.907	5	38	regulation of sister chromatid segregation	BP	1	SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:2000241	0.209	0.915	4	40	regulation of reproductive process	BP	1	SULF1,CTNNB1,INHBA,SPINK2	down_VSAP_EC
GO:0009063	0.209	0.918	4	25	cellular amino acid catabolic process	BP	1	ENOSF1,ENSCAFG00000002977,SARDH,PCYOX1	up_ACOR_VSMC
GO:0038202	0.209	0.918	4	24	TORC1 signaling	BP	1	CASTOR1,SESN3,SESN1,BMT2	up_ACOR_VSMC
GO:0023051	0.209	0.92	4	954	regulation of signaling	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0043407	0.209	0.932	3	19	negative regulation of MAP kinase activity	BP	1	HMGCR,CAV1,NUP62	down_ACOR_VSMC
GO:0044106	0.209	0.932	3	17	cellular amine metabolic process	BP	1	MOXD1,AZIN2,PARK7	up_ACOR_VSMC
GO:0006493	0.209	0.931	3	20	protein O-linked glycosylation	BP	1	GALNT18,MFNG,TET2	up_VCAV_EC
GO:0010647	0.209	0.93	3	460	positive regulation of cell communication	BP	1	NR1H4,CCL24,NEO1	up_VPUL_EC
GO:0120036	0.209	0.929	3	373	plasma membrane bounded cell projection	BP	1	EMP1,CAV1,SHOX2	up_VSAP_VSMC
GO:0060338	0.209	0.953	2	10	regulation of type I interferon-mediated	BP	1	SLC29A1,CACTIN	down_ACOR_VSMC
GO:0071158	0.209	0.952	2	10	positive regulation of cell cycle arrest	BP	1	CASP2,BRCA1	down_ACOR_VSMC
GO:0000266	0.209	0.949	2	17	mitochondrial fission	BP	1	DCN,MTFR1L	down_VCAV_EC
GO:1905207	0.209	0.949	2	17	regulation of cardiocyte differentiation	BP	1	SEMA3C,GREM1	down_VCAV_EC
GO:1901564	0.209	0.974	2	2053	organonitrogen compound metabolic	BP	1	PLCL1,USP12	down_VFEM_EC
GO:0032733	0.209	0.953	2	9	positive regulation of interleukin-10 production	BP	1	CD83,CD274	up_ACOR_VSMC
GO:0032680	0.209	0.947	2	36	regulation of tumor necrosis factor production	BP	1	LEP,BPI	up_AFEM_EC
GO:0002761	0.209	0.947	2	36	regulation of myeloid leukocyte differentiation	BP	1	HOXA7,EVI2B	up_AFEM_EC
GO:0001676	0.209	0.953	2	10	long-chain fatty acid metabolic process	BP	1	PTGS1,PTGS2	up_VCAV_EC
GO:0030072	0.209	0.978	1	48	peptide hormone secretion	BP	1	STX4	down_ACOR_EC

GO:0006203	0.209	0.984	1	3	dGTP catabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0009146	0.209	0.984	1	3	purine nucleoside triphosphate catabolic	BP	1	NUDT1	down_ACOR_VSMC
GO:0009155	0.209	0.984	1	3	purine deoxyribonucleotide	BP	1	NUDT1	down_ACOR_VSMC
GO:0009204	0.209	0.984	1	3	deoxyribonucleoside triphosphate catabolic	BP	1	NUDT1	down_ACOR_VSMC
GO:0009264	0.209	0.984	1	3	deoxyribonucleotide catabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0098532	0.209	0.984	1	3	histone H3-K27 trimethylation	BP	1	EZH2	down_ACOR_VSMC
GO:0009217	0.209	0.984	1	3	purine deoxyribonucleoside	BP	1	NUDT1	down_ACOR_VSMC
GO:0046386	0.209	0.984	1	3	deoxyribose phosphate catabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0051004	0.209	0.984	1	3	regulation of lipoprotein lipase activity	BP	1	ABHD5	down_ACOR_VSMC
GO:0097119	0.209	0.981	1	5	postsynaptic density protein 95 clustering	BP	1	CDH2	down_VCAV_EC
GO:0019220	0.209	0.984	1	525	regulation of phosphate metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0051174	0.209	0.984	1	525	regulation of phosphorus metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0008104	0.209	0.988	1	763	protein localization	BP	1	JUP	down_VFEM_VSMC
GO:1901621	0.209	0.982	1	4	negative regulation of smoothened signaling pathway involved in dorsal/ventral neural tube	BP	1	PRKACB	down_VSAP_EC
GO:1901668	0.209	0.988	1	2	regulation of superoxide dismutase activity	BP	1	PARK7	up_ACOR_VSMC
GO:0050877	0.209	0.979	1	164	nervous system process	BP	1	HOXC10	up_AFEM_VSMC
GO:0032870	0.209	0.979	1	162	cellular response to hormone stimulus	BP	1	CA2	up_VCAV_VSMC
GO:1901699	0.209	0.979	1	164	cellular response to nitrogen compound	BP	1	CA2	up_VCAV_VSMC
GO:0006140	0.209	0.978	1	28	regulation of nucleotide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:1901888	0.209	0.978	1	29	regulation of cell junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0034765	0.209	0.978	1	91	regulation of ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0003205	0.209	0.978	1	67	cardiac chamber development	BP	1	TBX5	up_VPUL_EC
GO:0072330	0.209	0.978	1	68	monocarboxylic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0001890	0.209	0.978	1	51	placenta development	BP	1	GJB5	up_VSAP_VSMC
GO:0050796	0.20942914	0.94745	2	33	regulation of insulin secretion	BP	1	NR1H4,KCNB1	up_ACOR_EC
GO:0001945	0.209448226	0.97891	1	9	lymph vessel development	BP	1	FOXC2	up_ACOR_EC
GO:0001946	0.209448226	0.97891	1	9	lymphangiogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0036303	0.209448226	0.97891	1	9	lymph vessel morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0048699	0.21	0.851	22	371	generation of neurons	BP	1	NDN,SDC4,BMPR1A,LMO4,TRPV2,NUMBL,NAGLU,SEMA3C,THY1,PEX5,TLX2,GLI3,NCDN,CDH2,GSDME,ENSCAFG00000017708,IRX5,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0065007	0.21	0.878	18	3499	biological regulation	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,NETO1,GATM,SALL1,HOXC10,IRX5,MAB21L1,PRR16,STIM1,TLR2,CAV1,SHOX2,F5,FGF5	up_VSAP_VSMC
GO:0043086	0.21	0.866	13	170	negative regulation of catalytic activity	BP	1	SOCS5,ERRFI1,TRIB3,PTGS2,PTPN2,CRYAB,APOE,LYN,CBLC,ARFGEF3,PAK2,CDKN1A,SPINK2	down_VSAP_EC
GO:0071396	0.21	0.872	11	134	cellular response to lipid	BP	1	NR1H4,SERPINE1,SMARCA4,MSN,YES1,MTDH,UBA5,LYN,REST,YWHAH,KDM3A	down_VSAP_EC
GO:0007018	0.21	0.874	11	82	microtubule-based movement	BP	1	RHOT1,DNAH7,TMEM108,IFT43,KIF1A,APP,DYNC1I2,KIF9,SUN1,DYNC1I1,ENSCAFG00000013536	up_ACOR_VSMC
GO:0052547	0.21	0.881	9	82	regulation of peptidase activity	BP	1	HMGB1,PRELID1,BIRC5,PDCD2,DHCR24,CYCS,ENSCAFG00000005299,AIFM1,DELE1	down_ACOR_VSMC
GO:0005996	0.21	0.88	9	85	monosaccharide metabolic process	BP	1	ATF3,FAM3C,PGM2,ENSCAFG00000010596,GALE,CHST1,ENSCAFG00000024323,APOD,PMAIP1	up_VCAV_EC
GO:0016358	0.21	0.886	8	58	dendrite development	BP	1	ZNF365,NRP1,SLITRK5,APP,PSEN1,SIPA1L1,ASAP1,WASL	up_ACOR_VSMC

GO:0010810	0.21	0.886	8	60	regulation of cell-substrate adhesion	BP	1	HOXA7,FAM107A,ABL1,EMP2,PIK3R1,ECM2,FBLN1,ACVRL1	up_VSAP_EC
GO:0048015	0.21	0.892	7	48	phosphatidylinositol-mediated signaling	BP	1	LEP,HTR2B,F2RL1,UNC5B,PIK3C3,EDN1,PIK3C2A	up_ACOR_VSMC
GO:0048017	0.21	0.892	7	48	inositol lipid-mediated signaling	BP	1	LEP,HTR2B,F2RL1,UNC5B,PIK3C3,EDN1,PIK3C2A	up_ACOR_VSMC
GO:0043170	0.21	0.925	6	2980	macromolecule metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0070661	0.21	0.904	5	63	leukocyte proliferation	BP	1	GPAM,PRNP,SDC4,GREM1,RAC2	down_VCAV_EC
GO:0048864	0.21	0.916	4	29	stem cell development	BP	1	EDNRB,EDN1,JAG1,HIF1A	up_VCAV_EC
GO:0031324	0.21	0.933	3	735	negative regulation of cellular metabolic process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0043551	0.21	0.931	3	17	regulation of phosphatidylinositol 3-	BP	1	AMBRA1,PIK3R1,PIK3IP1	up_VSAP_EC
GO:0072359	0.21	0.928	3	368	circulatory system development	BP	1	SALL1,CAV1,SHOX2	up_VSAP_VSMC
GO:0031344	0.21	0.947	2	161	regulation of cell projection organization	BP	1	LYN,PDPN	down_ACOR_EC
GO:0048799	0.21	0.952	2	10	animal organ maturation	BP	1	XYLT1,GREM1	down_ACOR_VSMC
GO:2000243	0.21	0.95	2	14	positive regulation of reproductive process	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0042476	0.21	0.947	2	36	odontogenesis	BP	1	CNNM4,AXIN2	up_AFEM_EC
GO:0072088	0.21	0.947	2	36	nephron epithelium morphogenesis	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0046883	0.21	0.977	1	49	regulation of hormone secretion	BP	1	STX4	down_ACOR_EC
GO:0050731	0.21	0.977	1	44	positive regulation of peptidyl-tyrosine	BP	1	LYN	down_ACOR_EC
GO:0050866	0.21	0.977	1	48	negative regulation of cell activation	BP	1	LYN	down_ACOR_EC
GO:0036265	0.21	0.984	1	3	RNA (guanine-N7)-methylation	BP	1	METTL1	down_ACOR_VSMC
GO:0009240	0.21	0.984	1	3	isopentenyl diphosphate biosynthetic process	BP	1	MVD	down_ACOR_VSMC
GO:0019287	0.21	0.984	1	3	isopentenyl diphosphate biosynthetic process, mevalonate pathway	BP	1	MVD	down_ACOR_VSMC
GO:0046490	0.21	0.984	1	3	isopentenyl diphosphate metabolic process	BP	1	MVD	down_ACOR_VSMC
GO:0097193	0.21	0.978	1	109	intrinsic apoptotic signaling pathway	BP	1	IVNS1ABP	down_AFEM_EC
GO:0072641	0.21	0.981	1	5	type I interferon secretion	BP	1	MAVS	down_VCAV_EC
GO:0072642	0.21	0.981	1	5	interferon-alpha secretion	BP	1	MAVS	down_VCAV_EC
GO:1902739	0.21	0.981	1	5	regulation of interferon-alpha secretion	BP	1	MAVS	down_VCAV_EC
GO:1902741	0.21	0.981	1	5	positive regulation of interferon-alpha secretion	BP	1	MAVS	down_VCAV_EC
GO:0060562	0.21	0.978	1	120	epithelial tube morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0010628	0.21	0.984	1	527	positive regulation of gene expression	BP	1	MOSPD1	down_VFEM_EC
GO:0032879	0.21	0.988	1	767	regulation of localization	BP	1	JUP	down_VFEM_VSMC
GO:0072358	0.21	0.98	1	268	cardiovascular system development	BP	1	TGFBI	down_VSAP_VSMC
GO:0050919	0.21	0.979	1	10	negative chemotaxis	BP	1	PLXNA4	up_AFEM_EC
GO:0050767	0.21	0.979	1	184	regulation of neurogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:1901617	0.21	0.977	1	60	organic hydroxy compound biosynthetic	BP	1	NR1H4	up_APUL_EC
GO:0003228	0.21	0.984	1	3	atrial cardiac muscle tissue development	BP	1	PROX1	up_VCAV_EC
GO:0048845	0.21	0.984	1	3	venous blood vessel morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0051315	0.21	0.984	1	3	attachment of mitotic spindle microtubules to	BP	1	CENPC	up_VCAV_EC
GO:0055009	0.21	0.984	1	3	atrial cardiac muscle tissue morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0071839	0.21	0.984	1	3	apoptotic process in bone marrow	BP	1	PLK2	up_VCAV_EC
GO:1901537	0.21	0.988	1	2	positive regulation of DNA demethylation	BP	1	OTUD4	up_VCAV_EC

GO:0070244	0.21	0.984	1	3	negative regulation of thymocyte apoptotic	BP	1	HIF1A	up_VCAV_EC
GO:0070997	0.21	0.978	1	93	neuron death	BP	1	CHL1	up_VPOR_VSMC
GO:0006470	0.21	0.977	1	54	protein dephosphorylation	BP	1	EYA1	up_VFEM_EC
GO:0001838	0.21	0.977	1	56	embryonic epithelial tube formation	BP	1	SIX1	up_VFEM_EC
GO:0060560	0.21	0.977	1	58	developmental growth involved in	BP	1	SIX1	up_VFEM_EC
GO:0030522	0.21	0.977	1	67	intracellular receptor signaling pathway	BP	1	NR1H4	up_VPUL_EC
GO:0001649	0.21	0.977	1	54	osteoblast differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0070588	0.21	0.977	1	54	calcium ion transmembrane transport	BP	1	STIM1	up_VSAP_VSMC
GO:0030855	0.210190106	0.88857	7	183	epithelial cell differentiation	BP	1	CDH3,TMOD1,GATA4,SOX9,DLX3,FOXC2,ARHGEF26	up_ACOR_EC
GO:0048199	0.210807262	0.97862	1	9	vesicle targeting, to, from or within Golgi	BP	1	PREB	up_ACOR_EC
GO:0002520	0.211	0.842	31	279	immune system development	BP	1	HOXA7,HOXA9,CD274,PPARGC1B,CRIP2,ABL1,DLL1,ANKRD54,ZBTB16,TOX,RARG,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,MYC,ZEB1,EEF2,TFE3,FBXO7,CD83,ZFP36L2,RAF1,PNP,PPP3CB,MAP2K2,TGFBR2,CITED2,PIR	up_VSAP_EC
GO:0010033	0.211	0.851	22	772	response to organic substance	BP	1	LEP,LBH,CRY2,RAB20,GAS1,CD40,DLL1,GPAM,FIBIN,CHRM2,TMEM100,GREM1,AVPR1A,CAMK2A,GREM2,CYLD,LRRC15,NR3C1,TBXA2R,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0019953	0.211	0.86	16	152	sexual reproduction	BP	1	KIT,TSPAN8,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,ARID4B,HIST1H1A,SPTBN4,AFF4,KDM3A,ATRX,SPATA6,FBXO5	up_VCAV_EC
GO:0022411	0.211	0.864	14	130	cellular component disassembly	BP	1	FSCN1,SREBF1,CAPG,LIMA1,STMN1,SMARCC1,PLK3,EIF5A,PDXP,SMARCB1,GRWD1,AIFM1,ARHGEF2,KIF24	down_ACOR_VSMC
GO:0016055	0.211	0.879	9	134	Wnt signaling pathway	BP	1	RECK,CLSTN1,ATP6V0C,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0198738	0.211	0.879	9	134	cell-cell signaling by wnt	BP	1	RECK,CLSTN1,ATP6V0C,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0090068	0.211	0.88	9	78	positive regulation of cell cycle process	BP	1	PDGFB,EDN1,RAB11A,UHRF2,SMC5,RAD21,CUL4A,ATRX,TMOD3	up_VCAV_EC
GO:0003205	0.211	0.885	8	67	cardiac chamber development	BP	1	MEF2C,CHD7,DLL4,GATA3,PROX1,JAG1,HIF1A,LUZP1	up_VCAV_EC
GO:0009617	0.211	0.902	5	133	response to bacterium	BP	1	CD40,BPI,SLC17A5,TBXA2R,ADAM17	up_AFEM_EC
GO:0050796	0.211	0.906	5	33	regulation of insulin secretion	BP	1	HNF4A,SLC8B1,KCNB1,STX4,PPP3CB	up_VSAP_EC
GO:0042472	0.211	0.916	4	27	inner ear morphogenesis	BP	1	CHD7,GATA3,ALDH1A3,ZEB1	up_VCAV_EC
GO:0097553	0.211	0.928	3	32	calcium ion transmembrane import	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0000266	0.211	0.931	3	17	mitochondrial fission	BP	1	MX1,MARCH5,BNIP3	up_ACOR_VSMC
GO:0023056	0.211	0.929	3	462	positive regulation of signaling	BP	1	NR1H4,CCL24,NEO1	up_VPUL_EC
GO:0097300	0.211	0.931	3	17	programmed necrotic cell death	BP	1	MAP3K5,RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:1903146	0.211	0.931	3	17	regulation of autophagy of mitochondrion	BP	1	MFN2,FBXO7,HTRA2	up_VSAP_EC
GO:0035773	0.211	0.949	2	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	NR1H4,HIF1A	down_VSAP_EC
GO:1901616	0.211	0.949	2	15	organic hydroxy compound catabolic	BP	1	TPI1,APOE	down_VSAP_EC
GO:0090276	0.211	0.947	2	36	regulation of peptide hormone secretion	BP	1	LEP,CCL5	up_AFEM_EC
GO:0031063	0.211	0.952	2	10	regulation of histone deacetylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0048646	0.211	0.948	2	349	anatomical structure formation involved in	BP	1	EYA1,HOXA11	up_VFEM_VSMC
GO:0016477	0.211	0.949	2	426	cell migration	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0005979	0.211	0.953	2	9	regulation of glycogen biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0010962	0.211	0.953	2	9	regulation of glucan biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0070873	0.211	0.953	2	9	regulation of glycogen metabolic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0030308	0.211	0.977	1	49	negative regulation of cell growth	BP	1	ACVRL1	down_ACOR_EC

GO:0032268	0.211	0.988	1	778	regulation of cellular protein metabolic process	BP	1	CST3	down_AORT_EC
GO:0002295	0.211	0.981	1	5	T-helper cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:0002363	0.211	0.981	1	5	alpha-beta T cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:0043373	0.211	0.981	1	5	CD4-positive, alpha-beta T cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:0048853	0.211	0.982	1	4	forebrain morphogenesis	BP	1	UCHL5	down_VSAP_EC
GO:0060767	0.211	0.982	1	4	epithelial cell proliferation involved in prostate gland development	BP	1	CTNNB1	down_VSAP_EC
GO:0072529	0.211	0.982	1	4	pyrimidine-containing compound catabolic	BP	1	ENTPD4	down_VSAP_EC
GO:0070091	0.211	0.988	1	2	glucagon secretion	BP	1	LEP	up_ACOR_VSMC
GO:0070092	0.211	0.988	1	2	regulation of glucagon secretion	BP	1	LEP	up_ACOR_VSMC
GO:0048486	0.211	0.978	1	10	parasympathetic nervous system development	BP	1	PLXNA4	up_AFEM_EC
GO:0045930	0.211	0.977	1	97	negative regulation of mitotic cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0000904	0.211	0.979	1	181	cell morphogenesis involved in differentiation	BP	1	WNT7A	up_AORT_VSMC
GO:0007267	0.211	0.981	1	332	cell-cell signaling	BP	1	TBX5	up_APUL_VSMC
GO:0042104	0.211	0.984	1	3	positive regulation of activated T cell	BP	1	HMGB1	up_VCAV_EC
GO:0071955	0.211	0.988	1	2	recycling endosome to Golgi transport	BP	1	GCC2	up_VCAV_EC
GO:1903223	0.211	0.988	1	2	positive regulation of oxidative stress-induced	BP	1	TLR4	up_VCAV_EC
GO:1904468	0.211	0.984	1	3	negative regulation of tumor necrosis factor	BP	1	ARG2	up_VCAV_EC
GO:0043271	0.211	0.977	1	28	negative regulation of ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0048864	0.211	0.977	1	29	stem cell development	BP	1	SEMA3A	up_VPOR_EC
GO:0051403	0.211	0.978	1	89	stress-activated MAPK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0090287	0.211	0.978	1	91	regulation of cellular response to growth factor	BP	1	BAMBI	up_VPOR_VSMC
GO:0033002	0.211	0.977	1	55	muscle cell proliferation	BP	1	SIX1	up_VFEM_EC
GO:0072522	0.211	0.977	1	91	purine-containing compound biosynthetic	BP	1	FBP1	up_VFEM_VSMC
GO:0071375	0.211	0.977	1	68	cellular response to peptide hormone stimulus	BP	1	NR1H4	up_VPUL_EC
GO:0032956	0.211	0.978	1	116	regulation of actin cytoskeleton organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0048732	0.211	0.978	1	116	gland development	BP	1	HOXA3	up_VPUL_VSMC
GO:0010894	0.211481962	0.97848	1	9	negative regulation of steroid biosynthetic	BP	1	NR1H4	up_ACOR_EC
GO:0045939	0.211481962	0.97848	1	9	negative regulation of steroid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0031328	0.212	0.831	49	512	positive regulation of cellular biosynthetic process	BP	1	ACSL3,HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,SLC29A1,CTDNEP1,RFC2,INSIG1,RFC5,RFC3,THRAP3,TRUB2,FAM129B,AURKB,GREM1,RFC4,NEK2,SMARCC1,PCNA,DHX33,CKS2,BRCA1,FASTKD3,EIF5A,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103	down_ACOR_VSMC
GO:0071704	0.212	0.874	20	3535	organic substance metabolic process	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0120031	0.212	0.856	18	154	plasma membrane bounded cell projection assembly	BP	1	WASF3,SLIT2,ABL1,EMP2,CDC42EP5,FUZ,RILPL2,CDC42EP2,F2RL1,FGD4,E2F4,KIF27,TMEM17,TTC8,EMP3,NCK1,CEP19,BAG4	up_VSAP_EC
GO:0048589	0.212	0.867	12	188	developmental growth	BP	1	GPAM,NDN,THBS3,BMPR1A,EVC,TRPV2,PEX5,GLI3,ZFP36L1,DDR2,RDH10,FOXO3	down_VCAV_EC
GO:0051249	0.212	0.878	9	107	regulation of lymphocyte activation	BP	1	SOCS5,FAM49B,PTPN2,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0001763	0.212	0.879	9	78	morphogenesis of a branching structure	BP	1	HOXB7,DLL4,EDN1,NTN4,BMP2,HHEX,PROX1,BTBD7,TIMELESS	up_VCAV_EC

GO:0050768	0.212	0.884	8	66	negative regulation of neurogenesis	BP	1	EDNRB,IFRD1,PPP3CA,HOOK3,HMG20A,JAG1,RAPGEF2,CTNNA1	up_VCAV_EC
GO:0001764	0.212	0.896	6	45	neuron migration	BP	1	RELN,MEF2C,GATA3,RAPGEF2,ARHGEF2,ZNF609	up_VCAV_EC
GO:0010976	0.212	0.896	6	47	positive regulation of neuron projection	BP	1	RELN,RAPGEF1,RAB11A,NCK1,FES,RAPGEF2	up_VCAV_EC
GO:0050870	0.212	0.897	6	42	positive regulation of T cell activation	BP	1	CD274,ZBTB16,CD83,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0030595	0.212	0.903	5	57	leukocyte chemotaxis	BP	1	VEGFA,SERPINE1,ADAM17,MMP28,LYN	down_VSAP_EC
GO:0007612	0.212	0.905	5	33	learning	BP	1	FGF13,HRH1,LRRN4,APP,CLN8	up_ACOR_VSMC
GO:0048645	0.212	0.905	5	33	animal organ formation	BP	1	HOXA11,AXIN2,MAP2K2,TGFBR2,CITED2	up_VSAP_EC
GO:0071230	0.212	0.917	4	23	cellular response to amino acid stimulus	BP	1	CASTOR1,UBR1,SESN3,SH3BP4	up_ACOR_VSMC
GO:0006790	0.212	0.912	4	99	sulfur compound metabolic process	BP	1	XYLT1,GPAM,TPST2,ACACB	up_AFEM_EC
GO:0050806	0.212	0.916	4	25	positive regulation of synaptic transmission	BP	1	FAM107A,ABL1,STX4,FLOT1	up_VSAP_EC
GO:0010562	0.212	0.927	3	312	positive regulation of phosphorus metabolic	BP	1	ACVRL1,LYN,ACSL3	down_ACOR_EC
GO:0019637	0.212	0.927	3	342	organophosphate metabolic process	BP	1	LYN,ACSL3,TNRC6B	down_ACOR_EC
GO:0045937	0.212	0.927	3	312	positive regulation of phosphate metabolic	BP	1	ACVRL1,LYN,ACSL3	down_ACOR_EC
GO:0046902	0.212	0.93	3	18	regulation of mitochondrial membrane	BP	1	RHOT1,BNIP3,NAIF1	up_ACOR_VSMC
GO:0002252	0.212	0.946	2	166	immune effector process	BP	1	LYN,STX4	down_ACOR_EC
GO:0001676	0.212	0.951	2	10	long-chain fatty acid metabolic process	BP	1	ELOVL6,ACADL	down_ACOR_VSMC
GO:0070198	0.212	0.951	2	10	protein localization to chromosome, telomeric	BP	1	TINF2,CCT4	down_ACOR_VSMC
GO:0010922	0.212	0.949	2	14	positive regulation of phosphatase activity	BP	1	PPP1R12A,CALM1	down_VSAP_EC
GO:0021904	0.212	0.952	2	9	dorsal/ventral neural tube patterning	BP	1	BMP4,PSEN1	up_ACOR_VSMC
GO:1903305	0.212	0.946	2	36	regulation of regulated secretory pathway	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:1900181	0.212	0.95	2	11	negative regulation of protein localization to	BP	1	FERMT1,APOD	up_VCAV_EC
GO:0045765	0.212	0.946	2	105	regulation of angiogenesis	BP	1	C3AR1,MTDH	up_VPOR_EC
GO:0002682	0.212	0.948	2	343	regulation of immune system process	BP	1	CYP26B1,C3AR1	up_VPOR_VSMC
GO:0010939	0.212	0.952	2	9	regulation of necrotic cell death	BP	1	RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0039528	0.212	0.952	2	9	cytoplasmic pattern recognition receptor signaling pathway in	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0045577	0.212	0.952	2	9	regulation of B cell differentiation	BP	1	ZFP36L1,ZFP36L2	up_VSAP_EC
GO:1901016	0.212	0.952	2	9	regulation of potassium ion transmembrane transporter activity	BP	1	KCNE3,KLHL24	up_VSAP_EC
GO:0070663	0.212	0.977	1	50	regulation of leukocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0008360	0.212	0.977	1	46	regulation of cell shape	BP	1	PDPN	down_ACOR_EC
GO:0016264	0.212	0.983	1	3	gap junction assembly	BP	1	CAV1	down_ACOR_VSMC
GO:0071455	0.212	0.983	1	3	cellular response to hyperoxia	BP	1	CAV1	down_ACOR_VSMC
GO:0035927	0.212	0.983	1	3	RNA import into mitochondrion	BP	1	MRPL18	down_ACOR_VSMC
GO:0055093	0.212	0.983	1	3	response to hyperoxia	BP	1	CAV1	down_ACOR_VSMC
GO:1902950	0.212	0.981	1	4	regulation of dendritic spine maintenance	BP	1	APOE	down_VSAP_EC
GO:0019320	0.212	0.981	1	4	hexose catabolic process	BP	1	GALE	down_VSAP_EC
GO:1901529	0.212	0.987	1	2	positive regulation of anion channel activity	BP	1	TCAF1	up_ACOR_VSMC
GO:0090259	0.212	0.987	1	2	regulation of retinal ganglion cell axon	BP	1	NRP1	up_ACOR_VSMC
GO:0019432	0.212	0.978	1	10	triglyceride biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:0042491	0.212	0.978	1	10	inner ear auditory receptor cell	BP	1	DLL1	up_AFEM_EC

GO:0046460	0.212	0.978	1	10	neutral lipid biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:0046463	0.212	0.978	1	10	acylglycerol biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:0048103	0.212	0.978	1	10	somatic stem cell division	BP	1	LBH	up_AFEM_EC
GO:0071402	0.212	0.978	1	10	cellular response to lipoprotein particle	BP	1	ADAM17	up_AFEM_EC
GO:1903530	0.212	0.978	1	165	regulation of secretion by cell	BP	1	TLR2	up_AFEM_VSMC
GO:0042180	0.212	0.977	1	61	cellular ketone metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0071216	0.212	0.977	1	61	cellular response to biotic stimulus	BP	1	NR1H4	up_APUL_EC
GO:0033211	0.212	0.983	1	3	adiponectin-activated signaling pathway	BP	1	ADIPOR2	up_VCAV_EC
GO:0070828	0.212	0.983	1	3	heterochromatin organization	BP	1	HP1BP3	up_VCAV_EC
GO:1905065	0.212	0.984	1	3	positive regulation of vascular smooth muscle	BP	1	KIT	up_VCAV_EC
GO:0070050	0.212	0.983	1	3	neuron cellular homeostasis	BP	1	TAOK1	up_VCAV_EC
GO:0090091	0.212	0.983	1	3	positive regulation of extracellular matrix	BP	1	FSCN1	up_VCAV_EC
GO:0043255	0.212	0.977	1	29	regulation of carbohydrate biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0048232	0.212	0.977	1	95	male gamete generation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006906	0.212	0.977	1	55	vesicle fusion	BP	1	TRIM9	up_VFEM_EC
GO:0030900	0.212	0.977	1	101	forebrain development	BP	1	EMX2	up_VFEM_VSMC
GO:0032103	0.212	0.977	1	69	positive regulation of response to external	BP	1	CCL24	up_VPUL_EC
GO:0002250	0.212	0.977	1	68	adaptive immune response	BP	1	IL18BP	up_VPUL_EC
GO:0045666	0.212	0.977	1	68	positive regulation of neuron differentiation	BP	1	ARHGEF2	up_VPUL_EC
GO:1904018	0.212	0.977	1	69	positive regulation of vasculature development	BP	1	CCL24	up_VPUL_EC
GO:0001655	0.212	0.978	1	116	urogenital system development	BP	1	SLIT2	up_VPUL_VSMC
GO:0060537	0.212	0.978	1	117	muscle tissue development	BP	1	TBX5	up_VPUL_VSMC
GO:0031103	0.212274602	0.97831	1	9	axon regeneration	BP	1	RGMA	up_ACOR_EC
GO:0019674	0.21245742	0.97827	1	9	NAD metabolic process	BP	1	NMNAT2	up_ACOR_EC
GO:0060716	0.212717923	0.97821	1	9	labyrinthine layer blood vessel development	BP	1	FZD5	up_ACOR_EC
GO:0006793	0.213	0.826	63	948	phosphorus metabolic process	BP	1	ARHGEF2,VEGFA,NR1H4,SOCS5,SGK1,ENPP1,ERRFI1,JCAD,SNX25,PGK1,BCAR3,NUAK1,PTPN11,TPI1,TRIB3,PGAM1,ILK,PPP1R12A,SESN2,PTGS2,HIF1A,DYNLL1,NMNAT2,DNAJC10,TNIK,PTPN2,ENTPD4,YES1,PLCL1,ADAM17,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,CDK8,APOE,LYN,STRAP,CCNYL1,MMD,CBLC,ATF3,GSK3B,VLDLR,AK5,GTF2H1,SH3GLB1,HTT,MAPK10,EIF2S1,ARFGEF3,CALM1,PAK2,INHBA,CAMK2D,BTK,CDKN1A,NRP1,SH3RF3,MADD,MID1,CMPK1	down_VSAP_EC
GO:0010608	0.213	0.855	18	154	posttranscriptional regulation of gene expression	BP	1	PRR16,AXIN2,TENT5C,PYM1,ZFP36L1,ZC3H10,EEF2,FBXO4,LARP6,ANKHD1,LIMD1,RPUSD4,SAMD4B,ZFP36L2,EIF3K,EIF3D,TNRC6C,NCK1	up_VSAP_EC
GO:0034248	0.213	0.86	15	125	regulation of cellular amide metabolic process	BP	1	PRR16,ENSCAFG00000000071,PYM1,PDK2,ZFP36L1,EEF2,LARP6,ANKHD1,RPUSD4,SAMD4B,ZFP36L2,EIF3K,EIF3D,TNRC6C,NCK1	up_VSAP_EC
GO:0016236	0.213	0.871	11	88	macroautophagy	BP	1	FEZ1,PRKAA2,TP53INP1,GABARAPL1,BNIP3,PSEN1,PIK3C3,LAMP2,ATG16L2,FEZ2,ZFYVE1	up_ACOR_VSMC
GO:0023061	0.213	0.874	10	95	signal release	BP	1	MEF2C,CHD7,GATA3,EDN1,SNCAIP,SNAP23,CREB1,STX11,MCU,HIF1A	up_VCAV_EC
GO:0051716	0.213	0.902	7	2001	cellular response to stimulus	BP	1	FGF5,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0043281	0.213	0.902	5	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	PTGS2,CRYAB,FAM162A,REST,PAK2	down_VSAP_EC
GO:0051090	0.213	0.901	5	134	regulation of DNA-binding transcription factor	BP	1	CMKLR1,GREM1,CAMK2A,CYLD,PPARGC1A	up_AFEM_EC

GO:0050848	0.213	0.915	4	30	regulation of calcium-mediated signaling	BP	1	PDE4D,HOMER3,PPP3CA,MTOR	up_VCAV_EC
GO:0051270	0.213	0.912	4	296	regulation of cellular component movement	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0002708	0.213	0.928	3	26	positive regulation of lymphocyte mediated	BP	1	FAM49B,PVR,TFRC	down_VSAP_EC
GO:0110111	0.213	0.93	3	17	negative regulation of animal organ	BP	1	BMP4,LIMS2,TNFRSF11B	up_ACOR_VSMC
GO:0043555	0.213	0.951	2	10	regulation of translation in response to stress	BP	1	PPP1R15B,RBM14	down_ACOR_VSMC
GO:0002763	0.213	0.948	2	17	positive regulation of myeloid leukocyte	BP	1	CLSTN1,ZFP36L1	down_VCAV_EC
GO:0044106	0.213	0.948	2	17	cellular amine metabolic process	BP	1	PARK7,NAPEPLD	down_VCAV_EC
GO:0071466	0.213	0.948	2	17	cellular response to xenobiotic stimulus	BP	1	NR3C1,CYP1B1	down_VCAV_EC
GO:0042221	0.213	0.956	2	1012	response to chemical	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0050704	0.213	0.95	2	11	regulation of interleukin-1 secretion	BP	1	ARG2,HMGB1	up_VCAV_EC
GO:0051894	0.213	0.951	2	10	positive regulation of focal adhesion assembly	BP	1	TEK,ENSCAFG00000002015	up_VCAV_EC
GO:0007204	0.213	0.977	1	46	positive regulation of cytosolic calcium ion	BP	1	LYN	down_ACOR_EC
GO:0007041	0.213	0.977	1	41	lysosomal transport	BP	1	NEDD4	down_ACOR_EC
GO:0021987	0.213	0.977	1	37	cerebral cortex development	BP	1	NRP2	down_ACOR_EC
GO:0032412	0.213	0.977	1	46	regulation of ion transmembrane	BP	1	NEDD4	down_ACOR_EC
GO:0090191	0.213	0.983	1	3	negative regulation of branching involved in ureteric bud	BP	1	GREM1	down_ACOR_VSMC
GO:0010863	0.213	0.98	1	5	positive regulation of phospholipase C activity	BP	1	PDGFRB	down_VCAV_EC
GO:0090130	0.213	0.977	1	121	tissue migration	BP	1	HDAC7	down_VPOR_EC
GO:0030854	0.213	0.981	1	4	positive regulation of granulocyte	BP	1	EVI2B	down_VSAP_EC
GO:0051645	0.213	0.981	1	4	Golgi localization	BP	1	HOOK3	down_VSAP_EC
GO:1904779	0.213	0.981	1	4	regulation of protein localization to	BP	1	GSK3B	down_VSAP_EC
GO:0006573	0.213	0.981	1	4	valine metabolic process	BP	1	BCAT1	down_VSAP_EC
GO:0007635	0.213	0.987	1	2	chemosensory behavior	BP	1	CHD7	up_ACOR_VSMC
GO:0042048	0.213	0.987	1	2	olfactory behavior	BP	1	CHD7	up_ACOR_VSMC
GO:0061478	0.213	0.987	1	2	response to platelet aggregation inhibitor	BP	1	ADCY6	up_ACOR_VSMC
GO:1904321	0.213	0.987	1	2	response to forskolin	BP	1	ADCY6	up_ACOR_VSMC
GO:1904322	0.213	0.987	1	2	cellular response to forskolin	BP	1	ADCY6	up_ACOR_VSMC
GO:0007176	0.213	0.978	1	10	regulation of epidermal growth factor-activated	BP	1	ADAM17	up_AFEM_EC
GO:0014037	0.213	0.978	1	10	Schwann cell differentiation	BP	1	LGI4	up_AFEM_EC
GO:0021680	0.213	0.978	1	10	cerebellar Purkinje cell layer development	BP	1	DLL1	up_AFEM_EC
GO:0031670	0.213	0.978	1	10	cellular response to nutrient	BP	1	POSTN	up_AFEM_EC
GO:0033688	0.213	0.978	1	10	regulation of osteoblast proliferation	BP	1	GREM1	up_AFEM_EC
GO:0045601	0.213	0.978	1	10	regulation of endothelial cell differentiation	BP	1	TMEM100	up_AFEM_EC
GO:0048678	0.213	0.978	1	10	response to axon injury	BP	1	TNC	up_AFEM_EC
GO:0071158	0.213	0.978	1	10	positive regulation of cell cycle arrest	BP	1	FAP	up_AFEM_EC
GO:0090278	0.213	0.978	1	10	negative regulation of peptide hormone	BP	1	LEP	up_AFEM_EC
GO:0010459	0.213	0.987	1	2	negative regulation of heart rate	BP	1	SPTBN4	up_VCAV_EC
GO:0002252	0.213	0.978	1	166	immune effector process	BP	1	C6	up_VCAV_VSMC
GO:0015672	0.213	0.977	1	89	monovalent inorganic cation transport	BP	1	NETO1	up_VFEM_VSMC

GO:0036230	0.213161283	0.97812	1	9	granulocyte activation	BP	1	PRKCD	up_ACOR_EC
GO:0007229	0.213936507	0.94566	2	32	integrin-mediated signaling pathway	BP	1	ADAMTS13,NRP1	up_ACOR_EC
GO:0009987	0.214	0.814	420	5086	cellular process	BP	1	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,RASGRP3,HCLS1,PCDH12,IL7R,GBP5,NPR1,ADGRF5,SELP,ST8SIA6,RGS16,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PANK3,F8,PTCHD1,PRKCH,ARHGEF15,IFRD1,LAPTM5,SHE,CP,CXCR4,FGD5,FRMD4B,ENSCAFG00000007112,DOCK4,CLEC14A,IL6,CALCRL,FLI1,TIE1,CDA,TNFAIP3,ADAMTS9,PPARG,ADGRL2,MAP3K11,ATP8A1,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,MALL,KIF21B,PODXL,STK10,SH2D3C,BAIAP2L1,TMEM173,ATP2B1,TSPAN8,EXOC3L2,RELN,VWF,CD34,ST6GAL1,SELL,FGD6,CTSC,LAMC2,KDR,CXHXorf36,PDE4D,MOV10,IWS1,OCLN,MEF2C,FERMT1,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NOS3,NLRC5,QKI,GPR4,TSPAN15,STC1,EIF2B2,GK5,GATA3,MMP28,USP33,EDN1,HOXB8,RAB11A,RALB,KIF3C,APLNR,ARAP3,RAB27A,TCF4,SLC39A8,SMAD1,EXOC6,CTTNBP2NL,NTN4,SNCAIP,FOXN2,MEOX1,HOMER3,PIPOX,PTGS1,TNFAIP8,TFPI,ENSCAFG00000017103,ZDHHC22,IGSF3,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SNAP91,ARHGAP28,SOX18,PIK3C2A,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,NASP,SERINC5,ADSS,YES1,RAPGEF3,FAM3C,MTSS1,GUCY1A1,ENSCAFG00000010893,TMEM150C,ODC1,SPTLC2,ARG2	up_VCAV_EC
GO:1901701	0.214	0.839	31	271	cellular response to oxygen-containing compound	BP	1	ACTN2,PRKAA2,ABCA1,CASTOR1,TP53INP1,SASH1,SLC2A5,FAM210B,ADCY6,ANKRD1,DAPK1,AKAP6,UBR1,PTPN22,APLP1,PTGDR,SESN3,PRKCE,AGRN,APP,PSEN1,JUP,NR3C1,RAB11B,OXR1,NOD2,DDIT4,GNAQ,INPP5K,SH3BP4,PARK7	up_ACOR_VSMC
GO:0072358	0.214	0.84	30	268	cardiovascular system development	BP	1	VEGFD,SMAD6,LEP,ANGPT1,RECK,BMP4,FGFR2,GJA1,TLR3,SEC24B,CITED2,SPINT1,SASH1,FGF18,EGLN1,NRP1,SLITRK5,TBX20,PSEN1,SYNJ2BP,CHD7,JUP,EDN1,HPGD,JAM3,AP2B1,ERAP1,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0030001	0.214	0.851	20	172	metal ion transport	BP	1	AMIGO1,SLC8B1,TPCN2,NIPAL3,ABL1,KCNE3,OSR1,CCS,KLHL24,RAB11B,SLC25A28,CRACR2B,SCARA5,NIPAL1,STEAP3,KCNB1,FTL,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0030003	0.214	0.857	16	157	cellular cation homeostasis	BP	1	CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0006413	0.214	0.896	6	42	translational initiation	BP	1	ANKHD1,EIF3G,EIF3K,EIF3L,EIF3D,NCK1	up_VSAP_EC
GO:0060349	0.214	0.904	5	38	bone morphogenesis	BP	1	NAB2,INSIG1,MMP14,POC1A,SERPINH1	down_ACOR_VSMC
GO:0051402	0.214	0.902	5	64	neuron apoptotic process	BP	1	PRNP,AKT2,PARK7,FOXO3,THRB	down_VCAV_EC
GO:0001952	0.214	0.904	5	34	regulation of cell-matrix adhesion	BP	1	FERMT1,NRP1,JUP,DUSP22,FAM107A	up_ACOR_VSMC
GO:0050851	0.214	0.904	5	34	antigen receptor-mediated signaling	BP	1	PLCG2,ELF1,PTPN22,PSEN1,DUSP22	up_ACOR_VSMC
GO:0022898	0.214	0.912	4	48	regulation of transmembrane	BP	1	PRNP,FXYD1,CACNB3,PARK7	down_VCAV_EC
GO:0034333	0.214	0.915	4	25	adherens junction assembly	BP	1	ACTN2,NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0007517	0.214	0.911	4	100	muscle organ development	BP	1	DLL1,CRYAB,GREM1,BVES	up_AFEM_EC
GO:0032989	0.214	0.926	3	292	cellular component morphogenesis	BP	1	SPG11,PDPN,NRP2	down_ACOR_EC
GO:0001909	0.214	0.929	3	18	leukocyte mediated cytotoxicity	BP	1	LEP,F2RL1,B2M	up_ACOR_VSMC
GO:0001666	0.214	0.925	3	67	response to hypoxia	BP	1	ANGPT4,CRYAB,ADAM17	up_AFEM_EC
GO:0036293	0.214	0.925	3	67	response to decreased oxygen levels	BP	1	ANGPT4,CRYAB,ADAM17	up_AFEM_EC
GO:0045010	0.214	0.929	3	19	actin nucleation	BP	1	NCKAP1,IQGAP2,ARPC5L	up_VCAV_EC
GO:0030030	0.214	0.927	3	377	cell projection organization	BP	1	EMP1,CAV1,SHOX2	up_VSAP_VSMC
GO:1903426	0.214	0.948	2	17	regulation of reactive oxygen species	BP	1	PARK7,CYBA	down_VCAV_EC
GO:0006807	0.214	1	2	3221	nitrogen compound metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC

GO:0006040	0.214	0.949	2	12	amino sugar metabolic process	BP	1	ST6GAL1,CHST7	up_VCAV_EC
GO:0010762	0.214	0.951	2	9	regulation of fibroblast migration	BP	1	DDR2,BAG4	up_VSAP_EC
GO:0022612	0.214	0.976	1	44	gland morphogenesis	BP	1	SULF1	down_ACOR_EC
GO:0016070	0.214	1	1	1479	RNA metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0048522	0.214	1	1	1484	positive regulation of cellular process	BP	1	GATA5	down_AFEM_VSMC
GO:0051136	0.214	0.98	1	5	regulation of NK T cell differentiation	BP	1	ZBTB16	down_VCAV_EC
GO:0007566	0.214	0.978	1	10	embryo implantation	BP	1	RECK	up_AFEM_EC
GO:0021696	0.214	0.978	1	10	cerebellar cortex morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:0046627	0.214	0.978	1	10	negative regulation of insulin receptor signaling	BP	1	KANK1	up_AFEM_EC
GO:0003337	0.214	0.978	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	GREM1	up_AFEM_EC
GO:0071715	0.214	0.978	1	10	icosanoid transport	BP	1	LEP	up_AFEM_EC
GO:1901223	0.214	0.978	1	10	negative regulation of NIK/NF-kappaB signaling	BP	1	CYLD	up_AFEM_EC
GO:1901571	0.214	0.978	1	10	fatty acid derivative transport	BP	1	LEP	up_AFEM_EC
GO:1903053	0.214	0.978	1	10	regulation of extracellular matrix organization	BP	1	FAP	up_AFEM_EC
GO:1903671	0.214	0.978	1	10	negative regulation of sprouting angiogenesis	BP	1	TBXA2R	up_AFEM_EC
GO:0007266	0.214	0.977	1	64	Rho protein signal transduction	BP	1	ARHGEF26	up_APUL_EC
GO:0035021	0.214	0.987	1	2	negative regulation of Rac protein signal	BP	1	ARAP3	up_VCAV_EC
GO:1904976	0.214	0.987	1	2	cellular response to bleomycin	BP	1	TIMELESS	up_VCAV_EC
GO:0035457	0.214	0.983	1	3	cellular response to interferon-alpha	BP	1	GATA3	up_VCAV_EC
GO:1904975	0.214	0.987	1	2	response to bleomycin	BP	1	TIMELESS	up_VCAV_EC
GO:0007420	0.214	0.978	1	169	brain development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0008406	0.214	0.976	1	57	gonad development	BP	1	HOXA9	up_VFEM_EC
GO:0045137	0.214	0.976	1	57	development of primary sexual characteristics	BP	1	HOXA9	up_VFEM_EC
GO:0010631	0.214	0.977	1	118	epithelial cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0090132	0.214	0.977	1	118	epithelium migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0043409	0.214	0.976	1	54	negative regulation of MAPK cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0043903	0.214164775	0.92492	3	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	TRIM8,MAVS,CHMP4B	up_ACOR_EC
GO:0010224	0.21466424	0.97779	1	9	response to UV-B	BP	1	MFAP4	up_ACOR_EC
GO:0060575	0.214687943	0.97779	1	9	intestinal epithelial cell differentiation	BP	1	GATA4	up_ACOR_EC
GO:0001952	0.214705721	0.94521	2	34	regulation of cell-matrix adhesion	BP	1	ARHGAP6,NRP1	up_ACOR_EC
GO:0038127	0.214721177	0.94533	2	32	ERBB signaling pathway	BP	1	SH3TC2,SOX9	up_ACOR_EC
GO:0070861	0.214729451	0.97778	1	9	regulation of protein exit from endoplasmic	BP	1	EDEM2	up_ACOR_EC
GO:0002021	0.214813983	0.97776	1	9	response to dietary excess	BP	1	PCSK1N	up_ACOR_EC
GO:0006520	0.215	0.881	8	114	cellular amino acid metabolic process	BP	1	THNSL2,PARK7,ENSCAFG00000002977,HPDL, CRTAP,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0006006	0.215	0.887	7	61	glucose metabolic process	BP	1	ATF3,FAM3C,PGM2,ENSCAFG00000010596,E NSCAFG00000024323,APOD,PMAIP1	up_VCAV_EC
GO:0016310	0.215	0.903	5	641	phosphorylation	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0045595	0.215	0.913	4	469	regulation of cell differentiation	BP	1	ACVRL1,LYN,PDPN,HOXA7	down_ACOR_EC
GO:0048585	0.215	0.912	4	475	negative regulation of response to stimulus	BP	1	LYN,IGF1R,SULF1,ASPN	down_ACOR_EC
GO:0042177	0.215	0.911	4	47	negative regulation of protein catabolic process	BP	1	TIMP2,PSMF1,PARK7,CLEC16A	down_VCAV_EC

GO:0003279	0.215	0.911	4	48	cardiac septum development	BP	1	NOTCH2,BMPR1A,LMO4,SEMA3C	down_VCAV_EC
GO:0043624	0.215	0.912	4	39	cellular protein complex disassembly	BP	1	ARHGEF2,WDR1,CAPG,MID1	down_VSAP_EC
GO:1904892	0.215	0.912	4	40	regulation of STAT cascade	BP	1	SOCS5,PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0051260	0.215	0.91	4	100	protein homooligomerization	BP	1	KCNC4,CRYAB,KCND1,ACACB	up_AFEM_EC
GO:0048477	0.215	0.928	3	19	oogenesis	BP	1	TRIP13,FBXO5,ASPM	down_ACOR_VSMC
GO:0010717	0.215	0.926	3	32	regulation of epithelial to mesenchymal transition	BP	1	VASN,GLIPR2,GREM1	down_VCAV_EC
GO:1902600	0.215	0.926	3	31	proton transmembrane transport	BP	1	ATP5MC1,ATP6V0C,PARK7	down_VCAV_EC
GO:0006446	0.215	0.926	3	27	regulation of translational initiation	BP	1	EIF4EBP1,EIF5,EIF2S1	down_VSAP_EC
GO:0098927	0.215	0.929	3	17	vesicle-mediated transport between endosomal compartments	BP	1	PIK3C3,AKTIP,LMTK2	up_ACOR_VSMC
GO:0001932	0.215	0.926	3	416	regulation of protein phosphorylation	BP	1	PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0048812	0.215	0.945	2	151	neuron projection morphogenesis	BP	1	SPG11,NRP2	down_ACOR_EC
GO:0006490	0.215	0.949	2	11	oligosaccharide-lipid intermediate biosynthetic	BP	1	MPDU1,NUS1	down_ACOR_VSMC
GO:0032757	0.215	0.948	2	14	positive regulation of interleukin-8 production	BP	1	SERPINE1,DDIT3	down_VSAP_EC
GO:0051336	0.215	0.946	2	251	regulation of hydrolase activity	BP	1	CCL24,PTGER2	up_VPUL_EC
GO:0032733	0.215	0.951	2	9	positive regulation of interleukin-10 production	BP	1	CD274,CD83	up_VSAP_EC
GO:0090022	0.215	0.951	2	9	regulation of neutrophil chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0045616	0.215	0.951	2	9	regulation of keratinocyte differentiation	BP	1	HOXA7,ZFP36L1	up_VSAP_EC
GO:0006907	0.215	0.983	1	3	pinocytosis	BP	1	CAV1	down_ACOR_VSMC
GO:0000188	0.215	0.983	1	3	inactivation of MAPK activity	BP	1	CAV1	down_ACOR_VSMC
GO:0035739	0.215	0.983	1	3	CD4-positive, alpha-beta T cell proliferation	BP	1	ARG2	down_ACOR_VSMC
GO:0060352	0.215	0.983	1	3	cell adhesion molecule production	BP	1	CAV1	down_ACOR_VSMC
GO:2000561	0.215	0.983	1	3	regulation of CD4-positive, alpha-beta T cell	BP	1	ARG2	down_ACOR_VSMC
GO:0033572	0.215	0.98	1	5	transferrin transport	BP	1	ARHGAP1	down_VCAV_EC
GO:0003002	0.215	0.977	1	118	regionalization	BP	1	CITED2	down_VPOR_EC
GO:0002717	0.215	0.981	1	4	positive regulation of natural killer cell	BP	1	PVR	down_VSAP_EC
GO:0045954	0.215	0.981	1	4	positive regulation of natural killer cell	BP	1	PVR	down_VSAP_EC
GO:0006521	0.215	0.981	1	4	regulation of cellular amino acid metabolic	BP	1	NR1H4	down_VSAP_EC
GO:0010715	0.215	0.981	1	4	regulation of extracellular matrix disassembly	BP	1	FSCN1	down_VSAP_EC
GO:0007167	0.215	0.979	1	274	enzyme linked receptor protein signaling pathway	BP	1	TGFBR1	down_VSAP_VSMC
GO:0042744	0.215	0.987	1	2	hydrogen peroxide catabolic process	BP	1	CAT	up_ACOR_VSMC
GO:0042059	0.215	0.977	1	10	negative regulation of epidermal growth factor receptor signaling	BP	1	RAB7A	up_AFEM_EC
GO:0060986	0.215	0.978	1	10	endocrine hormone secretion	BP	1	CRY2	up_AFEM_EC
GO:0090185	0.215	0.978	1	10	negative regulation of kidney development	BP	1	GREM1	up_AFEM_EC
GO:0090190	0.215	0.977	1	10	positive regulation of branching involved in ureteric bud	BP	1	GREM1	up_AFEM_EC
GO:1903541	0.215	0.977	1	10	regulation of exosomal secretion	BP	1	RAB7A	up_AFEM_EC
GO:1903543	0.215	0.977	1	10	positive regulation of exosomal secretion	BP	1	RAB7A	up_AFEM_EC
GO:1905517	0.215	0.977	1	10	macrophage migration	BP	1	CMKLR1	up_AFEM_EC
GO:0006811	0.215	0.98	1	330	ion transport	BP	1	HOXA3	up_APUL_VSMC

GO:0051241	0.215	0.98	1	336	negative regulation of multicellular organismal	BP	1	TBX5	up_APUL_VSMC
GO:0015734	0.215	0.987	1	2	taurine transport	BP	1	LRRC8D	up_VCAV_EC
GO:0002710	0.215	0.983	1	3	negative regulation of T cell mediated immunity	BP	1	IL7R	up_VCAV_EC
GO:0002685	0.215	0.976	1	55	regulation of leukocyte migration	BP	1	HOXA7	up_VFEM_EC
GO:0051099	0.215	0.976	1	70	positive regulation of binding	BP	1	HOXA3	up_VPUL_EC
GO:0034765	0.215179908	0.91021	4	91	regulation of ion transmembrane transport	BP	1	KCNB1,ACTN2,MAPK8IP2,PM20D1	up_ACOR_EC
GO:0032091	0.215285032	0.94497	2	34	negative regulation of protein binding	BP	1	IFIT2,CLSTN1	up_ACOR_EC
GO:0002230	0.215290574	0.97766	1	9	positive regulation of defense response to virus	BP	1	MAVS	up_ACOR_EC
GO:0033233	0.215539484	0.9776	1	9	regulation of protein sumoylation	BP	1	PIAS1	up_ACOR_EC
GO:0010573	0.215546058	0.9776	1	9	vascular endothelial growth factor production	BP	1	NDRG2	up_ACOR_EC
GO:0010574	0.215546058	0.9776	1	9	regulation of vascular endothelial growth factor	BP	1	NDRG2	up_ACOR_EC
GO:0010002	0.215647563	0.97758	1	9	cardioblast differentiation	BP	1	TBX5	up_ACOR_EC
GO:0046676	0.215822013	0.97754	1	9	negative regulation of insulin secretion	BP	1	KCNB1	up_ACOR_EC
GO:0002474	0.215889215	0.97753	1	9	antigen processing and presentation of peptide antigen via MHC class I	BP	1	TAPBP	up_ACOR_EC
GO:0048873	0.215964051	0.97751	1	9	homeostasis of number of cells within a tissue	BP	1	SOX9	up_ACOR_EC
GO:0007155	0.216	0.835	35	324	cell adhesion	BP	1	HOXA7,PCDH19,SERPINB8,FAM107A,CD274,ACKR3,AMIGO1,RADIL,LIMS2,HOXD3,CDH1,ABL1,EMP2,DLL1,HPSE,CLDN1,ZBTB16,PLPP3,ZFP36L1,PIK3R1,TIAM1,TFE3,ECM2,WISP2,CD83,FBLN1,PNP,STX4,ACVRL1,ASS1,FLOT1,NCK1,TGFBR2,CITED2,BAG4	up_VSAP_EC
GO:0050801	0.216	0.857	15	200	ion homeostasis	BP	1	SLC39A7,NR1H4,ERO1A,ENPP1,ATP2B1,TMTC2,HIF1A,NEO1,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0034220	0.216	0.859	14	188	ion transmembrane transport	BP	1	SLC39A7,ERO1A,LRRC8A,SLC38A1,REM1,WDR1,NDUFA4L2,LYN,DDIT3,CLCN3,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0051223	0.216	0.86	14	181	regulation of protein transport	BP	1	NR1H4,PLK3,PTPN14,PTPN11,MYO1C,HIF1A,IWS1,ZPR1,LYN,GSK3B,REST,RAB11FIP1,CDKN1A,RHBDF2	down_VSAP_EC
GO:0007265	0.216	0.862	13	121	Ras protein signal transduction	BP	1	ENSCAFG00000030005,PSD4,STMN1,RAP2C,ARHGDIA,NUP62,CDC42EP4,CDK2,CCNA2,PHACTR4,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:1904018	0.216	0.877	9	69	positive regulation of vasculature development	BP	1	ABL1,BTG1,HDAC7,DLL1,CCBE1,SASH1,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0030178	0.216	0.888	7	52	negative regulation of Wnt signaling pathway	BP	1	FZD1,WNT11,AXIN2,HIC1,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0033157	0.216	0.892	6	82	regulation of intracellular protein transport	BP	1	PRNP,ENSCAFG00000014978,AKT2,GLI3,PARK7,MAVS	down_VCAV_EC
GO:0032103	0.216	0.892	6	69	positive regulation of response to external	BP	1	VEGFA,SERPINE1,PTGS2,ADAM17,GBP5,NRP1	down_VSAP_EC
GO:0060401	0.216	0.894	6	42	cytosolic calcium ion transport	BP	1	PLCG2,HTR2B,MICU2,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0043491	0.216	0.893	6	50	protein kinase B signaling	BP	1	TEK,HCLS1,RAPGEF1,GATA3,MTOR,PEAR1	up_VCAV_EC
GO:0046165	0.216	0.894	6	42	alcohol biosynthetic process	BP	1	INSIG2,GOT1,PPIP5K1,PCBD1,MVK,CYB5R3	up_VSAP_EC
GO:0002062	0.216	0.911	4	48	chondrocyte differentiation	BP	1	BMPR1A,GLI3,GREM1,ZBTB16	down_VCAV_EC
GO:0045621	0.216	0.913	4	28	positive regulation of lymphocyte	BP	1	IL7R,GATA3,ITPKB,ATP11C	up_VCAV_EC
GO:1901863	0.216	0.914	4	25	positive regulation of muscle tissue	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0008283	0.216	0.913	4	545	cell proliferation	BP	1	EMX2,MAB21L1,CAV1,SHOX2	up_VSAP_VSMC
GO:0035904	0.216	0.926	3	25	aorta development	BP	1	PRICKLE1,LTBP1,ADAMTS6	down_VSAP_EC
GO:0031644	0.216	0.928	3	19	regulation of neurological system process	BP	1	RELN,HOMER3,ACPP	up_VCAV_EC
GO:0042116	0.216	0.928	3	18	macrophage activation	BP	1	ADGRF5,TLR4,CD200	up_VCAV_EC
GO:0060420	0.216	0.928	3	18	regulation of heart growth	BP	1	MEF2C,EDN1,PROX1	up_VCAV_EC

GO:0007007	0.216	0.949	2	11	inner mitochondrial membrane organization	BP	1	CHCHD3,SAMM50	down_ACOR_VSMC
GO:0015988	0.216	0.947	2	17	energy coupled proton transmembrane transport, against	BP	1	ATP5MC1,ATP6V0C	down_VCAV_EC
GO:0099132	0.216	0.947	2	17	ATP hydrolysis coupled cation transmembrane	BP	1	ATP5MC1,ATP6V0C	down_VCAV_EC
GO:0001569	0.216	0.948	2	14	branching involved in blood vessel	BP	1	CTNNB1,NRP1	down_VSAP_EC
GO:0030837	0.216	0.947	2	14	negative regulation of actin filament	BP	1	TWF1,CAPG	down_VSAP_EC
GO:0010224	0.216	0.951	2	9	response to UV-B	BP	1	MFAP4,CDKN1A	up_ACOR_VSMC
GO:0032309	0.216	0.951	2	9	icosanoid secretion	BP	1	LEP,CFI	up_ACOR_VSMC
GO:0046189	0.216	0.951	2	9	phenol-containing compound biosynthetic	BP	1	MOXD1,PARK7	up_ACOR_VSMC
GO:0048596	0.216	0.95	2	9	embryonic camera-type eye morphogenesis	BP	1	CITED2,FRS2	up_ACOR_VSMC
GO:0038179	0.216	0.95	2	10	neurotrophin signaling pathway	BP	1	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:0009161	0.216	0.944	2	103	ribonucleoside monophosphate	BP	1	AK5,FBP1	up_VPOR_EC
GO:1901293	0.216	0.944	2	106	nucleoside phosphate biosynthetic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0060284	0.216	0.945	2	212	regulation of cell development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0001568	0.216	0.945	2	252	blood vessel development	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:0033120	0.216	0.951	2	9	positive regulation of RNA splicing	BP	1	PIK3R1,NUP98	up_VSAP_EC
GO:0002230	0.216	0.951	2	9	positive regulation of defense response to virus	BP	1	PQBP1,MAVS	up_VSAP_EC
GO:1903204	0.216	0.951	2	9	negative regulation of oxidative stress-induced	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:0045683	0.216	0.951	2	9	negative regulation of epidermis development	BP	1	HOXA7,DLL1	up_VSAP_EC
GO:0007165	0.216	1	1	1496	signal transduction	BP	1	GATA5	down_AFEM_VSMC
GO:0044271	0.216	1	1	1501	cellular nitrogen compound biosynthetic	BP	1	GATA5	down_AFEM_VSMC
GO:0072396	0.216	0.98	1	5	response to cell cycle checkpoint signaling	BP	1	FBH1	down_VCAV_EC
GO:0072402	0.216	0.98	1	5	response to DNA integrity checkpoint signaling	BP	1	FBH1	down_VCAV_EC
GO:0072423	0.216	0.98	1	5	response to DNA damage checkpoint signaling	BP	1	FBH1	down_VCAV_EC
GO:0007413	0.216	0.98	1	5	axonal fasciculation	BP	1	NDN	down_VCAV_EC
GO:0106030	0.216	0.98	1	5	neuron projection fasciculation	BP	1	NDN	down_VCAV_EC
GO:0006468	0.216	0.983	1	544	protein phosphorylation	BP	1	PLCL1	down_VFEM_EC
GO:0010755	0.216	0.981	1	4	regulation of plasminogen activation	BP	1	SERPINE1	down_VSAP_EC
GO:0014850	0.216	0.981	1	4	response to muscle activity	BP	1	HIF1A	down_VSAP_EC
GO:0030212	0.216	0.981	1	4	hyaluronan metabolic process	BP	1	CEMIP2	down_VSAP_EC
GO:1902176	0.216	0.981	1	4	negative regulation of oxidative stress-induced intrinsic apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0006474	0.216	0.979	1	5	N-terminal protein amino acid acetylation	BP	1	NAA10	down_VSAP_EC
GO:0071941	0.216	0.981	1	4	nitrogen cycle metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0010459	0.216	0.987	1	2	negative regulation of heart rate	BP	1	RNLS	up_ACOR_VSMC
GO:0044703	0.216	0.977	1	172	multi-organism reproductive process	BP	1	HOXA9	up_AFEM_VSMC
GO:0060070	0.216	0.976	1	105	canonical Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:0001514	0.216	0.983	1	3	selenocysteine incorporation	BP	1	SECISBP2L	up_VCAV_EC
GO:0003365	0.216	0.987	1	2	establishment of cell polarity involved in ameboidal cell migration	BP	1	AMOT	up_VCAV_EC
GO:0006451	0.216	0.983	1	3	translational readthrough	BP	1	SECISBP2L	up_VCAV_EC

GO:0003376	0.216	0.983	1	3	sphingosine-1-phosphate receptor signaling	BP	1	SPNS3	up_VCAV_EC
GO:0006167	0.216	0.987	1	2	AMP biosynthetic process	BP	1	ADSS	up_VCAV_EC
GO:0006787	0.216	0.981	1	4	porphyrin-containing compound catabolic	BP	1	BLVRA	up_VCAV_EC
GO:0033015	0.216	0.981	1	4	tetrapyrrole catabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0042167	0.216	0.981	1	4	heme catabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0044208	0.216	0.987	1	2	'de novo' AMP biosynthetic process	BP	1	ADSS	up_VCAV_EC
GO:0046149	0.216	0.981	1	4	pigment catabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0051651	0.216	0.976	1	31	maintenance of location in cell	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0007163	0.216	0.976	1	60	establishment or maintenance of cell	BP	1	CYP26B1	up_VFEM_EC
GO:0009411	0.216	0.976	1	56	response to UV	BP	1	MME	up_VFEM_EC
GO:0090174	0.216	0.976	1	56	organelle membrane fusion	BP	1	TRIM9	up_VFEM_EC
GO:1901215	0.216	0.976	1	57	negative regulation of neuron death	BP	1	SIX1	up_VFEM_EC
GO:0045089	0.216	0.976	1	70	positive regulation of innate immune response	BP	1	NR1H4	up_VPUL_EC
GO:0051216	0.216	0.976	1	70	cartilage development	BP	1	HOXA3	up_VPUL_EC
GO:0008015	0.216	0.977	1	120	blood circulation	BP	1	SLIT2	up_VPUL_VSMC
GO:0015849	0.216	0.976	1	56	organic acid transport	BP	1	SLC16A12	up_VSAP_VSMC
GO:0046942	0.216	0.976	1	56	carboxylic acid transport	BP	1	SLC16A12	up_VSAP_VSMC
GO:0045683	0.216135176	0.97747	1	9	negative regulation of epidermis development	BP	1	CDH3	up_ACOR_EC
GO:0032897	0.216308762	0.97743	1	9	negative regulation of viral transcription	BP	1	TRIM8	up_ACOR_EC
GO:0018149	0.216358139	0.97742	1	9	peptide cross-linking	BP	1	PI3	up_ACOR_EC
GO:0051569	0.21638863	0.97742	1	9	regulation of histone H3-K4 methylation	BP	1	PYGO2	up_ACOR_EC
GO:0046189	0.216578836	0.97738	1	9	phenol-containing compound biosynthetic	BP	1	CDH3	up_ACOR_EC
GO:0072078	0.216602329	0.94448	2	33	nephron tubule morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0048596	0.216633497	0.97736	1	9	embryonic camera-type eye morphogenesis	BP	1	FZD5	up_ACOR_EC
GO:0071599	0.216666851	0.97736	1	9	otic vesicle development	BP	1	SOX9	up_ACOR_EC
GO:0007622	0.216802925	0.97733	1	9	rhythmic behavior	BP	1	PTGDS	up_ACOR_EC
GO:1904062	0.216864002	0.92349	3	62	regulation of cation transmembrane transport	BP	1	ACTN2,MAPK8IP2,PM20D1	up_ACOR_EC
GO:0080090	0.217	0.815	112	1734	regulation of primary metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,MEIS2,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,CBX5,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PGAM1,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,MSN,HIF1A,SLC45A3,IWS1,DNAJC10,TNIK,NXN,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,STRAP,DDIT3,FAM162A,BACH1,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,ARMCX3,SH3GLB1,HTT,REST,ABHD5,ZMYND8,EIF2S1,PRMT1,SPOP,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC

GO:0009056	0.217	0.819	79	755	catabolic process	BP	1	PEX7,DHDH,AXIN2,LIPC,ENPP2,PLEKHF1,RNPEP,PLBD1,ACAA1,FOXRED2,ACACB,TPCN2,RETREG1,GDA,ABTB1,PEX2,GOT1,INPP5E,CTSS,TENT5C,ADHFE1,HSD17B14,HPSE,PAFAH2,ALDH6A1,VPS36,EXOSC7,FAAH,PYM1,AMBRA1,LPL,DFFB,MFN2,ZFP36L1,GALK1,RBCK1,ENTPD3,PLA2G6,RNF24,FBXW4,GCDH,BCKDHB,FBXO4,RMND5A,POLDIP2,ATG2A,AZIN2,NCEH1,FBXW5,SMG9,FBXO7,UBA7,EHHADH,RNF166,LONP2,ABHD16A,PIP4K2B,LIPE,RNF216,OSBPL7,ENSCAFG00000002977,SAMD4B,ZFP36L2,PNP,TIMP2,IDH1,UBQLN2,CTSF,CDC26,HTRA2,TNRC6C,ULK1,HMOX1,NPRL3,GNPDA1,KEAP1,FUNDC2,DDIT4,IDO2	up_VSAP_EC
GO:2000147	0.217	0.867	11	169	positive regulation of cell motility	BP	1	PDGFRB,GLIPR2,RHOD,AKT2,SYDE1,SEMA3C,THY1,SASH1,TWIST2,DDR2,RAC2	down_VCAV_EC
GO:0061564	0.217	0.871	10	119	axon development	BP	1	SIPA1L1,PTPN11,IFRD1,KIF5B,ZPR1,NEO1,UST,CDH11,EXT1,NRP1	down_VSAP_EC
GO:0040011	0.217	0.892	6	505	locomotion	BP	1	C3AR1,ARHGEF2,SEMA3A,SEMA3D,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:0007040	0.217	0.902	5	33	lysosome organization	BP	1	ABCA1,CLN8,AKTIP,GAA,ACP2	up_ACOR_VSMC
GO:0080171	0.217	0.902	5	33	lytic vacuole organization	BP	1	ABCA1,CLN8,AKTIP,GAA,ACP2	up_ACOR_VSMC
GO:0000422	0.217	0.902	5	34	autophagy of mitochondrion	BP	1	AMBRA1,MFN2,FBXO7,HTRA2,FUNDC2	up_VSAP_EC
GO:0042471	0.217	0.902	5	34	ear morphogenesis	BP	1	OSR2,INSIG2,LRIG3,OSR1,ZEB1	up_VSAP_EC
GO:0061726	0.217	0.902	5	34	mitochondrion disassembly	BP	1	AMBRA1,MFN2,FBXO7,HTRA2,FUNDC2	up_VSAP_EC
GO:0001843	0.217	0.911	4	38	neural tube closure	BP	1	PRICKLE1,PRKACB,TMED2,SDC4	down_VSAP_EC
GO:0031529	0.217	0.927	3	20	ruffle organization	BP	1	CAV1,LIMA1,RAC1	down_ACOR_VSMC
GO:1901880	0.217	0.927	3	19	negative regulation of protein depolymerization	BP	1	CAPG,LIMA1,ARHGEF2	down_ACOR_VSMC
GO:0010605	0.217	0.929	3	745	negative regulation of macromolecule metabolic	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0019222	0.217	0.945	3	1934	regulation of metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0001954	0.217	0.928	3	17	positive regulation of cell-matrix adhesion	BP	1	FERMT1,NRP1,JUP	up_ACOR_VSMC
GO:0042981	0.217	0.926	3	471	regulation of apoptotic process	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0061028	0.217	0.947	2	14	establishment of endothelial barrier	BP	1	MSN,CTNNB1	down_VSAP_EC
GO:0007129	0.217	0.95	2	9	synapsis	BP	1	DMC1,SUN1	up_ACOR_VSMC
GO:0097435	0.217	0.945	2	230	supramolecular fiber organization	BP	1	TUBB4A,PDLIM3	up_APUL_EC
GO:1903361	0.217	0.983	1	3	protein localization to basolateral plasma	BP	1	CAV1	down_ACOR_VSMC
GO:0080154	0.217	0.983	1	3	regulation of fertilization	BP	1	B4GALT1	down_ACOR_VSMC
GO:0090091	0.217	0.983	1	3	positive regulation of extracellular matrix	BP	1	FSCN1	down_ACOR_VSMC
GO:0006357	0.217	0.983	1	547	regulation of transcription by RNA polymerase II	BP	1	MOSPD1	down_VFEM_EC
GO:0031118	0.217	0.981	1	4	rRNA pseudouridine synthesis	BP	1	MRPL1	down_VSAP_EC
GO:0036005	0.217	0.981	1	4	response to macrophage colony-stimulating factor	BP	1	PTPN2	down_VSAP_EC
GO:0036006	0.217	0.981	1	4	cellular response to macrophage colony-	BP	1	PTPN2	down_VSAP_EC
GO:0051085	0.217	0.981	1	4	chaperone cofactor-dependent protein	BP	1	ERO1A	down_VSAP_EC
GO:2001241	0.217	0.98	1	4	positive regulation of extrinsic apoptotic signaling pathway in	BP	1	INHBA	down_VSAP_EC
GO:0007517	0.217	0.976	1	100	muscle organ development	BP	1	SGCD	up_AORT_EC
GO:0048738	0.217	0.976	1	64	cardiac muscle tissue development	BP	1	TBX5	up_APUL_EC
GO:0032470	0.217	0.987	1	2	positive regulation of endoplasmic reticulum calcium ion concentration	BP	1	ATP2A1	up_VCAV_EC
GO:0035523	0.217	0.983	1	3	protein K29-linked deubiquitination	BP	1	USP13	up_VCAV_EC

GO:0071391	0.217	0.983	1	3	cellular response to estrogen stimulus	BP	1	ARID5A	up_VCAV_EC
GO:0032753	0.217	0.983	1	3	positive regulation of interleukin-4 production	BP	1	GATA3	up_VCAV_EC
GO:0070384	0.217	0.983	1	3	Harderian gland development	BP	1	ALDH1A3	up_VCAV_EC
GO:0070555	0.217	0.976	1	29	response to interleukin-1	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0003007	0.217	0.976	1	94	heart morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032984	0.217	0.976	1	70	protein-containing complex disassembly	BP	1	ARHGEF2	up_VPUL_EC
GO:0045861	0.217	0.976	1	71	negative regulation of proteolysis	BP	1	PTGER2	up_VPUL_EC
GO:0048863	0.217	0.976	1	70	stem cell differentiation	BP	1	TBX5	up_VPUL_EC
GO:0061564	0.217	0.976	1	119	axon development	BP	1	SLIT2	up_VPUL_VSMC
GO:0007179	0.217	0.976	1	57	transforming growth factor beta receptor	BP	1	CAV1	up_VSAP_VSMC
GO:0002724	0.217366049	0.9772	1	9	regulation of T cell cytokine production	BP	1	FZD5	up_ACOR_EC
GO:0097035	0.217659228	0.97714	1	9	regulation of membrane lipid distribution	BP	1	PRKCD	up_ACOR_EC
GO:0002688	0.217893551	0.94388	2	34	regulation of leukocyte chemotaxis	BP	1	MMP28,RARRES2	up_ACOR_EC
GO:1905476	0.217898897	0.97709	1	9	negative regulation of protein localization to	BP	1	LRRC15	up_ACOR_EC
GO:0045859	0.218	0.842	25	219	regulation of protein kinase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,LATS2,PDE5A,SASH1,FGF18,CDKN2B,CDKN1A,SMPD1,CCNT1,FRS2,APP,PSEN1,DDR2,DUSP22,EDN1,DUSP26,LRRC4,PRKAG3,MAP3K7,INPP5K,PARK7	up_ACOR_VSMC
GO:0010563	0.218	0.856	15	203	negative regulation of phosphorus metabolic process	BP	1	SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,DYNLL1,DNAJC10,PTPN2,APOE,LYN,STRAP,CBLC,ATF3,ARFGEF3,CDKN1A	down_VSAP_EC
GO:0045936	0.218	0.856	15	203	negative regulation of phosphate metabolic process	BP	1	SOCS5,ENPP1,ERRFI1,SNX25,TRIB3,DYNLL1,DNAJC10,PTPN2,APOE,LYN,STRAP,CBLC,ATF3,ARFGEF3,CDKN1A	down_VSAP_EC
GO:0016049	0.218	0.857	15	124	cell growth	BP	1	DCBLD2,CRIM1,GJA1,RERG,TMEM108,CDKN1A,CRLF3,NRP1,ULK2,APP,EDN1,FAM107A,IGFBP7,NAIF1,SH3BP4	up_ACOR_VSMC
GO:0031647	0.218	0.868	11	87	regulation of protein stability	BP	1	FAM107A,PEX2,SAV1,PLPP3,MORC3,PIK3R1,FBXO4,HPS4,FBXO7,FLOT1,PEX6	up_VSAP_EC
GO:0051099	0.218	0.875	9	70	positive regulation of binding	BP	1	PLCL1,BMP4,PARP9,APP,PSEN1,AKTIP,B2M,HERPUD1,PARK7	up_ACOR_VSMC
GO:0032103	0.218	0.876	9	69	positive regulation of response to external	BP	1	NAPEPLD,SLIT2,IL17RC,F2RL1,SASH1,MYD88,ZNF580,CYBA,STX4	up_VSAP_EC
GO:0030178	0.218	0.899	5	52	negative regulation of Wnt signaling pathway	BP	1	PRICKLE1,NXN,APOE,DDIT3,TAX1BP3	down_VSAP_EC
GO:0051261	0.218	0.902	5	33	protein depolymerization	BP	1	FGF13,DNAJC6,ACTN2,MID1,F2RL1	up_ACOR_VSMC
GO:0034614	0.218	0.901	5	39	cellular response to reactive oxygen species	BP	1	TNFAIP3,MAPK13,GUCY1B1,GCH1,RIPK1	up_VCAV_EC
GO:0060425	0.218	0.913	4	25	lung morphogenesis	BP	1	FGF7,NFIB,MAP2K2,TGFBR2	up_VSAP_EC
GO:0070534	0.218	0.927	3	19	protein K63-linked ubiquitination	BP	1	UBE2S,UBE2T,RNF152	down_ACOR_VSMC
GO:0032945	0.218	0.928	3	17	negative regulation of mononuclear cell	BP	1	BMP4,PDE5A,CD274	up_ACOR_VSMC
GO:0050672	0.218	0.928	3	17	negative regulation of lymphocyte proliferation	BP	1	BMP4,PDE5A,CD274	up_ACOR_VSMC
GO:1904894	0.218	0.928	3	17	positive regulation of STAT cascade	BP	1	LEP,CRLF3,PARP9	up_ACOR_VSMC
GO:0048661	0.218	0.928	3	17	positive regulation of smooth muscle cell	BP	1	IL6R,MFN2,HMOX1	up_VSAP_EC
GO:0055080	0.218	0.944	2	176	cation homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0005978	0.218	0.947	2	14	glycogen biosynthetic process	BP	1	ENPP1,PPP1R3C	down_VSAP_EC
GO:0009250	0.218	0.947	2	14	glucan biosynthetic process	BP	1	ENPP1,PPP1R3C	down_VSAP_EC
GO:0030901	0.218	0.947	2	14	midbrain development	BP	1	UCHL5,CTNNB1	down_VSAP_EC
GO:0045022	0.218	0.947	2	15	early endosome to late endosome transport	BP	1	HOOK3,MSN	down_VSAP_EC
GO:0010470	0.218	0.95	2	9	regulation of gastrulation	BP	1	MBP,DAG1	up_ACOR_VSMC

GO:1903555	0.218	0.944	2	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	LEP,BPI	up_AFEM_EC
GO:0043009	0.218	0.944	2	227	chordate embryonic development	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:1904036	0.218	0.949	2	10	negative regulation of epithelial cell apoptotic	BP	1	TNFAIP3,GATA3	up_VCAV_EC
GO:0006417	0.218	0.943	2	109	regulation of translation	BP	1	PUM3,EIF5	up_VPOR_EC
GO:0007178	0.218	0.943	2	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ASPN,ACVR2A	up_VPOR_EC
GO:0009144	0.218	0.943	2	103	purine nucleoside triphosphate metabolic	BP	1	AK5,FBP1	up_VPOR_EC
GO:0036230	0.218	0.95	2	9	granulocyte activation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0002062	0.218	0.976	1	48	chondrocyte differentiation	BP	1	SULF1	down_ACOR_EC
GO:0009128	0.218	0.982	1	3	purine nucleoside monophosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0009158	0.218	0.982	1	3	ribonucleoside monophosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0009169	0.218	0.982	1	3	purine ribonucleoside monophosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:1901666	0.218	0.982	1	3	positive regulation of NAD+ ADP-	BP	1	HMGN1	down_ACOR_VSMC
GO:0009125	0.218	0.982	1	3	nucleoside monophosphate catabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0045656	0.218	0.982	1	3	negative regulation of monocyte differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:1901664	0.218	0.982	1	3	regulation of NAD+ ADP-ribosyltransferase activity	BP	1	HMGN1	down_ACOR_VSMC
GO:0021873	0.218	0.979	1	5	forebrain neuroblast division	BP	1	NUMBL	down_VCAV_EC
GO:1900037	0.218	0.98	1	4	regulation of cellular response to hypoxia	BP	1	HYOU1	down_VSAP_EC
GO:1900038	0.218	0.98	1	4	negative regulation of cellular response to	BP	1	HYOU1	down_VSAP_EC
GO:0042118	0.218	0.98	1	4	endothelial cell activation	BP	1	TGFBR1	down_VSAP_EC
GO:0060123	0.218	0.987	1	2	regulation of growth hormone secretion	BP	1	CHD7	up_ACOR_VSMC
GO:2000394	0.218	0.987	1	2	positive regulation of lamellipodium	BP	1	RREB1	up_ACOR_VSMC
GO:0090200	0.218	0.977	1	10	positive regulation of release of cytochrome c	BP	1	MLLT11	up_AFEM_EC
GO:0098542	0.218	0.976	1	100	defense response to other organism	BP	1	BPI	up_AORT_EC
GO:1902532	0.218	0.977	1	204	negative regulation of intracellular signal	BP	1	ESR1	up_AORT_VSMC
GO:0043122	0.218	0.976	1	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	up_APUL_EC
GO:0016082	0.218	0.98	1	4	synaptic vesicle priming	BP	1	SNAP23	up_VCAV_EC
GO:0032485	0.218	0.982	1	3	regulation of Ral protein signal transduction	BP	1	RGL2	up_VCAV_EC
GO:1905563	0.218	0.987	1	2	negative regulation of vascular endothelial cell	BP	1	MEF2C	up_VCAV_EC
GO:0032484	0.218	0.982	1	3	Ral protein signal transduction	BP	1	RGL2	up_VCAV_EC
GO:0090557	0.218	0.983	1	3	establishment of endothelial intestinal	BP	1	RAPGEF2	up_VCAV_EC
GO:0014033	0.218	0.976	1	30	neural crest cell differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0035282	0.218	0.976	1	30	segmentation	BP	1	SEMA3A	up_VPOR_EC
GO:0044242	0.218	0.976	1	57	cellular lipid catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0009895	0.218	0.976	1	94	negative regulation of catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046034	0.218	0.976	1	88	ATP metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043414	0.218	0.976	1	70	macromolecule methylation	BP	1	NR1H4	up_VPUL_EC
GO:0003013	0.218	0.976	1	121	circulatory system process	BP	1	SLIT2	up_VPUL_VSMC
GO:0060562	0.218	0.976	1	120	epithelial tube morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0006575	0.218	0.975	1	53	cellular modified amino acid metabolic process	BP	1	GATM	up_VSAP_VSMC

GO:0034329	0.218	0.975	1	60	cell junction assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0006491	0.218073917	0.97705	1	9	N-glycan processing	BP	1	EDEM2	up_ACOR_EC
GO:0061564	0.218463758	0.89775	5	119	axon development	BP	1	BRSK1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0032309	0.21866598	0.97692	1	9	icosanoid secretion	BP	1	CFI	up_ACOR_EC
GO:0050789	0.219	0.872	17	3295	regulation of biological process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,NETO1,GATM,SALL1,HOXC10,IRX5,MAB21L1,PRR16,STIM1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0034641	0.219	0.875	12	2171	cellular nitrogen compound metabolic	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0009152	0.219	0.874	9	80	purine ribonucleotide biosynthetic process	BP	1	ACLY,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,ATP5F1D	down_ACOR_VSMC
GO:0046434	0.219	0.885	7	52	organophosphate catabolic process	BP	1	PLCG2,PDE5A,SMPD1,ALDOC,ENTPD3,DDIT4,INPP5K	up_ACOR_VSMC
GO:0001837	0.219	0.909	4	48	epithelial to mesenchymal transition	BP	1	VASN,GLIPR2,LOXL3,GREM1	down_VCAV_EC
GO:0043604	0.219	0.909	4	288	amide biosynthetic process	BP	1	RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:2000026	0.219	0.911	4	560	regulation of multicellular organismal development	BP	1	HOXA11,HOXA9,CAV1,SHOX2	up_VSAP_VSMC
GO:0010466	0.219	0.924	3	32	negative regulation of peptidase activity	BP	1	CST3,RECK,PARK7	down_VCAV_EC
GO:0010951	0.219	0.924	3	32	negative regulation of endopeptidase activity	BP	1	CST3,RECK,PARK7	down_VCAV_EC
GO:0065002	0.219	0.924	3	30	intracellular protein transmembrane transport	BP	1	TRAM1,SRP54,SRP72	down_VSAP_EC
GO:0071806	0.219	0.924	3	30	protein transmembrane transport	BP	1	TRAM1,SRP54,SRP72	down_VSAP_EC
GO:0001817	0.219	0.943	2	182	regulation of cytokine production	BP	1	LYN,SULF1	down_ACOR_EC
GO:0098657	0.219	0.943	2	181	import into cell	BP	1	SPG11,NEDD4	down_ACOR_EC
GO:1903827	0.219	0.944	2	164	regulation of cellular protein localization	BP	1	ACSL3,STX4	down_ACOR_EC
GO:0006821	0.219	0.945	2	18	chloride transport	BP	1	PRNP,CLIC4	down_VCAV_EC
GO:0010823	0.219	0.946	2	17	negative regulation of mitochondrion	BP	1	SLC35F6,CLEC16A	down_VCAV_EC
GO:0010518	0.219	0.949	2	9	positive regulation of phospholipase activity	BP	1	HTR2B,FGFR2	up_ACOR_VSMC
GO:0046850	0.219	0.949	2	9	regulation of bone remodeling	BP	1	LEP,GJA1	up_ACOR_VSMC
GO:0032635	0.219	0.943	2	37	interleukin-6 production	BP	1	LEP,BPI	up_AFEM_EC
GO:0060759	0.219	0.943	2	37	regulation of response to cytokine stimulus	BP	1	CYLD,ADAM17	up_AFEM_EC
GO:0072028	0.219	0.943	2	37	nephron morphogenesis	BP	1	IRX3,GREM1	up_AFEM_EC
GO:0001702	0.219	0.949	2	10	gastrulation with mouth forming second	BP	1	AMOT,HHEX	up_VCAV_EC
GO:0045736	0.219	0.948	2	11	negative regulation of cyclin-dependent protein serine/threonine kinase	BP	1	TNFAIP3,HHEX	up_VCAV_EC
GO:1904030	0.219	0.948	2	11	negative regulation of cyclin-dependent protein	BP	1	TNFAIP3,HHEX	up_VCAV_EC
GO:0003257	0.219	0.982	1	3	positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	down_ACOR_VSMC
GO:0034163	0.219	0.982	1	3	regulation of toll-like receptor 9 signaling	BP	1	HMGB1	down_ACOR_VSMC
GO:0035635	0.219	0.982	1	3	entry of bacterium into host cell	BP	1	CAV1	down_ACOR_VSMC
GO:0045617	0.219	0.982	1	3	negative regulation of keratinocyte	BP	1	HOXA7	down_ACOR_VSMC
GO:2000535	0.219	0.982	1	3	regulation of entry of bacterium into host cell	BP	1	CAV1	down_ACOR_VSMC
GO:0035562	0.219	0.979	1	5	negative regulation of chromatin binding	BP	1	FBH1	down_VCAV_EC
GO:0090085	0.219	0.979	1	5	regulation of protein deubiquitination	BP	1	PARK7	down_VCAV_EC
GO:1904469	0.219	0.979	1	5	positive regulation of tumor necrosis factor	BP	1	MAVS	down_VCAV_EC
GO:0048739	0.219	0.98	1	4	cardiac muscle fiber development	BP	1	NEXN	down_VSAP_EC

GO:0003433	0.219	0.98	1	4	chondrocyte development involved in endochondral bone morphogenesis	BP	1	SERPINH1	down_VSAP_EC
GO:2000641	0.219	0.98	1	4	regulation of early endosome to late	BP	1	MSN	down_VSAP_EC
GO:1901030	0.219	0.98	1	4	positive regulation of mitochondrial outer membrane permeabilization involved	BP	1	SH3GLB1	down_VSAP_EC
GO:0099403	0.219	0.987	1	2	maintenance of mitotic sister chromatid cohesion,	BP	1	ATRX	up_ACOR_VSMC
GO:0099404	0.219	0.987	1	2	mitotic sister chromatid cohesion, telomeric	BP	1	ATRX	up_ACOR_VSMC
GO:1904907	0.219	0.987	1	2	regulation of maintenance of mitotic sister chromatid cohesion, telomeric	BP	1	ATRX	up_ACOR_VSMC
GO:1904908	0.219	0.987	1	2	negative regulation of maintenance of mitotic sister chromatid cohesion,	BP	1	ATRX	up_ACOR_VSMC
GO:0002009	0.219	0.977	1	177	morphogenesis of an epithelium	BP	1	EYA1	up_AFEM_VSMC
GO:0043207	0.219	0.977	1	216	response to external biotic stimulus	BP	1	ARG2	up_AORT_VSMC
GO:0051707	0.219	0.977	1	216	response to other organism	BP	1	ARG2	up_AORT_VSMC
GO:0060322	0.219	0.977	1	193	head development	BP	1	WNT7A	up_AORT_VSMC
GO:2000628	0.219	0.982	1	3	regulation of miRNA metabolic process	BP	1	TENT2	up_VCAV_EC
GO:0060123	0.219	0.987	1	2	regulation of growth hormone secretion	BP	1	CHD7	up_VCAV_EC
GO:0043086	0.219	0.977	1	170	negative regulation of catalytic activity	BP	1	LIMK1	up_VCAV_VSMC
GO:0006638	0.219	0.975	1	30	neutral lipid metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0006639	0.219	0.975	1	30	acylglycerol metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0008625	0.219	0.975	1	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	ARHGEF2	up_VPOR_EC
GO:0043547	0.219	0.975	1	61	positive regulation of GTPase activity	BP	1	TIAM1	up_VFEM_EC
GO:0007249	0.219	0.975	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	NR1H4	up_VPUL_EC
GO:0002573	0.219	0.975	1	71	myeloid leukocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0090130	0.219	0.976	1	121	tissue migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0022409	0.219	0.975	1	56	positive regulation of cell-cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0048754	0.219	0.975	1	57	branching morphogenesis of an epithelial tube	BP	1	HOXA11	up_VSAP_VSMC
GO:0019377	0.219073412	0.97683	1	9	glycolipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0046479	0.219073412	0.97683	1	9	glycosphingolipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0046514	0.219073412	0.97683	1	9	ceramide catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:1904589	0.219178357	0.9434	2	33	regulation of protein import	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0070371	0.219244973	0.90784	4	91	ERK1 and ERK2 cascade	BP	1	SOX9,NDRG2,DUSP26,NRP1	up_ACOR_EC
GO:0030031	0.22	0.849	18	155	cell projection assembly	BP	1	WASF3,SLIT2,ABL1,EMP2,CDC42EP5,FUZ,RILPL2,CDC42EP2,F2RL1,FGD4,E2F4,KIF27,TMEM17,TTC8,EMP3,NCK1,CEP19,BAG4	up_VSAP_EC
GO:0006897	0.22	0.861	12	158	endocytosis	BP	1	VEGFA,MYH9,SERPINE1,ENSCAFG00000003477,CANX,PIK3C2A,TFRC,APOE,GPR107,MYO1E,LRRTM2,ICAM5	down_VSAP_EC
GO:0051348	0.22	0.866	11	90	negative regulation of transferase activity	BP	1	BMP4,EIF4A2,LATS2,CDKN1A,SMPD1,PSEN1,DUSP22,DUSP26,LRRC4,INPP5K,PARK7	up_ACOR_VSMC
GO:0023052	0.22	0.881	9	1602	signaling	BP	1	EYA1,MAP2K6,ENSCAFG00000018194,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,ADCY3	up_VFEM_EC
GO:0050890	0.22	0.89	6	67	cognition	BP	1	SLC1A4,HIF1A,UBA6,APOE,HTT,ARF4	down_VSAP_EC
GO:0002224	0.22	0.9	5	34	toll-like receptor signaling pathway	BP	1	TLR1,TLR3,F2RL1,PTPN22,PRKCE	up_ACOR_VSMC
GO:0050673	0.22	0.897	5	135	epithelial cell proliferation	BP	1	LEP,COL8A2,F3,FAP,ADAM17	up_AFEM_EC

GO:0032944	0.22	0.908	4	48	regulation of mononuclear cell	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0050670	0.22	0.908	4	48	regulation of lymphocyte proliferation	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0072091	0.22	0.912	4	24	regulation of stem cell proliferation	BP	1	FERMT1,SMARCD3,FZD3,DISC1	up_ACOR_VSMC
GO:1903363	0.22	0.924	3	32	negative regulation of cellular protein catabolic	BP	1	PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:0045682	0.22	0.924	3	27	regulation of epidermis development	BP	1	ERRFI1,CTNNB1,INHBA	down_VSAP_EC
GO:0043124	0.22	0.927	3	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	ABL1,NLRX1,MAPKBP1	up_VSAP_EC
GO:0035137	0.22	0.945	2	18	hindlimb morphogenesis	BP	1	BMPR1A,ZBTB16	down_VCAV_EC
GO:0061912	0.22	0.945	2	18	selective autophagy	BP	1	CLEC16A,RETREG1	down_VCAV_EC
GO:0031114	0.22	0.949	2	9	regulation of microtubule depolymerization	BP	1	FGF13,MID1	up_ACOR_VSMC
GO:0002376	0.22	0.948	2	622	immune system process	BP	1	TLR2,HOXA9	up_AFEM_VSMC
GO:0001910	0.22	0.947	2	12	regulation of leukocyte mediated cytotoxicity	BP	1	IL7R,NECTIN2	up_VCAV_EC
GO:0009123	0.22	0.943	2	104	nucleoside monophosphate	BP	1	AK5,FBP1	up_VPOR_EC
GO:0050801	0.22	0.943	2	200	ion homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0022898	0.22	0.975	1	48	regulation of transmembrane	BP	1	NEDD4	down_ACOR_EC
GO:0030595	0.22	0.975	1	57	leukocyte chemotaxis	BP	1	LYN	down_ACOR_EC
GO:0060122	0.22	0.979	1	5	inner ear receptor cell stereocilium organization	BP	1	SDC4	down_VCAV_EC
GO:0007220	0.22	0.98	1	4	Notch receptor processing	BP	1	ADAM17	down_VSAP_EC
GO:0045540	0.22	0.98	1	4	regulation of cholesterol biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:0106118	0.22	0.98	1	4	regulation of sterol biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:0003223	0.22	0.986	1	2	ventricular compact myocardium	BP	1	CHD7	up_ACOR_VSMC
GO:0042692	0.22	0.975	1	105	muscle cell differentiation	BP	1	SGCD	up_AORT_EC
GO:0046879	0.22	0.975	1	63	hormone secretion	BP	1	NR1H4	up_APUL_EC
GO:0032364	0.22	0.982	1	3	oxygen homeostasis	BP	1	HIF1A	up_VCAV_EC
GO:0071731	0.22	0.982	1	3	response to nitric oxide	BP	1	GUCY1B1	up_VCAV_EC
GO:0014070	0.22	0.976	1	172	response to organic cyclic compound	BP	1	CYP1A1	up_VCAV_VSMC
GO:0050769	0.22	0.975	1	95	positive regulation of neurogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051321	0.22	0.975	1	61	meiotic cell cycle	BP	1	CYP26B1	up_VFEM_EC
GO:0060047	0.22	0.975	1	57	heart contraction	BP	1	MAP2K6	up_VFEM_EC
GO:1900449	0.220398667	0.97653	1	9	regulation of glutamate receptor signaling	BP	1	MAPK8IP2	up_ACOR_EC
GO:0034694	0.22059496	0.97649	1	9	response to prostaglandin	BP	1	PTGER4	up_ACOR_EC
GO:0071320	0.220712807	0.97646	1	9	cellular response to cAMP	BP	1	AQP1	up_ACOR_EC
GO:0012501	0.220862132	0.84809	18	561	programmed cell death	BP	1	NR1H4,SOX9,AQP1,FZD5,IFI6,NOD2,CASP10,SMAD6,PAK3,BCL2,USP53,MAPK8IP2,FOXC2,FIGNL1,IFIT2,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0010557	0.221	0.824	47	492	positive regulation of macromolecule biosynthetic process	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,SLC29A1,RFC2,INSIG1,RFC5,RFC3,THRAP3,TRUB2,FAM129B,AURKB,GREM1,RFC4,NEK2,SMARCC1,PCNA,DHX33,CKS2,BRCA1,FASTKD3,EIF5A,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103	down_ACOR_VSMC
GO:0051094	0.221	0.84	23	388	positive regulation of developmental process	BP	1	GPAM,HSPB6,DCN,GLIPR2,BMPR1A,TRPV2,NUMBL,SYDE1,CLSTN1,SEMA3C,PEX5,B4GALT1,GLI3,ZFP36L1,MYDGF,SASH1,RAB7B,DDR2,GREM1,NAPEPLD,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC

GO:0061564	0.221	0.857	14	119	axon development	BP	1	AMIGO1,SLIT2,ABL1,PLXNA4,SHOX2,RTN4RL1,LRP4,DPYSL2,NFIB,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0030099	0.221	0.871	9	133	myeloid cell differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,ZFP36L1,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0030111	0.221	0.872	9	108	regulation of Wnt signaling pathway	BP	1	PRICKLE1,SULF1,ILK,SMARCA4,NXN,APOE,DDIT3,TAX1BP3,DISC1	down_VSAP_EC
GO:0046879	0.221	0.883	7	63	hormone secretion	BP	1	CHD7,GATA3,EDN1,SNAP23,CREB1,MCU,HIF1A	up_VCAV_EC
GO:0051246	0.221	0.892	6	832	regulation of protein metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN,NEDD4	down_ACOR_EC
GO:1903707	0.221	0.891	6	48	negative regulation of hemopoiesis	BP	1	HMGB1,HSPA9,PRMT1,HMGB3,HOXA7,HOXA9	down_ACOR_VSMC
GO:0006355	0.221	0.893	6	974	regulation of transcription, DNA-	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0043409	0.221	0.898	5	54	negative regulation of MAPK cascade	BP	1	PTPN2,APOE,LYN,CBLC,ATF3	down_VSAP_EC
GO:0012501	0.221	0.91	4	561	programmed cell death	BP	1	EYA1,MAP2K6,SIX1,CYP26B1	up_VFEM_EC
GO:0035329	0.221	0.927	3	16	hippo signaling	BP	1	LATS2,WWC2,TEAD1	up_ACOR_VSMC
GO:0019432	0.221	0.948	2	10	triglyceride biosynthetic process	BP	1	SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0046460	0.221	0.948	2	10	neutral lipid biosynthetic process	BP	1	SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0046463	0.221	0.948	2	10	acylglycerol biosynthetic process	BP	1	SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0045934	0.221	0.945	2	407	negative regulation of nucleobase-containing compound metabolic	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0048870	0.221	0.946	2	451	cell motility	BP	1	HDAC7,HSD3B7	down_VPOR_EC
GO:0051674	0.221	0.946	2	451	localization of cell	BP	1	HDAC7,HSD3B7	down_VPOR_EC
GO:0019674	0.221	0.949	2	9	NAD metabolic process	BP	1	NADK,PNP	up_VSAP_EC
GO:0001837	0.221	0.975	1	48	epithelial to mesenchymal transition	BP	1	PDPN	down_ACOR_EC
GO:0045017	0.221	0.975	1	52	glycerolipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0006627	0.221	0.982	1	3	protein processing involved in protein targeting to	BP	1	PMPCA	down_ACOR_VSMC
GO:0015959	0.221	0.982	1	3	diadenosine polyphosphate metabolic	BP	1	NUDT3	down_ACOR_VSMC
GO:0032627	0.221	0.982	1	3	interleukin-23 production	BP	1	RAC1	down_ACOR_VSMC
GO:0032667	0.221	0.982	1	3	regulation of interleukin-23 production	BP	1	RAC1	down_ACOR_VSMC
GO:0060216	0.221	0.982	1	3	definitive hemopoiesis	BP	1	HOXA9	down_ACOR_VSMC
GO:0070813	0.221	0.982	1	3	hydrogen sulfide metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0006002	0.221	0.979	1	5	fructose 6-phosphate metabolic process	BP	1	GFPT2	down_VCAV_EC
GO:0010763	0.221	0.979	1	5	positive regulation of fibroblast migration	BP	1	DDR2	down_VCAV_EC
GO:1901626	0.221	0.979	1	5	regulation of postsynaptic membrane organization	BP	1	CDH2	down_VCAV_EC
GO:0006027	0.221	0.98	1	4	glycosaminoglycan catabolic process	BP	1	CEMIP2	down_VSAP_EC
GO:0010819	0.221	0.98	1	4	regulation of T cell chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:0010820	0.221	0.98	1	4	positive regulation of T cell chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:0031295	0.221	0.982	1	3	T cell costimulation	BP	1	CD274	up_ACOR_VSMC
GO:0035303	0.221	0.975	1	65	regulation of dephosphorylation	BP	1	NPNT	up_APUL_EC
GO:0014820	0.221	0.982	1	3	tonic smooth muscle contraction	BP	1	EDN1	up_VCAV_EC
GO:0014824	0.221	0.982	1	3	artery smooth muscle contraction	BP	1	EDN1	up_VCAV_EC
GO:0055072	0.221	0.975	1	30	iron ion homeostasis	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0030833	0.221	0.975	1	59	regulation of actin filament polymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0010975	0.221	0.975	1	103	regulation of neuron projection development	BP	1	SHOX2	up_VFEM_VSMC

GO:0032259	0.221	0.975	1	71	methylation	BP	1	NR1H4	up_VPUL_EC
GO:0045926	0.221	0.975	1	72	negative regulation of growth	BP	1	TBX5	up_VPUL_EC
GO:0090092	0.221	0.975	1	72	regulation of transmembrane receptor protein serine/threonine	BP	1	NEO1	up_VPUL_EC
GO:0022604	0.221	0.976	1	122	regulation of cell morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0043112	0.221	0.975	1	57	receptor metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0002828	0.221172877	0.97636	1	9	regulation of type 2 immune response	BP	1	NOD2	up_ACOR_EC
GO:0010738	0.221254601	0.97634	1	9	regulation of protein kinase A signaling	BP	1	PDE4A	up_ACOR_EC
GO:0045596	0.221816492	0.88064	7	186	negative regulation of cell differentiation	BP	1	SOX9,DIXDC1,RGMA,SMAD6,LRP4,NRP1,EFEMP1	up_ACOR_EC
GO:0016311	0.222	0.859	13	106	dephosphorylation	BP	1	SH3RF2,PLPP2,NCEH1,PTPN22,NPNT,SMPD1,MARF1,PPP1R26,DUSP26,RPRD1B,INPP5K,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0072522	0.222	0.868	10	91	purine-containing compound biosynthetic process	BP	1	ACLY,PFAS,ELOVL1,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,ATP5F1D	down_ACOR_VSMC
GO:0030097	0.222	0.875	8	244	hemopoiesis	BP	1	HOXA9,LEP,HOXA7,DLL1,NFE2L1,CYLD,EVI2B,BVES	up_AFEM_EC
GO:0009156	0.222	0.889	6	50	ribonucleoside monophosphate	BP	1	PFAS,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:1902904	0.222	0.898	5	38	negative regulation of supramolecular fiber	BP	1	CAPG,LIMA1,STMN1,CORO1A,ARHGEF2	down_ACOR_VSMC
GO:0000079	0.222	0.91	4	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	LATS2,CDKN2B,CDKN1A,CCNT1	up_ACOR_VSMC
GO:2001244	0.222	0.91	4	27	positive regulation of intrinsic apoptotic	BP	1	NACC2,SIAH1,SERINC3,PARK7	up_ACOR_VSMC
GO:0034641	0.222	0.93	4	2171	cellular nitrogen compound metabolic	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0007040	0.222	0.922	3	33	lysosome organization	BP	1	NAGLU,ATP6V0C,ENSCAFG00000017708	down_VCAV_EC
GO:0080171	0.222	0.922	3	33	lytic vacuole organization	BP	1	NAGLU,ATP6V0C,ENSCAFG00000017708	down_VCAV_EC
GO:0036473	0.222	0.923	3	27	cell death in response to oxidative stress	BP	1	P4HB,HIF1A,CTNNB1	down_VSAP_EC
GO:0051897	0.222	0.925	3	20	positive regulation of protein kinase B signaling	BP	1	TEK,HCLS1,GATA3	up_VCAV_EC
GO:0050801	0.222	0.921	3	200	ion homeostasis	BP	1	C3AR1,HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0002066	0.222	0.926	3	17	columnar/cuboidal epithelial cell	BP	1	HNF4A,DLL1,RARG	up_VSAP_EC
GO:0032435	0.222	0.945	2	15	negative regulation of proteasomal ubiquitin-dependent protein	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0051932	0.222	0.948	2	9	synaptic transmission, GABAergic	BP	1	PLCL1,PRKCE	up_ACOR_VSMC
GO:0032878	0.222	0.95	2	8	regulation of establishment or	BP	1	TEK,GATA3	up_VCAV_EC
GO:0002376	0.222	0.947	2	622	immune system process	BP	1	LRRC17,C6	up_VCAV_VSMC
GO:0051962	0.222	0.941	2	112	positive regulation of nervous system	BP	1	ARHGEF2,SEMA3A	up_VPOR_EC
GO:0002262	0.222	0.974	1	54	myeloid cell homeostasis	BP	1	LYN	down_ACOR_EC
GO:0043401	0.222	0.974	1	46	steroid hormone mediated signaling	BP	1	NEDD4	down_ACOR_EC
GO:0046890	0.222	0.974	1	51	regulation of lipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0072531	0.222	0.982	1	3	pyrimidine-containing compound	BP	1	SLC25A19	down_ACOR_VSMC
GO:0048856	0.222	1	1	1533	anatomical structure development	BP	1	GATA5	down_AFEM_VSMC
GO:0048642	0.222	0.978	1	5	negative regulation of skeletal muscle tissue	BP	1	TSC22D3	down_VCAV_EC
GO:0031399	0.222	0.982	1	559	regulation of protein modification process	BP	1	PLCL1	down_VFEM_EC
GO:1900103	0.222	0.978	1	5	positive regulation of endoplasmic reticulum unfolded protein	BP	1	PTPN2	down_VSAP_EC
GO:1903817	0.222	0.982	1	3	negative regulation of voltage-gated potassium	BP	1	KCNE3	up_ACOR_VSMC
GO:0032101	0.222	0.976	1	173	regulation of response to external stimulus	BP	1	TLR2	up_AFEM_VSMC

GO:0050776	0.222	0.976	1	173	regulation of immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0030324	0.222	0.975	1	64	lung development	BP	1	TBX5	up_APUL_EC
GO:0021533	0.222	0.982	1	3	cell differentiation in hindbrain	BP	1	PROX1	up_VCAV_EC
GO:0030853	0.222	0.982	1	3	negative regulation of granulocyte	BP	1	CUL4A	up_VCAV_EC
GO:0051968	0.222	0.986	1	2	positive regulation of synaptic transmission,	BP	1	RELN	up_VCAV_EC
GO:0052200	0.222	0.982	1	3	response to host defenses	BP	1	GUCY1A1	up_VCAV_EC
GO:0075136	0.222	0.982	1	3	response to host	BP	1	GUCY1A1	up_VCAV_EC
GO:0052173	0.222	0.982	1	3	response to defenses of other organism involved in symbiotic interaction	BP	1	GUCY1A1	up_VCAV_EC
GO:1990441	0.222	0.98	1	4	negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP	1	NCK1	up_VCAV_EC
GO:0010817	0.222	0.975	1	102	regulation of hormone levels	BP	1	CYP26B1	up_VPOR_VSMC
GO:1903522	0.222	0.975	1	58	regulation of blood circulation	BP	1	AVPR1A	up_VFEM_EC
GO:2001236	0.222	0.975	1	59	regulation of extrinsic apoptotic signaling	BP	1	EYA1	up_VFEM_EC
GO:1902905	0.222	0.975	1	72	positive regulation of supramolecular fiber	BP	1	CCL24	up_VPUL_EC
GO:2000027	0.222	0.975	1	72	regulation of animal organ morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0006898	0.222	0.975	1	57	receptor-mediated endocytosis	BP	1	CAV1	up_VSAP_VSMC
GO:0042592	0.222275511	0.84862	17	522	homeostatic process	BP	1	CDH3,NR1H4,PLCL1,PKIB,SOX9,PTH1R,AQP1,KCNB1,IFI6,NOD2,FOXC2,SLC9A9,CHMP4B,TP53INP2,TMTC2,PRKACA,PM20D1	up_ACOR_EC
GO:0007612	0.222284462	0.94208	2	33	learning	BP	1	BRSK1,MAPK8IP2	up_ACOR_EC
GO:0048532	0.222571785	0.97604	1	9	anatomical structure arrangement	BP	1	NRP1	up_ACOR_EC
GO:0044091	0.222611712	0.97576	1	10	membrane biogenesis	BP	1	LRP4	up_ACOR_EC
GO:0044237	0.223	0.802	301	3491	cellular metabolic process	BP	1	ELK3,SCD,ACSL3,PRPSAP1,HMGB1,MCM6,RNPS1,SREBF1,ACLY,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,ENSCAFG00000016095,PPRC1,USP4,SF3B2,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,THOP1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,CTDNEP1,RAD54L,POLE,DDX23,HSPA9,NAB2,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,NF2,PFAS,EDC4,AURKB,NONO,HNRNPL,TK1,CDKN2C,TOPBP1,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,RNF152,DIS3,TKT,GMNN,DHCR24,BRCA1,NOC4L,MVD,WDR62,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,PRCP,ELOVL1,FARSA,SU	down_ACOR_VSMC

GO:0010467	0.223	0.805	158	1787	gene expression	BP	1	ELK3,HMGB1,RNPS1,SREBF1,IRAK1,PTBP1,IL F3,DDX39A,CBX5,PPRC1,USP4,SF3B2,ATAD2, HMGA1,EIF4A3,HNRNPUL1,HNRNPD,SREBF2, HINFP,VARS,NEDD4,SRSF2,MED17,U2AF2,IN TS7,MTDH,HEY1,HOXA3,RRBP1,SNRPB2,PPP 1R15B,SF1,SRRT,NOP56,DDX23,NAB2,SLC35 C2,MRPS18B,CDCA7L,FUS,BIRC5,MYBBP1A,I NSIG1,PRMT1,CAV1,CDK1,CASP2,U2AF1,TIM ELESS,THRAP3,TRUB2,FAM129B,TCEA1,AUR KB,NONO,MMP14,HNRNPL,EZH2,GREM1,FBL ,CDK4,SMARCC1,RNASEH2B,PLK3,SFSWAP,D HX33,HOXA7,SMG9,SF3B4,PHF5A,UHRF1,CK S2,DIS3,GMNN,DHCR24,BRCA1,NOC4L,WDR 62,FASTKD3,NOC2L,EIF5A,E2F8,FARSA,ENSC AFG00000015065,PPARD,YBX3,HNRNPF,NCL ,NUP62,MRPL37,FOSL1,SUV39H1,RSL1D1,TH UMPD2,RRP1,ZNF367,CACTIN,HMGB2,DMAP 1,DHX15,CDK2,SMARCB1,DDX39B,CCNA2,EN SCAFG00000005299,EZR,SF3A2,DHX38,RBM 14,RBM17,OSGEP,NOLC1,POLR3F,HOXA10,E RF,ENSCAFG00000019620,TCERG1,RARS,PU M3,SMARCAL1,NOP14,TBX15,ELF4,PRMT5,P SMC1,CTH,NOP58,ARHGEF2,ENSCAFG000000 015189,SUPT16H,TADA2A,PMPCA,WTAP,HA T1,HIST2H2AC,HOXA9,SERPINH1,GLI1,JMJD6 ,H2AFX,WDR33,MRPL18,ENSCAFG00000003	down_ACOR_VSMC
GO:0010558	0.223	0.834	28	392	negative regulation of macromolecule biosynthetic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,ENPP1,CBX5,FH L2,SMARCA4,SESN2,PTPN2,MORF4L2,PEG3, MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,E NSCAFG00000002015,WWC3,KLF5,STRAP,D DIT3,VLDLR,REST,ZMYND8,EIF2S1,HIF1AN,SI X4	down_VSAP_EC
GO:2000147	0.223	0.857	13	169	positive regulation of cell motility	BP	1	ARHGEF2,VEGFA,HSPA5,SERPINE1,SPARC,JC AD,MYO1C,PIK3C2A,HIF1A,ADAM17,PTP4A1, LYN,NRP1	down_VSAP_EC
GO:0007178	0.223	0.857	13	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD6,FERMT1,BMP4,CITED2,CDKN2B,NCE H1,NPNT,TBX20,FUT8,TGFBR1,DUSP22,HPG D,ENSCAFG00000018360	up_ACOR_VSMC
GO:0051272	0.223	0.862	11	170	positive regulation of cellular component	BP	1	PDGFRB,GLIPR2,RHOD,AKT2,SYDE1,SEMA3C, THY1,SASH1,TWIST2,DDR2,RAC2	down_VCAV_EC
GO:0031334	0.223	0.881	7	84	positive regulation of protein complex assembly	BP	1	VEGFA,FSCN1,MSN,ACTR3,CTNNB1,GSK3B,G BP5	down_VSAP_EC
GO:0021953	0.223	0.883	7	49	central nervous system neuron differentiation	BP	1	LEP,FGFR2,LMO4,NRP1,TBX20,PSEN1,CLN8	up_ACOR_VSMC
GO:1903506	0.223	0.892	6	977	regulation of nucleic acid-templated transcription	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0042129	0.223	0.899	5	35	regulation of T cell proliferation	BP	1	LEP,BMP4,PDE5A,CD274,PTPN22	up_ACOR_VSMC
GO:0051492	0.223	0.909	4	28	regulation of stress fiber assembly	BP	1	ARHGEF15,ARHGAP28,MTOR,STMN1	up_VCAV_EC
GO:0006518	0.223	0.907	4	290	peptide metabolic process	BP	1	RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:0043647	0.223	0.925	3	17	inositol phosphate metabolic process	BP	1	PLCG2,PPIP5K1,INPP5K	up_ACOR_VSMC
GO:0007417	0.223	0.942	2	235	central nervous system development	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0021983	0.223	0.946	2	11	pituitary gland development	BP	1	BMP2,CREB1	up_VCAV_EC
GO:2000378	0.223	0.946	2	12	negative regulation of reactive oxygen species	BP	1	CD34,HIF1A	up_VCAV_EC
GO:0031331	0.223	0.941	2	110	positive regulation of cellular catabolic process	BP	1	MTDH,ABHD5	up_VPOR_EC
GO:0060284	0.223	0.942	2	212	regulation of cell development	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0003279	0.223	0.974	1	48	cardiac septum development	BP	1	NRP2	down_ACOR_EC
GO:0010976	0.223	0.974	1	47	positive regulation of neuron projection	BP	1	LYN	down_ACOR_EC
GO:0071265	0.223	0.982	1	3	L-methionine biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0045653	0.223	0.982	1	3	negative regulation of megakaryocyte	BP	1	PRMT1	down_ACOR_VSMC
GO:0034645	0.223	1	1	1546	cellular macromolecule biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0042743	0.223	0.978	1	5	hydrogen peroxide metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0055091	0.223	0.978	1	5	phospholipid homeostasis	BP	1	GPAM	down_VCAV_EC
GO:0006518	0.223	0.977	1	290	peptide metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC

GO:0051046	0.223	0.976	1	174	regulation of secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0030111	0.223	0.975	1	108	regulation of Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:0009914	0.223	0.974	1	64	hormone transport	BP	1	NR1H4	up_APUL_EC
GO:0033500	0.223	0.974	1	64	carbohydrate homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0042593	0.223	0.974	1	64	glucose homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0048736	0.223	0.974	1	66	appendage development	BP	1	TBX5	up_APUL_EC
GO:0060173	0.223	0.974	1	66	limb development	BP	1	TBX5	up_APUL_EC
GO:0003223	0.223	0.986	1	2	ventricular compact myocardium	BP	1	CHD7	up_VCAV_EC
GO:0051105	0.223	0.982	1	3	regulation of DNA ligation	BP	1	HMGB1	up_VCAV_EC
GO:0051106	0.223	0.982	1	3	positive regulation of DNA ligation	BP	1	HMGB1	up_VCAV_EC
GO:2001025	0.223	0.982	1	3	positive regulation of response to drug	BP	1	RIPK1	up_VCAV_EC
GO:0032101	0.223	0.976	1	173	regulation of response to external stimulus	BP	1	C6	up_VCAV_VSMC
GO:0050776	0.223	0.976	1	173	regulation of immune response	BP	1	C6	up_VCAV_VSMC
GO:0003015	0.223	0.974	1	58	heart process	BP	1	MAP2K6	up_VFEM_EC
GO:0071478	0.223	0.974	1	58	cellular response to radiation	BP	1	MME	up_VFEM_EC
GO:0072175	0.223	0.974	1	60	epithelial tube formation	BP	1	SIX1	up_VFEM_EC
GO:0008064	0.223	0.974	1	72	regulation of actin polymerization or	BP	1	CCL24	up_VPUL_EC
GO:0030832	0.223	0.974	1	72	regulation of actin filament length	BP	1	CCL24	up_VPUL_EC
GO:0048511	0.223	0.974	1	72	rhythmic process	BP	1	HTR7	up_VPUL_EC
GO:0016049	0.223	0.975	1	124	cell growth	BP	1	SLIT2	up_VPUL_VSMC
GO:0051261	0.223068342	0.94175	2	33	protein depolymerization	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0060384	0.223076953	0.97593	1	9	innervation	BP	1	NRP1	up_ACOR_EC
GO:0048820	0.223109332	0.97592	1	9	hair follicle maturation	BP	1	CDH3	up_ACOR_EC
GO:0021783	0.22317437	0.97591	1	9	preganglionic parasympathetic fiber	BP	1	NRP1	up_ACOR_EC
GO:2001243	0.223501187	0.94156	2	33	negative regulation of intrinsic apoptotic	BP	1	FIGNL1,CLU	up_ACOR_EC
GO:0030041	0.223746264	0.91989	3	62	actin filament polymerization	BP	1	TMOD1,PAK3,PRKCD	up_ACOR_EC
GO:0045766	0.223922521	0.91976	3	63	positive regulation of angiogenesis	BP	1	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0048583	0.224	0.807	112	1095	regulation of response to stimulus	BP	1	FZD1,NAPEPLD,SEZ6L,CDON,WNT11,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,SLC8B1,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,ABL1,HDAC7,KLKB1,EMP2,DLL1,EPN2,SESN1,OSR1,MAP3K5,IL17RC,PDGFD,TRAFD1,KLF15,C1QTNF2,HPSE,PLXNA4,ANKRD54,CCBE1,STAT6,RECK,KLHL24,PLPP3,F2RL1,GLIS2,PDK2,MFN2,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,SULF2,SHOX2,HIC1,FGD4,RTN4RL1,SASH1,FBXO4,CREBRF,MYD88,LRP4,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,CFD,NPAS2,FBXO7,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CDK9,PRMT2,FBLN1,RNF216,IGFBP6,YPEL3,RAF1,MAPKBP1,ZNF580,CYBA,ZNF205,STX4,PSD4,PQBP1,QARS,ARHGAP12,ACVRL1,UBQLN2,UNC93B1,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,HMOX1,MAP2K2,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,LATS2	up_VSAP_EC

GO:0008219	0.224	0.818	54	611	cell death	BP	1	EPHB1,PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,MAP3K11,STK10,CD34,MEF2C,ATF3,TLR4,GATA3,SNCAIP,TNFAIP8,FIGNL1,PELI1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,ENSCAFG00000010596,MADD,PAK2,PRKD2,THOC1,SH3GLB1,TLR3,NCK1,CASP10,EXOC5,PTGS2,RAPGEF2,ENSCAFG00000005099,PLCG2,BCL10,USP28,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ATP2A1,ARHGEF2	up_VCAV_EC
GO:0043009	0.224	0.847	17	227	chordate embryonic development	BP	1	PRICKLE1,SULF1,PRKACB,SEC24D,TMED2,HOXB7,HIF1A,ZPR1,CTNNB1,PLOD3,MYO1E,SDC4,RBBP8,PRMT1,EXT1,SIX4,RTCB	down_VSAP_EC
GO:0001101	0.224	0.876	8	65	response to acid chemical	BP	1	TIE1,PPARG,PDGFB,YES1,MTOR,ABCA1,PDGFD,ZEB1	up_VCAV_EC
GO:0007599	0.224	0.888	6	48	hemostasis	BP	1	TFPI,TFPI2,CAV1,ITGB3,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0046467	0.224	0.889	6	45	membrane lipid biosynthetic process	BP	1	PIGN,PIGS,UGCG,PIGG,ORMDL3,SMPD1	up_ACOR_VSMC
GO:0002822	0.224	0.889	6	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	TP53BP1,CD274,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0044703	0.224	0.886	6	172	multi-organism reproductive process	BP	1	HOXA9,LEP,THRB,OVOL1,RECK,SPATA6	up_AFEM_EC
GO:1901135	0.224	0.895	5	390	carbohydrate derivative metabolic process	BP	1	OSTC,OGA,AK5,FBP1,GNPNAT1	up_VPOR_EC
GO:0009743	0.224	0.907	4	40	response to carbohydrate	BP	1	NR1H4,SMARCA4,SESN2,HIF1A	down_VSAP_EC
GO:0040012	0.224	0.906	4	303	regulation of locomotion	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1	up_VPOR_EC
GO:0006637	0.224	0.921	3	32	acyl-CoA metabolic process	BP	1	GPAM,ACSS2,ACAT1	down_VCAV_EC
GO:0035383	0.224	0.921	3	32	thioester metabolic process	BP	1	GPAM,ACSS2,ACAT1	down_VCAV_EC
GO:0030510	0.224	0.922	3	27	regulation of BMP signaling pathway	BP	1	SULF1,ILK,NEO1	down_VSAP_EC
GO:0051251	0.224	0.919	3	69	positive regulation of lymphocyte activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0051704	0.224	0.922	3	476	multi-organism process	BP	1	NR1H4,RGS1,MRC1	up_VPUL_EC
GO:0030154	0.224	0.952	2	1040	cell differentiation	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0071867	0.224	0.947	2	9	response to monoamine	BP	1	ADCY6,APLP1	up_ACOR_VSMC
GO:0071868	0.224	0.947	2	9	cellular response to monoamine stimulus	BP	1	ADCY6,APLP1	up_ACOR_VSMC
GO:0071869	0.224	0.947	2	9	response to catecholamine	BP	1	ADCY6,APLP1	up_ACOR_VSMC
GO:0071870	0.224	0.947	2	9	cellular response to catecholamine stimulus	BP	1	ADCY6,APLP1	up_ACOR_VSMC
GO:0009792	0.224	0.942	2	231	embryo development ending in birth or egg	BP	1	HOXA3,HOXA1	up_APUL_EC
GO:0007257	0.224	0.946	2	10	activation of JUN kinase activity	BP	1	MAP3K11,RIPK1	up_VCAV_EC
GO:0051960	0.224	0.942	2	216	regulation of nervous system development	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0002218	0.224	0.974	1	53	activation of innate immune response	BP	1	LYN	down_ACOR_EC
GO:0010921	0.224	0.974	1	46	regulation of phosphatase activity	BP	1	MYO1D	down_ACOR_EC
GO:1905330	0.224	0.974	1	48	regulation of morphogenesis of an	BP	1	SULF1	down_ACOR_EC
GO:0006520	0.224	0.975	1	114	cellular amino acid metabolic process	BP	1	DARS	down_AFEM_EC
GO:0050678	0.224	0.975	1	117	regulation of epithelial cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0048519	0.224	1	1	1554	negative regulation of biological process	BP	1	GATA5	down_AFEM_VSMC
GO:0051246	0.224	0.986	1	832	regulation of protein metabolic process	BP	1	CST3	down_AORT_EC
GO:0007618	0.224	0.978	1	5	mating	BP	1	THRB	down_VCAV_EC
GO:0030728	0.224	0.978	1	5	ovulation	BP	1	FOXO3	down_VCAV_EC
GO:0043584	0.224	0.978	1	5	nose development	BP	1	RDH10	down_VCAV_EC

GO:0051923	0.224	0.979	1	4	sulfation	BP	1	CHSY1	down_VSAP_EC
GO:0030238	0.224	0.979	1	4	male sex determination	BP	1	SIX4	down_VSAP_EC
GO:0043691	0.224	0.979	1	4	reverse cholesterol transport	BP	1	APOE	down_VSAP_EC
GO:0048514	0.224	0.976	1	214	blood vessel morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0071578	0.224	0.981	1	3	zinc ion import across plasma membrane	BP	1	SLC39A8	up_VCAV_EC
GO:2000726	0.224	0.981	1	3	negative regulation of cardiac muscle cell	BP	1	BMP2	up_VCAV_EC
GO:0002009	0.224	0.975	1	177	morphogenesis of an epithelium	BP	1	CA2	up_VCAV_VSMC
GO:0045637	0.224	0.974	1	73	regulation of myeloid cell differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0043583	0.224	0.974	1	59	ear development	BP	1	SALL1	up_VSAP_VSMC
GO:0032528	0.224032312	0.97571	1	9	microvillus organization	BP	1	PLS1	up_ACOR_EC
GO:0099054	0.224231256	0.97567	1	9	presynapse assembly	BP	1	LRP4	up_ACOR_EC
GO:0046879	0.224500351	0.91946	3	63	hormone secretion	BP	1	NR1H4,AQP1,KCNB1	up_ACOR_EC
GO:0006612	0.224625367	0.94095	2	35	protein targeting to membrane	BP	1	KCNB1,CHMP4B	up_ACOR_EC
GO:0048485	0.224791445	0.97554	1	9	sympathetic nervous system development	BP	1	NRP1	up_ACOR_EC
GO:0060562	0.225	0.856	13	120	epithelial tube morphogenesis	BP	1	HOXB7,PODXL,MEF2C,DLL4,GATA3,EDN1,MTSS1,BMP2,HHEX,TIMELESS,BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0002064	0.225	0.87	9	71	epithelial cell development	BP	1	HNF4A,DLL1,ADAMTSL4,RILPL2,RARG,F2RL1,MYD88,FRMD6,E2F4	up_VSAP_EC
GO:0021543	0.225	0.882	7	49	pallium development	BP	1	FGF13,TMEM108,NRP1,PSEN1,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:2001141	0.225	0.891	6	979	regulation of RNA biosynthetic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0061351	0.225	0.905	4	50	neural precursor cell proliferation	BP	1	NUMBL,GLI3,CDH2,FOXO3	down_VCAV_EC
GO:0010817	0.225	0.904	4	102	regulation of hormone levels	BP	1	LEP,CRY2,CCL5,GCNT4	up_AFEM_EC
GO:0007044	0.225	0.908	4	27	cell-substrate junction assembly	BP	1	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0006366	0.225	0.907	4	583	transcription by RNA polymerase II	BP	1	EYA1,HOXA9,HOXA7,SIX1	up_VFEM_EC
GO:0045010	0.225	0.923	3	19	actin nucleation	BP	1	IQGAP2,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0060411	0.225	0.921	3	33	cardiac septum morphogenesis	BP	1	NOTCH2,BMPR1A,SEMA3C	down_VCAV_EC
GO:1903825	0.225	0.924	3	17	organic acid transmembrane transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:1905039	0.225	0.924	3	17	carboxylic acid transmembrane transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:0043067	0.225	0.922	3	479	regulation of programmed cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:1903426	0.225	0.924	3	17	regulation of reactive oxygen species	BP	1	CYBA,ZNF205,ASS1	up_VSAP_EC
GO:0044106	0.225	0.924	3	17	cellular amine metabolic process	BP	1	NAPEPLD,AZIN2,IDO2	up_VSAP_EC
GO:0110111	0.225	0.924	3	17	negative regulation of animal organ	BP	1	THRB,LIMS2,NFIB	up_VSAP_EC
GO:0030224	0.225	0.943	2	18	monocyte differentiation	BP	1	CLSTN1,ZFP36L1	down_VCAV_EC
GO:1903131	0.225	0.943	2	18	mononuclear cell differentiation	BP	1	CLSTN1,ZFP36L1	down_VCAV_EC
GO:0006111	0.225	0.943	2	15	regulation of gluconeogenesis	BP	1	SESN2,PTPN2	down_VSAP_EC
GO:0046326	0.225	0.944	2	15	positive regulation of glucose import	BP	1	NR1H4,PTPN11	down_VSAP_EC
GO:0071364	0.225	0.944	2	14	cellular response to epidermal growth factor	BP	1	PTPN11,ZPR1	down_VSAP_EC
GO:0031343	0.225	0.946	2	10	positive regulation of cell killing	BP	1	F2RL1,B2M	up_ACOR_VSMC
GO:0009913	0.225	0.974	1	47	epidermal cell differentiation	BP	1	HOXA7	down_ACOR_EC
GO:0071219	0.225	0.974	1	50	cellular response to molecule of bacterial	BP	1	LYN	down_ACOR_EC
GO:0090557	0.225	0.981	1	3	establishment of endothelial intestinal	BP	1	RAP2C	down_ACOR_VSMC

GO:0009059	0.225	1	1	1563	macromolecule biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0009892	0.225	0.986	1	835	negative regulation of metabolic process	BP	1	CST3	down_AORT_EC
GO:0060363	0.225	0.978	1	5	cranial suture morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0061309	0.225	0.978	1	5	cardiac neural crest cell development involved in outflow tract	BP	1	SEMA3C	down_VCAV_EC
GO:0035372	0.225	0.979	1	4	protein localization to microtubule	BP	1	MID1	down_VSAP_EC
GO:0002829	0.225	0.979	1	4	negative regulation of type 2 immune response	BP	1	SOCS5	down_VSAP_EC
GO:0072106	0.225	0.979	1	4	regulation of ureteric bud formation	BP	1	SIX4	down_VSAP_EC
GO:0072107	0.225	0.979	1	4	positive regulation of ureteric bud formation	BP	1	SIX4	down_VSAP_EC
GO:1905278	0.225	0.979	1	4	positive regulation of epithelial tube formation	BP	1	SIX4	down_VSAP_EC
GO:2000831	0.225	0.979	1	4	regulation of steroid hormone secretion	BP	1	PTPN11	down_VSAP_EC
GO:0045837	0.225	0.981	1	3	negative regulation of membrane potential	BP	1	BNIP3	up_ACOR_VSMC
GO:0050767	0.225	0.975	1	184	regulation of neurogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0061061	0.225	0.975	1	179	muscle structure development	BP	1	BEND2	up_AFEM_VSMC
GO:0030323	0.225	0.974	1	65	respiratory tube development	BP	1	TBX5	up_APUL_EC
GO:0007494	0.225	0.981	1	3	midgut development	BP	1	EDNRB	up_VCAV_EC
GO:0032351	0.225	0.981	1	3	negative regulation of hormone metabolic	BP	1	BMP2	up_VCAV_EC
GO:0032353	0.225	0.981	1	3	negative regulation of hormone biosynthetic	BP	1	BMP2	up_VCAV_EC
GO:0060753	0.225	0.979	1	4	regulation of mast cell chemotaxis	BP	1	SWAP70	up_VCAV_EC
GO:1900118	0.225	0.981	1	3	negative regulation of execution phase of	BP	1	PAK2	up_VCAV_EC
GO:2001054	0.225	0.981	1	3	negative regulation of mesenchymal cell apoptotic process	BP	1	HIF1A	up_VCAV_EC
GO:0055080	0.225	0.975	1	176	cation homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0032271	0.225	0.974	1	73	regulation of protein polymerization	BP	1	CCL24	up_VPUL_EC
GO:0060541	0.225	0.974	1	73	respiratory system development	BP	1	TBX5	up_VPUL_EC
GO:1902903	0.225	0.974	1	125	regulation of supramolecular fiber	BP	1	SLIT2	up_VPUL_VSMC
GO:2001236	0.225	0.974	1	59	regulation of extrinsic apoptotic signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0022604	0.225047358	0.89356	5	122	regulation of cell morphogenesis	BP	1	BRSK1,RHOU,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0090101	0.225217426	0.94076	2	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:0050767	0.225296654	0.87826	7	184	regulation of neurogenesis	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0032781	0.225719679	0.97504	1	10	positive regulation of ATPase activity	BP	1	DYNC1I1	up_ACOR_EC
GO:0008045	0.225734717	0.97532	1	9	motor neuron axon guidance	BP	1	NRP1	up_ACOR_EC
GO:2001237	0.225777383	0.94059	2	33	negative regulation of extrinsic apoptotic	BP	1	IFI6,NRP1	up_ACOR_EC

GO:0006351	0.226	0.808	96	1069	transcription, DNA-templated	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,AHR,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0044271	0.226	0.856	15	1501	cellular nitrogen compound biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0031396	0.226	0.865	10	90	regulation of protein ubiquitination	BP	1	USP4,UBE2S,U2AF2,SLC29A1,CAV1,FANCI,CDC20,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0006820	0.226	0.869	9	109	anion transport	BP	1	SLC7A5,ENPP1,LRRC8A,SLC38A1,SLC20A1,APOE,CLCN3,SLC7A11,SLC20A2	down_VSAP_EC
GO:0009101	0.226	0.873	8	113	glycoprotein biosynthetic process	BP	1	KRTCAP2,DDOST,GFPT2,NECAB3,B4GALT1,FUT8,RPN2,SOAT1	down_VCAV_EC
GO:0030522	0.226	0.875	8	67	intracellular receptor signaling pathway	BP	1	PRCP,TNFAIP3,TLR4,RIOK3,SMARCA4,LSM14A,UFSP2,KDM3A	up_VCAV_EC
GO:0051262	0.226	0.896	5	40	protein tetramerization	BP	1	GBP5,CDA,ACPP,KCNJ2,ALDH1A3	up_VCAV_EC
GO:0097327	0.226	0.908	4	25	response to antineoplastic agent	BP	1	ATRX,JUP,NR3C1,DDIT4	up_ACOR_VSMC
GO:1904589	0.226	0.92	3	33	regulation of protein import	BP	1	ENSCAFG00000014978,GLI3,MAVS	down_VCAV_EC
GO:0046887	0.226	0.924	3	18	positive regulation of hormone secretion	BP	1	TM7SF3,PRKCE,EDN1	up_ACOR_VSMC
GO:0050863	0.226	0.919	3	69	regulation of T cell activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0035924	0.226	0.922	3	21	cellular response to vascular endothelial growth factor stimulus	BP	1	DLL4,PRKD2,JCAD	up_VCAV_EC
GO:0042310	0.226	0.922	3	21	vasoconstriction	BP	1	EDNRB,DOCK4,EDN1	up_VCAV_EC
GO:0097756	0.226	0.922	3	21	negative regulation of blood vessel diameter	BP	1	EDNRB,DOCK4,EDN1	up_VCAV_EC
GO:1902532	0.226	0.919	3	204	negative regulation of intracellular signal	BP	1	ARHGEF2,ASPN,FBP1	up_VPOR_EC
GO:0044088	0.226	0.924	3	17	regulation of vacuole organization	BP	1	PIP4K2B,UBQLN2,NPRL3	up_VSAP_EC
GO:0098771	0.226	0.941	2	180	inorganic ion homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0016192	0.226	0.943	2	452	vesicle-mediated transport	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:0002548	0.226	0.943	2	17	monocyte chemotaxis	BP	1	SERPINE1,LYN	down_VSAP_EC
GO:1902235	0.226	0.943	2	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	HYOU1,PTPN2	down_VSAP_EC
GO:0010033	0.226	0.948	2	772	response to organic substance	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0001541	0.226	0.944	2	12	ovarian follicle development	BP	1	KIT,EIF2B2	up_VCAV_EC
GO:0048050	0.226	0.981	1	3	post-embryonic eye morphogenesis	BP	1	HMGN1	down_ACOR_VSMC
GO:1900122	0.226	0.981	1	3	positive regulation of receptor binding	BP	1	HOXA3	down_ACOR_VSMC
GO:0032956	0.226	0.974	1	116	regulation of actin cytoskeleton organization	BP	1	FSCN1	down_AFEM_EC
GO:0045787	0.226	0.974	1	117	positive regulation of cell cycle	BP	1	GPSM2	down_AFEM_EC
GO:1901524	0.226	0.977	1	5	regulation of mitophagy	BP	1	CLEC16A	down_VCAV_EC
GO:0009306	0.226	0.974	1	127	protein secretion	BP	1	RAB11B	down_VPOR_EC
GO:0045940	0.226	0.979	1	4	positive regulation of steroid metabolic process	BP	1	APOE	down_VSAP_EC
GO:0060681	0.226	0.979	1	4	branch elongation involved in ureteric bud	BP	1	SIX4	down_VSAP_EC

GO:0006560	0.226	0.979	1	4	proline metabolic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0045944	0.226	0.977	1	287	positive regulation of transcription by RNA polymerase II	BP	1	GATA5	down_VSAP_VSMC
GO:0006172	0.226	0.981	1	3	ADP biosynthetic process	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0009133	0.226	0.981	1	3	nucleoside diphosphate biosynthetic process	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0009136	0.226	0.981	1	3	purine nucleoside diphosphate biosynthetic	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0009180	0.226	0.981	1	3	purine ribonucleoside diphosphate biosynthetic	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0009188	0.226	0.981	1	3	ribonucleoside diphosphate biosynthetic	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0032868	0.226	0.974	1	66	response to insulin	BP	1	NR1H4	up_APUL_EC
GO:0035148	0.226	0.974	1	66	tube formation	BP	1	HOXA1	up_APUL_EC
GO:0010212	0.226	0.974	1	60	response to ionizing radiation	BP	1	EYA1	up_VFEM_EC
GO:0007409	0.226	0.974	1	109	axonogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0070507	0.226	0.974	1	73	regulation of microtubule cytoskeleton organization	BP	1	ARHGEF2	up_VPUL_EC
GO:0003056	0.226	0.981	1	3	regulation of vascular smooth muscle	BP	1	CHRM1	up_VSAP_EC
GO:0071216	0.226	0.973	1	61	cellular response to biotic stimulus	BP	1	TLR2	up_VSAP_VSMC
GO:0009953	0.226222485	0.94033	2	34	dorsal/ventral pattern formation	BP	1	SMAD6,LRP4	up_ACOR_EC
GO:0032727	0.226557065	0.97513	1	9	positive regulation of interferon-alpha	BP	1	MAVS	up_ACOR_EC
GO:0022610	0.227	0.825	35	326	biological adhesion	BP	1	HOXA7,PCDH19,SERPINB8,FAM107A,CD274,ACKR3,AMIGO1,RADIL,LIMS2,HOXD3,CDH1,ABL1,EMP2,DLL1,HPSE,CLDN1,ZBTB16,PLPP3,ZFP36L1,PIK3R1,TIAM1,TFE3,ECM2,WISP2,CD83,FBLN1,PNP,STX4,ACVRL1,ASS1,FLOT1,NCK1,TGFBR2,CITED2,BAG4	up_VSAP_EC
GO:0006629	0.227	0.835	23	382	lipid metabolic process	BP	1	GPAM,PDGFRB,ENSCAFG00000014978,AKT2,LCAT,ACAA1,HSD3B7,SCP2,PLCL1,CYB5R3,THNSL2,PIGS,CYP1B1,PEX5,RETSAT,ABHD15,ORMDL3,ENSCAFG00000017708,RDH10,LONP2,NAPEPLD,SOAT1,ACAT1	down_VCAV_EC
GO:0008361	0.227	0.88	7	50	regulation of cell size	BP	1	CLCN3,SLC12A7,LRRC8C,NRP1,ULK2,CLN8,EDN1	up_ACOR_VSMC
GO:0032868	0.227	0.893	5	66	response to insulin	BP	1	ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0043270	0.227	0.894	5	56	positive regulation of ion transport	BP	1	KIF5B,APOE,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0070169	0.227	0.923	3	18	positive regulation of biomineral tissue	BP	1	BMP4,ISG15,SLC8A1	up_ACOR_VSMC
GO:0014013	0.227	0.923	3	19	regulation of gliogenesis	BP	1	PRKCH,MTOR,BMP2	up_VCAV_EC
GO:0048747	0.227	0.922	3	20	muscle fiber development	BP	1	PPP3CA,CAV2,P2RX2	up_VCAV_EC
GO:0032270	0.227	0.921	3	479	positive regulation of cellular protein metabolic	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0071466	0.227	0.923	3	17	cellular response to xenobiotic stimulus	BP	1	HNF4A,NCEH1,DDIT4	up_VSAP_EC
GO:0070830	0.227	0.943	2	14	bicellular tight junction assembly	BP	1	MYO1C,CTNNB1	down_VSAP_EC
GO:0120192	0.227	0.943	2	14	tight junction assembly	BP	1	MYO1C,CTNNB1	down_VSAP_EC
GO:0086003	0.227	0.946	2	10	cardiac muscle cell contraction	BP	1	KCNE3,JUP	up_ACOR_VSMC
GO:0016525	0.227	0.94	2	38	negative regulation of angiogenesis	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:1902904	0.227	0.94	2	38	negative regulation of supramolecular fiber	BP	1	CRYAB,KANK1	up_AFEM_EC
GO:2000181	0.227	0.94	2	38	negative regulation of blood vessel	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:0070887	0.227	0.948	2	775	cellular response to chemical stimulus	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0046465	0.227	0.981	1	3	dolichyl diphosphate metabolic process	BP	1	NUS1	down_ACOR_VSMC
GO:0006489	0.227	0.981	1	3	dolichyl diphosphate biosynthetic process	BP	1	NUS1	down_ACOR_VSMC
GO:0010878	0.227	0.981	1	3	cholesterol storage	BP	1	SREBF2	down_ACOR_VSMC

GO:0051315	0.227	0.981	1	3	attachment of mitotic spindle microtubules to	BP	1	NDC80	down_ACOR_VSMC
GO:0007501	0.227	0.977	1	5	mesodermal cell fate specification	BP	1	BMPR1A	down_VCAV_EC
GO:0045623	0.227	0.977	1	5	negative regulation of T-helper cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0050779	0.227	0.977	1	5	RNA destabilization	BP	1	ZFP36L1	down_VCAV_EC
GO:0061157	0.227	0.977	1	5	mRNA destabilization	BP	1	ZFP36L1	down_VCAV_EC
GO:0010875	0.227	0.979	1	4	positive regulation of cholesterol efflux	BP	1	APOE	down_VSAP_EC
GO:0032352	0.227	0.979	1	4	positive regulation of hormone metabolic	BP	1	HIF1A	down_VSAP_EC
GO:0045625	0.227	0.979	1	4	regulation of T-helper 1 cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0051890	0.227	0.979	1	4	regulation of cardioblast differentiation	BP	1	PRICKLE1	down_VSAP_EC
GO:2001222	0.227	0.974	1	11	regulation of neuron migration	BP	1	CAMK2A	up_AFEM_EC
GO:0051223	0.227	0.975	1	181	regulation of protein transport	BP	1	TLR2	up_AFEM_VSMC
GO:0031098	0.227	0.974	1	109	stress-activated protein kinase signaling cascade	BP	1	TAOK1	up_AORT_EC
GO:0060249	0.227	0.974	1	110	anatomical structure homeostasis	BP	1	TAOK1	up_AORT_EC
GO:0000122	0.227	0.975	1	218	negative regulation of transcription by RNA polymerase II	BP	1	ESR1	up_AORT_VSMC
GO:0042063	0.227	0.973	1	67	gliogenesis	BP	1	NTRK2	up_APUL_EC
GO:0002836	0.227	0.979	1	4	positive regulation of response to tumor cell	BP	1	NECTIN2	up_VCAV_EC
GO:0002839	0.227	0.979	1	4	positive regulation of immune response to	BP	1	NECTIN2	up_VCAV_EC
GO:0060509	0.227	0.981	1	3	type I pneumocyte differentiation	BP	1	CREB1	up_VCAV_EC
GO:0040008	0.227	0.975	1	179	regulation of growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0065002	0.227	0.973	1	30	intracellular protein transmembrane transport	BP	1	SRP54	up_VPOR_EC
GO:0071806	0.227	0.973	1	30	protein transmembrane transport	BP	1	SRP54	up_VPOR_EC
GO:0090100	0.227	0.973	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ACVR2A	up_VPOR_EC
GO:1901222	0.227	0.973	1	32	regulation of NIK/NF-kappaB signaling	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0045765	0.227	0.974	1	105	regulation of angiogenesis	BP	1	C3AR1	up_VPOR_VSMC
GO:0007369	0.227	0.973	1	63	gastrulation	BP	1	EYA1	up_VFEM_EC
GO:0010810	0.227	0.973	1	60	regulation of cell-substrate adhesion	BP	1	HOXA7	up_VFEM_EC
GO:0061041	0.227017773	0.93998	2	34	regulation of wound healing	BP	1	FOXC2,PRKCD	up_ACOR_EC
GO:0071482	0.227804137	0.93964	2	34	cellular response to light stimulus	BP	1	AQP1,MFAP4	up_ACOR_EC
GO:0071216	0.227936963	0.91769	3	61	cellular response to biotic stimulus	BP	1	NR1H4,FZD5,NOD2	up_ACOR_EC
GO:0003008	0.228	0.833	24	336	system process	BP	1	SULF1,SLC1A4,TPM4,PTPN11,AARS,PRCP,PTGS2,RPGR,HIF1A,HTR7,UBA6,ACTA2,APOE,PLOD3,UBA5,STRAP,MYO1E,HTT,CALM1,RAB11FIP1,INHBA,ARF4,MYBPC2,HOMER1	down_VSAP_EC
GO:0001816	0.228	0.837	22	194	cytokine production	BP	1	TLR1,PLCG2,LEP,CD83,HTR2B,MBP,FERMT1,ABCA1,ELF1,TLR3,ISG15,CD274,NDRG2,F2RL1,PTPN22,APP,NOD2,B2M,SCAMP5,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0014070	0.228	0.84	20	172	response to organic cyclic compound	BP	1	LBH,CD83,SKP2,BMP4,MED14,TLR3,AR,FAM210B,ADCY6,AKAP6,P2RX7,CREBRF,APLP1,PRKCE,JUP,NR3C1,FAM107A,DDIT4,INPP5K,PARK7	up_ACOR_VSMC
GO:0040013	0.228	0.877	7	100	negative regulation of locomotion	BP	1	DCN,BMPR1A,RECK,TRIM8,THY1,SPRED1,FOXO3	down_VCAV_EC
GO:0044260	0.228	0.9	7	2593	cellular macromolecule metabolic process	BP	1	CST3,HDAC7,CITED2,RAB11B,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:1903039	0.228	0.886	6	43	positive regulation of leukocyte cell-cell	BP	1	CD274,ZBTB16,CD83,PNP,NCK1,TGFBR2	up_VSAP_EC

GO:0090090	0.228	0.886	6	44	negative regulation of canonical Wnt signaling	BP	1	FZD1,WNT11,AXIN2,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0009953	0.228	0.896	5	34	dorsal/ventral pattern formation	BP	1	SMAD6,BMP4,TBX20,PSEN1,EDN1	up_ACOR_VSMC
GO:0009749	0.228	0.895	5	34	response to glucose	BP	1	PRKAA2,LPL,PRKCE,RAB11B,PFKL	up_ACOR_VSMC
GO:0030073	0.228	0.904	4	42	insulin secretion	BP	1	NR1H4,PTPN11,HIF1A,REST	down_VSAP_EC
GO:1901568	0.228	0.907	4	26	fatty acid derivative metabolic process	BP	1	CYP2J2,EDN1,HPGD,ELOVL7	up_ACOR_VSMC
GO:0051209	0.228	0.906	4	28	release of sequestered calcium ion into cytosol	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0051283	0.228	0.906	4	28	negative regulation of sequestering of calcium	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0006720	0.228	0.907	4	25	isoprenoid metabolic process	BP	1	DHRS4,RETSAT,DHRS9,MVK	up_VSAP_EC
GO:0042100	0.228	0.922	3	19	B cell proliferation	BP	1	MNDA,TFRC,CTPS1	down_ACOR_VSMC
GO:0032611	0.228	0.923	3	17	interleukin-1 beta production	BP	1	ABCA1,F2RL1,NOD2	up_ACOR_VSMC
GO:0090303	0.228	0.922	3	18	positive regulation of wound healing	BP	1	SELP,TLR4,MTOR	up_VCAV_EC
GO:2000113	0.228	0.92	3	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0007422	0.228	0.941	2	18	peripheral nervous system development	BP	1	NAB2,AKT2	down_VCAV_EC
GO:0021872	0.228	0.941	2	19	forebrain generation of neurons	BP	1	NUMBL,GLI3	down_VCAV_EC
GO:0050789	0.228	1	2	3295	regulation of biological process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0007498	0.228	0.939	2	38	mesoderm development	BP	1	IRX3,OVOL1	up_AFEM_EC
GO:0010906	0.228	0.939	2	38	regulation of glucose metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0003158	0.228	0.939	2	38	endothelium development	BP	1	DLL1,TMEM100	up_AFEM_EC
GO:0032879	0.228	0.947	2	767	regulation of localization	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0032940	0.228	0.94	2	231	secretion by cell	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0032024	0.228	0.944	2	12	positive regulation of insulin secretion	BP	1	MCU,HIF1A	up_VCAV_EC
GO:0090277	0.228	0.944	2	12	positive regulation of peptide hormone	BP	1	MCU,HIF1A	up_VCAV_EC
GO:0048666	0.228	0.941	2	258	neuron development	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0051480	0.228	0.973	1	50	regulation of cytosolic calcium ion concentration	BP	1	LYN	down_ACOR_EC
GO:1990481	0.228	0.981	1	3	mRNA pseudouridine synthesis	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0006449	0.228	0.981	1	3	regulation of translational termination	BP	1	EIF5A	down_ACOR_VSMC
GO:0060017	0.228	0.981	1	3	parathyroid gland development	BP	1	HOXA3	down_ACOR_VSMC
GO:0000377	0.228	0.974	1	119	RNA splicing, via transesterification reactions with bulged	BP	1	SRSF6	down_AFEM_EC
GO:0000398	0.228	0.974	1	119	mRNA splicing, via spliceosome	BP	1	SRSF6	down_AFEM_EC
GO:0010801	0.228	0.977	1	5	negative regulation of peptidyl-threonine	BP	1	SPRED1	down_VCAV_EC
GO:0002691	0.228	0.977	1	5	regulation of cellular extravasation	BP	1	THY1	down_VCAV_EC
GO:0021895	0.228	0.977	1	5	cerebral cortex neuron differentiation	BP	1	PEX5	down_VCAV_EC
GO:0035907	0.228	0.977	1	5	dorsal aorta development	BP	1	BMPR1A	down_VCAV_EC
GO:0035912	0.228	0.977	1	5	dorsal aorta morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0048261	0.228	0.977	1	5	negative regulation of receptor-mediated	BP	1	LRPAP1	down_VCAV_EC
GO:1900424	0.228	0.977	1	5	regulation of defense response to bacterium	BP	1	CYBA	down_VCAV_EC
GO:0048608	0.228	0.974	1	129	reproductive structure development	BP	1	CITED2	down_VPOR_EC
GO:0051656	0.228	0.974	1	129	establishment of organelle localization	BP	1	RAB11B	down_VPOR_EC
GO:0009892	0.228	0.985	1	835	negative regulation of metabolic process	BP	1	GATA5	down_VFEM_VSMC

GO:0002551	0.228	0.977	1	5	mast cell chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0045742	0.228	0.978	1	4	positive regulation of epidermal growth factor receptor signaling	BP	1	ADAM17	down_VSAP_EC
GO:0061046	0.228	0.978	1	4	regulation of branching involved in lung	BP	1	CTNNB1	down_VSAP_EC
GO:0061047	0.228	0.978	1	4	positive regulation of branching involved in lung	BP	1	CTNNB1	down_VSAP_EC
GO:0097531	0.228	0.977	1	5	mast cell migration	BP	1	VEGFA	down_VSAP_EC
GO:0034383	0.228	0.978	1	4	low-density lipoprotein particle clearance	BP	1	NR1H4	down_VSAP_EC
GO:0060685	0.228	0.978	1	4	regulation of prostatic bud formation	BP	1	SULF1	down_VSAP_EC
GO:0060686	0.228	0.978	1	4	negative regulation of prostatic bud formation	BP	1	SULF1	down_VSAP_EC
GO:0071073	0.228	0.978	1	4	positive regulation of phospholipid biosynthetic	BP	1	NR1H4	down_VSAP_EC
GO:0003205	0.228	0.973	1	67	cardiac chamber development	BP	1	TBX5	up_APUL_EC
GO:0030278	0.228	0.973	1	66	regulation of ossification	BP	1	NPNT	up_APUL_EC
GO:0030522	0.228	0.973	1	67	intracellular receptor signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0021683	0.228	0.981	1	3	cerebellar granular layer morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0045161	0.228	0.985	1	2	neuronal ion channel clustering	BP	1	SPTBN4	up_VCAV_EC
GO:0045162	0.228	0.985	1	2	clustering of voltage-gated sodium channels	BP	1	SPTBN4	up_VCAV_EC
GO:1901727	0.228	0.981	1	3	positive regulation of histone deacetylase	BP	1	PRKD2	up_VCAV_EC
GO:0097198	0.228	0.985	1	2	histone H3-K36 trimethylation	BP	1	IWS1	up_VCAV_EC
GO:0042493	0.228	0.975	1	178	response to drug	BP	1	CA2	up_VCAV_VSMC
GO:0000041	0.228	0.973	1	31	transition metal ion transport	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0006939	0.228	0.973	1	32	smooth muscle contraction	BP	1	HTR7	up_VPOR_EC
GO:2001237	0.228	0.973	1	33	negative regulation of extrinsic apoptotic	BP	1	ARHGEF2	up_VPOR_EC
GO:0007517	0.228	0.974	1	100	muscle organ development	BP	1	SHOX2	up_VFEM_VSMC
GO:0008356	0.228	0.981	1	3	asymmetric cell division	BP	1	ZBTB16	up_VSAP_EC
GO:0032941	0.228177587	0.97447	1	10	secretion by tissue	BP	1	AQP1	up_ACOR_EC
GO:0045927	0.228470051	0.91741	3	61	positive regulation of growth	BP	1	PLS1,TBX5,NRP1	up_ACOR_EC
GO:0051046	0.229	0.843	17	174	regulation of secretion	BP	1	MEF2C,FERMT1,CHD7,TLR4,STC1,GATA3,EDN1,RAB27A,SNCAIP,ARG2,RSC1A1,CD200,FES,CREB1,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0051272	0.229	0.852	13	170	positive regulation of cellular component movement	BP	1	ARHGEF2,VEGFA,HSPA5,SERPINE1,SPARC,JCAD,MYO1C,PIK3C2A,HIF1A,ADAM17,PTP4A1,LYN,NRP1	down_VSAP_EC
GO:0007033	0.229	0.883	6	82	vacuole organization	BP	1	NAGLU,GABARAP,WDR45,ATP6V0C,EMC6,ENSCAFG00000017708	down_VCAV_EC
GO:0033865	0.229	0.886	6	43	nucleoside bisphosphate metabolic process	BP	1	ACSM3,ACACB,PDK2,ACSS2,MVK,DCAKD	up_VSAP_EC
GO:0033875	0.229	0.886	6	43	ribonucleoside bisphosphate metabolic	BP	1	ACSM3,ACACB,PDK2,ACSS2,MVK,DCAKD	up_VSAP_EC
GO:0034032	0.229	0.886	6	43	purine nucleoside bisphosphate metabolic	BP	1	ACSM3,ACACB,PDK2,ACSS2,MVK,DCAKD	up_VSAP_EC
GO:0030879	0.229	0.895	5	34	mammary gland development	BP	1	LBH,BMP4,FGFR2,GJA1,RREB1	up_ACOR_VSMC
GO:0009743	0.229	0.894	5	40	response to carbohydrate	BP	1	CALCRL,MAPK13,SMARCA4,HIF1A,P2RX2	up_VCAV_EC
GO:0045185	0.229	0.906	4	25	maintenance of protein location	BP	1	OS9,DAG1,SUN1,PARK7	up_ACOR_VSMC
GO:0031623	0.229	0.905	4	31	receptor internalization	BP	1	SELE,CXCL8,CALCRL,PLCG2	up_VCAV_EC
GO:0006886	0.229	0.918	3	332	intracellular protein transport	BP	1	IPO7,STX4,NEDD4	down_ACOR_EC
GO:0045638	0.229	0.918	3	33	negative regulation of myeloid cell	BP	1	FBN1,ZFP36L1,ZBTB16	down_VCAV_EC
GO:0072078	0.229	0.919	3	33	nephron tubule morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC

GO:2001235	0.229	0.917	3	69	positive regulation of apoptotic signaling	BP	1	MLLT11,PLAGL2,CYLD	up_AFEM_EC
GO:0032507	0.229	0.922	3	18	maintenance of protein location in cell	BP	1	MORC3,CIZ1,TAF8	up_VSAP_EC
GO:0070252	0.229	0.922	3	17	actin-mediated cell contraction	BP	1	EMP2,KCNE3,FRMD6	up_VSAP_EC
GO:0048489	0.229	0.939	2	38	synaptic vesicle transport	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0097480	0.229	0.939	2	38	establishment of synaptic vesicle localization	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0009607	0.229	0.94	2	232	response to biotic stimulus	BP	1	NR1H4,BPI	up_APUL_EC
GO:0060260	0.229	0.943	2	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	IRF8,HMGB1	up_VCAV_EC
GO:0022618	0.229	0.939	2	111	ribonucleoprotein complex assembly	BP	1	RSL24D1,RPL10L	up_VPOR_EC
GO:0042127	0.229	0.942	2	452	regulation of cell proliferation	BP	1	HOXA3,TBX5	up_VPUL_VSMC
GO:0042104	0.229	0.98	1	3	positive regulation of activated T cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0033036	0.229	0.985	1	852	macromolecule localization	BP	1	SCAMP4	down_AORT_EC
GO:0007340	0.229	0.977	1	5	acrosome reaction	BP	1	B4GALT1	down_VCAV_EC
GO:0021670	0.229	0.977	1	5	lateral ventricle development	BP	1	NUMBL	down_VCAV_EC
GO:0043217	0.229	0.977	1	5	myelin maintenance	BP	1	AKT2	down_VCAV_EC
GO:0014014	0.229	0.978	1	4	negative regulation of gliogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0045603	0.229	0.977	1	5	positive regulation of endothelial cell	BP	1	CTNNB1	down_VSAP_EC
GO:0048102	0.229	0.98	1	3	autophagic cell death	BP	1	TP53INP1	up_ACOR_VSMC
GO:0040018	0.229	0.974	1	11	positive regulation of multicellular organism	BP	1	GPAM	up_AFEM_EC
GO:1901987	0.229	0.973	1	107	regulation of cell cycle phase transition	BP	1	TAOK1	up_AORT_EC
GO:0007254	0.229	0.973	1	67	JNK cascade	BP	1	MAPK10	up_APUL_EC
GO:0009952	0.229	0.973	1	66	anterior/posterior pattern specification	BP	1	HOXA3	up_APUL_EC
GO:0035587	0.229	0.981	1	3	purinergic receptor signaling pathway	BP	1	ACPP	up_VCAV_EC
GO:0071865	0.229	0.98	1	3	regulation of apoptotic process in bone marrow	BP	1	PLK2	up_VCAV_EC
GO:0071866	0.229	0.98	1	3	negative regulation of apoptotic process in bone	BP	1	PLK2	up_VCAV_EC
GO:0072393	0.229	0.981	1	3	microtubule anchoring at microtubule organizing	BP	1	HOOK3	up_VCAV_EC
GO:0099550	0.229	0.98	1	3	trans-synaptic signaling, modulating synaptic	BP	1	GUCY1A1	up_VCAV_EC
GO:0098609	0.229	0.974	1	181	cell-cell adhesion	BP	1	GATA5	up_VCAV_VSMC
GO:0042692	0.229	0.973	1	105	muscle cell differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0090235	0.229	0.981	1	3	regulation of metaphase plate congression	BP	1	TTL	up_VSAP_EC
GO:0046903	0.229686383	0.86478	9	255	secretion	BP	1	NR1H4,AQP1,KCNB1,FZD5,NOD2,CFI,PTGER4,PREB,MAVS	up_ACOR_EC
GO:0048869	0.23	0.812	61	1119	cellular developmental process	BP	1	NOTCH2,PDGFRB,LRP1,NAB2,NDN,ANGPT1,SDC4,VASN,FBN1,GLIPR2,BMPR1A,LMO4,TRPV2,ANPEP,COL6A1,CLIP3,NUMBL,NAGLU,AKT2,TFE3,LAMA3,CLSTN1,CSPG4,PRMT6,PRELP,SEMA3C,POLDIP2,THY1,PEX5,TLX2,B4GALT1,GLI3,ADAMTSL4,EEF2,ZFP36L1,NCDN,RBM38,CDH2,LOXL3,GSDME,CAMK2D,ENSCAFG00000017708,SPRED1,RAB7B,A2M,IRX5,UST,GLIS2,TWIST2,PRKCSH,DDR2,RDH10,GREM1,NAPEPLD,FOXO3,SOAT1,THRB,ZBTB16,ANKRD54,RGMA,BRSK1	down_VCAV_EC
GO:0008150	0.23	0.892	30	5646	biological_process	BP	1	ACVRL1,YEATS2,LYN,HOXA3,IGF1R,ACSL4,SPG11,PDPN,NRP2,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,IPO7,RPSA,ATRIP,ANPEP,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,STX4,MYO1D,HOXC4,TNRC6B,ASPN,NEDD4	down_ACOR_EC

GO:0006812	0.23	0.849	14	222	cation transport	BP	1	PRNP,FXYD1,TRPV2,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SCARA5,TPC3,CYBA,ARHGAP1,PACSIN3	down_VCAV_EC
GO:0002764	0.23	0.863	10	80	immune response-regulating signaling	BP	1	TLR1,PLCG2,ELF1,TLR3,F2RL1,PTPN22,PRKCE,PSEN1,DUSP22,NOD2	up_ACOR_VSMC
GO:0010595	0.23	0.878	7	52	positive regulation of endothelial cell migration	BP	1	ABL1,HDAC7,CCBE1,STAT5A,SASH1,ZNF580,HMOX1	up_VSAP_EC
GO:0006282	0.23	0.885	6	48	regulation of DNA repair	BP	1	HMGB1,USP1,PARPBP,RAD51,TIMELESS,PCNA	down_ACOR_VSMC
GO:0032101	0.23	0.882	6	173	regulation of response to external stimulus	BP	1	CMKLR1,LEP,PLXNA4,NAPEPLD,CCL5,ADAM17	up_AFEM_EC
GO:0043467	0.23	0.894	5	35	regulation of generation of precursor metabolites	BP	1	PPARGC1A,BNIP3,DDIT4,INPP5K,PARK7	up_ACOR_VSMC
GO:0060606	0.23	0.904	4	39	tube closure	BP	1	PRICKLE1,PRKACB,TMED2,SDC4	down_VSAP_EC
GO:0005977	0.23	0.919	3	26	glycogen metabolic process	BP	1	ENPP1,PPP1R3C,GSK3B	down_VSAP_EC
GO:0006073	0.23	0.919	3	26	cellular glucan metabolic process	BP	1	ENPP1,PPP1R3C,GSK3B	down_VSAP_EC
GO:0044042	0.23	0.919	3	26	glucan metabolic process	BP	1	ENPP1,PPP1R3C,GSK3B	down_VSAP_EC
GO:0045668	0.23	0.943	2	11	negative regulation of osteoblast differentiation	BP	1	GREM1,TWIST2	down_ACOR_VSMC
GO:0050854	0.23	0.941	2	16	regulation of antigen receptor-mediated	BP	1	PTPN2,LYN	down_VSAP_EC
GO:0032958	0.23	0.945	2	9	inositol phosphate biosynthetic process	BP	1	PLCG2,PPIP5K1	up_ACOR_VSMC
GO:0033137	0.23	0.944	2	10	negative regulation of peptidyl-serine	BP	1	RASSF2,INPP5K	up_ACOR_VSMC
GO:0001944	0.23	0.939	2	263	vasculature development	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:0048534	0.23	0.94	2	262	hematopoietic or lymphoid organ	BP	1	HOXA3,EVI2B	up_VPUL_EC
GO:0048870	0.23	0.942	2	451	cell motility	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0051674	0.23	0.942	2	451	localization of cell	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0001764	0.23	0.973	1	45	neuron migration	BP	1	NRP2	down_ACOR_EC
GO:0008654	0.23	0.973	1	58	phospholipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0006432	0.23	0.98	1	3	phenylalanyl-tRNA aminoacylation	BP	1	FARSA	down_ACOR_VSMC
GO:0006534	0.23	0.98	1	3	cysteine metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0034370	0.23	0.98	1	3	triglyceride-rich lipoprotein particle	BP	1	LIPC	down_ACOR_VSMC
GO:0034372	0.23	0.98	1	3	very-low-density lipoprotein particle	BP	1	LIPC	down_ACOR_VSMC
GO:0035234	0.23	0.98	1	3	ectopic germ cell programmed cell death	BP	1	CASP2	down_ACOR_VSMC
GO:0072526	0.23	0.98	1	3	pyridine-containing compound catabolic	BP	1	PDXP	down_ACOR_VSMC
GO:1902306	0.23	0.98	1	3	negative regulation of sodium ion	BP	1	NEDD4	down_ACOR_VSMC
GO:0000375	0.23	0.973	1	120	RNA splicing, via transesterification	BP	1	SRSF6	down_AFEM_EC
GO:0007265	0.23	0.973	1	121	Ras protein signal transduction	BP	1	GPSM2	down_AFEM_EC
GO:0009651	0.23	0.977	1	5	response to salt stress	BP	1	ZFP36L1	down_VCAV_EC
GO:0009713	0.23	0.977	1	5	catechol-containing compound biosynthetic	BP	1	PARK7	down_VCAV_EC
GO:0034375	0.23	0.977	1	5	high-density lipoprotein particle remodeling	BP	1	LCAT	down_VCAV_EC
GO:0042423	0.23	0.977	1	5	catecholamine biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0046532	0.23	0.977	1	5	regulation of photoreceptor cell	BP	1	THRB	down_VCAV_EC
GO:0071971	0.23	0.977	1	5	extracellular exosome assembly	BP	1	SDC4	down_VCAV_EC
GO:1903551	0.23	0.977	1	5	regulation of extracellular exosome assembly	BP	1	SDC4	down_VCAV_EC
GO:0006366	0.23	0.98	1	583	transcription by RNA polymerase II	BP	1	MOSPD1	down_VFEM_EC
GO:0009164	0.23	0.977	1	5	nucleoside catabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0042454	0.23	0.977	1	5	ribonucleoside catabolic process	BP	1	ENTPD4	down_VSAP_EC

GO:0051590	0.23	0.98	1	3	positive regulation of neurotransmitter	BP	1	PSEN1	up_ACOR_VSMC
GO:1905446	0.23	0.98	1	3	regulation of mitochondrial ATP synthesis coupled	BP	1	PARK7	up_ACOR_VSMC
GO:0006622	0.23	0.974	1	11	protein targeting to lysosome	BP	1	RAB7A	up_AFEM_EC
GO:0035315	0.23	0.974	1	11	hair cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0007178	0.23	0.973	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	LNPEP	up_AORT_EC
GO:0034093	0.23	0.98	1	3	positive regulation of maintenance of sister chromatid cohesion	BP	1	SMC5	up_VCAV_EC
GO:0034184	0.23	0.98	1	3	positive regulation of maintenance of mitotic sister chromatid cohesion	BP	1	SMC5	up_VCAV_EC
GO:0034145	0.23	0.98	1	3	positive regulation of toll-like receptor 4 signaling	BP	1	PELI1	up_VCAV_EC
GO:0098771	0.23	0.974	1	180	inorganic ion homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0009166	0.23	0.973	1	31	nucleotide catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0035296	0.23	0.973	1	32	regulation of tube diameter	BP	1	HTR7	up_VPOR_EC
GO:0097746	0.23	0.973	1	32	regulation of blood vessel diameter	BP	1	HTR7	up_VPOR_EC
GO:0001558	0.23	0.973	1	101	regulation of cell growth	BP	1	FBP1	up_VFEM_VSMC
GO:0062012	0.23	0.973	1	100	regulation of small molecule metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0071559	0.23	0.973	1	75	response to transforming growth factor beta	BP	1	MXRA5	up_VPUL_EC
GO:0010639	0.23	0.973	1	128	negative regulation of organelle organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0051098	0.23	0.973	1	129	regulation of binding	BP	1	HOXA3	up_VPUL_VSMC
GO:0033169	0.23	0.98	1	3	histone H3-K9 demethylation	BP	1	KDM3B	up_VSAP_EC
GO:1901673	0.230212284	0.97399	1	10	regulation of mitotic spindle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0043244	0.230682556	0.93839	2	34	regulation of protein complex disassembly	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0002253	0.230697795	0.90105	4	92	activation of immune response	BP	1	C7,NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0051258	0.230945169	0.90087	4	94	protein polymerization	BP	1	TMOD1,PAK3,PRKCD,TUBB4A	up_ACOR_EC
GO:0044281	0.231	0.812	57	622	small molecule metabolic process	BP	1	SCD,PRPSAP1,SQLE,LSS,SREBF1,ACLY,ENSCAFG00000016095,BCAT1,HMGCR,NNT,VARS,RRM1,RAN,INSIG1,CAV1,CDK1,XYLT1,PFAS,TK1,RNASEH2B,ARG2,DHCR24,BRCA1,MVD,B4GALT1,ELOVL1,FARSA,SUCLG1,PPARD,CYCS,PDXP,AADAT,GSTO1,ELOVL6,FDFT1,SGPL1,CYC1,RARS,ATP5F1A,DCK,PRPS1,ENSCAFG00000013366,CTH,GALE,ENSCAFG00000005637,PDHA1,GGH,LIPC,NUDT1,PGD,NUS1,GK5,CTPS1,PDSS1,ACADL,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0055086	0.231	0.845	15	237	nucleobase-containing small molecule metabolic process	BP	1	GPAM,ADCY6,H6PD,NT5C2,ENTPD3,PGLS,ATP5MC1,GFPT2,UQCR10,ADK,PARK7,AMPD2,FUT8,ACSS2,ACAT1	down_VCAV_EC
GO:0010631	0.231	0.849	14	118	epithelial cell migration	BP	1	ENPP2,SLIT2,FGF7,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0090132	0.231	0.849	14	118	epithelium migration	BP	1	ENPP2,SLIT2,FGF7,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0048878	0.231	0.864	9	283	chemical homeostasis	BP	1	LEP,CRY2,RAB20,GPAM,MLLT11,CNNM4,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0009914	0.231	0.876	7	64	hormone transport	BP	1	CHD7,GATA3,EDN1,SNAP23,CREB1,MCU,HIF1A	up_VCAV_EC
GO:0002688	0.231	0.904	4	34	regulation of leukocyte chemotaxis	BP	1	CXCL8,MMP28,SWAP70,HMGB1	up_VCAV_EC
GO:0002526	0.231	0.921	3	17	acute inflammatory response	BP	1	CLSTN1,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:1902807	0.231	0.921	3	18	negative regulation of cell cycle G1/S phase	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC
GO:2000134	0.231	0.921	3	18	negative regulation of G1/S transition of mitotic	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC

GO:0048863	0.231	0.916	3	70	stem cell differentiation	BP	1	LBH,HOXA7,GREM1	up_AFEM_EC
GO:0060078	0.231	0.921	3	17	regulation of postsynaptic membrane potential	BP	1	RELN,MEF2C,PPP3CA	up_VCAV_EC
GO:0099565	0.231	0.921	3	17	chemical synaptic transmission, postsynaptic	BP	1	RELN,MEF2C,PPP3CA	up_VCAV_EC
GO:0043457	0.231	0.943	2	11	regulation of cellular respiration	BP	1	PRELID1,CDK1	down_ACOR_VSMC
GO:0043388	0.231	0.941	2	16	positive regulation of DNA binding	BP	1	CTNNB1,CALM1	down_VSAP_EC
GO:0032941	0.231	0.944	2	10	secretion by tissue	BP	1	GJA1,PRKCE	up_ACOR_VSMC
GO:0010243	0.231	0.939	2	238	response to organonitrogen	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:1901838	0.231	0.945	2	9	positive regulation of transcription of nucleolar large rRNA by RNA	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:1903393	0.231	0.943	2	11	positive regulation of adherens junction	BP	1	TEK,ENSCAFG00000002015	up_VCAV_EC
GO:0007296	0.231	0.98	1	3	vitellogenesis	BP	1	FOSL1	down_ACOR_VSMC
GO:0019388	0.231	0.98	1	3	galactose catabolic process	BP	1	GALE	down_ACOR_VSMC
GO:0034374	0.231	0.98	1	3	low-density lipoprotein particle remodeling	BP	1	LIPC	down_ACOR_VSMC
GO:0071609	0.231	0.98	1	3	chemokine (C-C motif) ligand 5 production	BP	1	ARG2	down_ACOR_VSMC
GO:0071649	0.231	0.98	1	3	regulation of chemokine (C-C motif) ligand 5	BP	1	ARG2	down_ACOR_VSMC
GO:1903912	0.231	0.98	1	3	negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation	BP	1	PPP1R15B	down_ACOR_VSMC
GO:1903706	0.231	0.973	1	119	regulation of hemopoiesis	BP	1	GABPA	down_AFEM_EC
GO:0033145	0.231	0.977	1	5	positive regulation of intracellular steroid hormone receptor	BP	1	PARK7	down_VCAV_EC
GO:0006026	0.231	0.976	1	5	aminoglycan catabolic process	BP	1	CHID1	down_VCAV_EC
GO:0015872	0.231	0.976	1	5	dopamine transport	BP	1	PARK7	down_VCAV_EC
GO:0019430	0.231	0.976	1	5	removal of superoxide radicals	BP	1	PARK7	down_VCAV_EC
GO:0034975	0.231	0.976	1	5	protein folding in endoplasmic reticulum	BP	1	EMC6	down_VCAV_EC
GO:0048262	0.231	0.976	1	5	determination of dorsal/ventral asymmetry	BP	1	GREM1	down_VCAV_EC
GO:0051937	0.231	0.976	1	5	catecholamine transport	BP	1	PARK7	down_VCAV_EC
GO:0060431	0.231	0.976	1	5	primary lung bud formation	BP	1	RDH10	down_VCAV_EC
GO:0071450	0.231	0.976	1	5	cellular response to oxygen radical	BP	1	PARK7	down_VCAV_EC
GO:0071451	0.231	0.976	1	5	cellular response to superoxide	BP	1	PARK7	down_VCAV_EC
GO:1903792	0.231	0.977	1	5	negative regulation of anion transport	BP	1	AKT2	down_VCAV_EC
GO:0061458	0.231	0.973	1	131	reproductive system development	BP	1	CITED2	down_VPOR_EC
GO:0045628	0.231	0.978	1	4	regulation of T-helper 2 cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0030011	0.231	0.978	1	4	maintenance of cell polarity	BP	1	WDR1	down_VSAP_EC
GO:0035090	0.231	0.978	1	4	maintenance of apical/basal cell polarity	BP	1	WDR1	down_VSAP_EC
GO:0045199	0.231	0.978	1	4	maintenance of epithelial cell apical/basal polarity	BP	1	WDR1	down_VSAP_EC
GO:0002278	0.231	0.98	1	3	eosinophil activation involved in immune	BP	1	F2RL1	up_ACOR_VSMC
GO:0036353	0.231	0.98	1	3	histone H2A-K119 monoubiquitination	BP	1	PCGF5	up_ACOR_VSMC
GO:0002447	0.231	0.98	1	3	eosinophil mediated immunity	BP	1	F2RL1	up_ACOR_VSMC
GO:0030091	0.231	0.98	1	3	protein repair	BP	1	PARK7	up_ACOR_VSMC
GO:0043307	0.231	0.98	1	3	eosinophil activation	BP	1	F2RL1	up_ACOR_VSMC
GO:0043308	0.231	0.98	1	3	eosinophil degranulation	BP	1	F2RL1	up_ACOR_VSMC

GO:0008206	0.231	0.973	1	11	bile acid metabolic process	BP	1	LEP	up_AFEM_EC
GO:0010883	0.231	0.974	1	11	regulation of lipid storage	BP	1	ACACB	up_AFEM_EC
GO:0014002	0.231	0.974	1	11	astrocyte development	BP	1	DLL1	up_AFEM_EC
GO:0098868	0.231	0.974	1	11	bone growth	BP	1	LEP	up_AFEM_EC
GO:0090087	0.231	0.974	1	185	regulation of peptide transport	BP	1	TLR2	up_AFEM_VSMC
GO:0045666	0.231	0.972	1	68	positive regulation of neuron differentiation	BP	1	NTRK2	up_APUL_EC
GO:0099403	0.231	0.985	1	2	maintenance of mitotic sister chromatid cohesion,	BP	1	ATRX	up_VCAV_EC
GO:0099404	0.231	0.985	1	2	mitotic sister chromatid cohesion, telomeric	BP	1	ATRX	up_VCAV_EC
GO:1904907	0.231	0.985	1	2	regulation of maintenance of mitotic sister chromatid cohesion, telomeric	BP	1	ATRX	up_VCAV_EC
GO:1904908	0.231	0.985	1	2	negative regulation of maintenance of mitotic sister chromatid cohesion,	BP	1	ATRX	up_VCAV_EC
GO:0050767	0.231	0.974	1	184	regulation of neurogenesis	BP	1	LIMK1	up_VCAV_VSMC
GO:0034332	0.231	0.972	1	32	adherens junction organization	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0030041	0.231	0.972	1	62	actin filament polymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0060491	0.231	0.972	1	62	regulation of cell projection assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0120032	0.231	0.972	1	62	regulation of plasma membrane bounded cell	BP	1	CDC42EP5	up_VFEM_EC
GO:0032535	0.231	0.973	1	128	regulation of cellular component size	BP	1	SLIT2	up_VPUL_VSMC
GO:0048608	0.231	0.973	1	129	reproductive structure development	BP	1	SLIT2	up_VPUL_VSMC
GO:1903322	0.231	0.972	1	59	positive regulation of protein modification by small protein conjugation	BP	1	CAV1	up_VSAP_VSMC
GO:0043122	0.231086676	0.91597	3	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4,NOD2,TNFRSF19	up_ACOR_EC
GO:0010543	0.231183728	0.97376	1	10	regulation of platelet activation	BP	1	PRKCD	up_ACOR_EC
GO:0090190	0.231524878	0.97367	1	10	positive regulation of branching involved in ureteric bud	BP	1	SOX9	up_ACOR_EC
GO:0009914	0.231549753	0.91566	3	64	hormone transport	BP	1	NR1H4,AQP1,KCNB1	up_ACOR_EC
GO:0006576	0.231648965	0.97364	1	10	cellular biogenic amine metabolic process	BP	1	AZIN2	up_ACOR_EC
GO:0031589	0.231778939	0.90039	4	93	cell-substrate adhesion	BP	1	ARHGAP6,SMAD6,ACTN2,NRP1	up_ACOR_EC
GO:0030866	0.231971381	0.97357	1	10	cortical actin cytoskeleton organization	BP	1	PLS1	up_ACOR_EC
GO:2000113	0.232	0.819	37	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,ENC1,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,RAD17,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0010562	0.232	0.822	34	312	positive regulation of phosphorus metabolic process	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,IL6R,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,DDR2,TRAF7,SASH1,MYD88,LRP4,CDK9,RAF1,ACVRL1,FLOT1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0045937	0.232	0.822	34	312	positive regulation of phosphate metabolic process	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,IL6R,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,DDR2,TRAF7,SASH1,MYD88,LRP4,CDK9,RAF1,ACVRL1,FLOT1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0051960	0.232	0.831	24	216	regulation of nervous system development	BP	1	FZD1,THRB,CDON,WASF3,AMIGO1,LRRN3,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,CYB5D2,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC

GO:0070848	0.232	0.834	22	193	response to growth factor	BP	1	SMAD6,GATA5,FERMT1,BMP4,FGFR2,CITED2,TMEM108,FGF18,CDKN2B,ANKRD1,MXRA5,NRP1,NPNT,FRS2,FUT8,TGFBR1,NR3C1,DUSP22,HPGD,ENSCAFG00000018360,INPP5K,CRKL	up_ACOR_VSMC
GO:0097193	0.232	0.851	13	109	intrinsic apoptotic signaling pathway	BP	1	NACC2,ITPR1,BNIP3,CDKN1A,JMY,PERP,SIAH1,DDIT4,SERINC3,HERPUD1,WFS1,PARK7,ZMAT3	up_ACOR_VSMC
GO:0007154	0.232	0.873	9	1622	cell communication	BP	1	EYA1,MAP2K6,ENSCAFG00000018194,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,ADCY3	up_VFEM_EC
GO:0050808	0.232	0.869	8	93	synapse organization	BP	1	TUBB,CTNNB1,APOE,DISC1,LRRTM2,SIX4,NRP1,ARF4	down_VSAP_EC
GO:0042180	0.232	0.871	8	61	cellular ketone metabolic process	BP	1	INSIG2,ACACB,C1QTNF2,COQ9,PDK2,LONP2,DHRS9,IDO2	up_VSAP_EC
GO:0008152	0.232	0.918	7	3714	metabolic process	BP	1	HOXC10,TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0097164	0.232	0.883	6	44	ammonium ion metabolic process	BP	1	LCAT,MAOA,SMPD1,MOXD1,AZIN2,PARK7	up_ACOR_VSMC
GO:0016331	0.232	0.89	5	66	morphogenesis of embryonic epithelium	BP	1	SDC4,LMO4,IFT57,RDH10,GREM1	down_VCAV_EC
GO:0002429	0.232	0.893	5	35	immune response-activating cell surface receptor signaling	BP	1	PLCG2,ELF1,PTPN22,PSEN1,DUSP22	up_ACOR_VSMC
GO:0048839	0.232	0.901	4	50	inner ear development	BP	1	SDC4,NAGLU,GLI3,GSDME	down_VCAV_EC
GO:0017015	0.232	0.902	4	40	regulation of transforming growth factor beta receptor signaling	BP	1	HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:1903844	0.232	0.902	4	40	regulation of cellular response to transforming growth factor beta	BP	1	HSPA5,SNX25,ADAM17,STRAP	down_VSAP_EC
GO:0071326	0.232	0.905	4	26	cellular response to monosaccharide stimulus	BP	1	PRKAA2,SLC2A5,PRKCE,RAB11B	up_ACOR_VSMC
GO:0071331	0.232	0.905	4	26	cellular response to hexose stimulus	BP	1	PRKAA2,SLC2A5,PRKCE,RAB11B	up_ACOR_VSMC
GO:0016310	0.232	0.904	4	641	phosphorylation	BP	1	MAPK10,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0045892	0.232	0.917	3	328	negative regulation of transcription, DNA-	BP	1	HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0003073	0.232	0.92	3	20	regulation of systemic arterial blood pressure	BP	1	NAV2,PRCP,EMP2	down_ACOR_VSMC
GO:0051216	0.232	0.916	3	70	cartilage development	BP	1	GREM1,PTHLH,AXIN2	up_AFEM_EC
GO:0090183	0.232	0.919	3	21	regulation of kidney development	BP	1	HOXB7,PDGFB,GATA3	up_VCAV_EC
GO:0030279	0.232	0.939	2	19	negative regulation of ossification	BP	1	TWIST2,GREM1	down_VCAV_EC
GO:0051193	0.232	0.94	2	15	regulation of cofactor metabolic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0061437	0.232	0.943	2	10	renal system vasculature development	BP	1	BMP4,NRP1	up_ACOR_VSMC
GO:0061440	0.232	0.943	2	10	kidney vasculature development	BP	1	BMP4,NRP1	up_ACOR_VSMC
GO:0072359	0.232	0.94	2	368	circulatory system development	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0003351	0.232	0.98	1	3	epithelial cilium movement	BP	1	TTLL1	down_ACOR_VSMC
GO:1902035	0.232	0.98	1	3	positive regulation of hematopoietic stem cell proliferation	BP	1	PDCD2	down_ACOR_VSMC
GO:0005984	0.232	0.98	1	3	disaccharide metabolic process	BP	1	B4GALT1	down_ACOR_VSMC
GO:0031120	0.232	0.98	1	3	snRNA pseudouridine synthesis	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0046351	0.232	0.98	1	3	disaccharide biosynthetic process	BP	1	B4GALT1	down_ACOR_VSMC
GO:0048387	0.232	0.98	1	3	negative regulation of retinoic acid receptor	BP	1	EZH2	down_ACOR_VSMC
GO:0051016	0.232	0.98	1	3	barbed-end actin filament capping	BP	1	CAPG	down_ACOR_VSMC
GO:0052646	0.232	0.98	1	3	alditol phosphate metabolic process	BP	1	GK5	down_ACOR_VSMC
GO:0090481	0.232	0.98	1	3	pyrimidine nucleotide-sugar transmembrane	BP	1	SLC35C2	down_ACOR_VSMC
GO:0097384	0.232	0.98	1	3	cellular lipid biosynthetic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0023052	0.232	1	1	1602	signaling	BP	1	GATA5	down_AFEM_VSMC

GO:0018904	0.232	0.976	1	5	ether metabolic process	BP	1	EPHX1	down_VCAV_EC
GO:0070254	0.232	0.976	1	5	mucus secretion	BP	1	CYBA	down_VCAV_EC
GO:0070255	0.232	0.976	1	5	regulation of mucus secretion	BP	1	CYBA	down_VCAV_EC
GO:0033036	0.232	0.985	1	852	macromolecule localization	BP	1	JUP	down_VFEM_VSMC
GO:0002091	0.232	0.978	1	4	negative regulation of receptor internalization	BP	1	LRRTM2	down_VSAP_EC
GO:0034309	0.232	0.978	1	4	primary alcohol biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0002418	0.232	0.976	1	5	immune response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:0002834	0.232	0.976	1	5	regulation of response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:0002837	0.232	0.976	1	5	regulation of immune response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:1900227	0.232	0.978	1	4	positive regulation of NLRP3 inflammasome	BP	1	GBP5	down_VSAP_EC
GO:1902644	0.232	0.978	1	4	tertiary alcohol metabolic process	BP	1	REST	down_VSAP_EC
GO:0043649	0.232	0.978	1	4	dicarboxylic acid catabolic process	BP	1	ALDH1L2	down_VSAP_EC
GO:0070857	0.232	0.978	1	4	regulation of bile acid biosynthetic process	BP	1	NR1H4	down_VSAP_EC
GO:1904251	0.232	0.978	1	4	regulation of bile acid metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0071596	0.232	0.985	1	2	ubiquitin-dependent protein catabolic process via the N-end rule	BP	1	UBR1	up_ACOR_VSMC
GO:0046007	0.232	0.98	1	3	negative regulation of activated T cell	BP	1	CD274	up_ACOR_VSMC
GO:0010611	0.232	0.973	1	11	regulation of cardiac muscle hypertrophy	BP	1	LMCD1	up_AFEM_EC
GO:0014743	0.232	0.973	1	11	regulation of muscle hypertrophy	BP	1	LMCD1	up_AFEM_EC
GO:0022617	0.232	0.973	1	11	extracellular matrix disassembly	BP	1	FAP	up_AFEM_EC
GO:0001881	0.232	0.973	1	11	receptor recycling	BP	1	BVES	up_AFEM_EC
GO:0032715	0.232	0.973	1	11	negative regulation of interleukin-6 production	BP	1	BPI	up_AFEM_EC
GO:0060343	0.232	0.973	1	11	trabecula formation	BP	1	GREM1	up_AFEM_EC
GO:0060914	0.232	0.973	1	11	heart formation	BP	1	AXIN2	up_AFEM_EC
GO:1900077	0.232	0.973	1	11	negative regulation of cellular response to	BP	1	KANK1	up_AFEM_EC
GO:2001169	0.232	0.973	1	11	regulation of ATP biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0001817	0.232	0.974	1	182	regulation of cytokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0001781	0.232	0.98	1	3	neutrophil apoptotic process	BP	1	ITPKB	up_VCAV_EC
GO:0033029	0.232	0.98	1	3	regulation of neutrophil apoptotic process	BP	1	ITPKB	up_VCAV_EC
GO:2000402	0.232	0.98	1	3	negative regulation of lymphocyte migration	BP	1	APOD	up_VCAV_EC
GO:0034140	0.232	0.98	1	3	negative regulation of toll-like receptor 3 signaling	BP	1	TNFAIP3	up_VCAV_EC
GO:0051205	0.232	0.978	1	4	protein insertion into membrane	BP	1	SH3GLB1	up_VCAV_EC
GO:0007040	0.232	0.972	1	33	lysosome organization	BP	1	HOOK3	up_VPOR_EC
GO:0080171	0.232	0.972	1	33	lytic vacuole organization	BP	1	HOOK3	up_VPOR_EC
GO:0016054	0.232	0.972	1	61	organic acid catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0046395	0.232	0.972	1	61	carboxylic acid catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0051260	0.232	0.972	1	100	protein homooligomerization	BP	1	FBP1	up_VFEM_VSMC
GO:0048002	0.232119704	0.97353	1	10	antigen processing and presentation of peptide	BP	1	TAPBP	up_ACOR_EC
GO:0070997	0.232979804	0.89967	4	93	neuron death	BP	1	USP53,CHMP4B,NRP1,PM20D1	up_ACOR_EC
GO:0009611	0.233	0.85	13	122	response to wounding	BP	1	ELK3,TFPI,TFPI2,SDC1,CAV1,EZH2,ADIPOR2,B4GALT1,PRCP,PPARD,ITGB3,GLI1,PIK3CD	down_ACOR_VSMC

GO:0061351	0.233	0.876	7	50	neural precursor cell proliferation	BP	1	FGFR2,ACSL6,LIMS2,SMARCD3,FZD3,FRS2,DISC1	up_ACOR_VSMC
GO:0071345	0.233	0.873	7	210	cellular response to cytokine stimulus	BP	1	LEP,RAB20,GREM2,CYLD,LRRC15,CCL5,ADAM17	up_AFEM_EC
GO:0090596	0.233	0.88	6	84	sensory organ morphogenesis	BP	1	FBN1,NAGLU,THY1,GLI3,IRX5,THRB	down_VCAV_EC
GO:0007611	0.233	0.89	5	54	learning or memory	BP	1	HIF1A,UBA6,APOE,HTT,ARF4	down_VSAP_EC
GO:0043244	0.233	0.892	5	34	regulation of protein complex disassembly	BP	1	FGF13,ACTN2,MID1,F2RL1,BNIP3	up_ACOR_VSMC
GO:0002224	0.233	0.893	5	34	toll-like receptor signaling pathway	BP	1	F2RL1,MYD88,CYBA,UNC93B1,FLOT1	up_VSAP_EC
GO:0010770	0.233	0.903	4	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	RELN,RAB11A,NEDD9,ENSCAFG00000002015	up_VCAV_EC
GO:0042133	0.233	0.903	4	30	neurotransmitter metabolic process	BP	1	CD34,TLR4,NOS3,NOS2	up_VCAV_EC
GO:0009893	0.233	0.908	4	995	positive regulation of metabolic process	BP	1	NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:1902679	0.233	0.916	3	329	negative regulation of RNA biosynthetic process	BP	1	HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:1903507	0.233	0.916	3	329	negative regulation of nucleic acid-templated	BP	1	HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0048645	0.233	0.916	3	33	animal organ formation	BP	1	BMPR1A,GLI3,RDH10	down_VCAV_EC
GO:0051928	0.233	0.917	3	28	positive regulation of calcium ion transport	BP	1	HTT,CALM1,HOMER1	down_VSAP_EC
GO:0098876	0.233	0.917	3	29	vesicle-mediated transport to the plasma	BP	1	ANKRD50,EXOC5,BLZF1	down_VSAP_EC
GO:0010761	0.233	0.94	2	15	fibroblast migration	BP	1	ILK,SDC4	down_VSAP_EC
GO:0043537	0.233	0.94	2	15	negative regulation of blood vessel endothelial	BP	1	STARD13,APOE	down_VSAP_EC
GO:0000165	0.233	0.938	2	236	MAPK cascade	BP	1	MAPK10,NPNT	up_APUL_EC
GO:1902042	0.233	0.942	2	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	TNFAIP3,ARHGEF2	up_VCAV_EC
GO:0051053	0.233	0.972	1	45	negative regulation of DNA metabolic process	BP	1	ACVRL1	down_ACOR_EC
GO:0019627	0.233	0.98	1	3	urea metabolic process	BP	1	ARG2	down_ACOR_VSMC
GO:0035404	0.233	0.98	1	3	histone-serine phosphorylation	BP	1	AURKB	down_ACOR_VSMC
GO:0042983	0.233	0.98	1	3	amyloid precursor protein biosynthetic process	BP	1	NECAB3	down_ACOR_VSMC
GO:0042984	0.233	0.98	1	3	regulation of amyloid precursor protein	BP	1	NECAB3	down_ACOR_VSMC
GO:0042998	0.233	0.98	1	3	positive regulation of Golgi to plasma membrane protein	BP	1	ACSL3	down_ACOR_VSMC
GO:0070828	0.233	0.98	1	3	heterochromatin organization	BP	1	HMGA1	down_ACOR_VSMC
GO:1905065	0.233	0.98	1	3	positive regulation of vascular smooth muscle	BP	1	CTH	down_ACOR_VSMC
GO:0006108	0.233	0.976	1	5	malate metabolic process	BP	1	ME3	down_VCAV_EC
GO:0060449	0.233	0.976	1	5	bud elongation involved in lung branching	BP	1	RDH10	down_VCAV_EC
GO:0006616	0.233	0.976	1	5	SRP-dependent cotranslational protein targeting to membrane,	BP	1	SEC61B	down_VCAV_EC
GO:0010765	0.233	0.976	1	5	positive regulation of sodium ion transport	BP	1	FXYD1	down_VCAV_EC
GO:0034162	0.233	0.976	1	5	toll-like receptor 9 signaling pathway	BP	1	RAB7B	down_VCAV_EC
GO:0051641	0.233	0.985	1	858	cellular localization	BP	1	JUP	down_VFEM_VSMC
GO:0003306	0.233	0.977	1	4	Wnt signaling pathway involved in heart	BP	1	CTNNB1	down_VSAP_EC
GO:2001053	0.233	0.977	1	4	regulation of mesenchymal cell	BP	1	HIF1A	down_VSAP_EC
GO:0033623	0.233	0.977	1	4	regulation of integrin activation	BP	1	FBLIM1	down_VSAP_EC
GO:0035860	0.233	0.977	1	4	glial cell-derived neurotrophic factor	BP	1	SULF1	down_VSAP_EC
GO:0035239	0.233	0.975	1	299	tube morphogenesis	BP	1	TGFBI	down_VSAP_VSMC
GO:0009648	0.233	0.973	1	11	photoperiodism	BP	1	CRY2	up_AFEM_EC

GO:0031102	0.233	0.973	1	11	neuron projection regeneration	BP	1	TNC	up_AFEM_EC
GO:0032653	0.233	0.973	1	11	regulation of interleukin-10 production	BP	1	DLL1	up_AFEM_EC
GO:0043153	0.233	0.973	1	11	entrainment of circadian clock by photoperiod	BP	1	CRY2	up_AFEM_EC
GO:0043243	0.233	0.973	1	11	positive regulation of protein complex	BP	1	CLEC16A	up_AFEM_EC
GO:0043457	0.233	0.973	1	11	regulation of cellular respiration	BP	1	PPARGC1A	up_AFEM_EC
GO:0050850	0.233	0.973	1	11	positive regulation of calcium-mediated	BP	1	LMCD1	up_AFEM_EC
GO:0060351	0.233	0.973	1	11	cartilage development involved in endochondral bone morphogenesis	BP	1	AXIN2	up_AFEM_EC
GO:0045596	0.233	0.973	1	186	negative regulation of cell differentiation	BP	1	HOXA9	up_AFEM_VSMC
GO:0032102	0.233	0.972	1	67	negative regulation of response to external	BP	1	NR1H4	up_APUL_EC
GO:0072330	0.233	0.972	1	68	monocarboxylic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:1901605	0.233	0.972	1	67	alpha-amino acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0002182	0.233	0.98	1	3	cytoplasmic translational elongation	BP	1	DPH5	up_VCAV_EC
GO:1900247	0.233	0.98	1	3	regulation of cytoplasmic translational elongation	BP	1	DPH5	up_VCAV_EC
GO:0030855	0.233	0.973	1	183	epithelial cell differentiation	BP	1	GATA5	up_VCAV_VSMC
GO:0051261	0.233	0.972	1	33	protein depolymerization	BP	1	ARHGEF2	up_VPOR_EC
GO:0001101	0.233	0.972	1	65	response to acid chemical	BP	1	CYP26B1	up_VFEM_EC
GO:0032970	0.233	0.973	1	130	regulation of actin filament-based process	BP	1	SLIT2	up_VPUL_VSMC
GO:0007369	0.233	0.972	1	63	gastrulation	BP	1	HOXA11	up_VSAP_VSMC
GO:0007566	0.233002716	0.97332	1	10	embryo implantation	BP	1	ARHGDIB	up_ACOR_EC
GO:0051894	0.233688939	0.97315	1	10	positive regulation of focal adhesion assembly	BP	1	NRP1	up_ACOR_EC
GO:0034381	0.233715382	0.97315	1	10	plasma lipoprotein particle clearance	BP	1	NR1H4	up_ACOR_EC
GO:0048678	0.233803308	0.97313	1	10	response to axon injury	BP	1	RGMA	up_ACOR_EC
GO:0001568	0.234	0.825	28	252	blood vessel development	BP	1	VEGFD,SMAD6,LEP,ANGPT1,RECK,BMP4,FGFR2,GJA1,TLR3,SEC24B,CITED2,SPINT1,SASH1,FGF18,EGLN1,NRP1,TBX20,PSEN1,SYNJ2BP,CHD7,JUP,EDN1,HPGD,JAM3,AP2B1,ERAP1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0045089	0.234	0.864	9	70	positive regulation of innate immune response	BP	1	F2RL1,MYD88,NLRX1,TKFC,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0043010	0.234	0.867	8	96	camera-type eye development	BP	1	BCAR3,SMARCA4,HIF1A,CTNNB1,CRYAB,PDS5B,INHBA,NRP1	down_VSAP_EC
GO:2000116	0.234	0.874	7	67	regulation of cysteine-type endopeptidase	BP	1	CASP8,PAK2,PTGS2,BCL10,HMGB1,PMAIP1,PSMB9	up_VCAV_EC
GO:0070663	0.234	0.882	6	50	regulation of leukocyte proliferation	BP	1	HMGB1,MNDA,GREM1,ARG2,TFRC,CORO1A	down_ACOR_VSMC
GO:0001841	0.234	0.883	6	44	neural tube formation	BP	1	FZD1,ABL1,FUZ,RARG,KDM2B,CITED2	up_VSAP_EC
GO:0006606	0.234	0.889	5	67	protein import into nucleus	BP	1	ENSCAFG00000014978,SNUPN,GLI3,MAVS,SEC61B	down_VCAV_EC
GO:0048565	0.234	0.891	5	38	digestive tract development	BP	1	EDNRB,KIT,CXCL8,ITGA6,HIF1A	up_VCAV_EC
GO:0002688	0.234	0.892	5	34	regulation of leukocyte chemotaxis	BP	1	C5AR2,SLC8B1,SLIT2,F2RL1,ZNF580	up_VSAP_EC
GO:0003018	0.234	0.901	4	42	vascular process in circulatory system	BP	1	HTR7,ACTA2,APOE,PLOD3	down_VSAP_EC
GO:0019080	0.234	0.903	4	26	viral gene expression	BP	1	MON1B,EIF3G,EIF3L,EIF3D	up_VSAP_EC
GO:0021549	0.234	0.917	3	26	cerebellum development	BP	1	HSPA5,PTPN11,AARS	down_VSAP_EC
GO:0010558	0.234	0.916	3	392	negative regulation of macromolecule biosynthetic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0001522	0.234	0.942	2	11	pseudouridine synthesis	BP	1	TRUB2,ENSCAFG00000019620	down_ACOR_VSMC
GO:1901984	0.234	0.942	2	11	negative regulation of protein acetylation	BP	1	BRCA1,NOC2L	down_ACOR_VSMC

GO:0006576	0.234	0.942	2	10	cellular biogenic amine metabolic process	BP	1	MOXD1,AZIN2	up_ACOR_VSMC
GO:0009225	0.234	0.943	2	10	nucleotide-sugar metabolic process	BP	1	FUT8,EXTL2	up_ACOR_VSMC
GO:0097734	0.234	0.94	2	13	extracellular exosome biogenesis	BP	1	RAB11A,RAB27A	up_VCAV_EC
GO:1990182	0.234	0.94	2	13	exosomal secretion	BP	1	RAB11A,RAB27A	up_VCAV_EC
GO:0061564	0.234	0.936	2	119	axon development	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0007411	0.234	0.972	1	45	axon guidance	BP	1	NRP2	down_ACOR_EC
GO:0032409	0.234	0.972	1	52	regulation of transporter activity	BP	1	NEDD4	down_ACOR_EC
GO:0097485	0.234	0.972	1	45	neuron projection guidance	BP	1	NRP2	down_ACOR_EC
GO:0044030	0.234	0.98	1	3	regulation of DNA methylation	BP	1	MIS18A	down_ACOR_VSMC
GO:0009235	0.234	0.979	1	3	cobalamin metabolic process	BP	1	ENSCAFG00000005637	down_ACOR_VSMC
GO:0031115	0.234	0.98	1	3	negative regulation of microtubule	BP	1	STMN1	down_ACOR_VSMC
GO:0089700	0.234	0.979	1	3	protein kinase D signaling	BP	1	PRKD3	down_ACOR_VSMC
GO:1904468	0.234	0.979	1	3	negative regulation of tumor necrosis factor	BP	1	ARG2	down_ACOR_VSMC
GO:0051045	0.234	0.976	1	5	negative regulation of membrane protein	BP	1	TIMP2	down_VCAV_EC
GO:0001701	0.234	0.972	1	134	in utero embryonic development	BP	1	CITED2	down_VPOR_EC
GO:0002790	0.234	0.972	1	133	peptide secretion	BP	1	RAB11B	down_VPOR_EC
GO:0018027	0.234	0.977	1	4	peptidyl-lysine dimethylation	BP	1	KDM3A	down_VSAP_EC
GO:1905208	0.234	0.977	1	4	negative regulation of cardiocyte differentiation	BP	1	PRICKLE1	down_VSAP_EC
GO:0022603	0.234	0.975	1	301	regulation of anatomical structure morphogenesis	BP	1	GATA5	down_VSAP_VSMC
GO:0003203	0.234	0.973	1	11	endocardial cushion morphogenesis	BP	1	TMEM100	up_AFEM_EC
GO:0006584	0.234	0.973	1	11	catecholamine metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0009712	0.234	0.973	1	11	catechol-containing compound metabolic	BP	1	MOXD1	up_AFEM_EC
GO:0060317	0.234	0.973	1	11	cardiac epithelial to mesenchymal transition	BP	1	TMEM100	up_AFEM_EC
GO:0061213	0.234	0.973	1	11	positive regulation of mesonephros	BP	1	GREM1	up_AFEM_EC
GO:0071242	0.234	0.973	1	11	cellular response to ammonium ion	BP	1	CHRM2	up_AFEM_EC
GO:1901185	0.234	0.973	1	11	negative regulation of ERBB signaling pathway	BP	1	RAB7A	up_AFEM_EC
GO:0070201	0.234	0.973	1	187	regulation of establishment of protein	BP	1	TLR2	up_AFEM_VSMC
GO:0009607	0.234	0.974	1	232	response to biotic stimulus	BP	1	ARG2	up_AORT_VSMC
GO:0071375	0.234	0.972	1	68	cellular response to peptide hormone stimulus	BP	1	NR1H4	up_APUL_EC
GO:0033700	0.234	0.98	1	3	phospholipid efflux	BP	1	ABCA1	up_VCAV_EC
GO:0090087	0.234	0.973	1	185	regulation of peptide transport	BP	1	CA2	up_VCAV_VSMC
GO:2001243	0.234	0.971	1	33	negative regulation of intrinsic apoptotic	BP	1	ARHGEF2	up_VPOR_EC
GO:0043393	0.234	0.972	1	77	regulation of protein binding	BP	1	HOXA3	up_VPUL_EC
GO:0061458	0.234	0.972	1	131	reproductive system development	BP	1	SLIT2	up_VPUL_VSMC
GO:0015914	0.234152895	0.97304	1	10	phospholipid transport	BP	1	PRKCD	up_ACOR_EC
GO:0006929	0.234489272	0.97296	1	10	substrate-dependent cell migration	BP	1	NRP1	up_ACOR_EC
GO:0060713	0.234576772	0.97294	1	10	labyrinthine layer morphogenesis	BP	1	FZD5	up_ACOR_EC
GO:0048468	0.235	0.841	16	553	cell development	BP	1	IRX3,IRX5,LEP,DLL1,PLXNA4,NEFH,THRB,LGI4,CAMK2A,PTHLH,BVES,AXIN2,LRRN2,FOSL2,KANK1,TNC	up_AFEM_EC
GO:0071840	0.235	0.86	13	2059	cellular component organization or biogenesis	BP	1	ACVRL1,LYN,IGF1R,SPG11,PDPN,NRP2,RPSA,SULF1,CSGALNACT1,ACSL3,WDR12,STX4,NEDD4	down_ACOR_EC

GO:0006139	0.235	0.861	12	1909	nucleobase-containing compound metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,TNRC6B,NEDD4	down_ACOR_EC
GO:0002683	0.235	0.857	10	126	negative regulation of immune system process	BP	1	SOCS5,PTPN2,CNOT7,CTNNB1,MMP28,LYN,SDC4,PRMT1,A2M,BTK	down_VSAP_EC
GO:0032984	0.235	0.868	8	70	protein-containing complex disassembly	BP	1	TMOD1,STMN1,SWAP70,SMARCA4,MRRF,TAOK1,TMOD3,ARHGEF2	up_VCAV_EC
GO:0060284	0.235	0.871	7	212	regulation of cell development	BP	1	IRX3,DLL1,PLXNA4,THRB,CAMK2A,AXIN2,KANK1	up_AFEM_EC
GO:0050863	0.235	0.879	6	69	regulation of T cell activation	BP	1	SOCS5,FAM49B,PTPN2,CTNNB1,TFRC,SDC4	down_VSAP_EC
GO:0048518	0.235	0.892	6	1676	positive regulation of biological process	BP	1	EYA1,GATM,HOXA9,NETO1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0050731	0.235	0.882	6	44	positive regulation of peptidyl-tyrosine	BP	1	ENPP2,IL6R,FGF7,ABL1,PLPP3,LRP4	up_VSAP_EC
GO:1903900	0.235	0.89	5	40	regulation of viral life cycle	BP	1	ILF3,TRIM35,SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0016079	0.235	0.903	4	27	synaptic vesicle exocytosis	BP	1	FBXL20,STX11,PSEN1,PREPL	up_ACOR_VSMC
GO:0002088	0.235	0.903	4	26	lens development in camera-type eye	BP	1	BMP4,GJA1,CITED2,FRS2	up_ACOR_VSMC
GO:1902882	0.235	0.902	4	29	regulation of response to oxidative stress	BP	1	TLR4,GCH1,RIPK1,HIF1A	up_VCAV_EC
GO:0032007	0.235	0.902	4	27	negative regulation of TOR signaling	BP	1	SESN1,CASTOR1,NPRL3,DDIT4	up_VSAP_EC
GO:0006366	0.235	0.902	4	583	transcription by RNA polymerase II	BP	1	HOXA9,SALL1,CAV1,SHOX2	up_VSAP_VSMC
GO:0030100	0.235	0.914	3	70	regulation of endocytosis	BP	1	RAB20,DLL1,GREM1	up_AFEM_EC
GO:0022008	0.235	0.916	3	406	neurogenesis	BP	1	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0007169	0.235	0.937	2	178	transmembrane receptor protein tyrosine kinase	BP	1	LYN,SULF1	down_ACOR_EC
GO:0060706	0.235	0.941	2	11	cell differentiation involved in embryonic	BP	1	E2F8,PLK4	down_ACOR_VSMC
GO:0035994	0.235	0.942	2	10	response to muscle stretch	BP	1	ANKRD1,SLC8A1	up_ACOR_VSMC
GO:0032640	0.235	0.936	2	39	tumor necrosis factor production	BP	1	LEP,BPI	up_AFEM_EC
GO:0003382	0.235	0.942	2	11	epithelial cell morphogenesis	BP	1	STC1,FLNB	up_VCAV_EC
GO:0061024	0.235	0.937	2	215	membrane organization	BP	1	TRIM9,MTSS1	up_VFEM_EC
GO:0003418	0.235	0.979	1	3	growth plate cartilage chondrocyte	BP	1	POC1A	down_ACOR_VSMC
GO:0003431	0.235	0.979	1	3	growth plate cartilage chondrocyte development	BP	1	POC1A	down_ACOR_VSMC
GO:0032119	0.235	0.979	1	3	sequestering of zinc ion	BP	1	SLC30A1	down_ACOR_VSMC
GO:0033211	0.235	0.979	1	3	adiponectin-activated signaling pathway	BP	1	ADIPOR2	down_ACOR_VSMC
GO:0034379	0.235	0.979	1	3	very-low-density lipoprotein particle	BP	1	ACSL3	down_ACOR_VSMC
GO:0061088	0.235	0.979	1	3	regulation of sequestering of zinc ion	BP	1	SLC30A1	down_ACOR_VSMC
GO:0003376	0.235	0.979	1	3	sphingosine-1-phosphate receptor signaling	BP	1	EZR	down_ACOR_VSMC
GO:0061684	0.235	0.979	1	3	chaperone-mediated autophagy	BP	1	PLK3	down_ACOR_VSMC
GO:1903553	0.235	0.979	1	3	positive regulation of extracellular exosome	BP	1	SDC1	down_ACOR_VSMC
GO:0007154	0.235	1	1	1622	cell communication	BP	1	GATA5	down_AFEM_VSMC
GO:1903580	0.235	0.976	1	5	positive regulation of ATP metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0045725	0.235	0.976	1	5	positive regulation of glycogen biosynthetic	BP	1	AKT2	down_VCAV_EC
GO:0070875	0.235	0.976	1	5	positive regulation of glycogen metabolic	BP	1	AKT2	down_VCAV_EC
GO:1902991	0.235	0.976	1	5	regulation of amyloid precursor protein	BP	1	PRNP	down_VCAV_EC
GO:0030099	0.235	0.972	1	133	myeloid cell differentiation	BP	1	CITED2	down_VPOR_EC
GO:0003263	0.235	0.977	1	4	cardioblast proliferation	BP	1	CTNNB1	down_VSAP_EC
GO:1903121	0.235	0.979	1	3	regulation of TRAIL-activated apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:0060561	0.235	0.973	1	11	apoptotic process involved in	BP	1	CRYAB	up_AFEM_EC

GO:2000649	0.235	0.973	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	FXYD1	up_AFEM_EC
GO:0043414	0.235	0.971	1	70	macromolecule methylation	BP	1	NR1H4	up_APUL_EC
GO:0001833	0.235	0.977	1	4	inner cell mass cell proliferation	BP	1	GINS4	up_VCAV_EC
GO:0002675	0.235	0.979	1	3	positive regulation of acute inflammatory	BP	1	PTGS2	up_VCAV_EC
GO:0048589	0.235	0.973	1	188	developmental growth	BP	1	LIMK1	up_VCAV_VSMC
GO:1905952	0.235	0.971	1	33	regulation of lipid localization	BP	1	ABHD5	up_VPOR_EC
GO:0006469	0.235	0.971	1	78	negative regulation of protein kinase activity	BP	1	FLRT3	up_VPUL_EC
GO:0061762	0.235	0.979	1	3	CAMKK-AMPK signaling cascade	BP	1	CAMKK2	up_VSAP_EC
GO:0099004	0.235	0.979	1	3	calmodulin dependent kinase signaling pathway	BP	1	CAMKK2	up_VSAP_EC
GO:0021700	0.235	0.971	1	65	developmental maturation	BP	1	IRX5	up_VSAP_VSMC
GO:1901099	0.235030272	0.97283	1	10	negative regulation of signal transduction in	BP	1	IFI6	up_ACOR_EC
GO:2001240	0.235030272	0.97283	1	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	IFI6	up_ACOR_EC
GO:0002369	0.235241478	0.97278	1	10	T cell cytokine production	BP	1	FZD5	up_ACOR_EC
GO:0019362	0.235674719	0.93612	2	35	pyridine nucleotide metabolic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0046496	0.235674719	0.93612	2	35	nicotinamide nucleotide metabolic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0002520	0.236	0.821	31	279	immune system development	BP	1	TMEM176B,TMEM176A,PLCG2,LEP,CD83,RASSF2,BMP4,FGFR2,TP53BP1,CITED2,ISG15,CD274,LMO4,FAM210B,P4HTM,CDKN2B,F2RL1,CLSTN1,PTPN22,CHD2,APP,PSEN1,CHD7,RTKN2,JAM3,B2M,CNOT4,ENSCAFG00000003530,IL18R1,BVES,CRKL	up_ACOR_VSMC
GO:0120039	0.236	0.835	19	158	plasma membrane bounded cell projection morphogenesis	BP	1	EPYC,FEZ1,FGFR2,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL,RREB1	up_ACOR_VSMC
GO:0006417	0.236	0.847	13	109	regulation of translation	BP	1	PRR16,PYM1,ZFP36L1,EEF2,LARP6,ANKHD1,RPUSD4,SAMD4B,ZFP36L2,EIF3K,EIF3D,TNRC6C,NCK1	up_VSAP_EC
GO:0032787	0.236	0.853	11	144	monocarboxylic acid metabolic process	BP	1	ASNS,NR1H4,PGK1,TPI1,TRIB3,PGAM1,SESN2,PTGS2,HIF1A,SLC45A3,ALDOC	down_VSAP_EC
GO:0051716	0.236	0.875	9	2001	cellular response to stimulus	BP	1	NR1H4,RGS1,MRC1,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0045727	0.236	0.889	5	40	positive regulation of translation	BP	1	EIF4A3,HNRNPD,TRUB2,FASTKD3,EIF5A	down_ACOR_VSMC
GO:0010941	0.236	0.9	4	524	regulation of cell death	BP	1	LYN,IGF1R,PDPN,STX4	down_ACOR_EC
GO:0010821	0.236	0.899	4	49	regulation of mitochondrion	BP	1	SLC35F6,DCN,CLEC16A,MGARP	down_VCAV_EC
GO:0003008	0.236	0.915	3	336	system process	BP	1	ACVRL1,SULF1,HOXA1	down_ACOR_EC
GO:0001952	0.236	0.915	3	34	regulation of cell-matrix adhesion	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0021761	0.236	0.916	3	27	limbic system development	BP	1	UBA6,GSK3B,NRP1	down_VSAP_EC
GO:0044093	0.236	0.916	3	437	positive regulation of molecular function	BP	1	HOXA3,PLCL1,NPNT	up_APUL_EC
GO:0043243	0.236	0.941	2	11	positive regulation of protein complex	BP	1	EIF5A,PDXP	down_ACOR_VSMC
GO:0044238	0.236	1	2	3383	primary metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0071320	0.236	0.943	2	9	cellular response to cAMP	BP	1	AKAP6,INPP5K	up_ACOR_VSMC
GO:0097345	0.236	0.942	2	10	mitochondrial outer membrane	BP	1	RHOT1,BNIP3	up_ACOR_VSMC
GO:0000768	0.236	0.942	2	10	syncytium formation by plasma membrane fusion	BP	1	CDON,FLOT1	up_VSAP_EC
GO:0006949	0.236	0.942	2	10	syncytium formation	BP	1	CDON,FLOT1	up_VSAP_EC
GO:0140253	0.236	0.942	2	10	cell-cell fusion	BP	1	CDON,FLOT1	up_VSAP_EC
GO:0017144	0.236	0.936	2	199	drug metabolic process	BP	1	GATM,CAV1	up_VSAP_VSMC

GO:0071345	0.236	0.936	2	210	cellular response to cytokine stimulus	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0050663	0.236	0.971	1	52	cytokine secretion	BP	1	LYN	down_ACOR_EC
GO:0007008	0.236	0.977	1	4	outer mitochondrial membrane organization	BP	1	SAMM50	down_ACOR_VSMC
GO:0030953	0.236	0.979	1	3	astral microtubule organization	BP	1	EZR	down_ACOR_VSMC
GO:0051105	0.236	0.979	1	3	regulation of DNA ligation	BP	1	HMGB1	down_ACOR_VSMC
GO:0051106	0.236	0.979	1	3	positive regulation of DNA ligation	BP	1	HMGB1	down_ACOR_VSMC
GO:1904874	0.236	0.979	1	3	positive regulation of telomerase RNA	BP	1	CCT4	down_ACOR_VSMC
GO:0009611	0.236	0.972	1	122	response to wounding	BP	1	SRSF6	down_AFEM_EC
GO:0046597	0.236	0.975	1	5	negative regulation of viral entry into host cell	BP	1	TRIM8	down_VCAV_EC
GO:0090153	0.236	0.975	1	5	regulation of sphingolipid biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:1905038	0.236	0.975	1	5	regulation of membrane lipid metabolic process	BP	1	ORMDL3	down_VCAV_EC
GO:2000303	0.236	0.975	1	5	regulation of ceramide biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:0009966	0.236	0.984	1	868	regulation of signal transduction	BP	1	GATA5	down_VFEM_VSMC
GO:0007440	0.236	0.977	1	4	foregut morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0036302	0.236	0.977	1	4	atrioventricular canal development	BP	1	PTPN11	down_VSAP_EC
GO:0048617	0.236	0.977	1	4	embryonic foregut morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0042636	0.236	0.977	1	4	negative regulation of hair cycle	BP	1	INHBA	down_VSAP_EC
GO:0051799	0.236	0.977	1	4	negative regulation of hair follicle development	BP	1	INHBA	down_VSAP_EC
GO:0140058	0.236	0.977	1	4	neuron projection arborization	BP	1	NRP1	down_VSAP_EC
GO:0033275	0.236	0.979	1	3	actin-myosin filament sliding	BP	1	TNNT2	up_ACOR_VSMC
GO:0034382	0.236	0.979	1	3	chylomicron remnant clearance	BP	1	LMF1	up_ACOR_VSMC
GO:0045759	0.236	0.979	1	3	negative regulation of action potential	BP	1	KCNE3	up_ACOR_VSMC
GO:0045906	0.236	0.984	1	2	negative regulation of vasoconstriction	BP	1	DOCK5	up_ACOR_VSMC
GO:0060028	0.236	0.979	1	3	convergent extension involved in axis elongation	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0071500	0.236	0.979	1	3	cellular response to nitrosative stress	BP	1	PARK7	up_ACOR_VSMC
GO:0071830	0.236	0.979	1	3	triglyceride-rich lipoprotein particle	BP	1	LMF1	up_ACOR_VSMC
GO:1904672	0.236	0.979	1	3	regulation of somatic stem cell population	BP	1	LBH	up_ACOR_VSMC
GO:1904694	0.236	0.984	1	2	negative regulation of vascular smooth muscle	BP	1	DOCK5	up_ACOR_VSMC
GO:0016973	0.236	0.979	1	3	poly(A)+ mRNA export from nucleus	BP	1	HHEX	up_VCAV_EC
GO:0035584	0.236	0.977	1	4	calcium-mediated signaling using	BP	1	SELP	up_VCAV_EC
GO:0045596	0.236	0.973	1	186	negative regulation of cell differentiation	BP	1	LRRC17	up_VCAV_VSMC
GO:0009617	0.236	0.972	1	133	response to bacterium	BP	1	IL22RA1	up_VPUL_VSMC
GO:0060255	0.236215835	0.81225	52	1782	regulation of macromolecule metabolic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,PLCL1,PKIB,SOX9,PKNOX2,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,IFI6,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,RARRES2,GMEB2,RIOX2,RNF114,NRP1,AZIN2,PRKCD,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0070527	0.236349549	0.97251	1	10	platelet aggregation	BP	1	PRKCD	up_ACOR_EC
GO:0090102	0.236671181	0.97243	1	10	cochlea development	BP	1	SOX9	up_ACOR_EC
GO:0030195	0.236863024	0.97238	1	10	negative regulation of blood coagulation	BP	1	PRKCD	up_ACOR_EC

GO:1900047	0.236863024	0.97238	1	10	negative regulation of hemostasis	BP	1	PRKCD	up_ACOR_EC
GO:0032501	0.237	0.791	178	1782	multicellular organismal process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,NAPEPLD,PCDH19,TWIST2,HOXA9,SEZ6L,CDON,WNT11,HNF4A,FAM107A,CD274,ACKR3,AXIN2,C5AR2,LIPC,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PPARGC1B,CBR3,RNPEP,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,TPCN2,IL6R,IRX5,SLIT2,CRIP2,ZHX3,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,KLKB1,EMP2,KCNE3,CHRM1,DLL1,EPN2,HOXA6,OSR1,ZNF449,IL17RC,FUZ,PDGFD,WARS2,SAV1,HERPUD2,KLF15,ANXA4,HPSE,PLXNA4,ANKRD54,CLDN1,ZBTB16,TOX,RARG,CCBE1,STAT5A,STAT6,HOXC4,RECK,PATZ1,PLPP3,GTF3C5,AMBRA1,F2RL1,DLX3,LMF1,GLIS2,MORC3,DDR2,MFN2,ZFP36L1,PDE6D,FXN,PIK3R1,TIAM1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,TBXA2R,SULF2,SHOX2,ABAT,EEF2,RTN4RL1,SASH1,AGTR1,HOXC10,CREBRF,MYD88,LOX,TFE3,LRP4,PASK,DPYSL2,GDPD5,DAGLB,HPS4,CLCN2,E2F4,PRKAB1,SMG9,MCPH1,KIF27,FBXO7,NTN4,LCAT,LIMD1,NLRX1,TKFC,DOP1B,CD83,NR2F6,KDM2B,FBLN1,RNF216,ZFP36L2,HPGD,RAF1,PNP,MAPKBP1,TAF8,NFIB,ZNF580,CYBA,CYB5D2,NCOA2,CDNF,ZFAND5,ANPEP,PQBP1,TTL,PLEKHA5,QARS,ACVRL1,TPRA1,VANGL1,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,ULK1	up_VSAP_EC
GO:0007275	0.237	0.793	138	1370	multicellular organism development	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,PCDH19,HOXA9,SEZ6L,CDON,WNT11,HNF4A,CD274,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PPARGC1B,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,IL6R,IRX5,SLIT2,CRIP2,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,EPN2,HOXA6,OSR1,FUZ,WARS2,SAV1,KLF15,HPSE,PLXNA4,ANKRD54,CLDN1,ZBTB16,TOX,RARG,CCBE1,STAT6,HOXC4,RECK,PATZ1,PLPP3,GTF3C5,AMBRA1,F2RL1,DLX3,GLIS2,MORC3,DDR2,MFN2,ZFP36L1,FXN,PIK3R1,TIAM1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,TBXA2R,SULF2,SHOX2,EEF2,RTN4RL1,SASH1,HOXC10,LOX,TFE3,LRP4,DPYSL2,GDPD5,DAGLB,CLCN2,E2F4,PRKAB1,SMG9,MCPH1,KIF27,FBXO7,NTN4,CD83,NR2F6,KDM2B,ZFP36L2,HPGD,RAF1,PNP,TAF8,NFIB,CYB5D2,CDNF,ZFAND5,ANPEP,PQBP1,TTL,PLEKHA5,QARS,ACVRL1,TPRA1,VANGL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,OGN,TRADD,PIR,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0045597	0.237	0.822	28	253	positive regulation of cell differentiation	BP	1	HOXA11,NAPEPLD,CDON,AXIN2,PPARGC1B,ZHX3,HOXD3,ABL1,BTG1,MAP3K5,SAV1,ANKRD54,ZBTB16,TOX,DDR2,ZFP36L1,IRX3,ZEB1,SHOX2,GDPD5,CD83,PNP,CYB5D2,ACVRL1,FLOT1,NCK1,MAP2K2,TGFBR2	up_VSAP_EC
GO:0050778	0.237	0.852	11	141	positive regulation of immune response	BP	1	NR1H4,SOCS5,FAM49B,PTPN2,EIF2B1,PVR,SKAP2,TFRC,LYN,GBP5,A2M	down_VSAP_EC
GO:0032984	0.237	0.862	9	70	protein-containing complex disassembly	BP	1	FGF13,DNAJC6,ACTN2,MID1,F2RL1,BNIP3,SMARCD3,LAMP2,DDIT4	up_ACOR_VSMC
GO:0015931	0.237	0.872	7	59	nucleobase-containing compound transport	BP	1	DDX39A,SLC35C2,RAN,NUP62,NUP188,DDX39B,MRPL18	down_ACOR_VSMC
GO:0009124	0.237	0.88	6	51	nucleoside monophosphate	BP	1	PFAS,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0001890	0.237	0.879	6	51	placenta development	BP	1	SLC29A1,E2F8,PPARD,FOSL1,PLK4,RTCB	down_ACOR_VSMC
GO:0043412	0.237	0.886	6	1225	macromolecule modification	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0042471	0.237	0.89	5	34	ear morphogenesis	BP	1	FGFR2,SEC24B,FZD3,CHD7,EDN1	up_ACOR_VSMC
GO:0007224	0.237	0.898	4	50	smoothened signaling pathway	BP	1	EVC,GLI3,IFT57,GLIS2	down_VCAV_EC
GO:1904591	0.237	0.902	4	25	positive regulation of protein import	BP	1	LEP,PTPN22,PSEN1,JUP	up_ACOR_VSMC
GO:0009060	0.237	0.914	3	31	aerobic respiration	BP	1	ENSCAFG00000007260,HIF1A,BNIP3	down_VSAP_EC
GO:0010633	0.237	0.915	3	28	negative regulation of epithelial cell migration	BP	1	STARD13,APOE,STRAP	down_VSAP_EC
GO:0048146	0.237	0.918	3	18	positive regulation of fibroblast proliferation	BP	1	CDKN1A,DDR2,FOSL2	up_ACOR_VSMC

GO:0032392	0.237	0.917	3	19	DNA geometric change	BP	1	HMGB1,BLM,GINS4	up_VCAV_EC
GO:0002718	0.237	0.916	3	21	regulation of cytokine production involved in	BP	1	TLR4,GATA3,TLR3	up_VCAV_EC
GO:0007613	0.237	0.917	3	20	memory	BP	1	PLK2,RELN,CREB1	up_VCAV_EC
GO:0031111	0.237	0.941	2	11	negative regulation of microtubule polymerization or	BP	1	STMN1,ARHGEF2	down_ACOR_VSMC
GO:0043403	0.237	0.94	2	11	skeletal muscle tissue regeneration	BP	1	EZH2,PPARD	down_ACOR_VSMC
GO:0030219	0.237	0.938	2	16	megakaryocyte differentiation	BP	1	PTPN11,PRMT1	down_VSAP_EC
GO:1900408	0.237	0.939	2	15	negative regulation of cellular response to	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:1903202	0.237	0.939	2	15	negative regulation of oxidative stress-induced	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:0032365	0.237	0.943	2	9	intracellular lipid transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0016202	0.237	0.935	2	39	regulation of striated muscle tissue	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0051896	0.237	0.935	2	39	regulation of protein kinase B signaling	BP	1	LEP,F3	up_AFEM_EC
GO:0008284	0.237	0.936	2	238	positive regulation of cell proliferation	BP	1	TBX5,HOXA3	up_APUL_EC
GO:0034097	0.237	0.936	2	238	response to cytokine	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0021846	0.237	0.94	2	11	cell proliferation in forebrain	BP	1	HOOK3,HHEX	up_VCAV_EC
GO:0036475	0.237	0.941	2	11	neuron death in response to oxidative stress	BP	1	TLR4,HIF1A	up_VCAV_EC
GO:1903203	0.237	0.941	2	11	regulation of oxidative stress-induced neuron	BP	1	TLR4,HIF1A	up_VCAV_EC
GO:0000122	0.237	0.936	2	218	negative regulation of transcription by RNA polymerase II	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:1901698	0.237	0.936	2	266	response to nitrogen compound	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0072358	0.237	0.937	2	268	cardiovascular system development	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:1904816	0.237	0.979	1	3	positive regulation of protein localization to chromosome, telomeric	BP	1	CCT4	down_ACOR_VSMC
GO:0010836	0.237	0.979	1	3	negative regulation of protein ADP-ribosylation	BP	1	TINF2	down_ACOR_VSMC
GO:0021520	0.237	0.979	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	down_ACOR_VSMC
GO:0042090	0.237	0.979	1	3	interleukin-12 biosynthetic process	BP	1	MAST2	down_ACOR_VSMC
GO:0045075	0.237	0.979	1	3	regulation of interleukin-12 biosynthetic process	BP	1	MAST2	down_ACOR_VSMC
GO:0045647	0.237	0.979	1	3	negative regulation of erythrocyte	BP	1	HSPA9	down_ACOR_VSMC
GO:0072611	0.237	0.979	1	3	interleukin-13 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:2000665	0.237	0.979	1	3	regulation of interleukin-13 secretion	BP	1	ARG2	down_ACOR_VSMC
GO:0006465	0.237	0.975	1	5	signal peptide processing	BP	1	SEC11C	down_VCAV_EC
GO:0002551	0.237	0.975	1	5	mast cell chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0097531	0.237	0.975	1	5	mast cell migration	BP	1	RAC2	down_VCAV_EC
GO:1902415	0.237	0.975	1	5	regulation of mRNA binding	BP	1	LARP6	down_VCAV_EC
GO:1902416	0.237	0.975	1	5	positive regulation of mRNA binding	BP	1	LARP6	down_VCAV_EC
GO:0032386	0.237	0.972	1	137	regulation of intracellular transport	BP	1	RAB11B	down_VPOR_EC
GO:0000052	0.237	0.977	1	4	citrulline metabolic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0010869	0.237	0.977	1	4	regulation of receptor biosynthetic process	BP	1	HIF1A	down_VSAP_EC
GO:0032800	0.237	0.977	1	4	receptor biosynthetic process	BP	1	HIF1A	down_VSAP_EC
GO:0003334	0.237	0.977	1	4	keratinocyte development	BP	1	FLNB	down_VSAP_EC
GO:0044794	0.237	0.977	1	4	positive regulation by host of viral process	BP	1	APOE	down_VSAP_EC

GO:0072007	0.237	0.975	1	5	mesangial cell differentiation	BP	1	ACTA2	down_VSAP_EC
GO:0072143	0.237	0.975	1	5	mesangial cell development	BP	1	ACTA2	down_VSAP_EC
GO:1903897	0.237	0.975	1	5	regulation of PERK-mediated unfolded	BP	1	PTPN2	down_VSAP_EC
GO:1904238	0.237	0.975	1	5	pericyte cell differentiation	BP	1	ACTA2	down_VSAP_EC
GO:0009249	0.237	0.979	1	3	protein lipoylation	BP	1	LIPT2	up_ACOR_VSMC
GO:0009438	0.237	0.979	1	3	methylglyoxal metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0014706	0.237	0.971	1	112	striated muscle tissue development	BP	1	SGCD	up_AORT_EC
GO:0002070	0.237	0.979	1	3	epithelial cell maturation	BP	1	HIF1A	up_VCAV_EC
GO:0006930	0.237	0.979	1	3	substrate-dependent cell migration, cell extension	BP	1	NCK1	up_VCAV_EC
GO:0060749	0.237	0.979	1	3	mammary gland alveolus development	BP	1	HIF1A	up_VCAV_EC
GO:0061377	0.237	0.979	1	3	mammary gland lobule development	BP	1	HIF1A	up_VCAV_EC
GO:0051493	0.237	0.972	1	188	regulation of cytoskeleton organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0051051	0.237	0.971	1	112	negative regulation of transport	BP	1	HOXA3	up_VPOR_VSMC
GO:0030217	0.237	0.971	1	65	T cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0009165	0.237	0.971	1	104	nucleotide biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0002757	0.237	0.971	1	78	immune response-activating signal	BP	1	NR1H4	up_VPUL_EC
GO:1903532	0.237	0.971	1	78	positive regulation of secretion by cell	BP	1	NR1H4	up_VPUL_EC
GO:0060059	0.237	0.979	1	3	embryonic retina morphogenesis in camera-	BP	1	CDON	up_VSAP_EC
GO:0050918	0.237033337	0.97234	1	10	positive chemotaxis	BP	1	NRP1	up_ACOR_EC
GO:0061333	0.237415117	0.93535	2	35	renal tubule morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0046627	0.237725743	0.97217	1	10	negative regulation of insulin receptor signaling	BP	1	PRKCD	up_ACOR_EC
GO:0071604	0.23781586	0.97215	1	10	transforming growth factor beta production	BP	1	CDH3	up_ACOR_EC
GO:0071634	0.23781586	0.97215	1	10	regulation of transforming growth factor beta	BP	1	CDH3	up_ACOR_EC
GO:0043616	0.23784181	0.97214	1	10	keratinocyte proliferation	BP	1	CDH3	up_ACOR_EC
GO:0051338	0.23792704	0.85455	10	288	regulation of transferase activity	BP	1	PKIB,ENSCAFG00000004331,FZD5,DUSP26,PAK3,LRRC15,LRRC4,PRKCD,DBNDD2,CCNYL1	up_ACOR_EC
GO:0010629	0.238	0.815	35	502	negative regulation of gene expression	BP	1	PRICKLE1,NR1H4,PLK3,SERPINE1,ETV6,CBX5,FHL2,SMARCA4,SESN2,HIF1A,PTPN2,MORF4L2,PEG3,SMG7,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,APOE,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,EIF2S1,A2M,HIF1AN,SIX4,CDKN1A	down_VSAP_EC
GO:0031327	0.238	0.82	29	412	negative regulation of cellular biosynthetic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,ENPP1,CBX5,TRIB3,FHL2,SMARCA4,SESN2,PTPN2,MORF4L2,PEG3,MTDH,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,EIF2S1,HIF1AN,SIX4	down_VSAP_EC
GO:0048667	0.238	0.836	17	140	cell morphogenesis involved in neuron differentiation	BP	1	EPYC,FEZ1,FGFR2,SEC24B,ZNF365,NRP1,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL	up_ACOR_VSMC
GO:0007568	0.238	0.898	4	50	aging	BP	1	PRNP,BMPR1A,PRMT6,PRELP	down_VCAV_EC
GO:0045995	0.238	0.899	4	40	regulation of embryonic development	BP	1	SULF1,PRKACB,CTNNB1,SIX4	down_VSAP_EC
GO:0050770	0.238	0.899	4	39	regulation of axonogenesis	BP	1	SIPA1L1,IFRD1,UST,NRP1	down_VSAP_EC
GO:0042692	0.238	0.897	4	105	muscle cell differentiation	BP	1	DLL1,GREM1,BVES,DMPK	up_AFEM_EC
GO:0002088	0.238	0.901	4	26	lens development in camera-type eye	BP	1	CDON,CTNS,TGFBR2,CITED2	up_VSAP_EC
GO:0060021	0.238	0.913	3	34	roof of mouth development	BP	1	BMPR1A,GLI3,LOXL3	down_VCAV_EC

GO:0010594	0.238	0.912	3	71	regulation of endothelial cell migration	BP	1	ANGPT4,TBXA2R,ADAM17	up_AFEM_EC
GO:0009994	0.238	0.94	2	11	oocyte differentiation	BP	1	TRIP13,FBXO5	down_ACOR_VSMC
GO:0038066	0.238	0.937	2	19	p38MAPK cascade	BP	1	ZFP36L1,SASH1	down_VCAV_EC
GO:0042073	0.238	0.938	2	16	intraciliary transport	BP	1	RPGR,DYNLL1	down_VSAP_EC
GO:0032410	0.238	0.937	2	17	negative regulation of transporter activity	BP	1	REM1,CALM1	down_VSAP_EC
GO:0070884	0.238	0.938	2	16	regulation of calcineurin-NFAT signaling cascade	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:0106056	0.238	0.938	2	16	regulation of calcineurin-mediated signaling	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:1904063	0.238	0.937	2	17	negative regulation of cation transmembrane	BP	1	REM1,CALM1	down_VSAP_EC
GO:0009268	0.238	0.941	2	10	response to pH	BP	1	GJA1,RAB11B	up_ACOR_VSMC
GO:0042742	0.238	0.935	2	39	defense response to bacterium	BP	1	BPI,ADAM17	up_AFEM_EC
GO:0046425	0.238	0.935	2	39	regulation of JAK-STAT cascade	BP	1	LEP,LRRC15	up_AFEM_EC
GO:0048103	0.238	0.941	2	10	somatic stem cell division	BP	1	ZFP36L2,LBH	up_VSAP_EC
GO:0048678	0.238	0.941	2	10	response to axon injury	BP	1	RTN4RL1,MAP2K2	up_VSAP_EC
GO:0002440	0.238	0.971	1	51	production of molecular mediator of immune	BP	1	STX4	down_ACOR_EC
GO:0006346	0.238	0.979	1	3	methylation-dependent chromatin silencing	BP	1	UHRF1	down_ACOR_VSMC
GO:0022614	0.238	0.979	1	3	membrane to membrane docking	BP	1	EZR	down_ACOR_VSMC
GO:0071578	0.238	0.979	1	3	zinc ion import across plasma membrane	BP	1	SLC30A1	down_ACOR_VSMC
GO:0072095	0.238	0.979	1	3	regulation of branch elongation involved in ureteric bud branching	BP	1	SIX4	down_ACOR_VSMC
GO:1902965	0.238	0.979	1	3	regulation of protein localization to early	BP	1	EZR	down_ACOR_VSMC
GO:1902966	0.238	0.979	1	3	positive regulation of protein localization to	BP	1	EZR	down_ACOR_VSMC
GO:1903867	0.238	0.979	1	3	extraembryonic membrane development	BP	1	E2F8	down_ACOR_VSMC
GO:1905666	0.238	0.979	1	3	regulation of protein localization to endosome	BP	1	EZR	down_ACOR_VSMC
GO:1905668	0.238	0.979	1	3	positive regulation of protein localization to	BP	1	EZR	down_ACOR_VSMC
GO:1990414	0.238	0.979	1	3	replication-born double-strand break repair via sister chromatid exchange	BP	1	RAD51	down_ACOR_VSMC
GO:0009151	0.238	0.975	1	5	purine deoxyribonucleotide	BP	1	ADK	down_VCAV_EC
GO:0009200	0.238	0.975	1	5	deoxyribonucleoside triphosphate metabolic	BP	1	ADK	down_VCAV_EC
GO:0009215	0.238	0.975	1	5	purine deoxyribonucleoside	BP	1	ADK	down_VCAV_EC
GO:0019511	0.238	0.975	1	5	peptidyl-proline hydroxylation	BP	1	CRTAP	down_VCAV_EC
GO:1902337	0.238	0.975	1	5	regulation of apoptotic process involved in	BP	1	B4GALT1	down_VCAV_EC
GO:1904748	0.238	0.975	1	5	regulation of apoptotic process involved in	BP	1	B4GALT1	down_VCAV_EC
GO:0051173	0.238	0.984	1	874	positive regulation of nitrogen compound	BP	1	GATA5	down_VFEM_VSMC
GO:0033085	0.238	0.976	1	4	negative regulation of T cell differentiation in	BP	1	PTPN2	down_VSAP_EC
GO:0060315	0.238	0.975	1	5	negative regulation of ryanodine-sensitive calcium-release channel	BP	1	CALM1	down_VSAP_EC
GO:1903306	0.238	0.976	1	4	negative regulation of regulated secretory	BP	1	REST	down_VSAP_EC
GO:2000678	0.238	0.976	1	4	negative regulation of transcription regulatory region DNA binding	BP	1	DDIT3	down_VSAP_EC
GO:0051280	0.238	0.975	1	5	negative regulation of release of sequestered calcium ion into cytosol	BP	1	CALM1	down_VSAP_EC
GO:0051284	0.238	0.975	1	5	positive regulation of sequestering of calcium	BP	1	CALM1	down_VSAP_EC

GO:0003188	0.238	0.979	1	3	heart valve formation	BP	1	TBX20	up_ACOR_VSMC
GO:0051004	0.238	0.979	1	3	regulation of lipoprotein lipase activity	BP	1	LMF1	up_ACOR_VSMC
GO:0043009	0.238	0.973	1	227	chordate embryonic development	BP	1	HOXA9	up_AORT_VSMC
GO:0002064	0.238	0.971	1	71	epithelial cell development	BP	1	ARHGEF26	up_APUL_EC
GO:0032259	0.238	0.971	1	71	methylation	BP	1	NR1H4	up_APUL_EC
GO:0021516	0.238	0.976	1	4	dorsal spinal cord development	BP	1	HOXB8	up_VCAV_EC
GO:0030953	0.238	0.979	1	3	astral microtubule organization	BP	1	RAB11A	up_VCAV_EC
GO:0042574	0.238	0.976	1	4	retinal metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0009725	0.238	0.972	1	188	response to hormone	BP	1	CA2	up_VCAV_VSMC
GO:0038061	0.238	0.97	1	34	NIK/NF-kappaB signaling	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0050679	0.238	0.97	1	62	positive regulation of epithelial cell proliferation	BP	1	EYA1	up_VFEM_EC
GO:0009205	0.238	0.971	1	98	purine ribonucleoside triphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0006650	0.238	0.971	1	78	glycerophospholipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0051346	0.238	0.971	1	78	negative regulation of hydrolase activity	BP	1	PTGER2	up_VPUL_EC
GO:0021903	0.238	0.979	1	3	rostrocaudal neural tube patterning	BP	1	KDM2B	up_VSAP_EC
GO:0090278	0.238002363	0.9721	1	10	negative regulation of peptide hormone	BP	1	KCNB1	up_ACOR_EC
GO:0006855	0.238082446	0.97208	1	10	drug transmembrane transport	BP	1	AQP1	up_ACOR_EC
GO:1904375	0.238134471	0.93503	2	35	regulation of protein localization to cell	BP	1	PLS1,LRRC15	up_ACOR_EC
GO:0060338	0.238741514	0.97192	1	10	regulation of type I interferon-mediated	BP	1	MAVS	up_ACOR_EC
GO:0030154	0.239	0.794	108	1040	cell differentiation	BP	1	EXPH5,SH3TC2,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,LBH,GATA5,GATA4,CD83,ANGPT1,EPYC,HTR2B,RASSF2,FNDC5,SHROOM3,FEZ1,ITM2C,BMP4,LNPK,FGFR2,GJA1,ELF1,ATRX,TRPS1,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,ISG15,ACSL6,ZNF365,LMO4,TMEM108,FGF18,FAM210B,ARHGEF26,P4HTM,NEBL,CDKN2B,PLAC8B,ANKRD1,PLEKHB2,F2RL1,CAMK2D,CTSB,BNIP3,CLSTN1,LRRC8C,NRP1,PTPN22,GPM6A,CHD2,ULK2,DMPK,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,TBX20,TPT1,TBX5,CCDC3,MARF1,FZD3,AFF4,DKKL1,FRS2,RND1,DAG1,POMK,APP,LAMA3,PSEN1,TGFBR1,CHD7,SPINK2,SIPA1L1,DDR2,CLN8,FOSL2,SSH3,EDN1,ARID5B,ASAP1,DMC1,JAM3,B2M,DISC1,ATXN10,FEZ2,SUN1,CNOT4,WASL,DOCK5,ENSCAFG00000003530,IL18R1,BVES,RREB1,CRKL,MYOZ2	up_ACOR_VSMC
GO:1901698	0.239	0.819	30	266	response to nitrogen compound	BP	1	ACTN2,LEP,ABCA1,ATRX,CASTOR1,TLR3,GLRB,ADCY6,EGLN1,AKAP6,P2RX7,UBR1,PTPN22,OS9,STT3B,APLP1,SESN3,PRKCE,AGRN,APP,PSEN1,JUP,NOD2,HERPUD1,GNAQ,INPP5K,FAF2,WFS1,DZIP3,SH3BP4	up_ACOR_VSMC
GO:0098609	0.239	0.841	14	181	cell-cell adhesion	BP	1	SOCS5,FAM49B,FBLIM1,MSN,PTPN2,PVR,CDH11,CTNNB1,TFRC,LYN,SLC7A11,ITGB3,SDC4,ICAM5	down_VSAP_EC
GO:0032386	0.239	0.858	9	137	regulation of intracellular transport	BP	1	PRNP,ENSCAFG00000014978,AKT2,SCP2,GLI3,PARK7,MAVS,ARHGAP1,RAC2	down_VCAV_EC
GO:0032943	0.239	0.871	7	60	mononuclear cell proliferation	BP	1	HMGB1,MNDA,ARG2,TFRC,CORO1A,ELF4,CTPS1	down_ACOR_VSMC
GO:0046651	0.239	0.871	7	60	lymphocyte proliferation	BP	1	HMGB1,MNDA,ARG2,TFRC,CORO1A,ELF4,CTPS1	down_ACOR_VSMC
GO:0050794	0.239	0.91	6	3075	regulation of cellular process	BP	1	SLITRK5,LIMK1,GATA5,CA2,LRRC17,C6	up_VCAV_VSMC
GO:0002682	0.239	0.913	3	343	regulation of immune system process	BP	1	LYN,HOXA7,STX4	down_ACOR_EC
GO:0070664	0.239	0.917	3	18	negative regulation of leukocyte proliferation	BP	1	BMP4,PDE5A,CD274	up_ACOR_VSMC
GO:0030258	0.239	0.911	3	71	lipid modification	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC

GO:0033993	0.239	0.935	2	186	response to lipid	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0030032	0.239	0.936	2	19	lamellipodium assembly	BP	1	RHOD,RAC2	down_VCAV_EC
GO:1901796	0.239	0.937	2	18	regulation of signal transduction by p53 class	BP	1	PRMT6,SPRED1	down_VCAV_EC
GO:0034381	0.239	0.941	2	10	plasma lipoprotein particle clearance	BP	1	LRPAP1,LMF1	up_ACOR_VSMC
GO:0060135	0.239	0.941	2	10	maternal process involved in female pregnancy	BP	1	CITED2,CTSB	up_ACOR_VSMC
GO:0060384	0.239	0.942	2	9	innervation	BP	1	NRP1,CHD7	up_ACOR_VSMC
GO:0090140	0.239	0.941	2	10	regulation of mitochondrial fission	BP	1	MARCH5,BNIP3	up_ACOR_VSMC
GO:0008347	0.239	0.94	2	11	glial cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:1901342	0.239	0.934	2	114	regulation of vasculature development	BP	1	C3AR1,MTDH	up_VPOR_EC
GO:0030036	0.239	0.935	2	223	actin cytoskeleton organization	BP	1	CDC42EP5,MTSS1	up_VFEM_EC
GO:0033688	0.239	0.941	2	10	regulation of osteoblast proliferation	BP	1	ABL1,HPSE	up_VSAP_EC
GO:0033002	0.239	0.97	1	55	muscle cell proliferation	BP	1	SULF1	down_ACOR_EC
GO:0090150	0.239	0.97	1	64	establishment of protein localization to membrane	BP	1	ACSL3	down_ACOR_EC
GO:0009263	0.239	0.979	1	3	deoxyribonucleotide biosynthetic process	BP	1	RRM1	down_ACOR_VSMC
GO:1902932	0.239	0.979	1	3	positive regulation of alcohol biosynthetic	BP	1	SREBF1	down_ACOR_VSMC
GO:0018230	0.239	0.975	1	5	peptidyl-L-cysteine S-palmitoylation	BP	1	CLIP3	down_VCAV_EC
GO:0018231	0.239	0.975	1	5	peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-	BP	1	CLIP3	down_VCAV_EC
GO:0010714	0.239	0.975	1	5	positive regulation of collagen metabolic	BP	1	LARP6	down_VCAV_EC
GO:0014911	0.239	0.974	1	6	positive regulation of smooth muscle cell	BP	1	PDGFRB	down_VCAV_EC
GO:0032965	0.239	0.975	1	5	regulation of collagen biosynthetic process	BP	1	LARP6	down_VCAV_EC
GO:0032967	0.239	0.975	1	5	positive regulation of collagen biosynthetic	BP	1	LARP6	down_VCAV_EC
GO:0034114	0.239	0.975	1	5	regulation of heterotypic cell-cell adhesion	BP	1	THY1	down_VCAV_EC
GO:0042481	0.239	0.975	1	5	regulation of odontogenesis	BP	1	ASPN	down_VCAV_EC
GO:0060263	0.239	0.975	1	5	regulation of respiratory burst	BP	1	RAC2	down_VCAV_EC
GO:0002920	0.239	0.976	1	4	regulation of humoral immune response	BP	1	A2M	down_VSAP_EC
GO:0048670	0.239	0.976	1	4	regulation of collateral sprouting	BP	1	IFRD1	down_VSAP_EC
GO:0072217	0.239	0.976	1	4	negative regulation of metanephros	BP	1	CTNNB1	down_VSAP_EC
GO:0097090	0.239	0.976	1	4	presynaptic membrane organization	BP	1	APOE	down_VSAP_EC
GO:0006152	0.239	0.979	1	3	purine nucleoside catabolic process	BP	1	ENPP4	up_ACOR_VSMC
GO:0007603	0.239	0.979	1	3	phototransduction, visible light	BP	1	GNAQ	up_ACOR_VSMC
GO:0032020	0.239	0.979	1	3	ISG15-protein conjugation	BP	1	ISG15	up_ACOR_VSMC
GO:0033216	0.239	0.979	1	3	ferric iron import	BP	1	B2M	up_ACOR_VSMC
GO:0046130	0.239	0.979	1	3	purine ribonucleoside catabolic process	BP	1	ENPP4	up_ACOR_VSMC
GO:2001268	0.239	0.979	1	3	negative regulation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:0007507	0.239	0.972	1	194	heart development	BP	1	EYA1	up_AFEM_VSMC
GO:0051960	0.239	0.972	1	216	regulation of nervous system development	BP	1	WNT7A	up_AORT_VSMC
GO:0060284	0.239	0.973	1	212	regulation of cell development	BP	1	WNT7A	up_AORT_VSMC
GO:0048863	0.239	0.97	1	70	stem cell differentiation	BP	1	TBX5	up_APUL_EC

GO:0051216	0.239	0.97	1	70	cartilage development	BP	1	HOXA3	up_APUL_EC
GO:0010623	0.239	0.976	1	4	programmed cell death involved in cell	BP	1	KIT	up_VCAV_EC
GO:0050930	0.239	0.976	1	4	induction of positive chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:0071593	0.239	0.979	1	3	lymphocyte aggregation	BP	1	STK10	up_VCAV_EC
GO:0071363	0.239	0.972	1	188	cellular response to growth factor stimulus	BP	1	GATA5	up_VCAV_VSMC
GO:0044057	0.239	0.971	1	110	regulation of system process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051249	0.239	0.971	1	107	regulation of lymphocyte activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0051962	0.239	0.971	1	112	positive regulation of nervous system	BP	1	SHOX2	up_VFEM_VSMC
GO:0010959	0.239	0.97	1	79	regulation of metal ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0052548	0.239	0.97	1	80	regulation of endopeptidase activity	BP	1	PTGER2	up_VPUL_EC
GO:0010560	0.239	0.979	1	3	positive regulation of glycoprotein biosynthetic	BP	1	SOAT1	up_VSAP_EC
GO:1903020	0.239	0.979	1	3	positive regulation of glycoprotein metabolic	BP	1	SOAT1	up_VSAP_EC
GO:0060986	0.239201109	0.9718	1	10	endocrine hormone secretion	BP	1	AQP1	up_ACOR_EC
GO:0071715	0.239471236	0.97174	1	10	icosanoid transport	BP	1	CFI	up_ACOR_EC
GO:1901571	0.239471236	0.97174	1	10	fatty acid derivative transport	BP	1	CFI	up_ACOR_EC
GO:1903523	0.239793969	0.97166	1	10	negative regulation of blood circulation	BP	1	RNLS	up_ACOR_EC
GO:0051186	0.24	0.837	16	159	cofactor metabolic process	BP	1	ACLY,HMGCR,NNT,HSPA9,MVD,ELOVL1,PDXP,AADAT,GSTO1,ELOVL6,ENSCAFG00000006478,ENSCAFG00000005637,PDHA1,GGH,PGD,PDSS1	down_ACOR_VSMC
GO:1902903	0.24	0.853	10	125	regulation of supramolecular fiber	BP	1	ARHGEF2,WDR1,ACTR3,CRYAB,APOE,TWF1,PLEKHG2,CAPG,NRP1,MID1	down_VSAP_EC
GO:0002376	0.24	0.871	7	622	immune system process	BP	1	C3AR1,BARX1,HOXA3,ARHGEF2,OAS3,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0072331	0.24	0.897	4	49	signal transduction by p53 class mediator	BP	1	PRMT6,ZMAT3,SPRED1,FOXO3	down_VCAV_EC
GO:0065008	0.24	0.904	4	1056	regulation of biological quality	BP	1	HOXC10,ENSCAFG00000005494,LNPEP,TAOK1	up_AORT_EC
GO:0000422	0.24	0.912	3	34	autophagy of mitochondrion	BP	1	GABARAP,WDR45,CLEC16A	down_VCAV_EC
GO:0061726	0.24	0.912	3	34	mitochondrion disassembly	BP	1	GABARAP,WDR45,CLEC16A	down_VCAV_EC
GO:0071887	0.24	0.912	3	34	leukocyte apoptotic process	BP	1	GPAM,GLI3,TSC22D3	down_VCAV_EC
GO:0060351	0.24	0.939	2	11	cartilage development involved in endochondral bone morphogenesis	BP	1	POC1A,SERPINH1	down_ACOR_VSMC
GO:0009141	0.24	0.934	2	110	nucleoside triphosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0048732	0.24	0.933	2	116	gland development	BP	1	HOXA3,SEMA3A	up_VPOR_EC
GO:0002793	0.24	0.97	1	54	positive regulation of peptide secretion	BP	1	STX4	down_ACOR_EC
GO:0003206	0.24	0.97	1	51	cardiac chamber morphogenesis	BP	1	NRP2	down_ACOR_EC
GO:0050714	0.24	0.97	1	54	positive regulation of protein secretion	BP	1	STX4	down_ACOR_EC
GO:0002192	0.24	0.979	1	3	IRES-dependent translational initiation of	BP	1	RBM14	down_ACOR_VSMC
GO:0001781	0.24	0.978	1	3	neutrophil apoptotic process	BP	1	PIK3CD	down_ACOR_VSMC
GO:0110017	0.24	0.979	1	3	cap-independent translational initiation of	BP	1	RBM14	down_ACOR_VSMC
GO:0021615	0.24	0.978	1	3	glossopharyngeal nerve morphogenesis	BP	1	HOXA3	down_ACOR_VSMC
GO:0033029	0.24	0.978	1	3	regulation of neutrophil apoptotic process	BP	1	PIK3CD	down_ACOR_VSMC
GO:0070208	0.24	0.978	1	3	protein heterotrimerization	BP	1	C1QTNF6	down_ACOR_VSMC
GO:0070314	0.24	0.978	1	3	G1 to G0 transition	BP	1	EZH2	down_ACOR_VSMC
GO:0072718	0.24	0.978	1	3	response to cisplatin	BP	1	TIMELESS	down_ACOR_VSMC

GO:0072719	0.24	0.978	1	3	cellular response to cisplatin	BP	1	TIMELESS	down_ACOR_VSMC
GO:0090166	0.24	0.978	1	3	Golgi disassembly	BP	1	PLK3	down_ACOR_VSMC
GO:0032502	0.24	1	1	1661	developmental process	BP	1	GATA5	down_AFEM_VSMC
GO:0006166	0.24	0.974	1	5	purine ribonucleoside salvage	BP	1	ADK	down_VCAV_EC
GO:0043174	0.24	0.974	1	5	nucleoside salvage	BP	1	ADK	down_VCAV_EC
GO:0071636	0.24	0.974	1	5	positive regulation of transforming growth factor beta production	BP	1	LUM	down_VCAV_EC
GO:0043269	0.24	0.971	1	135	regulation of ion transport	BP	1	RAB11B	down_VPOR_EC
GO:0031650	0.24	0.976	1	4	regulation of heat generation	BP	1	PTGS2	down_VSAP_EC
GO:0031943	0.24	0.976	1	4	regulation of glucocorticoid metabolic	BP	1	REST	down_VSAP_EC
GO:0060742	0.24	0.976	1	4	epithelial cell differentiation involved in prostate gland	BP	1	CTNNB1	down_VSAP_EC
GO:0071850	0.24	0.974	1	5	mitotic cell cycle arrest	BP	1	CDKN1A	down_VSAP_EC
GO:0045780	0.24	0.976	1	4	positive regulation of bone resorption	BP	1	TFRC	down_VSAP_EC
GO:0046852	0.24	0.976	1	4	positive regulation of bone remodeling	BP	1	TFRC	down_VSAP_EC
GO:0060484	0.24	0.976	1	4	lung-associated mesenchyme	BP	1	CTNNB1	down_VSAP_EC
GO:1904396	0.24	0.976	1	4	regulation of neuromuscular junction	BP	1	SIX4	down_VSAP_EC
GO:0009435	0.24	0.978	1	3	NAD biosynthetic process	BP	1	NMNAT1	up_ACOR_VSMC
GO:0030431	0.24	0.978	1	3	sleep	BP	1	PTGDR	up_ACOR_VSMC
GO:0043497	0.24	0.979	1	3	regulation of protein heterodimerization	BP	1	CDON	up_VCAV_EC
GO:0055082	0.24	0.972	1	189	cellular chemical homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0043244	0.24	0.97	1	34	regulation of protein complex disassembly	BP	1	ARHGEF2	up_VPOR_EC
GO:0048645	0.24	0.97	1	33	animal organ formation	BP	1	HOXA3	up_VPOR_EC
GO:0097191	0.24	0.97	1	79	extrinsic apoptotic signaling pathway	BP	1	ARHGEF2	up_VPUL_EC
GO:0043269	0.24	0.971	1	135	regulation of ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0010172	0.24	0.978	1	3	embryonic body morphogenesis	BP	1	CDON	up_VSAP_EC
GO:0046322	0.24	0.978	1	3	negative regulation of fatty acid oxidation	BP	1	ACACB	up_VSAP_EC
GO:0050995	0.24	0.978	1	3	negative regulation of lipid catabolic process	BP	1	ACACB	up_VSAP_EC
GO:0021559	0.24	0.978	1	3	trigeminal nerve development	BP	1	PLXNA4	up_VSAP_EC
GO:0021636	0.24	0.978	1	3	trigeminal nerve morphogenesis	BP	1	PLXNA4	up_VSAP_EC
GO:0021637	0.24	0.978	1	3	trigeminal nerve structural organization	BP	1	PLXNA4	up_VSAP_EC
GO:0021785	0.24	0.978	1	3	branchiomotor neuron axon guidance	BP	1	PLXNA4	up_VSAP_EC
GO:1902287	0.24	0.978	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	PLXNA4	up_VSAP_EC
GO:2001242	0.24	0.97	1	62	regulation of intrinsic apoptotic signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0051298	0.240258845	0.93407	2	35	centrosome duplication	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0033363	0.240337108	0.97152	1	10	secretory granule organization	BP	1	AQP1	up_ACOR_EC

GO:0019222	0.240574708	0.8074	56	1934	regulation of metabolic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,PLCL1,PKIB,SOX9,PKNOX2,PCSK1N,NDRG2,ENSCAFG00000004331,EDEM2,FZD5,CCDC3,IFI6,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PAK3,TNFRSF19,CST3,PIAS1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,RIOX2,RNF114,NRP1,AZIN2,PRKCD,PPP1R26,PYGO2,DBNDD2,EFEMP1,CCNYL1,MFAP4,TLE2	up_ACOR_EC
GO:0051797	0.240974864	0.97136	1	10	regulation of hair follicle development	BP	1	CDH3	up_ACOR_EC
GO:0044238	0.241	0.853	19	3383	primary metabolic process	BP	1	ACVRL1,YEATS2,LYN,IGF1R,YBX3,HIVEP2,HOXA7,PRKAR2A,USP28,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,ACSL3,WDR12,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0051050	0.241	0.833	17	235	positive regulation of transport	BP	1	VEGFA,NR1H4,PLK3,SERPINE1,PTPN11,MYO1C,MSN,KIF5B,HIF1A,ZPR1,APOE,GSK3B,SH3GLB1,SDC4,HTT,CALM1,HOMER1	down_VSAP_EC
GO:0006873	0.241	0.836	16	160	cellular ion homeostasis	BP	1	CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0090087	0.241	0.84	14	185	regulation of peptide transport	BP	1	NR1H4,PLK3,PTPN14,PTPN11,MYO1C,HIF1A,IWS1,ZPR1,LYN,GSK3B,REST,RAB11FIP1,CDKN1A,RHBDF2	down_VSAP_EC
GO:0002443	0.241	0.859	9	71	leukocyte mediated immunity	BP	1	LEP,TP53BP1,TLR3,F2RL1,C1S,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0065009	0.241	0.864	8	735	regulation of molecular function	BP	1	HOXA3,ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,ABHD5,ENSCAFG00000032731	up_VPOR_EC
GO:0002009	0.241	0.874	6	177	morphogenesis of an epithelium	BP	1	IRX3,DLL1,GREM1,LUZP1,ADAM17,TNC	up_AFEM_EC
GO:0051240	0.241	0.898	4	489	positive regulation of multicellular organismal	BP	1	ACVRL1,LYN,PDPN,SULF1	down_ACOR_EC
GO:0035904	0.241	0.9	4	25	aorta development	BP	1	SMAD6,SEC24B,CHD7,AP2B1	up_ACOR_VSMC
GO:0006090	0.241	0.899	4	26	pyruvate metabolic process	BP	1	PDK2,GALK1,PC,DDIT4	up_VSAP_EC
GO:0043648	0.241	0.9	4	26	dicarboxylic acid metabolic process	BP	1	GOT1,ADHFE1,IDH1,ASS1	up_VSAP_EC
GO:1905332	0.241	0.915	3	20	positive regulation of morphogenesis of an	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0050868	0.241	0.913	3	28	negative regulation of T cell activation	BP	1	SOCS5,PTPN2,SDC4	down_VSAP_EC
GO:0007166	0.241	0.916	3	686	cell surface receptor signaling pathway	BP	1	EYA1,NETO1,SHOX2	up_VFEM_VSMC
GO:0000060	0.241	0.937	2	15	protein import into nucleus, translocation	BP	1	KPNB1,CDKN1A	down_VSAP_EC
GO:0002260	0.241	0.937	2	15	lymphocyte homeostasis	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0006884	0.241	0.937	2	14	cell volume homeostasis	BP	1	LRRC8A,CLCN3	down_VSAP_EC
GO:0030516	0.241	0.937	2	15	regulation of axon extension	BP	1	IFRD1,NRP1	down_VSAP_EC
GO:0030808	0.241	0.937	2	15	regulation of nucleotide biosynthetic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:1900371	0.241	0.937	2	15	regulation of purine nucleotide biosynthetic	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0048485	0.241	0.941	2	9	sympathetic nervous system development	BP	1	NRP1,FZD3	up_ACOR_VSMC
GO:0034067	0.241	0.939	2	11	protein localization to Golgi apparatus	BP	1	GBP5,GCC2	up_VCAV_EC
GO:0006929	0.241	0.94	2	10	substrate-dependent cell migration	BP	1	SLIT2,NCK1	up_VSAP_EC
GO:0000122	0.241	0.934	2	218	negative regulation of transcription by RNA polymerase II	BP	1	CAV1,SHOX2	up_VSAP_VSMC
GO:0010893	0.241	0.978	1	3	positive regulation of steroid biosynthetic	BP	1	SREBF1	down_ACOR_VSMC
GO:0045136	0.241	0.978	1	3	development of secondary sexual	BP	1	B4GALT1	down_ACOR_VSMC
GO:0061502	0.241	0.978	1	3	early endosome to recycling endosome	BP	1	CORO1A	down_ACOR_VSMC
GO:1901977	0.241	0.976	1	4	negative regulation of cell cycle checkpoint	BP	1	DDX39B	down_VSAP_EC
GO:2000002	0.241	0.976	1	4	negative regulation of DNA damage checkpoint	BP	1	DDX39B	down_VSAP_EC
GO:0032780	0.241	0.978	1	3	negative regulation of ATPase activity	BP	1	TNNT2	up_ACOR_VSMC

GO:0035025	0.241	0.978	1	3	positive regulation of Rho protein signal	BP	1	F2RL1	up_ACOR_VSMC
GO:0090191	0.241	0.978	1	3	negative regulation of branching involved in ureteric bud	BP	1	BMP4	up_ACOR_VSMC
GO:0009792	0.241	0.972	1	231	embryo development ending in birth or egg	BP	1	HOXA9	up_AORT_VSMC
GO:0002296	0.241	0.983	1	2	T-helper 1 cell lineage commitment	BP	1	MTOR	up_VCAV_EC
GO:0061218	0.241	0.976	1	4	negative regulation of mesonephros	BP	1	GATA3	up_VCAV_EC
GO:0060322	0.241	0.971	1	193	head development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0045639	0.241	0.97	1	33	positive regulation of myeloid cell	BP	1	ACVR2A	up_VPOR_EC
GO:0042110	0.241	0.97	1	109	T cell activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001503	0.241	0.97	1	109	ossification	BP	1	SHOX2	up_VFEM_VSMC
GO:0006820	0.241	0.97	1	109	anion transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:0009126	0.241	0.97	1	100	purine nucleoside monophosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0009167	0.241	0.97	1	100	purine ribonucleoside monophosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0010035	0.241	0.97	1	107	response to inorganic substance	BP	1	FBP1	up_VFEM_VSMC
GO:1901293	0.241	0.97	1	106	nucleoside phosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0090276	0.241254131	0.93356	2	36	regulation of peptide hormone secretion	BP	1	NR1H4,KCNB1	up_ACOR_EC
GO:0033500	0.241747964	0.91011	3	64	carbohydrate homeostasis	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0042593	0.241747964	0.91011	3	64	glucose homeostasis	BP	1	NR1H4,KCNB1,PRKACA	up_ACOR_EC
GO:0048232	0.241862948	0.89424	4	95	male gamete generation	BP	1	SOX9,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0014037	0.241955881	0.97112	1	10	Schwann cell differentiation	BP	1	SH3TC2	up_ACOR_EC
GO:0019438	0.242	0.791	113	1258	aromatic compound biosynthetic process	BP	1	ELK3,PRPSAP1,HMGB1,SREBF1,ACLY,IRAK1,IL F3,CBX5,PPRC1,ATAD2,HMGA1,HNRNPD,SRE BF2,HINFP,NEDD4,RRM1,MED17,SLC29A1,M TDH,HEY1,SRRT,POLE,NAB2,CDCA7L,FUS,RFC 2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5 ,RFC3,TIMELESS,THRAP3,FAM129B,TCEA1,PF AS,AURKB,NONO,TK1,EZH2,GREM1,RFC4,NE K2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHR F1,CKS2,GMNN,BRCA1,NOC2L,E2F8,ELOVL1, PPARD,POLH,YBX3,NCL,NUP62,DTL,FOSL1,SU V39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK 2,SMARCB1,DDX39B,CCNA2,ENSCAFG000000 005299,EZR,ELOVL6,RBM14,CYC1,POLR3F,H OXA10,ERF,TCERG1,ATP5F1A,SMARCAL1,PR PS1,ENSCAFG00000013366,TBX15,ELF4,PRM T5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,T ADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2, JMJD6,H2AFX,CDC5L,NUDT1,HMGN1,CCT4,SI X4,CTPS1,MED16,ENSCAFG00000017103,AT P5F1D,POLR1C,NUDT3	down_ACOR_VSMC
GO:0009888	0.242	0.801	58	545	tissue development	BP	1	EXPH5,TNNT2,SMAD6,ACTN2,LGR6,LEP,LBH, GATA5,GATA4,HTR2B,SHROOM3,MLLT3,FER MT1,BMP4,LNPK,FGFR2,GJA1,ATRX,SEC24B, PPARGC1A,LATS2,CITED2,SPINT1,ISG15,ZNRF 3,LMO4,FGF18,ARHGEF26,NEBL,ANKRD1,F2 RL1,CTSB,EGLN1,ENSCAFG00000006238,CLS TN1,NRP1,NPNT,SPINT2,TBX20,TBX5,FZD3,F RS2,DAG1,LAMA3,PSEN1,TGFBR1,CHD7,DDR 2,FOSL2,EDN1,ARID5B,SERPINB5,GAA,ATP2C 1,SLC8A1,BVES,RREB1,ZDHHC21	up_ACOR_VSMC
GO:0009888	0.242	0.815	31	545	tissue development	BP	1	SMAD9,NAB2,SDC4,VASN,GLIPR2,KANK2,TH BS3,BMPR1A,LMO4,COL6A1,HOXC4,LAMA3, CLSTN1,SEMA3C,ASPN,TLX2,B4GALT1,GLI3,A DAMTSL4,ZFP36L1,IFT57,CDH2,LOXL3,TSC22 D3,DDR2,RDH10,OMD,GREM1,THRB,ZBTB16, BRSK1	down_VCAV_EC

GO:0030335	0.242	0.829	19	165	positive regulation of cell migration	BP	1	VEGFD,LGR6,BMP4,SH3RF2,SASH1,FGF18,F2RL1,NRP1,PRKCE,APP,SEMA6D,CCL5,DDR2,EDN1,FAM107A,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:1901360	0.242	0.861	11	2016	organic cyclic compound metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,IRX5,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0010975	0.242	0.867	7	103	regulation of neuron projection development	BP	1	TRPV2,THY1,TLX2,UST,PRKCSH,RGMA,BRSK1	down_VCAV_EC
GO:0006606	0.242	0.875	6	67	protein import into nucleus	BP	1	PRICKLE1,ZPR1,KPNB1,KPNA4,KPNA1,CDKN1A	down_VSAP_EC
GO:0045017	0.242	0.876	6	52	glycerolipid biosynthetic process	BP	1	PDGFB,ENSCAFG00000010596,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0051924	0.242	0.876	6	53	regulation of calcium ion transport	BP	1	PDGFB,PDE4D,CHD7,STC1,APLNR,PLCG2	up_VCAV_EC
GO:0009855	0.242	0.896	4	42	determination of bilateral symmetry	BP	1	TMED2,HIF1A,CTNNB1,DDIT3	down_VSAP_EC
GO:0010469	0.242	0.899	4	26	regulation of signaling receptor activity	BP	1	DAPK1,APP,PSEN1,PARK7	up_ACOR_VSMC
GO:0021695	0.242	0.914	3	20	cerebellar cortex development	BP	1	EZH2,ARCN1,GLI1	down_ACOR_VSMC
GO:0048814	0.242	0.915	3	19	regulation of dendrite morphogenesis	BP	1	RELN,PPP3CA,RAPGEF2	up_VCAV_EC
GO:1903036	0.242	0.915	3	19	positive regulation of response to wounding	BP	1	SELP,TLR4,MTOR	up_VCAV_EC
GO:0001816	0.242	0.934	2	194	cytokine production	BP	1	LYN,SULF1	down_ACOR_EC
GO:0050704	0.242	0.938	2	11	regulation of interleukin-1 secretion	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:1902042	0.242	0.938	2	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	HMGB2,ARHGEF2	down_ACOR_VSMC
GO:0001706	0.242	0.935	2	20	endoderm formation	BP	1	COL6A1,LAMA3	down_VCAV_EC
GO:1900024	0.242	0.936	2	16	regulation of substrate adhesion-dependent cell	BP	1	ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0051128	0.242	0.942	2	790	regulation of cellular component organization	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0001881	0.242	0.939	2	11	receptor recycling	BP	1	ALS2,LMTK2	up_VCAV_EC
GO:0071402	0.242	0.939	2	10	cellular response to lipoprotein particle	BP	1	TLR4,ABCA1	up_VCAV_EC
GO:1901985	0.242	0.939	2	11	positive regulation of protein acetylation	BP	1	GATA3,TAOK1	up_VCAV_EC
GO:0007265	0.242	0.933	2	121	Ras protein signal transduction	BP	1	ARHGEF2,FBP1	up_VPOR_EC
GO:0007250	0.242	0.978	1	3	activation of NF-kappaB-inducing kinase activity	BP	1	IRAK1	down_ACOR_VSMC
GO:0010889	0.242	0.978	1	3	regulation of sequestering of triglyceride	BP	1	ABHD5	down_ACOR_VSMC
GO:0072757	0.242	0.978	1	3	cellular response to camptothecin	BP	1	RAD51	down_ACOR_VSMC
GO:1901563	0.242	0.978	1	3	response to camptothecin	BP	1	RAD51	down_ACOR_VSMC
GO:1903232	0.242	0.978	1	3	melanosome assembly	BP	1	TRAPPC6A	down_ACOR_VSMC
GO:0048518	0.242	1	1	1676	positive regulation of biological process	BP	1	GATA5	down_AFEM_VSMC
GO:0016339	0.242	0.973	1	6	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion	BP	1	CDH2	down_VCAV_EC
GO:0036342	0.242	0.974	1	5	post-anal tail morphogenesis	BP	1	TMED2	down_VSAP_EC
GO:0007214	0.242	0.976	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	down_VSAP_EC
GO:0021855	0.242	0.975	1	4	hypothalamus cell migration	BP	1	NRP1	down_VSAP_EC
GO:0046325	0.242	0.975	1	4	negative regulation of glucose import	BP	1	ENPP1	down_VSAP_EC
GO:0031640	0.242	0.978	1	3	killing of cells of other organism	BP	1	F2RL1	up_ACOR_VSMC
GO:0035739	0.242	0.978	1	3	CD4-positive, alpha-beta T cell proliferation	BP	1	CD274	up_ACOR_VSMC
GO:0044364	0.242	0.978	1	3	disruption of cells of other organism	BP	1	F2RL1	up_ACOR_VSMC
GO:2000561	0.242	0.978	1	3	regulation of CD4-positive, alpha-beta T cell	BP	1	CD274	up_ACOR_VSMC
GO:0002684	0.242	0.972	1	239	positive regulation of immune system process	BP	1	ESR1	up_AORT_VSMC
GO:0031346	0.242	0.97	1	73	positive regulation of cell projection organization	BP	1	NTRK2	up_APUL_EC

GO:0045089	0.242	0.969	1	70	positive regulation of innate immune response	BP	1	NR1H4	up_APUL_EC
GO:0002315	0.242	0.978	1	3	marginal zone B cell differentiation	BP	1	MFNG	up_VCAV_EC
GO:0099170	0.242	0.978	1	3	postsynaptic modulation of chemical synaptic	BP	1	PPP3CA	up_VCAV_EC
GO:0006596	0.242	0.978	1	3	polyamine biosynthetic process	BP	1	ODC1	up_VCAV_EC
GO:0009446	0.242	0.978	1	3	putrescine biosynthetic process	BP	1	ODC1	up_VCAV_EC
GO:0033387	0.242	0.978	1	3	putrescine biosynthetic process from ornithine	BP	1	ODC1	up_VCAV_EC
GO:0001503	0.242	0.97	1	109	ossification	BP	1	HOXA3	up_VPOR_VSMC
GO:0051402	0.242	0.97	1	64	neuron apoptotic process	BP	1	SIX1	up_VFEM_EC
GO:0009199	0.242	0.97	1	100	ribonucleoside triphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0018108	0.242	0.97	1	79	peptidyl-tyrosine phosphorylation	BP	1	ARHGEF2	up_VPUL_EC
GO:0002764	0.242	0.97	1	80	immune response-regulating signaling	BP	1	NR1H4	up_VPUL_EC
GO:0046578	0.242	0.97	1	77	regulation of Ras protein signal transduction	BP	1	ARHGEF2	up_VPUL_EC
GO:0060491	0.242	0.969	1	62	regulation of cell projection assembly	BP	1	CAV1	up_VSAP_VSMC
GO:0120032	0.242	0.969	1	62	regulation of plasma membrane bounded cell	BP	1	CAV1	up_VSAP_VSMC
GO:0009952	0.242249811	0.90977	3	66	anterior/posterior pattern specification	BP	1	FZD5,FOXC2,CLSTN1	up_ACOR_EC
GO:0032268	0.243	0.797	69	778	regulation of cellular protein metabolic process	BP	1	EPHB1,EDNRB,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,PDE4D,IWS1,ATF3,RAPGEF1,TLR4,QKI,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,CASP8,MTOR,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,SH3BP5,ENC1,PPP1R2,ITPKB,PROX1,SECISBP2L,MADD,PAK2,PRKD2,SWAP70,TLR3,NCK1,DPH5,OTUD4,NSD1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,CNOT7,HMGB1,PMAIP1,BLM,SPTBN4,RIPK1,PDGFD,UBE2D1,KDM5A,KDM3A,ATRX,IVNS1ABP,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0001944	0.243	0.816	29	263	vasculature development	BP	1	VEGFD,SMAD6,LEP,ANGPT1,RECK,BMP4,FGFR2,GJA1,TLR3,SEC24B,CITED2,SPINT1,SASH1,FGF18,EGLN1,NRP1,TBX20,PSEN1,SYNJ2BP,CHD7,JUP,EDN1,HPGD,JAM3,AP2B1,ERAP1,CRKL,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0048858	0.243	0.829	19	159	cell projection morphogenesis	BP	1	EPYC,FEZ1,FGFR2,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL,RREB1	up_ACOR_VSMC
GO:0006954	0.243	0.847	11	147	inflammatory response	BP	1	NR1H4,SERPINE1,SOCS5,PRCP,PTGS2,HIF1A,PTPN2,APOE,LYN,GBP5,A2M	down_VSAP_EC
GO:0071902	0.243	0.853	10	79	positive regulation of protein serine/threonine	BP	1	HTR2B,BMP4,PDE5A,SASH1,FGF18,CCNT1,FRS2,PSEN1,EDN1,MAP3K7	up_ACOR_VSMC
GO:0045766	0.243	0.862	8	63	positive regulation of angiogenesis	BP	1	VEGFD,TLR3,SASH1,FGF18,NRP1,JUP,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0045216	0.243	0.876	6	44	cell-cell junction organization	BP	1	WNT11,LIMS2,HDAC7,CLDN1,F2RL1,AJM1	up_VSAP_EC
GO:0060996	0.243	0.898	4	26	dendritic spine development	BP	1	ZNF365,PSEN1,ASAP1,WASL	up_ACOR_VSMC
GO:1901879	0.243	0.898	4	26	regulation of protein depolymerization	BP	1	FGF13,ACTN2,MID1,F2RL1	up_ACOR_VSMC
GO:2000756	0.243	0.914	3	20	regulation of peptidyl-lysine acetylation	BP	1	BRCA1,NOC2L,TADA2A	down_ACOR_VSMC
GO:0009953	0.243	0.911	3	34	dorsal/ventral pattern formation	BP	1	BMPR1A,GLI3,GREM1	down_VCAV_EC
GO:0006406	0.243	0.912	3	27	mRNA export from nucleus	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0071427	0.243	0.912	3	27	mRNA-containing ribonucleoprotein complex export from	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:1903311	0.243	0.909	3	72	regulation of mRNA metabolic process	BP	1	TENT5C,AXIN2,SAMD4B	up_AFEM_EC
GO:0022613	0.243	0.91	3	208	ribonucleoprotein complex biogenesis	BP	1	RSL24D1,RPL10L,RRP15	up_VPOR_EC
GO:0045893	0.243	0.911	3	413	positive regulation of transcription, DNA-	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0007435	0.243	0.914	3	18	salivary gland morphogenesis	BP	1	FGF7,NTN4,NFIB	up_VSAP_EC

GO:0030835	0.243	0.938	2	11	negative regulation of actin filament	BP	1	CAPG,LIMA1	down_ACOR_VSMC
GO:0032456	0.243	0.935	2	19	endocytic recycling	BP	1	MICALL2,ARHGAP1	down_VCAV_EC
GO:0019229	0.243	0.938	2	12	regulation of vasoconstriction	BP	1	DOCK4,EDN1	up_VCAV_EC
GO:0032715	0.243	0.938	2	11	negative regulation of interleukin-6 production	BP	1	TNFAIP3,TLR4	up_VCAV_EC
GO:0051148	0.243	0.937	2	12	negative regulation of muscle cell differentiation	BP	1	PDGFB,BMP2	up_VCAV_EC
GO:1900026	0.243	0.938	2	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	NEDD9,ENSCAFG00000002015	up_VCAV_EC
GO:0009755	0.243	0.969	1	52	hormone-mediated signaling pathway	BP	1	NEDD4	down_ACOR_EC
GO:0016579	0.243	0.969	1	49	protein deubiquitination	BP	1	USP28	down_ACOR_EC
GO:0048839	0.243	0.969	1	50	inner ear development	BP	1	HOXA1	down_ACOR_EC
GO:0001779	0.243	0.978	1	3	natural killer cell differentiation	BP	1	TOX	down_ACOR_VSMC
GO:0010457	0.243	0.978	1	3	centriole-centriole cohesion	BP	1	NEK2	down_ACOR_VSMC
GO:0032823	0.243	0.978	1	3	regulation of natural killer cell differentiation	BP	1	TOX	down_ACOR_VSMC
GO:0002683	0.243	0.97	1	126	negative regulation of immune system process	BP	1	GABPA	down_AFEM_EC
GO:0010635	0.243	0.978	1	3	regulation of mitochondrial fusion	BP	1	BNIP3	up_ACOR_VSMC
GO:0010637	0.243	0.978	1	3	negative regulation of mitochondrial fusion	BP	1	BNIP3	up_ACOR_VSMC
GO:0046476	0.243	0.978	1	3	glycosylceramide biosynthetic process	BP	1	UGCG	up_ACOR_VSMC
GO:0060754	0.243	0.978	1	3	positive regulation of mast cell chemotaxis	BP	1	VEGFD	up_ACOR_VSMC
GO:0072110	0.243	0.978	1	3	glomerular mesangial cell proliferation	BP	1	BMP4	up_ACOR_VSMC
GO:0072124	0.243	0.978	1	3	regulation of glomerular mesangial cell	BP	1	BMP4	up_ACOR_VSMC
GO:0090192	0.243	0.978	1	3	regulation of glomerulus development	BP	1	BMP4	up_ACOR_VSMC
GO:1903689	0.243	0.983	1	2	regulation of wound healing, spreading of	BP	1	RREB1	up_ACOR_VSMC
GO:1903691	0.243	0.983	1	2	positive regulation of wound healing, spreading of epidermal cells	BP	1	RREB1	up_ACOR_VSMC
GO:0048732	0.243	0.97	1	116	gland development	BP	1	HOXA9	up_AORT_EC
GO:0045861	0.243	0.969	1	71	negative regulation of proteolysis	BP	1	PCSK1N	up_APUL_EC
GO:0072540	0.243	0.978	1	3	T-helper 17 cell lineage commitment	BP	1	IL6	up_VCAV_EC
GO:2000121	0.243	0.978	1	3	regulation of removal of superoxide radicals	BP	1	GCH1	up_VCAV_EC
GO:0007507	0.243	0.971	1	194	heart development	BP	1	GATA5	up_VCAV_VSMC
GO:0021987	0.243	0.969	1	37	cerebral cortex development	BP	1	SEMA3A	up_VPOR_EC
GO:0032675	0.243	0.969	1	34	regulation of interleukin-6 production	BP	1	ARHGEF2	up_VPOR_EC
GO:0090101	0.243	0.969	1	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ASPN	up_VPOR_EC
GO:0008202	0.243	0.969	1	80	steroid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0034616	0.243	0.978	1	3	response to laminar fluid shear stress	BP	1	ASS1	up_VSAP_EC
GO:0097105	0.243	0.978	1	3	presynaptic membrane assembly	BP	1	LRP4	up_VSAP_EC
GO:0043903	0.243	0.969	1	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	CAV1	up_VSAP_VSMC
GO:0042180	0.243	0.969	1	61	cellular ketone metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0099601	0.24309842	0.97083	1	10	regulation of neurotransmitter	BP	1	MAPK8IP2	up_ACOR_EC

GO:0051171	0.244	0.791	109	1697	regulation of nitrogen compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,MEIS2,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,CBX5,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PGAM1,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,MSN,HIF1A,IWS1,DNAJC10,TNIK,NXN,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,STRAP,DDIT3,FAM162A,BACH1,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,ARMCX3,HTT,REST,ZMYND8,EIF2S1,PRMT1,SPOP,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0018209	0.244	0.836	15	125	peptidyl-serine modification	BP	1	GALNT3,PLCL1,CDC7,RASSF2,PRKAA2,LATS2,CAMK2D,DMPK,PRKCE,APP,PSKH1,LMTK2,INPP5K,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:1901990	0.244	0.851	10	94	regulation of mitotic cell cycle phase transition	BP	1	RAB11A,TAOK1,BLM,RAD21,RAD17,CUL4A,ZW10,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0002708	0.244	0.898	4	26	positive regulation of lymphocyte mediated	BP	1	TP53BP1,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0050773	0.244	0.897	4	29	regulation of dendrite development	BP	1	RELN,MEF2C,PPP3CA,RAPGEF2	up_VCAV_EC
GO:0051208	0.244	0.897	4	29	sequestering of calcium ion	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0051282	0.244	0.897	4	29	regulation of sequestering of calcium ion	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0032091	0.244	0.91	3	34	negative regulation of protein binding	BP	1	CLSTN1,LRPAP1,PARK7	down_VCAV_EC
GO:0035050	0.244	0.911	3	28	embryonic heart tube development	BP	1	TMED2,HIF1A,CTNNB1	down_VSAP_EC
GO:0032963	0.244	0.914	3	18	collagen metabolic process	BP	1	BMP4,MFAP4,CTSB	up_ACOR_VSMC
GO:0016070	0.244	0.926	3	1479	RNA metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:1905332	0.244	0.913	3	20	positive regulation of morphogenesis of an	BP	1	HOXB7,GATA3,MTOR	up_VCAV_EC
GO:0010883	0.244	0.938	2	11	regulation of lipid storage	BP	1	SREBF2,ABHD5	down_ACOR_VSMC
GO:0001958	0.244	0.938	2	11	endochondral ossification	BP	1	NAB2,MMP14	down_ACOR_VSMC
GO:0036075	0.244	0.938	2	11	replacement ossification	BP	1	NAB2,MMP14	down_ACOR_VSMC
GO:1901985	0.244	0.938	2	11	positive regulation of protein acetylation	BP	1	BRCA1,TADA2A	down_ACOR_VSMC
GO:0017004	0.244	0.935	2	18	cytochrome complex assembly	BP	1	COA1,CYBA	down_VCAV_EC
GO:0007064	0.244	0.936	2	15	mitotic sister chromatid cohesion	BP	1	NAA10,PDS5B	down_VSAP_EC
GO:0021879	0.244	0.935	2	15	forebrain neuron differentiation	BP	1	INHBA,NRP1	down_VSAP_EC
GO:0010803	0.244	0.939	2	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	F2RL1,CCDC3	up_ACOR_VSMC
GO:0010971	0.244	0.939	2	10	positive regulation of G2/M transition of mitotic	BP	1	CDC7,APP	up_ACOR_VSMC
GO:0050922	0.244	0.937	2	11	negative regulation of chemotaxis	BP	1	MMP28,ANGPT2	up_VCAV_EC
GO:0061217	0.244	0.936	2	13	regulation of mesonephros	BP	1	HOXB7,GATA3	up_VCAV_EC
GO:0042551	0.244	0.939	2	10	neuron maturation	BP	1	IRX5,NTN4	up_VSAP_EC
GO:0021936	0.244	0.978	1	3	regulation of cerebellar granule cell precursor	BP	1	GLI1	down_ACOR_VSMC
GO:0044528	0.244	0.978	1	3	regulation of mitochondrial mRNA	BP	1	FASTKD3	down_ACOR_VSMC
GO:1905097	0.244	0.978	1	3	regulation of guanyl-nucleotide exchange	BP	1	STMN1	down_ACOR_VSMC
GO:0051656	0.244	0.97	1	129	establishment of organelle localization	BP	1	GPSM2	down_AFEM_EC
GO:0007638	0.244	0.975	1	4	mechanosensory behavior	BP	1	HTT	down_VSAP_EC
GO:0017000	0.244	0.975	1	4	antibiotic biosynthetic process	BP	1	KDM3A	down_VSAP_EC

GO:0002645	0.244	0.978	1	3	positive regulation of tolerance induction	BP	1	CD274	up_ACOR_VSMC
GO:0007265	0.244	0.969	1	121	Ras protein signal transduction	BP	1	CTNNAL1	up_AORT_EC
GO:0032271	0.244	0.969	1	73	regulation of protein polymerization	BP	1	TUBB4A	up_APUL_EC
GO:0045926	0.244	0.969	1	72	negative regulation of growth	BP	1	TBX5	up_APUL_EC
GO:0000727	0.244	0.975	1	4	double-strand break repair via break-induced	BP	1	GINS4	up_VCAV_EC
GO:0060251	0.244	0.978	1	3	regulation of glial cell proliferation	BP	1	PRKCH	up_VCAV_EC
GO:0060252	0.244	0.978	1	3	positive regulation of glial cell proliferation	BP	1	PRKCH	up_VCAV_EC
GO:0015693	0.244	0.975	1	4	magnesium ion transport	BP	1	KCNJ2	up_VCAV_EC
GO:0050855	0.244	0.975	1	4	regulation of B cell receptor signaling	BP	1	PRKCH	up_VCAV_EC
GO:0050861	0.244	0.975	1	4	positive regulation of B cell receptor signaling	BP	1	PRKCH	up_VCAV_EC
GO:0070848	0.244	0.971	1	193	response to growth factor	BP	1	GATA5	up_VCAV_VSMC
GO:0016052	0.244	0.969	1	34	carbohydrate catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0001952	0.244	0.969	1	34	regulation of cell-matrix adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:1901342	0.244	0.97	1	114	regulation of vasculature development	BP	1	C3AR1	up_VPOR_VSMC
GO:0007254	0.244	0.969	1	67	JNK cascade	BP	1	CDC42EP5	up_VFEM_EC
GO:0016331	0.244	0.969	1	66	morphogenesis of embryonic epithelium	BP	1	SIX1	up_VFEM_EC
GO:0030522	0.244	0.969	1	67	intracellular receptor signaling pathway	BP	1	CYP26B1	up_VFEM_EC
GO:0035148	0.244	0.969	1	66	tube formation	BP	1	SIX1	up_VFEM_EC
GO:0052547	0.244	0.969	1	82	regulation of peptidase activity	BP	1	PTGER2	up_VPUL_EC
GO:1902105	0.244	0.969	1	80	regulation of leukocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0034380	0.244	0.978	1	3	high-density lipoprotein particle assembly	BP	1	LCAT	up_VSAP_EC
GO:0071397	0.244	0.978	1	3	cellular response to cholesterol	BP	1	OSBPL7	up_VSAP_EC
GO:0048486	0.244229944	0.97054	1	10	parasympathetic nervous system development	BP	1	NRP1	up_ACOR_EC
GO:0006536	0.244253881	0.97053	1	10	glutamate metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0007140	0.244264101	0.97053	1	10	male meiotic nuclear division	BP	1	FIGNL1	up_ACOR_EC
GO:0033036	0.244714782	0.81861	26	852	macromolecule localization	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,AGRN,NOD2,PLS1,ACTN2,CFI,TRIM8,PTGER4,PREB,DCLK2,MAVS,LRRC15,LRP4,LRRC4,CHMP4B,TP53INP2,VPS16,ABCB9,NRP1,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0001895	0.244781478	0.9704	1	10	retina homeostasis	BP	1	CDH3	up_ACOR_EC
GO:0048584	0.245	0.797	62	592	positive regulation of response to stimulus	BP	1	NAPEPLD,CDON,WNT11,CD274,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,LIMS2,IL6R,SLIT2,CRADD,ABL1,EMP2,DLL1,EPN2,MAP3K5,IL17RC,PDGFD,KLF15,C1QTNF2,HPSE,CCBE1,STAT6,F2RL1,TRAF7,PIK3R1,RBCK1,FAM53B,MYC,SULF2,SHOX2,SASH1,CREBRF,MYD88,S100A4,TSPAN5,CFD,NPAS2,NLRX1,ENSCAFG00000011993,TKFC,YPEL3,RAF1,ZNF580,CYBA,ZNF205,STX4,PQBP1,ACVRL1,UBQLN2,UNC93B1,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,CITED2,BAG4,TRADD,DEDD2	up_VSAP_EC
GO:0008283	0.245	0.799	57	545	cell proliferation	BP	1	VEGFD,SMAD6,LEP,LBH,CDC7,HTR2B,PRDX4,NACC2,FERMT1,BMP4,FGFR2,PDE5A,TP53INP1,RERG,ACSL6,ZNRF3,CD274,MARCKSL1,AR,PTGIR,FGF18,NDRG2,CDKN2B,PLAC8B,LIMS2,F2RL1,CDKN1A,CLSTN1,PTPN22,SMARCD3,TBX20,TBX5,FZD3,FRS2,CCPG1,APP,PSEN1,TGFBR1,SYNJ2BP,JUP,SPINK2,DDR2,FOSL2,DUSP22,EDN1,SERPINB5,DISC1,TNFRSF11B,KLF11,TACC1,RPRD1B,LHX9,WDR48,SH3BP4,RREB1,CRKL,PTPN14	up_ACOR_VSMC

GO:0009792	0.245	0.83	17	231	embryo development ending in birth or egg hatching	BP	1	PRICKLE1,SULF1,PRKACB,SEC24D,TMED2,HOXB7,HIF1A,ZPR1,CTNNB1,PLOD3,MYO1E,SDC4,RBBP8,PRMT1,EXT1,SIX4,RTCB	down_VSAP_EC
GO:1903829	0.245	0.85	10	91	positive regulation of cellular protein	BP	1	ACSL3,SLC29A1,RAN,CDK1,PLK3,NDC80,NUP62,DMAP1,EZR,CCT4	down_ACOR_VSMC
GO:0060562	0.245	0.859	8	120	epithelial tube morphogenesis	BP	1	SDC4,LMO4,CLSTN1,B4GALT1,GLI3,IFT57,RDH10,GREM1	down_VCAV_EC
GO:0002262	0.245	0.867	7	54	myeloid cell homeostasis	BP	1	BMP4,CITED2,ISG15,FAM210B,P4HTM,JAM3,B2M	up_ACOR_VSMC
GO:1901988	0.245	0.867	7	63	negative regulation of cell cycle phase transition	BP	1	TAOK1,BLM,RAD21,RAD17,ZW10,TOPBP1,FBXO5	up_VCAV_EC
GO:0030522	0.245	0.873	6	67	intracellular receptor signaling pathway	BP	1	NR1H4,PRCP,SMARCA4,UBA5,YWHAH,KDM3A	down_VSAP_EC
GO:0000302	0.245	0.874	6	52	response to reactive oxygen species	BP	1	TNFAIP3,MAPK13,APOD,GUCY1B1,GCH1,RIPK1	up_VCAV_EC
GO:0022904	0.245	0.875	6	43	respiratory electron transport chain	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,NDUFS2,NDUFV1	up_VSAP_EC
GO:0009201	0.245	0.884	5	41	ribonucleoside triphosphate biosynthetic	BP	1	CYC1,ATP5F1A,ENSCAFG00000013366,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0010769	0.245	0.881	5	69	regulation of cell morphogenesis involved	BP	1	TRPV2,THY1,TLX2,UST,BRSK1	down_VCAV_EC
GO:0003018	0.245	0.884	5	42	vascular process in circulatory system	BP	1	EDNRB,DOCK4,EDN1,GUCY1A1,NOS2	up_VCAV_EC
GO:0044272	0.245	0.884	5	35	sulfur compound biosynthetic process	BP	1	ACACB,PDK2,ACSS2,MPST,CHST7	up_VSAP_EC
GO:1901362	0.245	0.904	4	1293	organic cyclic compound biosynthetic process	BP	1	HDAC7,CITED2,HSD3B7,TBX15	down_VPOR_EC
GO:0042098	0.245	0.894	4	43	T cell proliferation	BP	1	MSN,CTNNB1,TFRC,SDC4	down_VSAP_EC
GO:0034763	0.245	0.897	4	27	negative regulation of transmembrane transport	BP	1	ACTN2,LEP,KCNE3,INPP5K	up_ACOR_VSMC
GO:0007267	0.245	0.91	3	332	cell-cell signaling	BP	1	SPG11,SULF1,STX4	down_ACOR_EC
GO:0046631	0.245	0.91	3	35	alpha-beta T cell activation	BP	1	GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0045926	0.245	0.908	3	72	negative regulation of growth	BP	1	MT2A,ENSCAFG00000009113,DCUN1D3	up_AFEM_EC
GO:0090092	0.245	0.908	3	72	regulation of transmembrane receptor protein serine/threonine	BP	1	GREM1,GREM2,ADAM17	up_AFEM_EC
GO:0055082	0.245	0.932	2	189	cellular chemical homeostasis	BP	1	LYN,STX4	down_ACOR_EC
GO:0000038	0.245	0.937	2	12	very long-chain fatty acid metabolic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0070206	0.245	0.937	2	11	protein trimerization	BP	1	C1QTNF6,SIGMAR1	down_ACOR_VSMC
GO:0032526	0.245	0.934	2	19	response to retinoic acid	BP	1	SLC10A3,TMEM161A	down_VCAV_EC
GO:0070849	0.245	0.935	2	15	response to epidermal growth factor	BP	1	PTPN11,ZPR1	down_VSAP_EC
GO:0010565	0.245	0.931	2	40	regulation of cellular ketone metabolic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0071706	0.245	0.932	2	40	tumor necrosis factor superfamily cytokine	BP	1	LEP,BPI	up_AFEM_EC
GO:0006911	0.245	0.937	2	11	phagocytosis, engulfment	BP	1	ABCA1,ELMO1	up_VCAV_EC
GO:0097742	0.245	0.978	1	3	de novo centriole assembly	BP	1	PLK4	down_ACOR_VSMC
GO:0098535	0.245	0.978	1	3	de novo centriole assembly involved in multi-ciliated epithelial cell	BP	1	PLK4	down_ACOR_VSMC
GO:1902775	0.245	0.978	1	3	mitochondrial large ribosomal subunit	BP	1	DDX28	down_ACOR_VSMC
GO:1903251	0.245	0.978	1	3	multi-ciliated epithelial cell differentiation	BP	1	PLK4	down_ACOR_VSMC
GO:0061196	0.245	0.977	1	3	fungiform papilla development	BP	1	SIX4	down_ACOR_VSMC
GO:0061197	0.245	0.977	1	3	fungiform papilla morphogenesis	BP	1	SIX4	down_ACOR_VSMC
GO:0061668	0.245	0.978	1	3	mitochondrial ribosome assembly	BP	1	DDX28	down_ACOR_VSMC
GO:0051171	0.245	1	1	1697	regulation of nitrogen compound metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0090304	0.245	1	1	1694	nucleic acid metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0002360	0.245	0.972	1	6	T cell lineage commitment	BP	1	LOXL3	down_VCAV_EC
GO:0043369	0.245	0.972	1	6	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BP	1	LOXL3	down_VCAV_EC

GO:0007389	0.245	0.97	1	137	pattern specification process	BP	1	CITED2	down_VPOR_EC
GO:0006688	0.245	0.973	1	5	glycosphingolipid biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0042219	0.245	0.975	1	4	cellular modified amino acid catabolic process	BP	1	ALDH1L2	down_VSAP_EC
GO:0046653	0.245	0.973	1	5	tetrahydrofolate metabolic process	BP	1	ALDH1L2	down_VSAP_EC
GO:0050927	0.245	0.973	1	5	positive regulation of positive chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0051124	0.245	0.975	1	4	synaptic growth at neuromuscular junction	BP	1	SIX4	down_VSAP_EC
GO:0021978	0.245	0.978	1	3	telencephalon regionalization	BP	1	BMP4	up_ACOR_VSMC
GO:0042095	0.245	0.977	1	3	interferon-gamma biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0045072	0.245	0.977	1	3	regulation of interferon-gamma biosynthetic	BP	1	TLR3	up_ACOR_VSMC
GO:0045078	0.245	0.977	1	3	positive regulation of interferon-gamma	BP	1	TLR3	up_ACOR_VSMC
GO:0072677	0.245	0.978	1	3	eosinophil migration	BP	1	HRH1	up_ACOR_VSMC
GO:0001816	0.245	0.97	1	194	cytokine production	BP	1	TLR2	up_AFEM_VSMC
GO:0007249	0.245	0.969	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	NR1H4	up_APUL_EC
GO:0007600	0.245	0.969	1	73	sensory perception	BP	1	HOXA1	up_APUL_EC
GO:0046578	0.245	0.969	1	77	regulation of Ras protein signal transduction	BP	1	ARHGEF26	up_APUL_EC
GO:0070507	0.245	0.969	1	73	regulation of microtubule cytoskeleton organization	BP	1	TUBB4A	up_APUL_EC
GO:0045176	0.245	0.977	1	3	apical protein localization	BP	1	SHROOM2	up_VCAV_EC
GO:0006820	0.245	0.969	1	109	anion transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0007162	0.245	0.969	1	66	negative regulation of cell adhesion	BP	1	HOXA7	up_VFEM_EC
GO:1903708	0.245	0.969	1	65	positive regulation of hemopoiesis	BP	1	TOX	up_VFEM_EC
GO:0043434	0.245	0.969	1	80	response to peptide hormone	BP	1	NR1H4	up_VPUL_EC
GO:1900748	0.245	0.977	1	3	positive regulation of vascular endothelial growth factor signaling	BP	1	CCBE1	up_VSAP_EC
GO:0048251	0.245	0.977	1	3	elastic fiber assembly	BP	1	LOX	up_VSAP_EC
GO:0051650	0.245038553	0.90825	3	65	establishment of vesicle localization	BP	1	CDH3,DYNC1I1,PREB	up_ACOR_EC
GO:0032647	0.245668844	0.97017	1	10	regulation of interferon-alpha production	BP	1	MAVS	up_ACOR_EC
GO:0030317	0.245680074	0.96989	1	11	flagellated sperm motility	BP	1	CCNYL1	up_ACOR_EC
GO:0097722	0.245680074	0.96989	1	11	sperm motility	BP	1	CCNYL1	up_ACOR_EC
GO:0010604	0.246	0.79	94	919	positive regulation of macromolecule metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PTGFR,PPARGC1B,IL6R,CRADD,HOXD3,CDH1,SLC6A4,FGF7,ABL1,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,KLF15,C1QTNF2,ZBTB16,RARG,CCBE1,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,ICE1,ZFP36L1,TRAF7,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,ZC3H10,CIZ1,EEF2,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,PHF1,NPAS2,PRKAB1,RNF166,RPUSD4,CDK9,PRMT2,OSBPL7,ZFP36L2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,NCOA2,SMARCA2,EIF3D,ACVRL1,UBQLN2,HTRA2,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,SOAT1	up_VSAP_EC

GO:0009966	0.246	0.79	89	868	regulation of signal transduction	BP	1	FZD1,SEZ6L,CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,ABL1,HDAC7,EMP2,DLL1,EPN2,SESN1,MAP3K5,PDGFD,C1QTNF2,HPSE,ANKRD54,CCBE1,RECK,KLHL24,PLPP3,F2RL1,GLIS2,PDK2,MFN2,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,SULF2,SHOX2,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,PRMT2,FBLN1,IGFBP6,RAF1,MAPKBP1,CYBA,ZNF205,STX4,PSD4,QARS,ARHGAP12,ACVRL1,UBQLN2,HTRA2,FLOT1,NCK1,MAVS,HMOX1,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0044093	0.246	0.805	41	437	positive regulation of molecular function	BP	1	HMGB1,IRAK1,PPRC1,HNRNPD,UBE2S,SLC29A1,MTDH,HOXA3,PRELID1,RFC2,CAV1,RFC5,RFC3,FAM129B,AURKB,ABHD5,EZH2,STMN1,GREM1,MAP3K20,RFC4,NEK2,PCNA,DHX33,CKS2,PDCD2,GMNN,YWHAB,CYCS,EMP2,HMGB2,GSTO1,CLSPN,CDC20,CTH,AIFM1,ARHGEF2,NUS1,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC
GO:0051248	0.246	0.81	34	316	negative regulation of protein metabolic process	BP	1	SMAD6,RASSF2,RECK,PRKAA2,ITM2C,BMP4,SH3RF2,LATS2,ISG15,PTPN3,NDRG2,CST3,F2RL1,FAM129A,DAPK1,CDKN1A,PTPN22,OS9,SMPD1,SH3RF1,PRKCE,DAG1,PSEN1,SYNJ2BP,SPINK2,DUSP22,EDN1,OXR1,DUSP26,LRRC4,INPP5K,AZIN2,PARK7,CRKL	up_ACOR_VSMC
GO:0071310	0.246	0.828	18	634	cellular response to organic substance	BP	1	LEP,LBH,CRY2,RAB20,GAS1,DLL1,CHRM2,TMEM100,GREM1,AVPR1A,CAMK2A,GREM2,CYLD,LRRC15,NR3C1,CCL5,ADAM17,KANK1	up_AFEM_EC
GO:0006935	0.246	0.845	11	143	chemotaxis	BP	1	VEGFA,SERPINE1,KIF5B,PTPN2,NEO1,ADAM17,MMP28,LYN,EXT1,NRP1,USP14	down_VSAP_EC
GO:0042330	0.246	0.845	11	143	taxis	BP	1	VEGFA,SERPINE1,KIF5B,PTPN2,NEO1,ADAM17,MMP28,LYN,EXT1,NRP1,USP14	down_VSAP_EC
GO:0007517	0.246	0.859	8	100	muscle organ development	BP	1	ACTN1,FLNB,CTNNB1,CRYAB,KLF5,ATF3,SIX4,HOMER1	down_VSAP_EC
GO:0098660	0.246	0.88	5	141	inorganic ion transmembrane transport	BP	1	KCNC4,ATP6V1B2,FXYD1,ATP6V0B,CLIC4	up_AFEM_EC
GO:0010507	0.246	0.896	4	26	negative regulation of autophagy	BP	1	LEP,HTR2B,FEZ1,FEZ2	up_ACOR_VSMC
GO:0048644	0.246	0.895	4	31	muscle organ morphogenesis	BP	1	CHD7,DLL4,BMP2,PROX1	up_VCAV_EC
GO:0071322	0.246	0.91	3	29	cellular response to carbohydrate stimulus	BP	1	NR1H4,SMARCA4,HIF1A	down_VSAP_EC
GO:1902680	0.246	0.91	3	415	positive regulation of RNA biosynthetic process	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:1903508	0.246	0.91	3	415	positive regulation of nucleic acid-templated	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:1901216	0.246	0.933	2	19	positive regulation of neuron death	BP	1	PRNP,FOXO3	down_VCAV_EC
GO:0048634	0.246	0.931	2	40	regulation of muscle organ development	BP	1	DLL1,GREM1	up_AFEM_EC
GO:0010611	0.246	0.937	2	11	regulation of cardiac muscle hypertrophy	BP	1	EDN1,PPP3CA	up_VCAV_EC
GO:0014743	0.246	0.937	2	11	regulation of muscle hypertrophy	BP	1	EDN1,PPP3CA	up_VCAV_EC
GO:0032727	0.246	0.939	2	9	positive regulation of interferon-alpha	BP	1	TLR4,TLR3	up_VCAV_EC
GO:0071826	0.246	0.931	2	117	ribonucleoprotein complex subunit	BP	1	RSL24D1,RPL10L	up_VPOR_EC
GO:0006536	0.246	0.938	2	10	glutamate metabolic process	BP	1	GOT1,ADHFE1	up_VSAP_EC
GO:1903053	0.246	0.938	2	10	regulation of extracellular matrix organization	BP	1	ABL1,DDR2	up_VSAP_EC
GO:0030177	0.246	0.968	1	51	positive regulation of Wnt signaling pathway	BP	1	SULF1	down_ACOR_EC
GO:0043112	0.246	0.968	1	57	receptor metabolic process	BP	1	NEDD4	down_ACOR_EC
GO:0042753	0.246	0.977	1	3	positive regulation of circadian rhythm	BP	1	THRAP3	down_ACOR_VSMC
GO:0031053	0.246	0.977	1	3	primary miRNA processing	BP	1	SRRT	down_ACOR_VSMC
GO:0016266	0.246	0.977	1	3	O-glycan processing	BP	1	GALNT10	up_ACOR_VSMC
GO:0009313	0.246	0.977	1	3	oligosaccharide catabolic process	BP	1	NEU3	up_ACOR_VSMC

GO:0051955	0.246	0.977	1	3	regulation of amino acid transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0080154	0.246	0.977	1	3	regulation of fertilization	BP	1	SPINK2	up_ACOR_VSMC
GO:1903371	0.246	0.977	1	3	regulation of endoplasmic reticulum tubular network organization	BP	1	LNPK	up_ACOR_VSMC
GO:0060537	0.246	0.969	1	117	muscle tissue development	BP	1	SGCD	up_AORT_EC
GO:0051094	0.246	0.973	1	388	positive regulation of developmental process	BP	1	TBX5	up_APUL_VSMC
GO:0032792	0.246	0.977	1	3	negative regulation of CREB transcription factor	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0042573	0.246	0.975	1	4	retinoic acid metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0072189	0.246	0.975	1	4	ureter development	BP	1	GATA3	up_VCAV_EC
GO:0061564	0.246	0.969	1	119	axon development	BP	1	SHOX2	up_VFEM_VSMC
GO:0034330	0.246	0.969	1	80	cell junction organization	BP	1	NR1H4	up_VPUL_EC
GO:0045088	0.246	0.969	1	81	regulation of innate immune response	BP	1	NR1H4	up_VPUL_EC
GO:0006955	0.246851978	0.84406	11	327	immune response	BP	1	C7,NR1H4,FZD5,NOD2,IL33,SMAD6,TRIM8,PTGER4,MAVS,RARRES2,PRKCD	up_ACOR_EC
GO:0070887	0.247	0.791	80	775	cellular response to chemical stimulus	BP	1	FZD1,ENSCAFG00000009113,HNF4A,FAM107A,ARHGEF5,C5AR2,PTGFR,SLC8B1,PPARGC1B,SLIT2,CDH1,SLC6A4,FGF7,ABL1,GOT1,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,IL17RC,PDGFD,KLF15,PLXNA4,CDC42EP2,HSD3B7,RARG,CCBE1,MGST1,STAT5A,STAT6,F2RL1,RAB11B,NFE2L2,PDK2,ZFP36L1,MT2A,FXN,PIK3R1,GAS1,ZEB1,SULF2,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,STK16,CASTOR1,NCEH1,FBXO7,KCNB1,CDK9,PRMT2,OSBPL7,ZFP36L2,HPGD,RAF1,ZNF580,NCOA2,STX4,PQBP1,ACVRL1,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,HMOX1,TGFBR2,CITED2,SAA1,BAG4,LBH,KEAP1,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC
GO:0045595	0.247	0.8	50	469	regulation of cell differentiation	BP	1	TMEM176B,TMEM176A,SMAD6,LEP,LBH,GATA5,CD83,RASSF2,FNDC5,ITM2C,BMP4,LNPK,FGFR2,GJA1,PDE5A,TP53INP1,ISG15,ZNF365,LMO4,FGF18,FAM210B,P4HTM,PLEKHB2,CLSTN1,NRP1,ULK2,DMPK,NPNT,SMARCD3,TBX5,CCDC3,FZD3,DKKL1,FRS2,DAG1,APP,PSEN1,TGFBR1,CHD7,SIPA1L1,DDR2,SSH3,EDN1,ASAP1,B2M,DISC1,CNOT4,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0009987	0.247	0.869	24	5086	cellular process	BP	1	HOXC10,TBX15,EYA1,HOXA9,TOX,MAP2K6,MME,AVPR1A,HOXA10,TRIM9,HOXB7,HOXA7,ENSCAFG00000018194,SIX1,YBX3,MAB21L1,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3,CHST7	up_VFEM_EC
GO:0055082	0.247	0.835	14	189	cellular chemical homeostasis	BP	1	SLC39A7,NR1H4,ERO1A,ENPP1,ATP2B1,SMARCA4,HIF1A,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0051051	0.247	0.839	13	112	negative regulation of transport	BP	1	ACTN2,LEP,KCNE3,FERMT1,ATXN2,F2RL1,PTPN22,LRPAP1,OS9,SCAMP5,INPP5K,PFKL,PARK7	up_ACOR_VSMC
GO:0007169	0.247	0.87	6	178	transmembrane receptor protein tyrosine kinase	BP	1	DLL1,F3,HCK,RAB7A,ADAM17,KANK1	up_AFEM_EC
GO:0001894	0.247	0.873	6	49	tissue homeostasis	BP	1	ADGRF5,CD34,TLR4,EXOC5,LDB2,VPS54	up_VCAV_EC
GO:0071375	0.247	0.88	5	68	cellular response to peptide hormone stimulus	BP	1	ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0010001	0.247	0.881	5	54	glial cell differentiation	BP	1	PTPN11,ILK,SLC45A3,EIF2B1,CTNNB1	down_VSAP_EC
GO:0045778	0.247	0.883	5	35	positive regulation of ossification	BP	1	OSR2,ZHX3,OSR1,ZBTB16,DDR2	up_VSAP_EC
GO:0033135	0.247	0.893	4	40	regulation of peptidyl-serine phosphorylation	BP	1	VEGFA,BCAR3,PTGS2,PLCL1	down_VSAP_EC
GO:0044070	0.247	0.911	3	22	regulation of anion transport	BP	1	ATP8A1,STC1,RIPK1	up_VCAV_EC
GO:1903201	0.247	0.912	3	20	regulation of oxidative stress-induced cell death	BP	1	TLR4,RIPK1,HIF1A	up_VCAV_EC
GO:2000059	0.247	0.933	2	19	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	PARK7,CLEC16A	down_VCAV_EC

GO:0009954	0.247	0.934	2	16	proximal/distal pattern formation	BP	1	CHSY1,CTNNB1	down_VSAP_EC
GO:0045620	0.247	0.934	2	15	negative regulation of lymphocyte	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:1904892	0.247	0.931	2	40	regulation of STAT cascade	BP	1	LEP,LRRC15	up_AFEM_EC
GO:0048699	0.247	0.933	2	371	generation of neurons	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0031670	0.247	0.937	2	10	cellular response to nutrient	BP	1	PDK2,CASTOR1	up_VSAP_EC
GO:0007566	0.247	0.937	2	10	embryo implantation	BP	1	EMP2,RECK	up_VSAP_EC
GO:0071897	0.247	0.968	1	54	DNA biosynthetic process	BP	1	ACVRL1	down_ACOR_EC
GO:0006297	0.247	0.977	1	3	nucleotide-excision repair, DNA gap filling	BP	1	POLE	down_ACOR_VSMC
GO:2001015	0.247	0.977	1	3	negative regulation of skeletal muscle cell	BP	1	SIX4	down_ACOR_VSMC
GO:1900274	0.247	0.972	1	6	regulation of phospholipase C activity	BP	1	PDGFRB	down_VCAV_EC
GO:0006935	0.247	0.969	1	143	chemotaxis	BP	1	HSD3B7	down_VPOR_EC
GO:0042330	0.247	0.969	1	143	taxis	BP	1	HSD3B7	down_VPOR_EC
GO:0055015	0.247	0.973	1	5	ventricular cardiac muscle cell development	BP	1	FHL2	down_VSAP_EC
GO:0034163	0.247	0.977	1	3	regulation of toll-like receptor 9 signaling	BP	1	PTPN22	up_ACOR_VSMC
GO:0042416	0.247	0.977	1	3	dopamine biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0060017	0.247	0.977	1	3	parathyroid gland development	BP	1	CRKL	up_ACOR_VSMC
GO:0098902	0.247	0.977	1	3	regulation of membrane depolarization during action potential	BP	1	PTPN3	up_ACOR_VSMC
GO:0071526	0.247	0.969	1	12	semaphorin-plexin signaling pathway	BP	1	PLXNA4	up_AFEM_EC
GO:0043588	0.247	0.968	1	74	skin development	BP	1	SLITRK5	up_APUL_EC
GO:0061138	0.247	0.968	1	73	morphogenesis of a branching epithelium	BP	1	NPNT	up_APUL_EC
GO:0071560	0.247	0.968	1	72	cellular response to transforming growth	BP	1	NPNT	up_APUL_EC
GO:0090092	0.247	0.968	1	72	regulation of transmembrane receptor protein serine/threonine	BP	1	NPNT	up_APUL_EC
GO:2000027	0.247	0.968	1	72	regulation of animal organ morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0006346	0.247	0.977	1	3	methylation-dependent chromatin silencing	BP	1	UHRF2	up_VCAV_EC
GO:0045117	0.247	0.973	1	5	azole transport	BP	1	SNAP23	up_VCAV_EC
GO:0060052	0.247	0.977	1	3	neurofilament cytoskeleton organization	BP	1	VPS54	up_VCAV_EC
GO:0071947	0.247	0.977	1	3	protein deubiquitination involved in ubiquitin-dependent protein	BP	1	TNFAIP3	up_VCAV_EC
GO:1900151	0.247	0.977	1	3	regulation of nuclear-transcribed mRNA catabolic process,	BP	1	CNOT7	up_VCAV_EC
GO:1900153	0.247	0.977	1	3	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	CNOT7	up_VCAV_EC
GO:0008154	0.247	0.968	1	81	actin polymerization or depolymerization	BP	1	CCL24	up_VPUL_EC
GO:0018212	0.247	0.968	1	81	peptidyl-tyrosine modification	BP	1	ARHGEF2	up_VPUL_EC
GO:0032886	0.247	0.968	1	81	regulation of microtubule-based process	BP	1	ARHGEF2	up_VPUL_EC
GO:0010499	0.247	0.977	1	3	proteasomal ubiquitin-independent protein catabolic process	BP	1	KEAP1	up_VSAP_EC
GO:0050665	0.247	0.977	1	3	hydrogen peroxide biosynthetic process	BP	1	ZNF205	up_VSAP_EC
GO:0071359	0.247372267	0.96945	1	11	cellular response to dsRNA	BP	1	MAVS	up_ACOR_EC
GO:0072088	0.247679079	0.93062	2	36	nephron epithelium morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC

GO:0031399	0.248	0.796	59	559	regulation of protein modification process	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,SKP2,PRKAA2,BMP4,FGFR2,ATRX,TLR3,SH3RF2,LATS2,PDE5A,ISG15,SASH1,FGF18,NDRG2,CDKN2B,F2RL1,FAM129A,CDKN1A,NRP1,PTPN22,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,CCL5,DDR2,DUSP22,EDN1,OXR1,AKTIP,DUSP26,NOD2,LRRC4,FAM107A,PRKAG3,SH3RF3,DCUN1D4,HERPUD1,MAP3K7,INPP5K,WFS1,WDR48,ENSCAFG00000029553,PARK7,CRKL	up_ACOR_VSMC
GO:0051726	0.248	0.806	37	393	regulation of cell cycle	BP	1	PLK2,CXCL8,TNFAIP3,MX2,PDGFB,STK10,GATA3,EDN1,RAB11A,FIGNL1,MAP3K3,BMP2,HHEX,SLK,GDPD5,PROX1,UHRF2,ENSCAFG00000010596,MADD,PAK2,THOC1,ETAA1,SENP6,USP28,TAOK1,BLM,SMC5,RAD21,RAD17,SKIL,CUL4A,ZW10,ATRX,NR4A1,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:1901564	0.248	0.852	12	2053	organonitrogen compound metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,RPSA,SULF1,CSGALNACT1,ACSL3,TNRC6B,ASPN,NEDD4	down_ACOR_EC
GO:0030001	0.248	0.843	11	172	metal ion transport	BP	1	PRNP,FXYD1,TRPV2,SLC39A6,CACNB3,THY1,SCARA5,TPC3,CYBA,ARHGAP1,PACSIN3	down_VCAV_EC
GO:0006399	0.248	0.863	7	87	tRNA metabolic process	BP	1	CARS,SARS,AARS,YARS,TARS,NARS,RTCB	down_VSAP_EC
GO:0050920	0.248	0.865	7	53	regulation of chemotaxis	BP	1	C5AR2,SLC8B1,SLIT2,PLXNA4,F2RL1,ZNF580,STX4	up_VSAP_EC
GO:0000086	0.248	0.872	6	52	G2/M transition of mitotic cell cycle	BP	1	RAB11A,TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0016571	0.248	0.892	4	39	histone methylation	BP	1	NR1H4,IWS1,PRMT1,KDM3A	down_VSAP_EC
GO:0035051	0.248	0.893	4	41	cardiocyte differentiation	BP	1	PRICKLE1,FHL2,NEXN,REST	down_VSAP_EC
GO:0048483	0.248	0.912	3	19	autonomic nervous system development	BP	1	EDNRB,GATA3,NAV2	up_VCAV_EC
GO:0051247	0.248	0.91	3	502	positive regulation of protein metabolic process	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0009581	0.248	0.912	3	18	detection of external stimulus	BP	1	CHRM1,NR2F6,DENND5A	up_VSAP_EC
GO:0009582	0.248	0.912	3	18	detection of abiotic stimulus	BP	1	CHRM1,NR2F6,DENND5A	up_VSAP_EC
GO:0051279	0.248	0.933	2	19	regulation of release of sequestered calcium ion into cytosol	BP	1	THY1,CYBA	down_VCAV_EC
GO:0003179	0.248	0.933	2	19	heart valve morphogenesis	BP	1	NOTCH2,BMPR1A	down_VCAV_EC
GO:0010828	0.248	0.933	2	16	positive regulation of glucose transmembrane	BP	1	NR1H4,PTPN11	down_VSAP_EC
GO:0031341	0.248	0.935	2	13	regulation of cell killing	BP	1	IL7R,NECTIN2	up_VCAV_EC
GO:0021680	0.248	0.937	2	10	cerebellar Purkinje cell layer development	BP	1	SEZ6L,DLL1	up_VSAP_EC
GO:0070588	0.248	0.968	1	54	calcium ion transmembrane transport	BP	1	LYN	down_ACOR_EC
GO:0006898	0.248	0.968	1	57	receptor-mediated endocytosis	BP	1	NEDD4	down_ACOR_EC
GO:0007219	0.248	0.968	1	59	Notch signaling pathway	BP	1	WDR12	down_ACOR_EC
GO:0006610	0.248	0.977	1	3	ribosomal protein import into nucleus	BP	1	IPO4	down_ACOR_VSMC
GO:0014816	0.248	0.977	1	3	skeletal muscle satellite cell differentiation	BP	1	SIX4	down_ACOR_VSMC
GO:0019896	0.248	0.977	1	3	axonal transport of mitochondrion	BP	1	TRAK1	down_ACOR_VSMC
GO:0038180	0.248	0.977	1	3	nerve growth factor signaling pathway	BP	1	CORO1A	down_ACOR_VSMC
GO:0032970	0.248	0.969	1	130	regulation of actin filament-based process	BP	1	FSCN1	down_AFEM_EC
GO:0007398	0.248	0.971	1	6	ectoderm development	BP	1	BMPR1A	down_VCAV_EC
GO:0097106	0.248	0.972	1	6	postsynaptic density organization	BP	1	CDH2	down_VCAV_EC
GO:0099084	0.248	0.972	1	6	postsynaptic specialization	BP	1	CDH2	down_VCAV_EC
GO:2000273	0.248	0.972	1	6	positive regulation of signaling receptor activity	BP	1	PARK7	down_VCAV_EC
GO:0031325	0.248	0.982	1	914	positive regulation of cellular metabolic process	BP	1	GATA5	down_VFEM_VSMC
GO:0051000	0.248	0.973	1	5	positive regulation of nitric-oxide synthase	BP	1	APOE	down_VSAP_EC

GO:1990403	0.248	0.974	1	4	embryonic brain development	BP	1	CTNNB1	down_VSAP_EC
GO:0030035	0.248	0.974	1	4	microspike assembly	BP	1	FSCN1	down_VSAP_EC
GO:0031290	0.248	0.974	1	4	retinal ganglion cell axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0003140	0.248	0.977	1	3	determination of left/right asymmetry in	BP	1	CITED2	up_ACOR_VSMC
GO:0003183	0.248	0.977	1	3	mitral valve morphogenesis	BP	1	SMAD6	up_ACOR_VSMC
GO:0006107	0.248	0.977	1	3	oxaloacetate metabolic process	BP	1	NIT2	up_ACOR_VSMC
GO:0032693	0.248	0.977	1	3	negative regulation of interleukin-10 production	BP	1	CD274	up_ACOR_VSMC
GO:1902993	0.248	0.977	1	3	positive regulation of amyloid precursor protein catabolic process	BP	1	APP	up_ACOR_VSMC
GO:0044319	0.248	0.969	1	12	wound healing, spreading of cells	BP	1	ADAM17	up_AFEM_EC
GO:0090504	0.248	0.969	1	12	epiboly	BP	1	ADAM17	up_AFEM_EC
GO:0090505	0.248	0.969	1	12	epiboly involved in wound healing	BP	1	ADAM17	up_AFEM_EC
GO:1903706	0.248	0.968	1	119	regulation of hemopoiesis	BP	1	HOXA9	up_AORT_EC
GO:0060541	0.248	0.968	1	73	respiratory system development	BP	1	TBX5	up_APUL_EC
GO:0060013	0.248	0.977	1	3	righting reflex	BP	1	ALDH1A3	up_VCAV_EC
GO:0072216	0.248	0.974	1	4	positive regulation of metanephros	BP	1	PDGFB	up_VCAV_EC
GO:0061299	0.248	0.977	1	3	retina vasculature morphogenesis in camera-	BP	1	ARHGEF15	up_VCAV_EC
GO:0072224	0.248	0.974	1	4	metanephric glomerulus development	BP	1	PDGFB	up_VCAV_EC
GO:0072239	0.248	0.974	1	4	metanephric glomerulus vasculature development	BP	1	PDGFB	up_VCAV_EC
GO:0010720	0.248	0.968	1	110	positive regulation of cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007548	0.248	0.968	1	68	sex differentiation	BP	1	HOXA9	up_VFEM_EC
GO:0009161	0.248	0.968	1	103	ribonucleoside monophosphate	BP	1	FBP1	up_VFEM_VSMC
GO:0001826	0.248	0.977	1	3	inner cell mass cell differentiation	BP	1	LATS2	up_VSAP_EC
GO:0009187	0.248193343	0.96952	1	10	cyclic nucleotide metabolic process	BP	1	GUCY1B1	up_ACOR_EC
GO:0016053	0.248355291	0.89021	4	97	organic acid biosynthetic process	BP	1	NR1H4,THNSL2,PTGDS,ALDOC	up_ACOR_EC
GO:0046394	0.248355291	0.89021	4	97	carboxylic acid biosynthetic process	BP	1	NR1H4,THNSL2,PTGDS,ALDOC	up_ACOR_EC
GO:1903393	0.248415979	0.96918	1	11	positive regulation of adherens junction	BP	1	NRP1	up_ACOR_EC
GO:0032502	0.249	0.78	166	1661	developmental process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,NAPEPLD,PCDH19,TWIST2,HOXA9,SEZ6L,CDON,WNT11,HNF4A,CD274,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,RADIL,PPARGC1B,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,DDHD1,IL6R,IRX5,SLIT2,CRIP2,ZHX3,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,EPN2,HOXA6,OSR1,MAP3K5,CDC42EP5,FUZ,ADAMTSL4,WARS2,SAV1,KLF15,ANXA4,HPSE,PLXNA4,ARL4A,RILPL2,ANKRD54,CLDN1,CDC42EP2,ZBTB16,TOX,ALDH6A1,RARG,CCBE1,STAT6,HOXC4,RECK,PATZ1,PLPP3,GTF3C5,AMBRA1,F2RL1,DLX3,GLIS2,MORC3,DDR2,MFN2,ZFP36L1,FXN,PIK3R1,TIAM1,GAS1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,TBXA2R,SULF2,SHOX2,EEF2,RTN4RL1,SASH1,FBXO4,HOXC10,POLDIP2,MYD88,LOX,TFE3,LRP4,DPYSL2,GDPD5,ZADH2,DAGLB,HPS4,FRMD6,CLCN2,E2F4,PRKAB1,SMG9,MCPH1,KIF27,FBXO7,NTN4,LIMD1,CDK9,CD83,NR2F6,KDM2B,FBLN1,ZFP36L2,HPGD,PLEKHB2,YPEL3,RAF1,PNP,TAF8,NFIB,CYB5D2,CDNF,PRELP,ZFAND5,ANPEP,PQBP1,TTL,PLEKHA5,QARS,ARHGAP12,ACVRL1,TPRA1,VANGL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,OGN,TRADD,PIR	up_VSAP_EC

GO:0009891	0.249	0.799	49	521	positive regulation of biosynthetic process	BP	1	ACSL3,HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,SLC29A1,CTDNEP1,RFC2,INSIG1,RFC5,RFC3,THRAP3,TRUB2,FAM129B,AURKB,GREM1,RFC4,NEK2,SMARCC1,PCNA,DHX33,CKS2,BRCA1,FASTKD3,EIF5A,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103	down_ACOR_VSMC
GO:0050776	0.249	0.836	13	173	regulation of immune response	BP	1	NR1H4,SOCS5,FAM49B,PTPN2,EIF2B1,PVR,SKAP2,CNOT7,TFRC,LYN,CDC37,GBP5,A2M	down_VSAP_EC
GO:0042098	0.249	0.881	5	43	T cell proliferation	BP	1	PELI1,ARG2,ELF4,NCK1,HMGB1	up_VCAV_EC
GO:0045580	0.249	0.908	3	35	regulation of T cell differentiation	BP	1	GLI3,LOXL3,ZBTB16	down_VCAV_EC
GO:0045747	0.249	0.911	3	18	positive regulation of Notch signaling pathway	BP	1	DLL1,EPN2,TSPAN5	up_VSAP_EC
GO:1901379	0.249	0.935	2	12	regulation of potassium ion transmembrane	BP	1	NEDD4,CAV1	down_ACOR_VSMC
GO:0007010	0.249	0.933	2	441	cytoskeleton organization	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0046902	0.249	0.932	2	18	regulation of mitochondrial membrane	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0120193	0.249	0.933	2	15	tight junction organization	BP	1	MYO1C,CTNNB1	down_VSAP_EC
GO:0034063	0.249	0.938	2	9	stress granule assembly	BP	1	PRKAA2,ATXN2	up_ACOR_VSMC
GO:0050820	0.249	0.936	2	10	positive regulation of coagulation	BP	1	ENPP4,PSEN1	up_ACOR_VSMC
GO:0007166	0.249	0.936	2	686	cell surface receptor signaling pathway	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0003016	0.249	0.936	2	10	respiratory system process	BP	1	CCBE1,ZFAND5	up_VSAP_EC
GO:1903671	0.249	0.937	2	10	negative regulation of sprouting angiogenesis	BP	1	EPN2,TBXA2R	up_VSAP_EC
GO:0043207	0.249	0.931	2	216	response to external biotic stimulus	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0051707	0.249	0.931	2	216	response to other organism	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0010970	0.249	0.968	1	48	transport along microtubule	BP	1	SPG11	down_ACOR_EC
GO:0099111	0.249	0.968	1	48	microtubule-based transport	BP	1	SPG11	down_ACOR_EC
GO:0071407	0.249	0.968	1	129	cellular response to organic cyclic compound	BP	1	GABPA	down_AFEM_EC
GO:0022411	0.249	0.968	1	130	cellular component disassembly	BP	1	FSCN1	down_AFEM_EC
GO:0048841	0.249	0.974	1	4	regulation of axon extension involved in	BP	1	NRP1	down_VSAP_EC
GO:1902668	0.249	0.974	1	4	negative regulation of axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0021859	0.249	0.977	1	3	pyramidal neuron differentiation	BP	1	FGFR2	up_ACOR_VSMC
GO:0021860	0.249	0.977	1	3	pyramidal neuron development	BP	1	FGFR2	up_ACOR_VSMC
GO:0007063	0.249	0.969	1	12	regulation of sister chromatid cohesion	BP	1	AXIN2	up_AFEM_EC
GO:0021517	0.249	0.969	1	12	ventral spinal cord development	BP	1	HOXC10	up_AFEM_EC
GO:0030201	0.249	0.969	1	12	heparan sulfate proteoglycan metabolic	BP	1	XYLT1	up_AFEM_EC
GO:0043030	0.249	0.969	1	12	regulation of macrophage activation	BP	1	BPI	up_AFEM_EC
GO:0045058	0.249	0.969	1	12	T cell selection	BP	1	CYLD	up_AFEM_EC
GO:0072283	0.249	0.969	1	12	metanephric renal vesicle morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:0016485	0.249	0.968	1	73	protein processing	BP	1	PCSK1N	up_APUL_EC
GO:0045792	0.249	0.977	1	3	negative regulation of cell size	BP	1	MTOR	up_VCAV_EC
GO:0089700	0.249	0.977	1	3	protein kinase D signaling	BP	1	PRKD2	up_VCAV_EC
GO:2000767	0.249	0.977	1	3	positive regulation of cytoplasmic translation	BP	1	NCK1	up_VCAV_EC
GO:1901292	0.249	0.968	1	34	nucleoside phosphate catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0051301	0.249	0.968	1	117	cell division	BP	1	FGF5	up_VPOR_VSMC

GO:0044057	0.249	0.968	1	110	regulation of system process	BP	1	NETO1	up_VFEM_VSMC
GO:0051495	0.249	0.968	1	82	positive regulation of cytoskeleton organization	BP	1	CCL24	up_VPUL_EC
GO:0060534	0.249	0.977	1	3	trachea cartilage development	BP	1	RARG	up_VSAP_EC
GO:0061086	0.249	0.977	1	3	negative regulation of histone H3-K27	BP	1	PHF1	up_VSAP_EC
GO:0010038	0.249	0.968	1	62	response to metal ion	BP	1	CAV1	up_VSAP_VSMC
GO:0003205	0.249	0.968	1	67	cardiac chamber development	BP	1	SHOX2	up_VSAP_VSMC
GO:0048856	0.249344744	0.80302	45	1533	anatomical structure development	BP	1	SH3TC2,MYOZ2,CPAMD8,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TBX18,SOX9,RHOU,PTH1R,NDRG2,AQP1,ENSCAFG00000004331,FZD5,SEMA6D,DIXDC1,PDLIM3,RGMA,LHX9,SMAD6,ACTN2,ESM1,PAK3,IL11RA,DLX3,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,MAPK8IP2,FOXC2,TBX5,LRP4,CLSTN1,RBM38,C23H3orf58,RARRES2,NRP1,ARHGEF26,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:1900181	0.249450451	0.96891	1	11	negative regulation of protein localization to	BP	1	DCLK2	up_ACOR_EC
GO:0018130	0.25	0.784	113	1261	heterocycle biosynthetic process	BP	1	ELK3,PRPSAP1,HMGB1,SREBF1,ACLY,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,HNRNPD,SREBF2,HINFP,NEDD4,RRM1,MED17,SLC29A1,MTDH,HEY1,SRRT,POLE,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,ELOVL1,PPARD,POLH,YBX3,NCL,NUP62,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,RBM14,CYC1,POLR3F,HOXA10,ERF,TCERG1,ATP5F1A,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,NUDT1,HMGN1,CCT4,SIX4,CTPS1,MED16,ENSCAFG00000017103,ATP5F1D,POLR1C,NUDT3	down_ACOR_VSMC
GO:0006793	0.25	0.785	97	948	phosphorus metabolic process	BP	1	FGF13,ADRA1B,SMAD6,PIP5K1B,PLCG2,LEP,PLCL1,MAP3K8,MID1,CDC7,HTR2B,RASSF2,MBP,PRKAA2,BMP4,LCAT,CHPT1,FGFR2,TLR3,SH3RF2,PPARGC1A,LATS2,PIGN,PDE5A,PIGS,PLPP2,AR,SASH1,LMO4,PFKM,FGF18,NDRG2,CDKN2B,ADCY6,PPIP5K1,GRK7,PIGG,F2RL1,FAM129A,CAMK2D,DAPK1,NCEH1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,MARF1,CRLS1,FRS2,DAG1,FUT8,ENSCAFG00000018611,PPP1R26,PARP9,APP,PSEN1,SYNJ2BP,PIK3C3,CCL5,DDR2,CLN8,PSKH1,DUSP22,EDN1,ALDOC,AKTIP,DUSP26,NOD2,LRRC4,ENTPD3,LMTK2,PRKAG3,DDIT4,SH3RF3,SERINC3,EXTL2,SERINC1,CFI,RPRD1B,MAP3K7,INPP5K,PFKL,NT5C2,ENSCAFG00000029553,NMNAT1,PARK7,ELOVL7,GPATCH2,ZFYVE1,CRKL,CDKL2	up_ACOR_VSMC
GO:0009056	0.25	0.789	78	755	catabolic process	BP	1	PLCG2,LEP,PLCL1,HTR2B,ENOSF1,ZRANB1,FBXL20,FEZ1,ENSCAFG00000002977,SKP2,PRKAA2,PNRC1,SH3RF2,LPL,PDE5A,TP53INP1,MAOA,ISG15,ZNRF3,CTSS,PTPN3,FMO4,KLHL20,ACAD11,ENPP4,GABARAPL1,DAPK1,CTSB,BNIP3,EGLN1,NCEH1,LIPE,DCP1B,UBR1,ULK2,OS9,STT3B,SMPD1,UBE2H,MOXD1,PYGM,RNF24,PRKCE,SARDH,RNF19A,LYPLAL1,PSEN1,PIK3C3,LAMP2,CLN8,SIAH1,ALDOC,CTSF,ENTPD3,ATG16L2,PCYOX1,DDIT4,DISC1,RNF181,NEU3,USP20,HERPUD1,CFI,GAA,FEZ2,INPP5K,FAF2,CNOT4,WFS1,AZIN2,CTIF,CAT,DZIP3,SH3BP4,ERAP1,ENSCAFG00000029553,PARK7,ZFYVE1	up_ACOR_VSMC

GO:0048534	0.25	0.811	29	262	hematopoietic or lymphoid organ development	BP	1	TMEM176B,TMEM176A,PLCG2,LEP,CD83,RASSF2,BMP4,FGFR2,CITED2,ISG15,LMO4,FAM210B,P4HTM,CDKN2B,F2RL1,CLSTN1,PTPN22,CHD2,APP,PSEN1,CHD7,RTKN2,JAM3,B2M,CNOT4,ENSCAFG00000003530,IL18R1,BVES,CRKL	up_ACOR_VSMC
GO:0060562	0.25	0.834	14	120	epithelial tube morphogenesis	BP	1	HOXA11,FZD1,WNT11,SLIT2,ABL1,DLL1,OSR1,FUZ,RARG,IRX3,KDM2B,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0051960	0.25	0.861	7	216	regulation of nervous system development	BP	1	IRX3,DLL1,PLXNA4,THRB,LGI4,CAMK2A,KANK1	up_AFEM_EC
GO:0030100	0.25	0.863	7	70	regulation of endocytosis	BP	1	SELE,RAB27A,PPP3CA,BMP2K,HIST1H1A,PLCG2,HMGB1	up_VCAV_EC
GO:0034101	0.25	0.872	6	45	erythrocyte homeostasis	BP	1	BMP4,CITED2,ISG15,FAM210B,P4HTM,B2M	up_ACOR_VSMC
GO:0002695	0.25	0.872	6	44	negative regulation of leukocyte activation	BP	1	BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0031214	0.25	0.872	6	45	biomineral tissue development	BP	1	BMP4,FGFR2,GJA1,ISG15,DDR2,SLC8A1	up_ACOR_VSMC
GO:0006405	0.25	0.881	5	39	RNA export from nucleus	BP	1	DDX39A,RAN,NUP62,NUP188,DDX39B	down_ACOR_VSMC
GO:0034341	0.25	0.88	5	43	response to interferon-gamma	BP	1	GBP5,NLRC5,IRF8,FLNB,GCH1	up_VCAV_EC
GO:0007259	0.25	0.891	4	42	JAK-STAT cascade	BP	1	SOCS5,PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0007178	0.25	0.889	4	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	TMEM100,GREM1,GREM2,ADAM17	up_AFEM_EC
GO:0007600	0.25	0.905	3	73	sensory perception	BP	1	THRB,TMEM100,REEP2	up_AFEM_EC
GO:0045069	0.25	0.909	3	22	regulation of viral genome replication	BP	1	CXCL8,PROX1,CNOT7	up_VCAV_EC
GO:0048514	0.25	0.906	3	214	blood vessel morphogenesis	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0034605	0.25	0.911	3	18	cellular response to heat	BP	1	SCARA5,HTRA2,HMOX1	up_VSAP_EC
GO:0061178	0.25	0.934	2	12	regulation of insulin secretion involved in cellular response to	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0048599	0.25	0.936	2	10	oocyte development	BP	1	PDE5A,DMC1	up_ACOR_VSMC
GO:1903053	0.25	0.936	2	10	regulation of extracellular matrix organization	BP	1	DAG1,DDR2	up_ACOR_VSMC
GO:0023014	0.25	0.93	2	248	signal transduction by protein phosphorylation	BP	1	MAPK10,NPNT	up_APUL_EC
GO:0021799	0.25	0.935	2	11	cerebral cortex radially oriented cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0007417	0.25	0.93	2	235	central nervous system development	BP	1	HOXC10,SIX1	up_VFEM_EC
GO:0040007	0.25	0.931	2	276	growth	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0043534	0.25	0.967	1	57	blood vessel endothelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0080090	0.25	1	1	1734	regulation of primary metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0021801	0.25	0.971	1	6	cerebral cortex radial glia guided migration	BP	1	GLI3	down_VCAV_EC
GO:0022030	0.25	0.971	1	6	telencephalon glial cell migration	BP	1	GLI3	down_VCAV_EC
GO:0001865	0.25	0.971	1	6	NK T cell differentiation	BP	1	ZBTB16	down_VCAV_EC
GO:0010604	0.25	0.982	1	919	positive regulation of macromolecule metabolic	BP	1	GATA5	down_VFEM_VSMC
GO:0030859	0.25	0.972	1	5	polarized epithelial cell differentiation	BP	1	MSN	down_VSAP_EC
GO:0035744	0.25	0.976	1	3	T-helper 1 cell cytokine production	BP	1	IL18R1	up_ACOR_VSMC
GO:0006621	0.25	0.976	1	3	protein retention in ER lumen	BP	1	OS9	up_ACOR_VSMC
GO:0034370	0.25	0.977	1	3	triglyceride-rich lipoprotein particle	BP	1	LCAT	up_ACOR_VSMC
GO:0034372	0.25	0.977	1	3	very-low-density lipoprotein particle	BP	1	LCAT	up_ACOR_VSMC
GO:0048169	0.25	0.977	1	3	regulation of long-term neuronal synaptic	BP	1	APP	up_ACOR_VSMC
GO:0001754	0.25	0.968	1	12	eye photoreceptor cell differentiation	BP	1	THRB	up_AFEM_EC
GO:0045922	0.25	0.968	1	12	negative regulation of fatty acid metabolic	BP	1	ACACB	up_AFEM_EC

GO:0003333	0.25	0.969	1	12	amino acid transmembrane transport	BP	1	SLC6A6	up_AFEM_EC
GO:0061098	0.25	0.968	1	12	positive regulation of protein tyrosine kinase	BP	1	ADAM17	up_AFEM_EC
GO:0071825	0.25	0.969	1	12	protein-lipid complex subunit organization	BP	1	PLAGL2	up_AFEM_EC
GO:0071827	0.25	0.969	1	12	plasma lipoprotein particle organization	BP	1	PLAGL2	up_AFEM_EC
GO:0072604	0.25	0.969	1	12	interleukin-6 secretion	BP	1	LEP	up_AFEM_EC
GO:0072606	0.25	0.969	1	12	interleukin-8 secretion	BP	1	LEP	up_AFEM_EC
GO:0120033	0.25	0.968	1	12	negative regulation of plasma membrane bounded cell projection	BP	1	KANK1	up_AFEM_EC
GO:2000036	0.25	0.968	1	12	regulation of stem cell population maintenance	BP	1	LBH	up_AFEM_EC
GO:0006281	0.25	0.969	1	208	DNA repair	BP	1	EYA1	up_AFEM_VSMC
GO:0072017	0.25	0.976	1	3	distal tubule development	BP	1	JAG1	up_VCAV_EC
GO:0010457	0.25	0.976	1	3	centriole-centriole cohesion	BP	1	CEP68	up_VCAV_EC
GO:0010811	0.25	0.967	1	36	positive regulation of cell-substrate adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0032680	0.25	0.967	1	36	regulation of tumor necrosis factor production	BP	1	ARHGEF2	up_VPOR_EC
GO:0062014	0.25	0.967	1	35	negative regulation of small molecule metabolic	BP	1	FBP1	up_VPOR_EC
GO:0009123	0.25	0.968	1	104	nucleoside monophosphate	BP	1	FBP1	up_VFEM_VSMC
GO:0009144	0.25	0.968	1	103	purine nucleoside triphosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0051181	0.250635356	0.9686	1	11	cofactor transport	BP	1	SLC25A42	up_ACOR_EC
GO:0042110	0.251	0.836	13	109	T cell activation	BP	1	LEP,CD83,BMP4,PDE5A,CD274,F2RL1,PTPN22,PSEN1,CHD7,DUSP22,B2M,IL18R1,PAG1	up_ACOR_VSMC
GO:0072594	0.251	0.845	10	155	establishment of protein localization to organelle	BP	1	NABP2,ENSCAFG00000014978,SNUPN,SSR3,PEX5,GLI3,MAVS,SEC61B,LONP2,SEC61A1	down_VCAV_EC
GO:0048608	0.251	0.845	10	129	reproductive structure development	BP	1	SULF1,PTPN11,TMED2,PTGS2,HIF1A,CTNNB1,INHBA,SIX4,SPINK2,RTCB	down_VSAP_EC
GO:0001659	0.251	0.863	7	54	temperature homeostasis	BP	1	NAPEPLD,PPARGC1B,EBF2,STAT6,MFN2,HOXC10,PRKAB1	up_VSAP_EC
GO:0031398	0.251	0.87	6	51	positive regulation of protein ubiquitination	BP	1	UBE2S,CAV1,FANCI,CDC20,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0050817	0.251	0.87	6	50	coagulation	BP	1	TFPI,TFPI2,CAV1,ANXA5,ITGB3,PIK3CD	down_ACOR_VSMC
GO:0061061	0.251	0.867	6	179	muscle structure development	BP	1	DLL1,CRYAB,GREM1,BVES,DMPK,HSPB2	up_AFEM_EC
GO:0044774	0.251	0.893	4	30	mitotic DNA integrity checkpoint	BP	1	TAOK1,BLM,RAD17,TOPBP1	up_VCAV_EC
GO:0048660	0.251	0.907	3	35	regulation of smooth muscle cell proliferation	BP	1	PDGFRB,BMPR1A,CLSTN1	down_VCAV_EC
GO:0110110	0.251	0.907	3	34	positive regulation of animal organ	BP	1	SEMA3C,B4GALT1,GREM1	down_VCAV_EC
GO:0046513	0.251	0.91	3	19	ceramide biosynthetic process	BP	1	UGCG,ORMDL3,SMPD1	up_ACOR_VSMC
GO:0043618	0.251	0.909	3	22	regulation of transcription from RNA polymerase II promoter in response to	BP	1	ATF3,NCK1,HIF1A	up_VCAV_EC
GO:0045934	0.251	0.907	3	407	negative regulation of nucleobase-containing compound metabolic	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0007264	0.251	0.929	2	164	small GTPase mediated signal transduction	BP	1	PDPN,USP28	down_ACOR_EC
GO:0051240	0.251	0.933	2	489	positive regulation of multicellular organismal	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0044237	0.251	1	2	3491	cellular metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048869	0.251	0.942	2	1119	cellular developmental process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0071715	0.251	0.936	2	10	icosanoid transport	BP	1	LEP,CFI	up_ACOR_VSMC
GO:1901571	0.251	0.936	2	10	fatty acid derivative transport	BP	1	LEP,CFI	up_ACOR_VSMC
GO:0045685	0.251	0.935	2	11	regulation of glial cell differentiation	BP	1	MTOR,BMP2	up_VCAV_EC
GO:0001676	0.251	0.936	2	10	long-chain fatty acid metabolic process	BP	1	DAGLB,ENSCAFG00000023820	up_VSAP_EC

GO:0032743	0.251	0.935	2	10	positive regulation of interleukin-2 production	BP	1	ABL1,CD83	up_VSAP_EC
GO:0043616	0.251	0.936	2	10	keratinocyte proliferation	BP	1	FGF7,ZFP36L1	up_VSAP_EC
GO:0030299	0.251	0.976	1	3	intestinal cholesterol absorption	BP	1	LIMA1	down_ACOR_VSMC
GO:0098856	0.251	0.976	1	3	intestinal lipid absorption	BP	1	LIMA1	down_ACOR_VSMC
GO:0009950	0.251	0.971	1	6	dorsal/ventral axis specification	BP	1	BMPR1A	down_VCAV_EC
GO:0016310	0.251	0.976	1	641	phosphorylation	BP	1	PLCL1	down_VFEM_EC
GO:0035331	0.251	0.974	1	4	negative regulation of hippo signaling	BP	1	WWC3	down_VSAP_EC
GO:0038203	0.251	0.976	1	3	TORC2 signaling	BP	1	SESN3	up_ACOR_VSMC
GO:0070244	0.251	0.976	1	3	negative regulation of thymocyte apoptotic	BP	1	BMP4	up_ACOR_VSMC
GO:0090091	0.251	0.976	1	3	positive regulation of extracellular matrix	BP	1	DDR2	up_ACOR_VSMC
GO:0002067	0.251	0.968	1	12	glandular epithelial cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0002686	0.251	0.968	1	12	negative regulation of leukocyte migration	BP	1	HOXA7	up_AFEM_EC
GO:0030101	0.251	0.968	1	12	natural killer cell activation	BP	1	LEP	up_AFEM_EC
GO:0032768	0.251	0.968	1	12	regulation of monooxygenase activity	BP	1	LEP	up_AFEM_EC
GO:0042461	0.251	0.968	1	12	photoreceptor cell development	BP	1	THRB	up_AFEM_EC
GO:0060231	0.251	0.968	1	12	mesenchymal to epithelial transition	BP	1	GREM1	up_AFEM_EC
GO:0097352	0.251	0.968	1	12	autophagosome maturation	BP	1	CLEC16A	up_AFEM_EC
GO:1905953	0.251	0.968	1	12	negative regulation of lipid localization	BP	1	CRY2	up_AFEM_EC
GO:0031175	0.251	0.97	1	224	neuron projection development	BP	1	WNT7A	up_AORT_VSMC
GO:0019320	0.251	0.974	1	4	hexose catabolic process	BP	1	GALE	up_VCAV_EC
GO:0034350	0.251	0.976	1	3	regulation of glial cell apoptotic process	BP	1	PRKCH	up_VCAV_EC
GO:0034351	0.251	0.976	1	3	negative regulation of glial cell apoptotic process	BP	1	PRKCH	up_VCAV_EC
GO:0048520	0.251	0.976	1	3	positive regulation of behavior	BP	1	MEF2C	up_VCAV_EC
GO:0042476	0.251	0.967	1	36	odontogenesis	BP	1	ASPN	up_VPOR_EC
GO:0048284	0.251	0.967	1	66	organelle fusion	BP	1	TRIM9	up_VFEM_EC
GO:0033673	0.251	0.967	1	84	negative regulation of kinase activity	BP	1	FLRT3	up_VPUL_EC
GO:0048667	0.251	0.968	1	140	cell morphogenesis involved in neuron	BP	1	SLIT2	up_VPUL_VSMC
GO:0045719	0.251	0.976	1	3	negative regulation of glycogen biosynthetic	BP	1	PASK	up_VSAP_EC
GO:0070874	0.251	0.976	1	3	negative regulation of glycogen metabolic	BP	1	PASK	up_VSAP_EC
GO:1903037	0.251	0.967	1	65	regulation of leukocyte cell-cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0070848	0.251162258	0.86002	7	193	response to growth factor	BP	1	SOX9,FNDC4,RGMA,SMAD6,ADAMTSL2,LRP4,NRP1	up_ACOR_EC
GO:0045668	0.25139718	0.9684	1	11	negative regulation of osteoblast differentiation	BP	1	SMAD6	up_ACOR_EC
GO:0009069	0.251435537	0.96839	1	11	serine family amino acid metabolic process	BP	1	THNSL2	up_ACOR_EC

GO:0008150	0.252	0.782	478	5646	biological_process	BP	1	FADS2,ELK3,SCD,ACSL3,PRPSAP1,SQLE,FSCN1,FADS1,HMGB1,MCM6,RNPS1,LSS,SREBF1,ACLY,ARSI,MCM4,FLNB,POLE3,USP1,IRAK1,MCM7,RPA1,NCAPD2,ANLN,PTBP1,ILF3,DDX39A,STXBP6,CBX5,ENSCAFG00000016095,PPRC1,USP4,FMNL3,RACGAP1,SF3B2,ACSL4,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,TFPI,HNRNPD,SREBF2,MCM3,SMC1A,TFPI2,HINFP,VARS,RALY,KIF2A,UBE2S,NEDD4,SRSF2,RRM1,WDR76,THOP1,MED17,U2AF2,ZW10,INTS7,QSOX2,ENSCAFG00000016482,MNDA,CAPG,SMC4,CENPA,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,HOXA3,ENSCAFG00000017264,NDC1,PPM1G,RRBP1,SNRPB2,CENPN,TOP3A,TRIP13,COLGALT1,SLC25A5,PPP1R15B,TIMM44,SF1,PARPBP,SGO1,POLA2,MPDU1,SRRT,GINS4,C1QTNF6,NOP56,SDC1,ARFGAP1,CTDNEP1,RAD54L,RANGAP1,POLE,FBXO5,DDX23,HSPA9,NAB2,SLC35C2,TENT4A,HNRNPH3,MRPS18B,SLC25A15,RAN,B3GNT2,CFAP298,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,ENSCAFG00000030005,CAV1,CDK1,RFC5,CENPE,RFC3,RAD51,CASP2,RANBP1,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,LIMA1,TRUB2,ENSCAFG0000001	down_ACOR_VSMC
GO:0080135	0.252	0.811	27	240	regulation of cellular response to stress	BP	1	LEP,MID1,RASSF2,NACC2,TP53BP1,TLR3,SH3RF2,ZNF365,SASH1,ANKRD1,F2RL1,PTPN22,OS9,SH3RF1,FUT8,PARP9,APP,DUSP22,EDN1,OXR1,NOD2,SH3RF3,SERINC3,HERPUD1,MAP3K7,WFS1,PARK7	up_ACOR_VSMC
GO:0048568	0.252	0.826	17	148	embryonic organ development	BP	1	BMP4,FGFR2,GJA1,SEC24B,CITED2,SPINT1,EGLN1,ENSCAFG00000006238,SPINT2,TBX20,FZD3,FRS2,PSEN1,CHD7,EDN1,WDR48,TEAD1	up_ACOR_VSMC
GO:0031349	0.252	0.842	11	90	positive regulation of defense response	BP	1	NAPEPLD,IL17RC,F2RL1,MYD88,NLRX1,TKFC,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0051258	0.252	0.845	10	94	protein polymerization	BP	1	UBE2S,CAPG,FBXO5,STMN1,RAC1,IQGAP2,CDC42EP4,CORO1A,ARPC1B,UBE2C	down_ACOR_VSMC
GO:0002449	0.252	0.863	7	53	lymphocyte mediated immunity	BP	1	LEP,TP53BP1,C1S,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051170	0.252	0.877	5	69	import into nucleus	BP	1	ENSCAFG00000014978,SNUPN,GLI3,MAVS,SEC61B	down_VCAV_EC
GO:0060402	0.252	0.88	5	35	calcium ion transport into cytosol	BP	1	PLCG2,HTR2B,ITPR1,PRKCE,CHD7	up_ACOR_VSMC
GO:0006935	0.252	0.876	5	143	chemotaxis	BP	1	CMKLR1,PLXNA4,ACKR4,CCL5,ADAM17	up_AFEM_EC
GO:0042330	0.252	0.876	5	143	taxis	BP	1	CMKLR1,PLXNA4,ACKR4,CCL5,ADAM17	up_AFEM_EC
GO:2001257	0.252	0.892	4	30	regulation of cation channel activity	BP	1	RELN,PDE4D,MEF2C,PLCG2	up_VCAV_EC
GO:0090183	0.252	0.908	3	21	regulation of kidney development	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0032527	0.252	0.909	3	19	protein exit from endoplasmic reticulum	BP	1	OS9,HERPUD1,FAF2	up_ACOR_VSMC
GO:0009725	0.252	0.929	2	188	response to hormone	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0032727	0.252	0.936	2	9	positive regulation of interferon-alpha	BP	1	TLR3,PTPN22	up_ACOR_VSMC
GO:0072678	0.252	0.935	2	10	T cell migration	BP	1	APP,CCL5	up_ACOR_VSMC
GO:0060039	0.252	0.934	2	11	pericardium development	BP	1	DLL4,BMP2	up_VCAV_EC
GO:0008015	0.252	0.928	2	120	blood circulation	BP	1	HTR7,SEMA3A	up_VPOR_EC
GO:0002520	0.252	0.93	2	279	immune system development	BP	1	HOXA3,EVI2B	up_VPUL_EC
GO:0051797	0.252	0.935	2	10	regulation of hair follicle development	BP	1	HPSE,TRADD	up_VSAP_EC
GO:0016051	0.252	0.967	1	63	carbohydrate biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0022409	0.252	0.967	1	56	positive regulation of cell-cell adhesion	BP	1	PDPN	down_ACOR_EC
GO:0021953	0.252	0.967	1	49	central nervous system neuron differentiation	BP	1	NRP2	down_ACOR_EC
GO:0050679	0.252	0.967	1	62	positive regulation of epithelial cell proliferation	BP	1	ACVRL1	down_ACOR_EC
GO:0030099	0.252	0.967	1	133	myeloid cell differentiation	BP	1	GABPA	down_AFEM_EC

GO:0033273	0.252	0.971	1	6	response to vitamin	BP	1	KANK2	down_VCAV_EC
GO:0036445	0.252	0.971	1	6	neuronal stem cell division	BP	1	NUMBL	down_VCAV_EC
GO:0055057	0.252	0.971	1	6	neuroblast division	BP	1	NUMBL	down_VCAV_EC
GO:0060872	0.252	0.971	1	6	semicircular canal development	BP	1	GLI3	down_VCAV_EC
GO:0021562	0.252	0.973	1	4	vestibulocochlear nerve development	BP	1	NRP1	down_VSAP_EC
GO:0043268	0.252	0.973	1	4	positive regulation of potassium ion transport	BP	1	KIF5B	down_VSAP_EC
GO:0007182	0.252	0.976	1	3	common-partner SMAD protein phosphorylation	BP	1	BMP4	up_ACOR_VSMC
GO:0039689	0.252	0.976	1	3	negative stranded viral RNA replication	BP	1	ATG16L2	up_ACOR_VSMC
GO:1990144	0.252	0.976	1	3	intrinsic apoptotic signaling pathway in	BP	1	BNIP3	up_ACOR_VSMC
GO:0006221	0.252	0.968	1	12	pyrimidine nucleotide biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:0033146	0.252	0.968	1	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	LBH	up_AFEM_EC
GO:0050856	0.252	0.968	1	12	regulation of T cell receptor signaling	BP	1	CYLD	up_AFEM_EC
GO:0051148	0.252	0.968	1	12	negative regulation of muscle cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0071384	0.252	0.968	1	12	cellular response to corticosteroid stimulus	BP	1	NR3C1	up_AFEM_EC
GO:0071385	0.252	0.968	1	12	cellular response to glucocorticoid stimulus	BP	1	NR3C1	up_AFEM_EC
GO:0071480	0.252	0.968	1	12	cellular response to gamma radiation	BP	1	CRYAB	up_AFEM_EC
GO:0016322	0.252	0.973	1	4	neuron remodeling	BP	1	NTN4	up_VCAV_EC
GO:0021564	0.252	0.982	1	2	vagus nerve development	BP	1	NAV2	up_VCAV_EC
GO:0044501	0.252	0.973	1	4	modulation of signal transduction in other	BP	1	TNIP1	up_VCAV_EC
GO:0052250	0.252	0.973	1	4	modulation of signal transduction in other organism involved in	BP	1	TNIP1	up_VCAV_EC
GO:0050801	0.252	0.968	1	200	ion homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0043467	0.252	0.966	1	35	regulation of generation of precursor metabolites	BP	1	FBP1	up_VPOR_EC
GO:0002688	0.252	0.967	1	34	regulation of leukocyte chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0045778	0.252	0.967	1	35	positive regulation of ossification	BP	1	ACVR2A	up_VPOR_EC
GO:0007409	0.252	0.967	1	109	axonogenesis	BP	1	CHL1	up_VPOR_VSMC
GO:0031098	0.252	0.967	1	109	stress-activated protein kinase signaling cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0007265	0.252	0.967	1	121	Ras protein signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0045444	0.252	0.967	1	84	fat cell differentiation	BP	1	WIF1	up_VPUL_EC
GO:0048638	0.252	0.967	1	82	regulation of developmental growth	BP	1	TBX5	up_VPUL_EC
GO:0051047	0.252	0.967	1	84	positive regulation of secretion	BP	1	NR1H4	up_VPUL_EC
GO:0060326	0.252	0.967	1	84	cell chemotaxis	BP	1	CCL24	up_VPUL_EC
GO:0003406	0.252	0.976	1	3	retinal pigment epithelium development	BP	1	RARG	up_VSAP_EC
GO:0021957	0.252	0.976	1	3	corticospinal tract morphogenesis	BP	1	SLIT2	up_VSAP_EC
GO:1901660	0.252	0.976	1	3	calcium ion export	BP	1	SLC8B1	up_VSAP_EC
GO:0010769	0.252	0.967	1	69	regulation of cell morphogenesis involved	BP	1	SHOX2	up_VSAP_VSMC
GO:0003382	0.25216829	0.96819	1	11	epithelial cell morphogenesis	BP	1	ARHGEF26	up_ACOR_EC
GO:0061213	0.252173993	0.96819	1	11	positive regulation of mesonephros	BP	1	SOX9	up_ACOR_EC
GO:0042476	0.252297707	0.92848	2	36	odontogenesis	BP	1	DLX3,LRP4	up_ACOR_EC
GO:0090314	0.252627792	0.96807	1	11	positive regulation of protein targeting to	BP	1	KCNB1	up_ACOR_EC

GO:1900026	0.252650665	0.96806	1	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	NRP1	up_ACOR_EC
GO:0003094	0.252801099	0.96802	1	11	glomerular filtration	BP	1	AQP1	up_ACOR_EC
GO:0031102	0.252852561	0.96801	1	11	neuron projection regeneration	BP	1	RGMA	up_ACOR_EC
GO:0050730	0.25297802	0.90377	3	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0051128	0.253	0.788	72	790	regulation of cellular component organization	BP	1	FSCN1,HMGB1,SREBF1,ANLN,STXBP6,FMNL3,ATAD2,HNRNPD,SMC1A,ZW10,CAPG,TRIP13,COLGALT1,SLC25A5,SDC1,ARFGAP1,FBXO5,PRELID1,BIRC5,INSIG1,CAV1,LIMA1,NF2,AURKB,MMP14,CDKN2C,STMN1,GREM1,NEK2,FEN1,RCC1,DHX33,UHRF1,POC1A,BRCA1,NOC2L,EIF5A,PREB,CDC6,NDC80,HIST1H1A,RAC1,NUP62,PDXP,FOSL1,PLK4,IQGAP2,CDC42EP4,SMC3,STAG1,ENSCAFG00000005299,EZR,BUB1,RBM14,CORO1A,CDC20,TTK,BAP1,ARPC1B,PSMC1,AIFM1,ARHGEF2,KIF11,TADA2A,TINF2,UBE2C,CCT4,SIX4,MTBP,TPBG,GEN1,ANXA7	down_ACOR_VSMC
GO:0006366	0.253	0.799	40	583	transcription by RNA polymerase II	BP	1	ARHGEF2,VEGFA,SULF1,NR1H4,PLK3,ETV6,CBX5,ILK,FHL2,PPP1R12A,SMARCA4,ANKRA2,SESN2,HIF1A,PTPN2,YES1,NEO1,PEG3,MTDH,BRD2,CNOT7,MAGED1,CTNNB1,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,ZMYND8,GLO1,INHBA,NR4A1,ENSCAFG00000018360,HIF1AN,ARF4,KDM3A	down_VSAP_EC
GO:0018105	0.253	0.832	14	116	peptidyl-serine phosphorylation	BP	1	PLCL1,CDC7,RASSF2,PRKAA2,LATS2,CAMK2D,DMPK,PRKCE,APP,PSKH1,LMTK2,INPP5K,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0110053	0.253	0.837	12	98	regulation of actin filament organization	BP	1	SYNPO2L,ARHGAP28,ACTN2,SYNPO2,F2RL1,JMY,NRP1,EVL,PRKCE,SSH3,INPP5K,WASL	up_ACOR_VSMC
GO:0032101	0.253	0.84	11	173	regulation of response to external stimulus	BP	1	KANK2,CHID1,RNF216,PARK7,SASH1,CYBA,MAVS,A2M,RAC2,NAPEPLD,RGMA	down_VCAV_EC
GO:0071417	0.253	0.848	9	142	cellular response to organonitrogen	BP	1	LRP1,PRNP,ADCY6,COL6A1,ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0007409	0.253	0.848	9	109	axonogenesis	BP	1	SIPA1L1,PTPN11,IFRD1,KIF5B,NEO1,UST,CDH11,EXT1,NRP1	down_VSAP_EC
GO:0044403	0.253	0.848	9	116	symbiont process	BP	1	P4HB,SMARCA4,DDX39B,CNOT7,TFRC,APOE,REST,CALM1,RAD23A	down_VSAP_EC
GO:0045597	0.253	0.852	8	253	positive regulation of cell differentiation	BP	1	CMKLR1,IRX3,TMEM100,GREM1,CYLD,EVI2B,AXIN2,NAPEPLD	up_AFEM_EC
GO:0030336	0.253	0.867	6	86	negative regulation of cell migration	BP	1	DCN,BMPR1A,RECK,THY1,SPRED1,FOXO3	down_VCAV_EC
GO:0032409	0.253	0.868	6	52	regulation of transporter activity	BP	1	RELN,PDE4D,MEF2C,CTTNBP2NL,PLCG2,RIPK1	up_VCAV_EC
GO:0016477	0.253	0.877	5	426	cell migration	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:0017148	0.253	0.879	5	36	negative regulation of translation	BP	1	ZFP36L1,ANKHD1,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0061333	0.253	0.905	3	35	renal tubule morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0043255	0.253	0.906	3	29	regulation of carbohydrate biosynthetic	BP	1	ENPP1,SESN2,PTPN2	down_VSAP_EC
GO:0045786	0.253	0.928	2	195	negative regulation of cell cycle	BP	1	USP28,ATRIP	down_ACOR_EC
GO:0033043	0.253	0.932	2	446	regulation of organelle organization	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0001909	0.253	0.931	2	18	leukocyte mediated cytotoxicity	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0015914	0.253	0.935	2	10	phospholipid transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0002886	0.253	0.935	2	10	regulation of myeloid leukocyte mediated	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0010216	0.253	0.976	1	3	maintenance of DNA methylation	BP	1	UHRF1	down_ACOR_VSMC
GO:0044331	0.253	0.97	1	6	cell-cell adhesion mediated by cadherin	BP	1	CDH2	down_VCAV_EC
GO:0001667	0.253	0.967	1	146	ameboidal-type cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0001886	0.253	0.971	1	5	endothelial cell morphogenesis	BP	1	PLOD3	down_VSAP_EC
GO:0034162	0.253	0.971	1	5	toll-like receptor 9 signaling pathway	BP	1	NR1H4	down_VSAP_EC
GO:0002318	0.253	0.976	1	3	myeloid progenitor cell differentiation	BP	1	JAM3	up_ACOR_VSMC

GO:0045112	0.253	0.976	1	3	integrin biosynthetic process	BP	1	AR	up_ACOR_VSMC
GO:0070940	0.253	0.976	1	3	dephosphorylation of RNA polymerase II C-terminal	BP	1	RPRD1B	up_ACOR_VSMC
GO:0006574	0.253	0.976	1	3	valine catabolic process	BP	1	ENSCAFG00000002977	up_ACOR_VSMC
GO:0045113	0.253	0.976	1	3	regulation of integrin biosynthetic process	BP	1	AR	up_ACOR_VSMC
GO:0003254	0.253	0.968	1	12	regulation of membrane depolarization	BP	1	MLLT11	up_AFEM_EC
GO:0001910	0.253	0.968	1	12	regulation of leukocyte mediated cytotoxicity	BP	1	LEP	up_AFEM_EC
GO:0032459	0.253	0.968	1	12	regulation of protein oligomerization	BP	1	CRYAB	up_AFEM_EC
GO:0050830	0.253	0.968	1	12	defense response to Gram-positive bacterium	BP	1	ADAM17	up_AFEM_EC
GO:0090189	0.253	0.968	1	12	regulation of branching involved in ureteric bud	BP	1	GREM1	up_AFEM_EC
GO:1902305	0.253	0.968	1	12	regulation of sodium ion transmembrane transport	BP	1	FXYD1	up_AFEM_EC
GO:0051146	0.253	0.966	1	76	striated muscle cell differentiation	BP	1	TBX5	up_APUL_EC
GO:0071559	0.253	0.966	1	75	response to transforming growth factor beta	BP	1	NPNT	up_APUL_EC
GO:0030810	0.253	0.976	1	3	positive regulation of nucleotide biosynthetic	BP	1	NOS2	up_VCAV_EC
GO:1900373	0.253	0.976	1	3	positive regulation of purine nucleotide	BP	1	NOS2	up_VCAV_EC
GO:2001198	0.253	0.973	1	4	regulation of dendritic cell differentiation	BP	1	HMGB1	up_VCAV_EC
GO:0006435	0.253	0.976	1	3	threonyl-tRNA aminoacylation	BP	1	TARSL2	up_VCAV_EC
GO:0030854	0.253	0.973	1	4	positive regulation of granulocyte	BP	1	HCLS1	up_VCAV_EC
GO:0034380	0.253	0.976	1	3	high-density lipoprotein particle assembly	BP	1	ABCA1	up_VCAV_EC
GO:0035270	0.253	0.966	1	35	endocrine system development	BP	1	HOXA3	up_VPOR_EC
GO:0051251	0.253	0.966	1	69	positive regulation of lymphocyte activation	BP	1	TOX	up_VFEM_EC
GO:0048732	0.253	0.967	1	116	gland development	BP	1	HOXA9	up_VFEM_VSMC
GO:0031334	0.253	0.967	1	84	positive regulation of protein complex assembly	BP	1	CCL24	up_VPUL_EC
GO:0006935	0.253	0.967	1	143	chemotaxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0009314	0.253	0.967	1	143	response to radiation	BP	1	LRRN4	up_VPUL_VSMC
GO:0042330	0.253	0.967	1	143	taxis	BP	1	SLIT2	up_VPUL_VSMC
GO:0014816	0.253	0.976	1	3	skeletal muscle satellite cell differentiation	BP	1	CDON	up_VSAP_EC
GO:0048311	0.253	0.976	1	3	mitochondrion distribution	BP	1	CLUH	up_VSAP_EC
GO:0048312	0.253	0.976	1	3	intracellular distribution of mitochondria	BP	1	CLUH	up_VSAP_EC
GO:0072718	0.253	0.976	1	3	response to cisplatin	BP	1	HMOX1	up_VSAP_EC
GO:0072719	0.253	0.976	1	3	cellular response to cisplatin	BP	1	HMOX1	up_VSAP_EC
GO:0097421	0.253	0.976	1	3	liver regeneration	BP	1	SULF2	up_VSAP_EC
GO:0140052	0.253	0.976	1	3	cellular response to oxidised low-density lipoprotein particle	BP	1	MYD88	up_VSAP_EC
GO:0050730	0.253	0.966	1	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0035493	0.253424929	0.96786	1	11	SNARE complex assembly	BP	1	VPS16	up_ACOR_EC
GO:0051098	0.25376356	0.87481	5	129	regulation of binding	BP	1	PLCL1,ARHGAP28,IFIT2,CLSTN1,PYGO2	up_ACOR_EC
GO:0003203	0.253863943	0.96774	1	11	endocardial cushion morphogenesis	BP	1	SOX9	up_ACOR_EC

GO:0044085	0.254	0.783	93	1076	cellular component biogenesis	BP	1	EPHB1,PLK2,TEK,HCLS1,GBP5,SELP,KIT,PRKCH,ARHGEF15,CDA,MX2,PODXL,BAIAP2L1,VWF,LAMC2,OCLN,MEF2C,RAPGEF1,TLR4,EDN1,RAB11A,RALB,RAB27A,SMAD1,SNCAIP,IRF8,SNAP91,ARHGAP28,TMOD1,NASP,NECTIN2,MTOR,ACPP,SAMD8,SNAP23,LRRC8C,TJP1,LNX2,CAV2,SLK,SCAF11,CNOT6,ABCA1,NCKAP1,MZT1,RIOK3,PROX1,IQGAP2,ENSCAFG00000010224,STMN1,SNX2,SH3GLB1,SWAP70,APOD,CENPC,NCK1,KCNJ2,EXOC5,LDB2,FES,HIST1H1A,EHD4,RAPGEF2,BCL10,SENP6,PAN3,PRPF39,CTNNA1,CNOT7,GCH1,ASF1A,HMGB1,PMAIP1,ARPC5L,BLM,RIPK1,LSM14A,ITGA6,MCU,ZW10,IQUB,ATRX,HAUS3,ALDH1A3,HP1BP3,ENSCAFG00000002015,P2RX2,TNFAIP1,SPATA6,TMOD3,FSCN1,FBXO5,SASS6	up_VCAV_EC
GO:1903530	0.254	0.825	16	165	regulation of secretion by cell	BP	1	MEF2C,FERMT1,CHD7,TLR4,GATA3,EDN1,RAB27A,SNCAIP,ARG2,RSC1A1,CD200,FES,CREB1,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0022411	0.254	0.828	15	130	cellular component disassembly	BP	1	RETREG1,CTSS,SMARCD2,PYM1,AMBRA1,F2RL1,DFFB,DDR2,MFN2,FBXO7,HTRA2,FLOT1,DEDD2,FUNDC2,DDIT4	up_VSAP_EC
GO:0007163	0.254	0.86	7	60	establishment or maintenance of cell	BP	1	FSCN1,ZW10,CENPA,SLC29A1,NDC80,EZR,AMOTL1	down_ACOR_VSMC
GO:0002685	0.254	0.861	7	55	regulation of leukocyte migration	BP	1	VEGFD,F2RL1,PTPN22,APP,CCL5,JAM3,WASL	up_ACOR_VSMC
GO:0042476	0.254	0.878	5	36	odontogenesis	BP	1	AXIN2,OSR2,OSR1,DLX3,LRP4	up_VSAP_EC
GO:0001656	0.254	0.905	3	35	metanephros development	BP	1	GLI3,RDH10,GREM1	down_VCAV_EC
GO:0060402	0.254	0.905	3	35	calcium ion transport into cytosol	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0022037	0.254	0.906	3	27	metencephalon development	BP	1	HSPA5,PTPN11,AARS	down_VSAP_EC
GO:1902807	0.254	0.909	3	18	negative regulation of cell cycle G1/S phase	BP	1	FAM107A,CRADD,FBXO7	up_VSAP_EC
GO:2000134	0.254	0.909	3	18	negative regulation of G1/S transition of mitotic	BP	1	FAM107A,CRADD,FBXO7	up_VSAP_EC
GO:1903901	0.254	0.93	2	19	negative regulation of viral life cycle	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0051653	0.254	0.931	2	15	spindle localization	BP	1	KPNB1,HTT	down_VSAP_EC
GO:0032941	0.254	0.934	2	10	secretion by tissue	BP	1	CHRM1,CYBA	up_VSAP_EC
GO:0007034	0.254	0.966	1	55	vacuolar transport	BP	1	NEDD4	down_ACOR_EC
GO:0003222	0.254	0.97	1	6	ventricular trabecula myocardium	BP	1	BMPR1A	down_VCAV_EC
GO:0072657	0.254	0.967	1	144	protein localization to membrane	BP	1	RAB11B	down_VPOR_EC
GO:2001279	0.254	0.973	1	4	regulation of unsaturated fatty acid biosynthetic	BP	1	PTGS2	down_VSAP_EC
GO:0007530	0.254	0.971	1	5	sex determination	BP	1	SIX4	down_VSAP_EC
GO:0035404	0.254	0.976	1	3	histone-serine phosphorylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0048729	0.254	0.968	1	209	tissue morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0060284	0.254	0.968	1	212	regulation of cell development	BP	1	EYA1	up_AFEM_VSMC
GO:0050727	0.254	0.966	1	74	regulation of inflammatory response	BP	1	NR1H4	up_APUL_EC
GO:0042640	0.254	0.976	1	3	anagen	BP	1	FERMT1	up_VCAV_EC
GO:0051884	0.254	0.976	1	3	regulation of timing of anagen	BP	1	FERMT1	up_VCAV_EC
GO:1903025	0.254	0.976	1	3	regulation of RNA polymerase II regulatory region sequence-specific	BP	1	NSD1	up_VCAV_EC
GO:0017144	0.254	0.968	1	199	drug metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0006612	0.254	0.966	1	35	protein targeting to membrane	BP	1	SRP54	up_VPOR_EC
GO:0046916	0.254	0.966	1	35	cellular transition metal ion homeostasis	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:0006520	0.254	0.967	1	114	cellular amino acid metabolic process	BP	1	GATM	up_VFEM_VSMC
GO:0006816	0.254	0.966	1	84	calcium ion transport	BP	1	HOXA3	up_VPUL_EC

GO:0071417	0.254	0.967	1	142	cellular response to organonitrogen	BP	1	SLIT2	up_VPUL_VSMC
GO:0022028	0.254	0.976	1	3	tangential migration from the subventricular zone to the olfactory bulb	BP	1	SLIT2	up_VSAP_EC
GO:1904526	0.254	0.976	1	3	regulation of microtubule binding	BP	1	ABL1	up_VSAP_EC
GO:1902170	0.254	0.976	1	3	cellular response to reactive nitrogen species	BP	1	MAP3K5	up_VSAP_EC
GO:0019058	0.254	0.966	1	64	viral life cycle	BP	1	CAV1	up_VSAP_VSMC
GO:0045666	0.254	0.966	1	68	positive regulation of neuron differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0071375	0.254	0.966	1	68	cellular response to peptide hormone stimulus	BP	1	CAV1	up_VSAP_VSMC
GO:0072524	0.254420964	0.92742	2	37	pyridine-containing compound metabolic	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0006664	0.254475885	0.92739	2	37	glycolipid metabolic process	BP	1	PIGS,PRKCD	up_ACOR_EC
GO:1903509	0.254475885	0.92739	2	37	liposaccharide metabolic process	BP	1	PIGS,PRKCD	up_ACOR_EC
GO:0022414	0.254494153	0.84197	10	294	reproductive process	BP	1	GATA4,SOX9,FZD5,LHX9,DLX3,ARHGDIB,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0009593	0.254674791	0.96752	1	11	detection of chemical stimulus	BP	1	NOD2	up_ACOR_EC
GO:0010458	0.25499005	0.96719	1	12	exit from mitosis	BP	1	CHMP4B	up_ACOR_EC
GO:1901575	0.255	0.787	67	643	organic substance catabolic process	BP	1	PEX7,DHDH,AXIN2,LIPC,ENPP2,RNPEP,PLBD1,ACAA1,FOXRED2,ACACB,GDA,ABTB1,PEX2,GOT1,INPP5E,CTSS,TENT5C,ADHFE1,HSD17B14,HPSE,PAFAH2,ALDH6A1,VPS36,EXOSC7,FAAH,PYM1,LPL,DFFB,ZFP36L1,GALK1,RBCK1,ENTPD3,PLA2G6,RNF24,FBXW4,GCDH,BCKDHB,FBXO4,RMND5A,AZIN2,FBXW5,SMG9,FBXO7,UBA7,EHHADH,RNF166,LONP2,ABHD16A,LIPE,RNF216,OSBPL7,ENSCAFG00000002977,SAMD4B,ZFP36L2,PNP,TIMP2,IDH1,UBQLN2,CTSF,CDC26,HTRA2,TNRC6C,HMOX1,GNPDA1,KEAP1,DDIT4,IDO2	up_VSAP_EC
GO:0010558	0.255	0.8	37	392	negative regulation of macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,PDGFB,MEF2C,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,BMP2,HMG20A,HHEX,CREM,ENC1,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,RAD17,MTA2,KDM5A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0048812	0.255	0.821	18	151	neuron projection morphogenesis	BP	1	EPYC,FEZ1,FGFR2,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL	up_ACOR_VSMC
GO:0045088	0.255	0.843	10	81	regulation of innate immune response	BP	1	TRAFD1,F2RL1,MYD88,NLRX1,TKFC,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0006164	0.255	0.847	9	86	purine nucleotide biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,NOS2,HIF1A	up_VCAV_EC
GO:0051216	0.255	0.866	6	70	cartilage development	BP	1	SULF1,SERPINH1,CHSY1,HIF1A,CTNNB1,CREB3L2	down_VSAP_EC
GO:1902531	0.255	0.867	6	536	regulation of intracellular signal transduction	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,FBP1,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:1901657	0.255	0.877	5	43	glycosyl compound metabolic process	BP	1	PRPSAP1,RAN,TK1,PRPS1,CTPS1	down_ACOR_VSMC
GO:0045664	0.255	0.874	5	144	regulation of neuron differentiation	BP	1	IRX3,DLL1,PLXNA4,THRB,KANK1	up_AFEM_EC
GO:0009799	0.255	0.888	4	43	specification of symmetry	BP	1	TMED2,HIF1A,CTNNB1,DDIT3	down_VSAP_EC
GO:0019722	0.255	0.888	4	45	calcium-mediated signaling	BP	1	FHL2,GSK3B,HTT,CALM1	down_VSAP_EC
GO:0055076	0.255	0.888	4	44	transition metal ion homeostasis	BP	1	SLC39A7,HIF1A,NEO1,TFRC	down_VSAP_EC
GO:0071260	0.255	0.908	3	19	cellular response to mechanical stimulus	BP	1	TLR3,ANKRD1,BNIP3	up_ACOR_VSMC
GO:0021795	0.255	0.929	2	20	cerebral cortex cell migration	BP	1	PEX5,GLI3	down_VCAV_EC
GO:0006024	0.255	0.93	2	16	glycosaminoglycan biosynthetic process	BP	1	CHSY1,EXT1	down_VSAP_EC
GO:0032743	0.255	0.934	2	10	positive regulation of interleukin-2 production	BP	1	CD83,MAP3K7	up_ACOR_VSMC
GO:0071346	0.255	0.927	2	41	cellular response to interferon-gamma	BP	1	RAB20,CCL5	up_AFEM_EC
GO:0097479	0.255	0.927	2	41	synaptic vesicle localization	BP	1	CHRM2,CAMK2A	up_AFEM_EC

GO:0071702	0.255	0.934	2	687	organic substance transport	BP	1	TLR2,SLC16A12	up_AFEM_VSMC
GO:0003013	0.255	0.926	2	121	circulatory system process	BP	1	HTR7,SEMA3A	up_VPOR_EC
GO:0021543	0.255	0.966	1	49	pallium development	BP	1	NRP2	down_ACOR_EC
GO:0050803	0.255	0.966	1	55	regulation of synapse structure or activity	BP	1	NRP2	down_ACOR_EC
GO:0050807	0.255	0.966	1	55	regulation of synapse organization	BP	1	NRP2	down_ACOR_EC
GO:0050673	0.255	0.967	1	135	epithelial cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0009886	0.255	0.97	1	6	post-embryonic animal morphogenesis	BP	1	FBN1	down_VCAV_EC
GO:0002521	0.255	0.967	1	149	leukocyte differentiation	BP	1	CITED2	down_VPOR_EC
GO:0008090	0.255	0.975	1	3	retrograde axonal transport	BP	1	TMEM108	up_ACOR_VSMC
GO:0014022	0.255	0.975	1	3	neural plate elongation	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0022007	0.255	0.975	1	3	convergent extension involved in neural plate	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0032930	0.255	0.975	1	3	positive regulation of superoxide anion	BP	1	F2RL1	up_ACOR_VSMC
GO:0033148	0.255	0.976	1	3	positive regulation of intracellular estrogen receptor signaling	BP	1	SKP2	up_ACOR_VSMC
GO:0042983	0.255	0.976	1	3	amyloid precursor protein biosynthetic process	BP	1	ITM2C	up_ACOR_VSMC
GO:0042984	0.255	0.976	1	3	regulation of amyloid precursor protein	BP	1	ITM2C	up_ACOR_VSMC
GO:0043589	0.255	0.975	1	3	skin morphogenesis	BP	1	PSEN1	up_ACOR_VSMC
GO:0046500	0.255	0.976	1	3	S-adenosylmethionine metabolic process	BP	1	MAT2B	up_ACOR_VSMC
GO:0048845	0.255	0.975	1	3	venous blood vessel morphogenesis	BP	1	TBX20	up_ACOR_VSMC
GO:0051891	0.255	0.976	1	3	positive regulation of cardioblast differentiation	BP	1	TBX5	up_ACOR_VSMC
GO:0072138	0.255	0.975	1	3	mesenchymal cell proliferation involved in ureteric bud development	BP	1	BMP4	up_ACOR_VSMC
GO:0032808	0.255	0.975	1	3	lacrimal gland development	BP	1	IGSF3	up_VCAV_EC
GO:0033005	0.255	0.973	1	4	positive regulation of mast cell activation	BP	1	NECTIN2	up_VCAV_EC
GO:0071248	0.255	0.966	1	35	cellular response to metal ion	BP	1	FBP1	up_VPOR_EC
GO:0051962	0.255	0.966	1	112	positive regulation of nervous system	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006732	0.255	0.966	1	107	coenzyme metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0070372	0.255	0.966	1	85	regulation of ERK1 and ERK2 cascade	BP	1	CCL24	up_VPUL_EC
GO:0007015	0.255	0.967	1	144	actin filament organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0045664	0.255	0.967	1	144	regulation of neuron differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0055065	0.255	0.967	1	145	metal ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0021889	0.255	0.976	1	3	olfactory bulb interneuron	BP	1	SLIT2	up_VSAP_EC
GO:0021891	0.255	0.976	1	3	olfactory bulb interneuron development	BP	1	SLIT2	up_VSAP_EC
GO:1903589	0.255	0.976	1	3	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	HMOX1	up_VSAP_EC
GO:1901381	0.255	0.975	1	3	positive regulation of potassium ion	BP	1	AMIGO1	up_VSAP_EC
GO:0031111	0.255605438	0.96727	1	11	negative regulation of microtubule polymerization or	BP	1	TUBB4A	up_ACOR_EC
GO:0060706	0.255672896	0.96725	1	11	cell differentiation involved in embryonic	BP	1	FZD5	up_ACOR_EC
GO:0022414	0.256	0.806	28	294	reproductive process	BP	1	PCDH12,KIT,PDGFB,TSPAN8,CHD7,TIPARP,EIF2B2,GATA3,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,MDFI,ARID4B,CENPC,HIST1H1A,PTGS2,SPTBN4,AFF4,ARHGDIB,HIF1A,KDM3A,ATRX,VASH1,SPATA6,FBXO5	up_VCAV_EC

GO:1901137	0.256	0.809	25	232	carbohydrate derivative biosynthetic process	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,ITM2C,B3GNT7,CCDC126,PPARGC1A,PIGN,PIGS,UGCG,ADCY6,PIGG,MAGT1,STT3B,FUT11,FUT8,ENSCAFG00000018611,POMK,PSEN1,ALDOC,DDIT4,EOGT,ELOVL7,LMF1	up_ACOR_VSMC
GO:0009725	0.256	0.815	21	188	response to hormone	BP	1	FAM107A,PTGFR,PPARGC1B,SLIT2,GOT1,CHRM1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,CREBRF,PRMT2,ZFP36L2,NCOA2,TIMP2,NCK1,BGLAP,LBH,DDIT4,LATS2	up_VSAP_EC
GO:1903827	0.256	0.818	19	164	regulation of cellular protein localization	BP	1	SH3TC2,ACTN2,LEP,TCAF1,PRKAA2,FERMT1,BMP4,AR,CDKN1A,PTPN22,OS9,DAG1,PARP9,PSEN1,JUP,RAB11B,INPP5K,PARK7,PTPN14	up_ACOR_VSMC
GO:0034641	0.256	0.844	13	2171	cellular nitrogen compound metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,RPSA,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,TNRC6B,NEDD4	down_ACOR_EC
GO:0046483	0.256	0.846	12	1948	heterocycle metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,TNRC6B,NEDD4	down_ACOR_EC
GO:0065004	0.256	0.852	8	81	protein-DNA complex assembly	BP	1	NASP,CENPC,HIST1H1A,SENP6,ASF1A,HMGB1,ATRX,HP1BP3	up_VCAV_EC
GO:0060070	0.256	0.857	7	105	canonical Wnt signaling pathway	BP	1	RECK,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0007568	0.256	0.867	6	50	aging	BP	1	HMGA1,RAD54L,ARG2,NUP62,RSL1D1,SMC6	down_ACOR_VSMC
GO:1901135	0.256	0.904	3	390	carbohydrate derivative metabolic process	BP	1	SULF1,CSGALNACT1,TNRC6B	down_ACOR_EC
GO:1905268	0.256	0.907	3	20	negative regulation of chromatin organization	BP	1	ATAD2,BRCA1,NOC2L	down_ACOR_VSMC
GO:0032680	0.256	0.903	3	36	regulation of tumor necrosis factor production	BP	1	BPI,CYBA,MAVS	down_VCAV_EC
GO:0001678	0.256	0.905	3	29	cellular glucose homeostasis	BP	1	NR1H4,SMARCA4,HIF1A	down_VSAP_EC
GO:0001909	0.256	0.908	3	18	leukocyte mediated cytotoxicity	BP	1	EMP2,F2RL1,PPP3CB	up_VSAP_EC
GO:0045321	0.256	0.927	2	191	leukocyte activation	BP	1	LYN,STX4	down_ACOR_EC
GO:0098609	0.256	0.927	2	181	cell-cell adhesion	BP	1	LYN,PDPN	down_ACOR_EC
GO:1901224	0.256	0.929	2	20	positive regulation of NIK/NF-kappaB signaling	BP	1	SASH1,GREM1	down_VCAV_EC
GO:0048662	0.256	0.929	2	18	negative regulation of smooth muscle cell	BP	1	ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:0031670	0.256	0.933	2	10	cellular response to nutrient	BP	1	CASTOR1,CDKN2B	up_ACOR_VSMC
GO:0042551	0.256	0.934	2	10	neuron maturation	BP	1	RND1,APP	up_ACOR_VSMC
GO:0048013	0.256	0.932	2	11	ephrin receptor signaling pathway	BP	1	EFNB2,SIPA1L1	up_ACOR_VSMC
GO:0009892	0.256	0.936	2	835	negative regulation of metabolic process	BP	1	HOXC10,ESR1	up_AORT_VSMC
GO:0072577	0.256	0.932	2	11	endothelial cell apoptotic process	BP	1	TNFAIP3,GATA3	up_VCAV_EC
GO:1905314	0.256	0.932	2	12	semi-lunar valve development	BP	1	GATA3,JAG1	up_VCAV_EC
GO:2000351	0.256	0.932	2	11	regulation of endothelial cell apoptotic process	BP	1	TNFAIP3,GATA3	up_VCAV_EC
GO:0051094	0.256	0.929	2	388	positive regulation of developmental process	BP	1	HOXA11,SHOX2	up_VFEM_VSMC
GO:0032943	0.256	0.966	1	60	mononuclear cell proliferation	BP	1	LYN	down_ACOR_EC
GO:0046651	0.256	0.966	1	60	lymphocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0046879	0.256	0.965	1	63	hormone secretion	BP	1	STX4	down_ACOR_EC
GO:0001701	0.256	0.966	1	134	in utero embryonic development	BP	1	GABPA	down_AFEM_EC
GO:0000737	0.256	0.97	1	6	DNA catabolic process, endonucleolytic	BP	1	FBH1	down_VCAV_EC
GO:0048143	0.256	0.97	1	6	astrocyte activation	BP	1	LRP1	down_VCAV_EC
GO:0009065	0.256	0.97	1	6	glutamine family amino acid catabolic process	BP	1	GLS2	down_VCAV_EC
GO:0060379	0.256	0.97	1	6	cardiac muscle cell myoblast differentiation	BP	1	GREM1	down_VCAV_EC
GO:0010646	0.256	0.981	1	945	regulation of cell communication	BP	1	GATA5	down_VFEM_VSMC
GO:0010793	0.256	0.972	1	4	regulation of mRNA export from nucleus	BP	1	IWS1	down_VSAP_EC

GO:0021819	0.256	0.972	1	4	layer formation in cerebral cortex	BP	1	CTNNB1	down_VSAP_EC
GO:0006531	0.256	0.971	1	5	aspartate metabolic process	BP	1	NMNAT2	down_VSAP_EC
GO:0048261	0.256	0.971	1	5	negative regulation of receptor-mediated	BP	1	LRRTM2	down_VSAP_EC
GO:0090330	0.256	0.971	1	5	regulation of platelet aggregation	BP	1	LYN	down_VSAP_EC
GO:0051954	0.256	0.975	1	3	positive regulation of amine transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0031115	0.256	0.975	1	3	negative regulation of microtubule	BP	1	TUBB4A	up_ACOR_VSMC
GO:1902903	0.256	0.966	1	125	regulation of supramolecular fiber	BP	1	TAOK1	up_AORT_EC
GO:0030097	0.256	0.968	1	244	hemopoiesis	BP	1	HOXA9	up_AORT_VSMC
GO:0080135	0.256	0.968	1	240	regulation of cellular response to stress	BP	1	ARG2	up_AORT_VSMC
GO:0045906	0.256	0.981	1	2	negative regulation of vasoconstriction	BP	1	DOCK4	up_VCAV_EC
GO:0048714	0.256	0.975	1	3	positive regulation of oligodendrocyte	BP	1	MTOR	up_VCAV_EC
GO:1904694	0.256	0.981	1	2	negative regulation of vascular smooth muscle	BP	1	DOCK4	up_VCAV_EC
GO:0036480	0.256	0.975	1	3	neuron intrinsic apoptotic signaling pathway in response to oxidative	BP	1	HIF1A	up_VCAV_EC
GO:0042730	0.256	0.975	1	3	fibrinolysis	BP	1	KLKB1	up_VCAV_EC
GO:0051917	0.256	0.975	1	3	regulation of fibrinolysis	BP	1	KLKB1	up_VCAV_EC
GO:1903376	0.256	0.975	1	3	regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	HIF1A	up_VCAV_EC
GO:0019362	0.256	0.965	1	35	pyridine nucleotide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0035150	0.256	0.965	1	36	regulation of tube size	BP	1	HTR7	up_VPOR_EC
GO:0046496	0.256	0.965	1	35	nicotinamide nucleotide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0050880	0.256	0.965	1	36	regulation of blood vessel size	BP	1	HTR7	up_VPOR_EC
GO:0043087	0.256	0.966	1	83	regulation of GTPase activity	BP	1	CCL24	up_VPUL_EC
GO:0001933	0.256	0.966	1	146	negative regulation of protein phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0001922	0.256	0.975	1	3	B-1 B cell homeostasis	BP	1	ABL1	up_VSAP_EC
GO:0003351	0.256	0.975	1	3	epithelial cilium movement	BP	1	KIF27	up_VSAP_EC
GO:0021678	0.256	0.975	1	3	third ventricle development	BP	1	KDM2B	up_VSAP_EC
GO:0042730	0.256	0.975	1	3	fibrinolysis	BP	1	KLKB1	up_VSAP_EC
GO:0043497	0.256	0.975	1	3	regulation of protein heterodimerization	BP	1	CDON	up_VSAP_EC
GO:0051917	0.256	0.975	1	3	regulation of fibrinolysis	BP	1	KLKB1	up_VSAP_EC
GO:0060916	0.256	0.975	1	3	mesenchymal cell proliferation involved in	BP	1	NFIB	up_VSAP_EC
GO:0061087	0.256	0.975	1	3	positive regulation of histone H3-K27	BP	1	PHF1	up_VSAP_EC
GO:2000767	0.256	0.975	1	3	positive regulation of cytoplasmic translation	BP	1	NCK1	up_VSAP_EC
GO:0010694	0.256	0.975	1	3	positive regulation of alkaline phosphatase	BP	1	PPARGC1B	up_VSAP_EC
GO:0014831	0.256	0.975	1	3	gastro-intestinal system smooth muscle	BP	1	SULF2	up_VSAP_EC
GO:0032989	0.256069509	0.84077	10	292	cellular component morphogenesis	BP	1	MYOZ2,TMOD1,BRSK1,RHOU,ACTN2,PAK3, MAPK8IP2,LRP4,NRP1,ARHGEF26	up_ACOR_EC
GO:0007569	0.256146595	0.92667	2	36	cell aging	BP	1	PRELP,PRKCD	up_ACOR_EC
GO:0035303	0.256185212	0.90198	3	65	regulation of dephosphorylation	BP	1	DUSP26,PRKCD,PPP1R26	up_ACOR_EC
GO:0043243	0.256309389	0.96708	1	11	positive regulation of protein complex	BP	1	ACTN2	up_ACOR_EC
GO:0070306	0.256849701	0.96693	1	11	lens fiber cell differentiation	BP	1	TMOD1	up_ACOR_EC

GO:0055080	0.257	0.83	13	176	cation homeostasis	BP	1	SLC39A7,ERO1A,ATP2B1,TMTC2,HIF1A,NEO1,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0006873	0.257	0.833	12	160	cellular ion homeostasis	BP	1	SLC39A7,ERO1A,ENPP1,ATP2B1,HIF1A,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0007389	0.257	0.845	9	137	pattern specification process	BP	1	BMPR1A,HOXC4,CLSTN1,SEMA3C,GLI3,IFT57,PCSK6,GREM1,ZBTB16	down_VCAV_EC
GO:1902905	0.257	0.852	8	72	positive regulation of supramolecular fiber	BP	1	COLGALT1,NF2,RAC1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0001649	0.257	0.859	7	54	osteoblast differentiation	BP	1	SMAD6,RASSF2,BMP4,GJA1,CLSTN1,NPNT,DDR2	up_ACOR_VSMC
GO:0048863	0.257	0.865	6	70	stem cell differentiation	BP	1	PRICKLE1,HIF1A,REST,A2M,NRP1,KDM3A	down_VSAP_EC
GO:0002819	0.257	0.867	6	44	regulation of adaptive immune response	BP	1	TP53BP1,CD274,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0001823	0.257	0.867	6	45	mesonephros development	BP	1	HOXA11,WNT11,OSR2,SLIT2,OSR1,ZBTB16	up_VSAP_EC
GO:0032680	0.257	0.876	5	36	regulation of tumor necrosis factor production	BP	1	C5AR2,PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC
GO:1901992	0.257	0.905	3	23	positive regulation of mitotic cell cycle phase	BP	1	RAB11A,CUL4A,TMOD3	up_VCAV_EC
GO:0007200	0.257	0.907	3	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	C5AR2,CHRM1,F2RL1	up_VSAP_EC
GO:0045922	0.257	0.931	2	12	negative regulation of fatty acid metabolic	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:0032527	0.257	0.928	2	19	protein exit from endoplasmic reticulum	BP	1	SEC61B,HM13	down_VCAV_EC
GO:0065007	0.257	1	2	3499	biological regulation	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0042558	0.257	0.932	2	11	pteridine-containing compound metabolic	BP	1	PCBD1,PTS	up_ACOR_VSMC
GO:0030514	0.257	0.931	2	12	negative regulation of BMP signaling pathway	BP	1	CTDSPL2,SKIL	up_VCAV_EC
GO:0001819	0.257	0.925	2	120	positive regulation of cytokine production	BP	1	C3AR1,ARHGEF2	up_VPOR_EC
GO:0009968	0.257	0.929	2	392	negative regulation of signal transduction	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0046822	0.257	0.965	1	53	regulation of nucleocytoplasmic	BP	1	NEDD4	down_ACOR_EC
GO:2001212	0.257	0.972	1	4	regulation of vasculogenesis	BP	1	EMP2	down_ACOR_VSMC
GO:0010467	0.257	1	1	1787	gene expression	BP	1	GATA5	down_AFEM_VSMC
GO:0060255	0.257	1	1	1782	regulation of macromolecule metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0097320	0.257	0.969	1	6	plasma membrane tubulation	BP	1	PACSIN3	down_VCAV_EC
GO:1905146	0.257	0.969	1	6	lysosomal protein catabolic process	BP	1	LRP1	down_VCAV_EC
GO:0034105	0.257	0.969	1	6	positive regulation of tissue remodeling	BP	1	B4GALT1	down_VCAV_EC
GO:0043586	0.257	0.969	1	6	tongue development	BP	1	GLI3	down_VCAV_EC
GO:0097091	0.257	0.972	1	4	synaptic vesicle clustering	BP	1	CTNNB1	down_VSAP_EC
GO:1903749	0.257	0.971	1	5	positive regulation of establishment of protein localization to	BP	1	SH3GLB1	down_VSAP_EC
GO:0006977	0.257	0.971	1	5	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BP	1	CDKN1A	down_VSAP_EC
GO:0010642	0.257	0.97	1	5	negative regulation of platelet-derived growth factor receptor signaling	BP	1	PTPN2	down_VSAP_EC
GO:0070243	0.257	0.97	1	5	regulation of thymocyte apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:0071680	0.257	0.972	1	4	response to indole-3-methanol	BP	1	CTNNB1	down_VSAP_EC
GO:0071681	0.257	0.972	1	4	cellular response to indole-3-methanol	BP	1	CTNNB1	down_VSAP_EC
GO:0072431	0.257	0.971	1	5	signal transduction involved in mitotic G1	BP	1	CDKN1A	down_VSAP_EC
GO:1902400	0.257	0.971	1	5	DNA damage checkpoint intracellular signal transduction involved in G1 DNA damage	BP	1	CDKN1A	down_VSAP_EC
GO:0072044	0.257	0.975	1	3	collecting duct development	BP	1	BMP4	up_ACOR_VSMC

GO:0032740	0.257	0.975	1	3	positive regulation of interleukin-17 production	BP	1	NOD2	up_ACOR_VSMC
GO:0035523	0.257	0.975	1	3	protein K29-linked deubiquitination	BP	1	ZRANB1	up_ACOR_VSMC
GO:0051580	0.257	0.975	1	3	regulation of neurotransmitter uptake	BP	1	PSEN1	up_ACOR_VSMC
GO:0060099	0.257	0.975	1	3	regulation of phagocytosis, engulfment	BP	1	F2RL1	up_ACOR_VSMC
GO:0060100	0.257	0.975	1	3	positive regulation of phagocytosis, engulfment	BP	1	F2RL1	up_ACOR_VSMC
GO:0060391	0.257	0.975	1	3	positive regulation of SMAD protein signal	BP	1	BMP4	up_ACOR_VSMC
GO:1900028	0.257	0.975	1	3	negative regulation of ruffle assembly	BP	1	EVL	up_ACOR_VSMC
GO:1905153	0.257	0.975	1	3	regulation of membrane invagination	BP	1	F2RL1	up_ACOR_VSMC
GO:1905155	0.257	0.975	1	3	positive regulation of membrane invagination	BP	1	F2RL1	up_ACOR_VSMC
GO:0001568	0.257	0.968	1	252	blood vessel development	BP	1	WNT7A	up_AORT_VSMC
GO:0033234	0.257	0.972	1	4	negative regulation of protein sumoylation	BP	1	HMG20A	up_VCAV_EC
GO:0035630	0.257	0.972	1	4	bone mineralization involved in bone	BP	1	BMP2	up_VCAV_EC
GO:0061626	0.257	0.975	1	3	pharyngeal arch artery morphogenesis	BP	1	ADGRF5	up_VCAV_EC
GO:0006573	0.257	0.972	1	4	valine metabolic process	BP	1	BCAT1	up_VCAV_EC
GO:0051645	0.257	0.972	1	4	Golgi localization	BP	1	HOOK3	up_VCAV_EC
GO:1903003	0.257	0.975	1	3	positive regulation of protein deubiquitination	BP	1	TNIP1	up_VCAV_EC
GO:0030162	0.257	0.967	1	202	regulation of proteolysis	BP	1	C6	up_VCAV_VSMC
GO:1903555	0.257	0.965	1	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	up_VPOR_EC
GO:0008015	0.257	0.966	1	120	blood circulation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0050863	0.257	0.965	1	69	regulation of T cell activation	BP	1	CYP26B1	up_VFEM_EC
GO:0022604	0.257	0.966	1	122	regulation of cell morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0021520	0.257	0.975	1	3	spinal cord motor neuron cell fate specification	BP	1	HOXC10	up_VSAP_EC
GO:0051251	0.257	0.965	1	69	positive regulation of lymphocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:0048545	0.257	0.965	1	68	response to steroid hormone	BP	1	CAV1	up_VSAP_VSMC
GO:0050691	0.257092168	0.96686	1	11	regulation of defense response to virus by host	BP	1	MAVS	up_ACOR_EC
GO:0071242	0.257139061	0.96685	1	11	cellular response to ammonium ion	BP	1	AGRN	up_ACOR_EC
GO:0021799	0.257497811	0.96675	1	11	cerebral cortex radially oriented cell migration	BP	1	DIXDC1	up_ACOR_EC
GO:1904355	0.257515385	0.96675	1	11	positive regulation of telomere capping	BP	1	PKIB	up_ACOR_EC
GO:0006633	0.257573448	0.92586	2	38	fatty acid biosynthetic process	BP	1	THNSL2,PTGDS	up_ACOR_EC
GO:0032459	0.257632493	0.96646	1	12	regulation of protein oligomerization	BP	1	CLU	up_ACOR_EC
GO:0061036	0.257660062	0.96671	1	11	positive regulation of cartilage development	BP	1	SOX9	up_ACOR_EC
GO:0072028	0.257671485	0.92588	2	37	nephron morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0060351	0.257754759	0.96668	1	11	cartilage development involved in endochondral bone morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0048608	0.257768569	0.87214	5	129	reproductive structure development	BP	1	GATA4,SOX9,FZD5,LHX9,DLX3	up_ACOR_EC
GO:0000003	0.257790309	0.83944	10	295	reproduction	BP	1	GATA4,SOX9,FZD5,LHX9,DLX3,ARHGDIB,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0071901	0.257933342	0.92576	2	37	negative regulation of protein serine/threonine	BP	1	PKIB,PRKCD	up_ACOR_EC

GO:0009889	0.258	0.777	107	1190	regulation of biosynthetic process	BP	1	ELK3,ACSL3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,PPP1R15B,SF1,SRRT,CTDNEP1,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,RFC4,NEK2,CDK4,SMARCC1,PLK3,PCNA,DHX33,HOXA7,ARG2,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,HMGN1,CCT4,SIX4,NECAB3,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:2000112	0.258	0.778	101	1119	regulation of cellular macromolecule biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,PPP1R15B,SRRT,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,HOXA10,ERF,TCERG1,PUM3,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,HMGN1,CCT4,SIX4,NECAB3,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:0019693	0.258	0.836	11	172	ribose phosphate metabolic process	BP	1	GPAM,ADCY6,H6PD,NT5C2,PGLS,ATP5MC1,UQCR10,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:1901652	0.258	0.856	7	105	response to peptide	BP	1	LRP1,PRNP,ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0002443	0.258	0.864	6	71	leukocyte mediated immunity	BP	1	FAM49B,WDR1,PVR,TFRC,LYN,BTK	down_VSAP_EC
GO:0045216	0.258	0.866	6	44	cell-cell junction organization	BP	1	GJA1,PKP4,LIMS2,F2RL1,JUP,PERP	up_ACOR_VSMC
GO:0098609	0.258	0.863	6	181	cell-cell adhesion	BP	1	LEP,CDH18,GPAM,CYLD,ICAM5,BVES	up_AFEM_EC
GO:1903725	0.258	0.888	4	30	regulation of phospholipid metabolic process	BP	1	TEK,ADGRF5,PDGFB,SH3GLB1	up_VCAV_EC
GO:0061005	0.258	0.904	3	28	cell differentiation involved in kidney	BP	1	ACTA2,CTNNB1,MYO1E	down_VSAP_EC
GO:0007422	0.258	0.906	3	18	peripheral nervous system development	BP	1	SH3TC2,CITED2,DAG1	up_ACOR_VSMC
GO:0043407	0.258	0.906	3	19	negative regulation of MAP kinase activity	BP	1	BMP4,SMPD1,INPP5K	up_ACOR_VSMC
GO:0010524	0.258	0.931	2	12	positive regulation of calcium ion transport into	BP	1	CAV1,GSTO1	down_ACOR_VSMC
GO:0071704	0.258	1	2	3535	organic substance metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0021575	0.258	0.929	2	15	hindbrain morphogenesis	BP	1	HSPA5,PTPN11	down_VSAP_EC
GO:0021587	0.258	0.929	2	15	cerebellum morphogenesis	BP	1	HSPA5,PTPN11	down_VSAP_EC
GO:0006855	0.258	0.933	2	10	drug transmembrane transport	BP	1	PSEN1,CLN8	up_ACOR_VSMC
GO:0007176	0.258	0.933	2	10	regulation of epidermal growth factor-activated	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0048799	0.258	0.933	2	10	animal organ maturation	BP	1	GATA3,BMP2	up_VCAV_EC
GO:0060713	0.258	0.932	2	10	labyrinthine layer morphogenesis	BP	1	GJB5,ZFP36L1	up_VSAP_EC
GO:0031294	0.258	0.972	1	4	lymphocyte costimulation	BP	1	CAV1	down_ACOR_VSMC
GO:0031323	0.258	1	1	1788	regulation of cellular metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0032501	0.258	1	1	1782	multicellular organismal process	BP	1	GATA5	down_AFEM_VSMC

GO:0023051	0.258	0.981	1	954	regulation of signaling	BP	1	GATA5	down_VFEM_VSMC
GO:0010818	0.258	0.97	1	5	T cell chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:1901620	0.258	0.97	1	5	regulation of smoothened signaling pathway involved in dorsal/ventral neural tube patterning	BP	1	PRKACB	down_VSAP_EC
GO:0003008	0.258	0.969	1	336	system process	BP	1	GATA5	down_VSAP_VSMC
GO:0051241	0.258	0.969	1	336	negative regulation of multicellular organismal	BP	1	GATA5	down_VSAP_VSMC
GO:0032892	0.258	0.975	1	3	positive regulation of organic acid transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0032364	0.258	0.975	1	3	oxygen homeostasis	BP	1	EGLN1	up_ACOR_VSMC
GO:0033240	0.258	0.975	1	3	positive regulation of cellular amine metabolic	BP	1	PARK7	up_ACOR_VSMC
GO:0051583	0.258	0.975	1	3	dopamine uptake involved in synaptic	BP	1	PARK7	up_ACOR_VSMC
GO:0051934	0.258	0.975	1	3	catecholamine uptake involved in synaptic	BP	1	PARK7	up_ACOR_VSMC
GO:0061684	0.258	0.975	1	3	chaperone-mediated autophagy	BP	1	LAMP2	up_ACOR_VSMC
GO:0071731	0.258	0.975	1	3	response to nitric oxide	BP	1	EGLN1	up_ACOR_VSMC
GO:0090493	0.258	0.975	1	3	catecholamine uptake	BP	1	PARK7	up_ACOR_VSMC
GO:0090494	0.258	0.975	1	3	dopamine uptake	BP	1	PARK7	up_ACOR_VSMC
GO:0097070	0.258	0.975	1	3	ductus arteriosus closure	BP	1	HPGD	up_ACOR_VSMC
GO:1902459	0.258	0.975	1	3	positive regulation of stem cell population	BP	1	LBH	up_ACOR_VSMC
GO:0014832	0.258	0.975	1	3	urinary bladder smooth muscle contraction	BP	1	P2RX2	up_VCAV_EC
GO:0014848	0.258	0.975	1	3	urinary tract smooth muscle contraction	BP	1	P2RX2	up_VCAV_EC
GO:0072757	0.258	0.975	1	3	cellular response to camptothecin	BP	1	BLM	up_VCAV_EC
GO:1901563	0.258	0.975	1	3	response to camptothecin	BP	1	BLM	up_VCAV_EC
GO:0061469	0.258	0.972	1	4	regulation of type B pancreatic cell	BP	1	NR4A1	up_VCAV_EC
GO:0048863	0.258	0.965	1	70	stem cell differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0061025	0.258	0.965	1	69	membrane fusion	BP	1	TRIM9	up_VFEM_EC
GO:1903706	0.258	0.965	1	119	regulation of hemopoiesis	BP	1	HOXA9	up_VFEM_VSMC
GO:0001667	0.258	0.966	1	146	ameboidal-type cell migration	BP	1	SLIT2	up_VPUL_VSMC
GO:0007610	0.258	0.966	1	146	behavior	BP	1	LRRN4	up_VPUL_VSMC
GO:0001955	0.258	0.975	1	3	blood vessel maturation	BP	1	RECK	up_VSAP_EC
GO:0032891	0.258	0.975	1	3	negative regulation of organic acid transport	BP	1	OSR1	up_VSAP_EC
GO:0070602	0.258	0.975	1	3	regulation of centromeric sister chromatid cohesion	BP	1	AXIN2	up_VSAP_EC
GO:0090557	0.258	0.975	1	3	establishment of endothelial intestinal	BP	1	MYD88	up_VSAP_EC
GO:1903960	0.258	0.975	1	3	negative regulation of anion transmembrane	BP	1	OSR1	up_VSAP_EC
GO:2000697	0.258	0.975	1	3	negative regulation of epithelial cell differentiation involved in	BP	1	OSR1	up_VSAP_EC
GO:0038189	0.258	0.975	1	3	neuropilin signaling pathway	BP	1	ABL1	up_VSAP_EC
GO:0021846	0.258208238	0.96656	1	11	cell proliferation in forebrain	BP	1	DIXDC1	up_ACOR_EC
GO:0001101	0.258384774	0.90073	3	65	response to acid chemical	BP	1	NR1H4,AQP1,PTGER4	up_ACOR_EC
GO:1900077	0.258804773	0.9664	1	11	negative regulation of cellular response to	BP	1	PRKCD	up_ACOR_EC
GO:0006692	0.258928974	0.96636	1	11	prostanoid metabolic process	BP	1	PTGDS	up_ACOR_EC
GO:0006693	0.258928974	0.96636	1	11	prostaglandin metabolic process	BP	1	PTGDS	up_ACOR_EC

GO:0007049	0.259	0.789	52	560	cell cycle	BP	1	PLK2,CXCL8,TNFAIP3,MX2,PDGFB,STK10,GATA3,EDN1,RAB11A,FIGNL1,PPP3CA,MAP3K3,BMP2,HHEX,SLK,CEP68,GDPD5,MZT1,PROX1,UHRF2,ENSCAFG00000010596,MADD,EPB41,STMN1,PAK2,THOC1,CENPC,ESCO1,TIMELESS,FES,ETAA1,SENP6,USP28,TAOK1,PPP1CB,BLM,SMC5,RAD21,RAD17,SKIL,USP37,CUL4A,ZW10,ATRX,NR4A1,HAUS3,TOPBP1,TMOD3,RABGAP1,ARHGEF2,FBXO5,SASS6	up_VCAV_EC
GO:0006163	0.259	0.819	17	174	purine nucleotide metabolic process	BP	1	ACLY,HMGCR,RAN,CDK1,PFAS,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0031334	0.259	0.844	9	84	positive regulation of protein complex assembly	BP	1	FSCN1,DHX33,RAC1,FOSL1,IQGAP2,CDC42EP4,CORO1A,ARPC1B,PSMC1	down_ACOR_VSMC
GO:0044419	0.259	0.844	9	117	interspecies interaction between organisms	BP	1	P4HB,SMARCA4,DDX39B,CNOT7,TFRC,APOE,REST,CALM1,RAD23A	down_VSAP_EC
GO:0055123	0.259	0.874	5	40	digestive system development	BP	1	EDNRB,KIT,CXCL8,ITGA6,HIF1A	up_VCAV_EC
GO:0010629	0.259	0.886	4	502	negative regulation of gene expression	BP	1	ACVRL1,HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0043280	0.259	0.887	4	33	positive regulation of cysteine-type endopeptidase activity	BP	1	HMGB1,PDCD2,CYCS,AIFM1	down_ACOR_VSMC
GO:0032409	0.259	0.885	4	52	regulation of transporter activity	BP	1	PRNP,FXYD1,CACNB3,PARK7	down_VCAV_EC
GO:0046822	0.259	0.885	4	53	regulation of nucleocytoplasmic	BP	1	ENSCAFG00000014978,GLI3,PARK7,MAVS	down_VCAV_EC
GO:0030902	0.259	0.886	4	41	hindbrain development	BP	1	HSPA5,PTPN11,AARS,CTNNB1	down_VSAP_EC
GO:0003014	0.259	0.888	4	27	renal system process	BP	1	EMP2,F2RL1,SULF2,JCHAIN	up_VSAP_EC
GO:0042632	0.259	0.888	4	27	cholesterol homeostasis	BP	1	HNF4A,LIPC,LCAT,SOAT1	up_VSAP_EC
GO:0046916	0.259	0.902	3	35	cellular transition metal ion homeostasis	BP	1	SLC39A6,SCARA5,ATOX1	down_VCAV_EC
GO:0034645	0.259	0.919	3	1546	cellular macromolecule biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0017004	0.259	0.906	3	18	cytochrome complex assembly	BP	1	CYBA,SMIM20,COA1	up_VSAP_EC
GO:0031327	0.259	0.903	3	412	negative regulation of cellular biosynthetic	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0060260	0.259	0.93	2	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	HMGB1,PSMC1	down_ACOR_VSMC
GO:2000649	0.259	0.931	2	11	regulation of sodium ion transmembrane transporter activity	BP	1	PTPN3,FXYD1	up_ACOR_VSMC
GO:0043066	0.259	0.926	2	253	negative regulation of apoptotic process	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0002686	0.259	0.931	2	12	negative regulation of leukocyte migration	BP	1	MMP28,APOD	up_VCAV_EC
GO:0015696	0.259	0.929	2	14	ammonium transport	BP	1	SNAP23,RALBP1	up_VCAV_EC
GO:0042088	0.259	0.931	2	12	T-helper 1 type immune response	BP	1	MTOR,HMGB1	up_VCAV_EC
GO:0051240	0.259	0.929	2	489	positive regulation of multicellular organismal	BP	1	TBX5,GATA5	up_VPUL_VSMC
GO:0001913	0.259	0.932	2	10	T cell mediated cytotoxicity	BP	1	EMP2,PPP3CB	up_VSAP_EC
GO:0009914	0.259	0.965	1	64	hormone transport	BP	1	STX4	down_ACOR_EC
GO:0000423	0.259	0.969	1	6	mitophagy	BP	1	CLEC16A	down_VCAV_EC
GO:0051172	0.259	0.975	1	663	negative regulation of nitrogen compound	BP	1	MOSPD1	down_VFEM_EC
GO:0060431	0.259	0.97	1	5	primary lung bud formation	BP	1	CTNNB1	down_VSAP_EC
GO:0021670	0.259	0.97	1	5	lateral ventricle development	BP	1	UCHL5	down_VSAP_EC
GO:1902237	0.259	0.97	1	5	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	PTPN2	down_VSAP_EC
GO:2001138	0.259	0.97	1	5	regulation of phospholipid transport	BP	1	APOE	down_VSAP_EC
GO:2001140	0.259	0.97	1	5	positive regulation of phospholipid transport	BP	1	APOE	down_VSAP_EC

GO:0002710	0.259	0.975	1	3	negative regulation of T cell mediated immunity	BP	1	DUSP22	up_ACOR_VSMC
GO:0061343	0.259	0.975	1	3	cell adhesion involved in heart morphogenesis	BP	1	GATA5	up_ACOR_VSMC
GO:0050765	0.259	0.97	1	5	negative regulation of phagocytosis	BP	1	HMGB1	up_VCAV_EC
GO:0033483	0.259	0.972	1	4	gas homeostasis	BP	1	HIF1A	up_VCAV_EC
GO:0072718	0.259	0.975	1	3	response to cisplatin	BP	1	TIMELESS	up_VCAV_EC
GO:0072719	0.259	0.975	1	3	cellular response to cisplatin	BP	1	TIMELESS	up_VCAV_EC
GO:0090336	0.259	0.972	1	4	positive regulation of brown fat cell	BP	1	PTGS2	up_VCAV_EC
GO:0010638	0.259	0.967	1	207	positive regulation of organelle organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0031400	0.259	0.967	1	205	negative regulation of protein modification	BP	1	LIMK1	up_VCAV_VSMC
GO:0001819	0.259	0.965	1	120	positive regulation of cytokine production	BP	1	C3AR1	up_VPOR_VSMC
GO:0003013	0.259	0.965	1	121	circulatory system process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007186	0.259	0.965	1	124	G protein-coupled receptor signaling	BP	1	C3AR1	up_VPOR_VSMC
GO:0046578	0.259	0.965	1	77	regulation of Ras protein signal transduction	BP	1	TIAM1	up_VFEM_EC
GO:0030336	0.259	0.965	1	86	negative regulation of cell migration	BP	1	TBX5	up_VPUL_EC
GO:0010878	0.259	0.975	1	3	cholesterol storage	BP	1	SOAT1	up_VSAP_EC
GO:0055118	0.259	0.975	1	3	negative regulation of cardiac muscle	BP	1	KCNE3	up_VSAP_EC
GO:1902914	0.259037046	0.96633	1	11	regulation of protein polyubiquitination	BP	1	NOD2	up_ACOR_EC
GO:1903793	0.259127816	0.96631	1	11	positive regulation of anion transport	BP	1	PRKCD	up_ACOR_EC
GO:0021700	0.259485672	0.9001	3	65	developmental maturation	BP	1	CDH3,PTH1R,FZD5	up_ACOR_EC
GO:0003254	0.25962053	0.96591	1	12	regulation of membrane depolarization	BP	1	IFI6	up_ACOR_EC
GO:0030835	0.25994793	0.96608	1	11	negative regulation of actin filament	BP	1	TMOD1	up_ACOR_EC
GO:0071495	0.26	0.796	35	365	cellular response to endogenous stimulus	BP	1	KIT,PRCP,CXCL8,PPARG,BAIAP2L1,PDE4D,MEF2C,FERMT1,DLL4,RAPGEF1,GATA3,SMAD1,TFPI,YES1,MTOR,BMP2,MAPK13,ENSCAFG00000010596,PRKD2,SMARCA4,NCK1,TIMELESS,RAPGEF2,CTDSPL2,CTNNA1,ADIPOR2,BLM,SKIL,PDGFD,UFSP2,KDM3A,NR4A1,ENSCAFG00000002015,ZEB1,ARHGEF2	up_VCAV_EC
GO:0003006	0.26	0.816	18	180	developmental process involved in reproduction	BP	1	SLC29A1,TRIP13,SF1,FBXO5,CASP2,DHCR24,E2F8,B4GALT1,PPARD,FOSL1,PLK4,HMGB2,SGPL1,ASPM,HOXA9,RTCB,SIX4,TTLL1	down_ACOR_VSMC
GO:0007264	0.26	0.816	18	164	small GTPase mediated signal transduction	BP	1	CDON,ARHGEF5,ARHGEF6,SLIT2,ABL1,CDC42EP5,RASGRP2,CDC42EP2,F2RL1,MFN2,RGL1,TIAM1,DLC1,FGD4,PSD4,ARHGAP12,RAPGEF3,FLOT1	up_VSAP_EC
GO:0033673	0.26	0.839	10	84	negative regulation of kinase activity	BP	1	BMP4,LATS2,CDKN1A,SMPD1,PSEN1,DUSP22,DUSP26,LRRC4,INPP5K,PARK7	up_ACOR_VSMC
GO:0045927	0.26	0.85	8	61	positive regulation of growth	BP	1	LEP,FGFR2,NRP1,TBX20,TBX5,CHD7,EDN1,WFS1	up_ACOR_VSMC
GO:0044267	0.26	0.859	8	1583	cellular protein metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2	up_APUL_EC
GO:0002793	0.26	0.856	7	54	positive regulation of peptide secretion	BP	1	CD274,ABL1,IL17RC,F2RL1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0050714	0.26	0.856	7	54	positive regulation of protein secretion	BP	1	CD274,ABL1,IL17RC,F2RL1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0006164	0.26	0.862	6	86	purine nucleotide biosynthetic process	BP	1	ADCY6,ATP5MC1,ADK,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0030010	0.26	0.885	4	41	establishment of cell polarity	BP	1	FSCN1,MSN,UST,HTT	down_VSAP_EC
GO:0006820	0.26	0.883	4	109	anion transport	BP	1	LEP,SLC17A5,SLC6A6,CLIC4	up_AFEM_EC
GO:0042552	0.26	0.887	4	30	myelination	BP	1	MALL,EIF2B2,SERINC5,MTOR	up_VCAV_EC
GO:0017148	0.26	0.901	3	36	negative regulation of translation	BP	1	SAMD4B,ZFP36L1,EIF4EBP1	down_VCAV_EC
GO:0021987	0.26	0.901	3	37	cerebral cortex development	BP	1	PEX5,GLI3,CDH2	down_VCAV_EC
GO:0055072	0.26	0.902	3	30	iron ion homeostasis	BP	1	HIF1A,NEO1,TFRC	down_VSAP_EC

GO:0001755	0.26	0.928	2	16	neural crest cell migration	BP	1	HIF1A,NRP1	down_VSAP_EC
GO:0014037	0.26	0.932	2	10	Schwann cell differentiation	BP	1	SH3TC2,DAG1	up_ACOR_VSMC
GO:0098911	0.26	0.972	1	4	regulation of ventricular cardiac muscle cell action	BP	1	CAV1	down_ACOR_VSMC
GO:0016486	0.26	0.969	1	6	peptide hormone processing	BP	1	PCSK6	down_VCAV_EC
GO:0090051	0.26	0.969	1	6	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	SPRED1	down_VCAV_EC
GO:1905048	0.26	0.969	1	6	regulation of metallopeptidase activity	BP	1	RECK	down_VCAV_EC
GO:0022607	0.26	0.981	1	969	cellular component assembly	BP	1	JUP	down_VFEM_VSMC
GO:0021825	0.26	0.972	1	4	substrate-dependent cerebral cortex tangential	BP	1	NRP1	down_VSAP_EC
GO:0046697	0.26	0.97	1	5	decidualization	BP	1	PTGS2	down_VSAP_EC
GO:1902285	0.26	0.972	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	NRP1	down_VSAP_EC
GO:2000574	0.26	0.969	1	6	regulation of microtubule motor activity	BP	1	DYNLL1	down_VSAP_EC
GO:0019637	0.26	0.969	1	342	organophosphate metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0006678	0.26	0.974	1	3	glucosylceramide metabolic process	BP	1	UGCG	up_ACOR_VSMC
GO:0009134	0.26	0.974	1	3	nucleoside diphosphate catabolic process	BP	1	ENTPD3	up_ACOR_VSMC
GO:0016255	0.26	0.974	1	3	attachment of GPI anchor to protein	BP	1	PIGS	up_ACOR_VSMC
GO:0032351	0.26	0.974	1	3	negative regulation of hormone metabolic	BP	1	DKKL1	up_ACOR_VSMC
GO:0032353	0.26	0.974	1	3	negative regulation of hormone biosynthetic	BP	1	DKKL1	up_ACOR_VSMC
GO:0035844	0.26	0.974	1	3	cloaca development	BP	1	BMP4	up_ACOR_VSMC
GO:0051960	0.26	0.966	1	216	regulation of nervous system development	BP	1	EYA1	up_AFEM_VSMC
GO:0046512	0.26	0.971	1	4	sphingosine biosynthetic process	BP	1	SPTLC2	up_VCAV_EC
GO:0010544	0.26	0.971	1	4	negative regulation of platelet activation	BP	1	PDGFB	up_VCAV_EC
GO:0031652	0.26	0.974	1	3	positive regulation of heat generation	BP	1	PTGS2	up_VCAV_EC
GO:0048853	0.26	0.971	1	4	forebrain morphogenesis	BP	1	HHEX	up_VCAV_EC
GO:0072578	0.26	0.974	1	3	neurotransmitter-gated ion channel clustering	BP	1	RELN	up_VCAV_EC
GO:0032635	0.26	0.964	1	37	interleukin-6 production	BP	1	ARHGEF2	up_VPOR_EC
GO:0008064	0.26	0.964	1	72	regulation of actin polymerization or	BP	1	CDC42EP5	up_VFEM_EC
GO:0030832	0.26	0.964	1	72	regulation of actin filament length	BP	1	CDC42EP5	up_VFEM_EC
GO:0018205	0.26	0.965	1	122	peptidyl-lysine modification	BP	1	EYA1	up_VFEM_VSMC
GO:0002315	0.26	0.974	1	3	marginal zone B cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0045217	0.26	0.974	1	3	cell-cell junction maintenance	BP	1	F2RL1	up_VSAP_EC
GO:1902259	0.26	0.974	1	3	regulation of delayed rectifier potassium	BP	1	KCNE3	up_VSAP_EC
GO:1902498	0.26	0.975	1	3	regulation of protein autoubiquitination	BP	1	SASH1	up_VSAP_EC
GO:0072497	0.26	0.974	1	3	mesenchymal stem cell differentiation	BP	1	FZD1	up_VSAP_EC
GO:0035176	0.260202692	0.96601	1	11	social behavior	BP	1	MAPK8IP2	up_ACOR_EC
GO:0051703	0.260202692	0.96601	1	11	intraspecies interaction between organisms	BP	1	MAPK8IP2	up_ACOR_EC
GO:0045123	0.260272108	0.96599	1	11	cellular extravasation	BP	1	PTGER4	up_ACOR_EC
GO:0003158	0.260543445	0.92445	2	38	endothelium development	BP	1	FOXC2,ARHGEF26	up_ACOR_EC

GO:0043603	0.261	0.793	40	372	cellular amide metabolic process	BP	1	PRR16,NAPEPLD,ACSM3,RNPEP,MRPL37,ACACB,ENSCAFG00000013986,CERS4,WARS2,ENSCAFG00000000071,PYM1,PDK2,ZFP36L1,CTNS,EEF2,LARP6,RPL13,ANKHD1,FARS2,UBA52,RPUSD4,RPL15,ACSS2,MVK,EIF3G,SAMD4B,ZFP36L2,EIF3K,EIF3L,QARS,EIF3D,IDH1,ASS1,TNRC6C,COA1,NCK1,MRPL4,LARS2,B3GALT4,ENSCAFG00000006478	up_VSAP_EC
GO:0000003	0.261	0.802	28	295	reproduction	BP	1	PCDH12,KIT,PDGFB,TSPAN8,CHD7,TIPARP,EIF2B2,GATA3,PSME4,FIGNL1,NECTIN2,MTOR,CDYL,CREM,MDFI,ARID4B,CENPC,HIST1H1A,PTGS2,SPTBN4,AFF4,ARHGDIB,HIF1A,KDM3A,ATRX,VASH1,SPATA6,FBXO5	up_VCAV_EC
GO:0009611	0.261	0.825	14	122	response to wounding	BP	1	HNF4A,KLKB1,PDGFD,HPSE,F2RL1,ZFP36L1,SULF2,RTN4RL1,HPS4,FBLN1,ZFP36L2,ACVRL1,HMOX1,MAP2K2	up_VSAP_EC
GO:0090130	0.261	0.825	14	121	tissue migration	BP	1	ENPP2,SLIT2,FGF7,ABL1,HDAC7,EMP2,CCBE1,STAT5A,TBXA2R,SASH1,ZNF580,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0006725	0.261	0.843	12	1956	cellular aromatic compound metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,TNRC6B,NEDD4	down_ACOR_EC
GO:0070371	0.261	0.835	11	91	ERK1 and ERK2 cascade	BP	1	ACKR3,C5AR2,TBC1D10C,ABL1,PDGFD,F2RL1,ZFP36L1,FBLN1,ZFP36L2,RAF1,MAP2K2	up_VSAP_EC
GO:0009966	0.261	0.845	9	868	regulation of signal transduction	BP	1	BARX1,ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0006664	0.261	0.874	5	37	glycolipid metabolic process	BP	1	PIGN,PIGS,UGCG,PIGG,NEU3	up_ACOR_VSMC
GO:1903509	0.261	0.874	5	37	liposaccharide metabolic process	BP	1	PIGN,PIGS,UGCG,PIGG,NEU3	up_ACOR_VSMC
GO:0002822	0.261	0.884	4	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	SOCS5,FAM49B,PVR,TFRC	down_VSAP_EC
GO:0042306	0.261	0.886	4	31	regulation of protein import into nucleus	BP	1	HCLS1,TMEM173,FERMT1,APOD	up_VCAV_EC
GO:1903510	0.261	0.903	3	22	mucopolysaccharide metabolic process	BP	1	PDGFB,CHST7,CHST1	up_VCAV_EC
GO:0050801	0.261	0.925	2	200	ion homeostasis	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0010591	0.261	0.93	2	12	regulation of lamellipodium assembly	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:0070129	0.261	0.929	2	12	regulation of mitochondrial translation	BP	1	TRUB2,FASTKD3	down_ACOR_VSMC
GO:0007405	0.261	0.926	2	21	neuroblast proliferation	BP	1	NUMBL,GLI3	down_VCAV_EC
GO:0016239	0.261	0.926	2	20	positive regulation of macroautophagy	BP	1	DCN,CLEC16A	down_VCAV_EC
GO:0018958	0.261	0.926	2	20	phenol-containing compound metabolic	BP	1	MAOA,PARK7	down_VCAV_EC
GO:0040011	0.261	0.928	2	505	locomotion	BP	1	HDAC7,HSD3B7	down_VPOR_EC
GO:1902883	0.261	0.927	2	16	negative regulation of response to oxidative	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:0030518	0.261	0.924	2	42	intracellular steroid hormone receptor	BP	1	LBH,CRY2	up_AFEM_EC
GO:0070536	0.261	0.931	2	10	protein K63-linked deubiquitination	BP	1	TNFAIP3,USP13	up_VCAV_EC
GO:0010212	0.261	0.964	1	60	response to ionizing radiation	BP	1	USP28	down_ACOR_EC
GO:0003417	0.261	0.968	1	6	growth plate cartilage development	BP	1	THBS3	down_VCAV_EC
GO:0033160	0.261	0.968	1	6	positive regulation of protein import into	BP	1	MAVS	down_VCAV_EC
GO:0070486	0.261	0.968	1	6	leukocyte aggregation	BP	1	RAC2	down_VCAV_EC
GO:0032504	0.261	0.965	1	152	multicellular organism reproduction	BP	1	CITED2	down_VPOR_EC
GO:0048609	0.261	0.965	1	152	multicellular organismal reproductive process	BP	1	CITED2	down_VPOR_EC
GO:0007340	0.261	0.97	1	5	acrosome reaction	BP	1	SPINK2	down_VSAP_EC
GO:0090239	0.261	0.969	1	5	regulation of histone H4 acetylation	BP	1	IWS1	down_VSAP_EC
GO:0023058	0.261	0.97	1	5	adaptation of signaling pathway	BP	1	RDH11	down_VSAP_EC

GO:0032482	0.261	0.971	1	4	Rab protein signal transduction	BP	1	MADD	down_VSAP_EC
GO:0035766	0.261	0.974	1	3	cell chemotaxis to fibroblast growth factor	BP	1	FGF18	up_ACOR_VSMC
GO:0035768	0.261	0.974	1	3	endothelial cell chemotaxis to fibroblast	BP	1	FGF18	up_ACOR_VSMC
GO:1904847	0.261	0.974	1	3	regulation of cell chemotaxis to fibroblast	BP	1	FGF18	up_ACOR_VSMC
GO:2000544	0.261	0.974	1	3	regulation of endothelial cell chemotaxis to fibroblast growth factor	BP	1	FGF18	up_ACOR_VSMC
GO:0014820	0.261	0.974	1	3	tonic smooth muscle contraction	BP	1	EDN1	up_ACOR_VSMC
GO:0014824	0.261	0.974	1	3	artery smooth muscle contraction	BP	1	EDN1	up_ACOR_VSMC
GO:0061325	0.261	0.974	1	3	cell proliferation involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:1900165	0.261	0.974	1	3	negative regulation of interleukin-6 secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:1905292	0.261	0.974	1	3	regulation of neural crest cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:1905294	0.261	0.974	1	3	positive regulation of neural crest cell	BP	1	BMP4	up_ACOR_VSMC
GO:1905310	0.261	0.974	1	3	regulation of cardiac neural crest cell migration involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:1905312	0.261	0.974	1	3	positive regulation of cardiac neural crest cell migration involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:0002694	0.261	0.965	1	126	regulation of leukocyte activation	BP	1	BPI	up_AORT_EC
GO:0001763	0.261	0.964	1	78	morphogenesis of a branching structure	BP	1	NPNT	up_APUL_EC
GO:0032496	0.261	0.964	1	77	response to lipopolysaccharide	BP	1	NR1H4	up_APUL_EC
GO:0051346	0.261	0.964	1	78	negative regulation of hydrolase activity	BP	1	PCSK1N	up_APUL_EC
GO:0015780	0.261	0.971	1	4	nucleotide-sugar transmembrane transport	BP	1	SLC35A3	up_VCAV_EC
GO:0060579	0.261	0.974	1	3	ventral spinal cord interneuron fate	BP	1	DLL4	up_VCAV_EC
GO:0060581	0.261	0.974	1	3	cell fate commitment involved in pattern	BP	1	DLL4	up_VCAV_EC
GO:0009068	0.261	0.971	1	4	aspartate family amino acid catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0001955	0.261	0.974	1	3	blood vessel maturation	BP	1	CDH5	up_VCAV_EC
GO:0034616	0.261	0.974	1	3	response to laminar fluid shear stress	BP	1	ABCA1	up_VCAV_EC
GO:0071941	0.261	0.971	1	4	nitrogen cycle metabolic process	BP	1	ARG2	up_VCAV_EC
GO:0140052	0.261	0.974	1	3	cellular response to oxidised low-density lipoprotein particle	BP	1	TLR4	up_VCAV_EC
GO:0060284	0.261	0.966	1	212	regulation of cell development	BP	1	LIMK1	up_VCAV_VSMC
GO:0002687	0.261	0.964	1	36	positive regulation of leukocyte migration	BP	1	C3AR1	up_VPOR_EC
GO:0002573	0.261	0.964	1	71	myeloid leukocyte differentiation	BP	1	HOXA7	up_VFEM_EC
GO:0017121	0.261	0.974	1	3	phospholipid scrambling	BP	1	XKR8	up_VSAP_EC
GO:0023019	0.261	0.974	1	3	signal transduction involved in regulation of	BP	1	HNF4A	up_VSAP_EC
GO:0001666	0.261	0.964	1	67	response to hypoxia	BP	1	CAV1	up_VSAP_VSMC
GO:0036293	0.261	0.964	1	67	response to decreased oxygen levels	BP	1	CAV1	up_VSAP_VSMC
GO:0007249	0.261	0.964	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	TLR2	up_VSAP_VSMC
GO:1902230	0.261423103	0.96567	1	11	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	CLU	up_ACOR_EC

GO:0001932	0.262	0.789	44	416	regulation of protein phosphorylation	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,F2RL1,DDR2,TRAF7,MYC,RTN4RL1,SASH1,MYD88,LRP4,FBXO7,CDK9,FBLN1,RAF1,QARS,ACVRL1,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0034330	0.262	0.838	10	80	cell junction organization	BP	1	ACTN2,GJA1,PKP4,LIMS2,F2RL1,NRP1,JUP,PERP,DUSP22,FAM107A	up_ACOR_VSMC
GO:0046903	0.262	0.846	8	255	secretion	BP	1	LEP,KCNC4,CRY2,GPAM,CHRM2,CAMK2A,RAB7A,CCL5	up_AFEM_EC
GO:1901564	0.262	0.879	6	2053	organonitrogen compound metabolic	BP	1	IVNS1ABP,DARS,SUCLG2,EIF3M,USP33,NDUFA10	down_AFEM_EC
GO:0051170	0.262	0.861	6	69	import into nucleus	BP	1	PRICKLE1,ZPR1,KPNB1,KPNA4,KPNA1,CDKN1A	down_VSAP_EC
GO:0032103	0.262	0.87	5	69	positive regulation of response to external	BP	1	PARK7,SASH1,CYBA,RAC2,NAPEPLD	down_VCAV_EC
GO:0048706	0.262	0.871	5	59	embryonic skeletal system development	BP	1	SULF1,HOXB7,CTNNB1,EXT1,SIX4	down_VSAP_EC
GO:0001824	0.262	0.887	4	27	blastocyst development	BP	1	MFN2,TAF8,CITED2,LATS2	up_VSAP_EC
GO:0044706	0.262	0.886	4	27	multi-multicellular organism process	BP	1	EMP2,RECK,HPGD,CITED2	up_VSAP_EC
GO:0008286	0.262	0.9	3	36	insulin receptor signaling pathway	BP	1	ENSCAFG00000014978,AKT2,SHC1	down_VCAV_EC
GO:0030216	0.262	0.901	3	29	keratinocyte differentiation	BP	1	ERRFI1,CASP3,FLNB	down_VSAP_EC
GO:0001906	0.262	0.903	3	20	cell killing	BP	1	LEP,F2RL1,B2M	up_ACOR_VSMC
GO:0043207	0.262	0.899	3	216	response to external biotic stimulus	BP	1	OAS3,MTDH,NAALADL2	up_VPOR_EC
GO:0051707	0.262	0.899	3	216	response to other organism	BP	1	OAS3,MTDH,NAALADL2	up_VPOR_EC
GO:0072079	0.262	0.929	2	12	nephron tubule formation	BP	1	GREM1,SIX4	down_ACOR_VSMC
GO:1905953	0.262	0.929	2	12	negative regulation of lipid localization	BP	1	SREBF2,ABHD5	down_ACOR_VSMC
GO:0046324	0.262	0.926	2	20	regulation of glucose import	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0060393	0.262	0.926	2	19	regulation of pathway-restricted SMAD protein	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0033173	0.262	0.927	2	17	calcineurin-NFAT signaling cascade	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:0097720	0.262	0.927	2	17	calcineurin-mediated signaling	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:0071158	0.262	0.931	2	10	positive regulation of cell cycle arrest	BP	1	CDKN1A,CRLF3	up_ACOR_VSMC
GO:0098656	0.262	0.924	2	42	anion transmembrane transport	BP	1	SLC6A6,CLIC4	up_AFEM_EC
GO:1901343	0.262	0.923	2	42	negative regulation of vasculature development	BP	1	ANGPT4,TBXA2R	up_AFEM_EC
GO:1902903	0.262	0.923	2	125	regulation of supramolecular fiber	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0071383	0.262	0.964	1	58	cellular response to steroid hormone stimulus	BP	1	NEDD4	down_ACOR_EC
GO:0019098	0.262	0.968	1	6	reproductive behavior	BP	1	THRB	down_VCAV_EC
GO:0033689	0.262	0.968	1	6	negative regulation of osteoblast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0003184	0.262	0.968	1	6	pulmonary valve morphogenesis	BP	1	NOTCH2	down_VCAV_EC
GO:0055083	0.262	0.968	1	6	monovalent inorganic anion homeostasis	BP	1	ENSCAFG00000018277	down_VCAV_EC
GO:0097062	0.262	0.968	1	6	dendritic spine maintenance	BP	1	PRNP	down_VCAV_EC
GO:0032460	0.262	0.969	1	5	negative regulation of protein oligomerization	BP	1	CRYAB	down_VSAP_EC
GO:0032463	0.262	0.969	1	5	negative regulation of protein	BP	1	CRYAB	down_VSAP_EC
GO:0060429	0.262	0.968	1	341	epithelium development	BP	1	GATA5	down_VSAP_VSMC
GO:0044387	0.262	0.974	1	3	negative regulation of protein kinase activity by regulation of protein	BP	1	DUSP26	up_ACOR_VSMC
GO:0003214	0.262	0.974	1	3	cardiac left ventricle morphogenesis	BP	1	TBX5	up_ACOR_VSMC
GO:0060737	0.262	0.974	1	3	prostate gland morphogenetic growth	BP	1	FGFR2	up_ACOR_VSMC

GO:0072513	0.262	0.974	1	3	positive regulation of secondary heart field cardioblast proliferation	BP	1	TBX5	up_ACOR_VSMC
GO:1900118	0.262	0.974	1	3	negative regulation of execution phase of	BP	1	FZD3	up_ACOR_VSMC
GO:1902498	0.262	0.974	1	3	regulation of protein autoubiquitination	BP	1	SASH1	up_ACOR_VSMC
GO:2001025	0.262	0.974	1	3	positive regulation of response to drug	BP	1	PSEN1	up_ACOR_VSMC
GO:0010639	0.262	0.964	1	128	negative regulation of organelle organization	BP	1	TAOK1	up_AORT_EC
GO:0071888	0.262	0.974	1	3	macrophage apoptotic process	BP	1	MEF2C	up_VCAV_EC
GO:2000601	0.262	0.974	1	3	positive regulation of Arp2/3 complex-mediated actin nucleation	BP	1	NCKAP1	up_VCAV_EC
GO:0032461	0.262	0.969	1	5	positive regulation of protein oligomerization	BP	1	PMAIP1	up_VCAV_EC
GO:2000109	0.262	0.974	1	3	regulation of macrophage apoptotic process	BP	1	MEF2C	up_VCAV_EC
GO:0006754	0.262	0.964	1	36	ATP biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:1903706	0.262	0.965	1	119	regulation of hemopoiesis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048511	0.262	0.964	1	72	rhythmic process	BP	1	ENOX1	up_VFEM_EC
GO:0006975	0.262	0.974	1	3	DNA damage induced protein phosphorylation	BP	1	ABL1	up_VSAP_EC
GO:0017196	0.262	0.974	1	3	N-terminal peptidyl-methionine acetylation	BP	1	NAA60	up_VSAP_EC
GO:0018206	0.262	0.974	1	3	peptidyl-methionine modification	BP	1	NAA60	up_VSAP_EC
GO:0031987	0.262	0.974	1	3	locomotion involved in locomotory behavior	BP	1	PPP3CB	up_VSAP_EC
GO:0032020	0.262	0.974	1	3	ISG15-protein conjugation	BP	1	UBA7	up_VSAP_EC
GO:0061140	0.262	0.974	1	3	lung secretory cell differentiation	BP	1	NFIB	up_VSAP_EC
GO:0072393	0.262	0.974	1	3	microtubule anchoring at microtubule organizing	BP	1	CEP19	up_VSAP_EC
GO:0006930	0.262	0.974	1	3	substrate-dependent cell migration, cell extension	BP	1	NCK1	up_VSAP_EC
GO:1902713	0.262	0.974	1	3	regulation of interferon-gamma secretion	BP	1	ABL1	up_VSAP_EC
GO:1901605	0.262	0.964	1	67	alpha-amino acid metabolic process	BP	1	GATM	up_VSAP_VSMC
GO:0042634	0.262527419	0.96536	1	11	regulation of hair cycle	BP	1	CDH3	up_ACOR_EC
GO:0006497	0.262590216	0.92346	2	38	protein lipidation	BP	1	PORCN,PIGS	up_ACOR_EC
GO:1901136	0.262830124	0.92335	2	38	carbohydrate derivative catabolic process	BP	1	EDEM2,PRKCD	up_ACOR_EC
GO:0050830	0.262959596	0.96498	1	12	defense response to Gram-positive bacterium	BP	1	RARRES2	up_ACOR_EC
GO:0002065	0.262989321	0.92334	2	37	columnar/cuboidal epithelial cell	BP	1	GATA4,DLX3	up_ACOR_EC
GO:0071363	0.263	0.809	21	188	cellular response to growth factor stimulus	BP	1	FZD1,SLIT2,FGF7,ABL1,DLL1,EPN2,CCBE1,ZFP36L1,GAS1,ZEB1,SULF2,LRP4,STK16,ZFP36L2,HPGD,RAF1,ACVRL1,HTRA2,TGFBR2,CITED2,BAG4	up_VSAP_EC
GO:0007276	0.263	0.836	10	130	gamete generation	BP	1	CELF1,ETV6,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0022414	0.263	0.84	9	294	reproductive process	BP	1	HOXA9,IRX5,LEP,THRB,OVOL1,AVPR1A,RECK,SPATA6,TNC	up_AFEM_EC
GO:0001775	0.263	0.852	7	219	cell activation	BP	1	HOXA9,LEP,CD40,DLL1,BPI,GPAM,CYLD	up_AFEM_EC
GO:0007088	0.263	0.854	7	64	regulation of mitotic nuclear division	BP	1	PDGFB,EDN1,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0043535	0.263	0.862	6	45	regulation of blood vessel endothelial cell migration	BP	1	ABL1,HDAC7,STAT5A,TBXA2R,ACVRL1,HMOX1	up_VSAP_EC
GO:0046474	0.263	0.871	5	44	glycerophospholipid biosynthetic process	BP	1	PDGFB,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0097696	0.263	0.883	4	43	STAT cascade	BP	1	SOCS5,PTPN2,CNOT7,LYN	down_VSAP_EC
GO:0034332	0.263	0.884	4	32	adherens junction organization	BP	1	TEK,SLK,APOD,ENSCAFG00000002015	up_VCAV_EC
GO:0120034	0.263	0.885	4	28	positive regulation of plasma membrane bounded cell projection	BP	1	CDC42EP5,FUZ,CDC42EP2,F2RL1	up_VSAP_EC

GO:0033138	0.263	0.901	3	28	positive regulation of peptidyl-serine	BP	1	VEGFA,BCAR3,PTGS2	down_VSAP_EC
GO:0007435	0.263	0.904	3	18	salivary gland morphogenesis	BP	1	FGFR2,NRP1,DAG1	up_ACOR_VSMC
GO:0060038	0.263	0.904	3	18	cardiac muscle cell proliferation	BP	1	FGFR2,TBX20,TBX5	up_ACOR_VSMC
GO:0050878	0.263	0.898	3	75	regulation of body fluid levels	BP	1	F5,F3,TFPI2	up_AFEM_EC
GO:0010647	0.263	0.901	3	460	positive regulation of cell communication	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0030048	0.263	0.902	3	23	actin filament-based movement	BP	1	PDE4D,STC1,KCNJ2	up_VCAV_EC
GO:0098927	0.263	0.926	2	17	vesicle-mediated transport between endosomal compartments	BP	1	HOOK3,MSN	down_VSAP_EC
GO:0090278	0.263	0.93	2	10	negative regulation of peptide hormone	BP	1	LEP,PFKL	up_ACOR_VSMC
GO:0099504	0.263	0.923	2	42	synaptic vesicle cycle	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0046903	0.263	0.924	2	255	secretion	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0042531	0.263	0.928	2	13	positive regulation of tyrosine phosphorylation	BP	1	HCLS1,KIT	up_VCAV_EC
GO:0050771	0.263	0.929	2	11	negative regulation of axonogenesis	BP	1	SLIT2,LRP4	up_VSAP_EC
GO:0070661	0.263	0.963	1	63	leukocyte proliferation	BP	1	LYN	down_ACOR_EC
GO:0071229	0.263	0.964	1	51	cellular response to acid chemical	BP	1	LYN	down_ACOR_EC
GO:0021513	0.263	0.968	1	6	spinal cord dorsal/ventral patterning	BP	1	GLI3	down_VCAV_EC
GO:0021871	0.263	0.968	1	6	forebrain regionalization	BP	1	GLI3	down_VCAV_EC
GO:1904263	0.263	0.968	1	6	positive regulation of TORC1 signaling	BP	1	CLEC16A	down_VCAV_EC
GO:0014823	0.263	0.969	1	5	response to activity	BP	1	HIF1A	down_VSAP_EC
GO:2001256	0.263	0.969	1	5	regulation of store-operated calcium entry	BP	1	HOMER1	down_VSAP_EC
GO:0003175	0.263	0.974	1	3	tricuspid valve development	BP	1	TBX20	up_ACOR_VSMC
GO:0072095	0.263	0.974	1	3	regulation of branch elongation involved in ureteric bud branching	BP	1	BMP4	up_ACOR_VSMC
GO:2000402	0.263	0.974	1	3	negative regulation of lymphocyte migration	BP	1	WASL	up_ACOR_VSMC
GO:2000726	0.263	0.974	1	3	negative regulation of cardiac muscle cell	BP	1	FRS2	up_ACOR_VSMC
GO:0048514	0.263	0.966	1	214	blood vessel morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0006650	0.263	0.963	1	78	glycerophospholipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0001562	0.263	0.971	1	4	response to protozoan	BP	1	IRF8	up_VCAV_EC
GO:0021631	0.263	0.974	1	3	optic nerve morphogenesis	BP	1	EPHB1	up_VCAV_EC
GO:0042832	0.263	0.971	1	4	defense response to protozoan	BP	1	IRF8	up_VCAV_EC
GO:0007368	0.263	0.963	1	37	determination of left/right symmetry	BP	1	ACVR2A	up_VPOR_EC
GO:0031346	0.263	0.963	1	73	positive regulation of cell projection organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0051099	0.263	0.964	1	70	positive regulation of binding	BP	1	TIAM1	up_VFEM_EC
GO:0009141	0.263	0.964	1	110	nucleoside triphosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0051091	0.263	0.964	1	87	positive regulation of DNA-binding transcription factor activity	BP	1	ARHGEF2	up_VPUL_EC
GO:0001779	0.263	0.974	1	3	natural killer cell differentiation	BP	1	TOX	up_VSAP_EC
GO:0006777	0.263	0.974	1	3	Mo-molybdopterin cofactor biosynthetic	BP	1	MOCOS	up_VSAP_EC
GO:0019720	0.263	0.974	1	3	Mo-molybdopterin cofactor metabolic	BP	1	MOCOS	up_VSAP_EC
GO:0032823	0.263	0.974	1	3	regulation of natural killer cell differentiation	BP	1	TOX	up_VSAP_EC
GO:0043553	0.263	0.974	1	3	negative regulation of phosphatidylinositol 3-kinase activity	BP	1	PIK3IP1	up_VSAP_EC

GO:0070208	0.263	0.974	1	3	protein heterotrimerization	BP	1	C1QTNF2	up_VSAP_EC
GO:0099010	0.263	0.974	1	3	modification of postsynaptic structure	BP	1	WASF3	up_VSAP_EC
GO:1900242	0.263	0.974	1	3	regulation of synaptic vesicle endocytosis	BP	1	PPP3CB	up_VSAP_EC
GO:1903232	0.263	0.974	1	3	melanosome assembly	BP	1	HPS4	up_VSAP_EC
GO:1903421	0.263	0.974	1	3	regulation of synaptic vesicle recycling	BP	1	PPP3CB	up_VSAP_EC
GO:0006596	0.263	0.974	1	3	polyamine biosynthetic process	BP	1	AZIN2	up_VSAP_EC
GO:0009446	0.263	0.974	1	3	putrescine biosynthetic process	BP	1	AZIN2	up_VSAP_EC
GO:0033387	0.263	0.974	1	3	putrescine biosynthetic process from ornithine	BP	1	AZIN2	up_VSAP_EC
GO:0034350	0.263	0.974	1	3	regulation of glial cell apoptotic process	BP	1	DLL1	up_VSAP_EC
GO:0034351	0.263	0.974	1	3	negative regulation of glial cell apoptotic process	BP	1	DLL1	up_VSAP_EC
GO:0050863	0.263	0.963	1	69	regulation of T cell activation	BP	1	CAV1	up_VSAP_VSMC
GO:0033598	0.263300074	0.96515	1	11	mammary gland epithelial cell proliferation	BP	1	PYGO2	up_ACOR_EC
GO:0032715	0.263305719	0.96515	1	11	negative regulation of interleukin-6 production	BP	1	NR1H4	up_ACOR_EC
GO:0008206	0.263371488	0.96513	1	11	bile acid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0032940	0.263496323	0.84481	8	231	secretion by cell	BP	1	NR1H4,AQP1,KCNB1,FZD5,NOD2,PTGER4,PREB,MAVS	up_ACOR_EC
GO:1904018	0.263909195	0.89742	3	69	positive regulation of vasculature development	BP	1	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0019222	0.264	0.771	123	1934	regulation of metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,MEIS2,PRKACB,ENPP1,ERRFI1,JCAD,SNX25,CBX5,BCAR3,NUAK1,PTPN11,AARS,TRIB3,PGAM1,TMED2,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,MSN,HIF1A,DYNLL1,SLC45A3,IWS1,DNAJC10,ACTG2,TNIK,NXN,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YES1,NEO1,PLCL1,PEG3,SMG7,MTDH,DDX39B,ADAM17,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,TFRC,APOE,WWC3,KLF5,LYN,BNIP3,STRAP,DDIT3,FAM162A,BACH1,CCNYL1,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,SH3GLB1,HTT,REST,ABHD5,ZMYND8,MAPK10,EIF2S1,PRMT1,ARFGEF3,SPOP,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,LRRTM2,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,TMTC3,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0046903	0.264	0.799	28	255	secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,FGF7,ABL1,CHRM1,IL17RC,ANXA4,ABCB11,F2RL1,LMF1,RAB11B,PASK,SCFD2,STEAP3,KCNB1,RAF1,PNP,MAPKBP1,CYBA,STX4,VPS11,KCNC4,PPP3CB,MAVS,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0071363	0.264	0.808	21	188	cellular response to growth factor stimulus	BP	1	SMAD6,GATA5,FERMT1,BMP4,FGFR2,CITED2,TMEM108,FGF18,CDKN2B,ANKRD1,NRP1,NPNT,FRS2,FUT8,TGFBR1,NR3C1,DUSP22,HPGD,ENSCAFG00000018360,INPP5K,CRKL	up_ACOR_VSMC
GO:0055080	0.264	0.815	17	176	cation homeostasis	BP	1	EDNRB,CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0050678	0.264	0.828	12	117	regulation of epithelial cell proliferation	BP	1	HMGB1,BIRC5,CAV1,B4GALT1,NRAS,PPARD,HMGB2,ENSCAFG00000005299,GLI1,TINF2,HMGN1,SIX4	down_ACOR_VSMC
GO:0010975	0.264	0.828	12	103	regulation of neuron projection development	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,RTN4RL1,LRP4,DPYSL2,FBXO7,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC
GO:0000956	0.264	0.854	7	55	nuclear-transcribed mRNA catabolic process	BP	1	EXOSC7,PYM1,ZFP36L1,SMG9,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0016241	0.264	0.871	5	41	regulation of macroautophagy	BP	1	RALB,SPTLC2,MTOR,SH3GLB1,HIF1A	up_VCAV_EC
GO:0048167	0.264	0.885	4	28	regulation of synaptic plasticity	BP	1	HRH1,APP,PSEN1,FAM107A	up_ACOR_VSMC
GO:1904029	0.264	0.885	4	28	regulation of cyclin-dependent protein kinase	BP	1	LATS2,CDKN2B,CDKN1A,CCNT1	up_ACOR_VSMC

GO:0006952	0.264	0.881	4	319	defense response	BP	1	C3AR1,ARHGEF2,OAS3,ENSCAFG00000032731	up_VPOR_EC
GO:0030199	0.264	0.902	3	21	collagen fibril organization	BP	1	COLGALT1,GREM1,SERPINH1	down_ACOR_VSMC
GO:0007569	0.264	0.899	3	36	cell aging	BP	1	BMPR1A,PRMT6,PRELP	down_VCAV_EC
GO:0035137	0.264	0.903	3	18	hindlimb morphogenesis	BP	1	AFF3,BMP4,CHD7	up_ACOR_VSMC
GO:0009059	0.264	0.916	3	1563	macromolecule biosynthetic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0042325	0.264	0.9	3	463	regulation of phosphorylation	BP	1	PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0051254	0.264	0.9	3	431	positive regulation of RNA metabolic process	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0035088	0.264	0.928	2	12	establishment or maintenance of	BP	1	FSCN1,EZR	down_ACOR_VSMC
GO:0061245	0.264	0.928	2	12	establishment or maintenance of bipolar	BP	1	FSCN1,EZR	down_ACOR_VSMC
GO:0048103	0.264	0.93	2	10	somatic stem cell division	BP	1	LBH,FGFR2	up_ACOR_VSMC
GO:0007259	0.264	0.922	2	42	JAK-STAT cascade	BP	1	LEP,LRRC15	up_AFEM_EC
GO:0045766	0.264	0.963	1	63	positive regulation of angiogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0000303	0.264	0.968	1	6	response to superoxide	BP	1	PARK7	down_VCAV_EC
GO:0000305	0.264	0.968	1	6	response to oxygen radical	BP	1	PARK7	down_VCAV_EC
GO:1901032	0.264	0.968	1	6	negative regulation of response to reactive	BP	1	PARK7	down_VCAV_EC
GO:1903206	0.264	0.968	1	6	negative regulation of hydrogen peroxide-	BP	1	PARK7	down_VCAV_EC
GO:2001039	0.264	0.968	1	6	negative regulation of cellular response to drug	BP	1	PARK7	down_VCAV_EC
GO:0045773	0.264	0.968	1	6	positive regulation of axon extension	BP	1	TRPV2	down_VCAV_EC
GO:0072201	0.264	0.968	1	6	negative regulation of mesenchymal cell	BP	1	CLSTN1	down_VCAV_EC
GO:1903055	0.264	0.968	1	6	positive regulation of extracellular matrix	BP	1	DDR2	down_VCAV_EC
GO:0014003	0.264	0.969	1	5	oligodendrocyte development	BP	1	EIF2B1	down_VSAP_EC
GO:0046461	0.264	0.969	1	5	neutral lipid catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0046464	0.264	0.969	1	5	acylglycerol catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0090197	0.264	0.974	1	3	positive regulation of chemokine secretion	BP	1	MBP	up_ACOR_VSMC
GO:1902525	0.264	0.974	1	3	regulation of protein monoubiquitination	BP	1	WDR48	up_ACOR_VSMC
GO:0071865	0.264	0.974	1	3	regulation of apoptotic process in bone marrow	BP	1	FGFR2	up_ACOR_VSMC
GO:0071866	0.264	0.974	1	3	negative regulation of apoptotic process in bone	BP	1	FGFR2	up_ACOR_VSMC
GO:1900222	0.264	0.974	1	3	negative regulation of amyloid-beta clearance	BP	1	LRPAP1	up_ACOR_VSMC
GO:0021952	0.264	0.964	1	13	central nervous system projection neuron	BP	1	PLXNA4	up_AFEM_EC
GO:0010959	0.264	0.963	1	79	regulation of metal ion transport	BP	1	HOXA3	up_APUL_EC
GO:0034330	0.264	0.963	1	80	cell junction organization	BP	1	NR1H4	up_APUL_EC
GO:0016477	0.264	0.969	1	426	cell migration	BP	1	TBX5	up_APUL_VSMC
GO:0002323	0.264	0.971	1	4	natural killer cell activation involved in	BP	1	RAB27A	up_VCAV_EC
GO:0043320	0.264	0.971	1	4	natural killer cell degranulation	BP	1	RAB27A	up_VCAV_EC
GO:1903689	0.264	0.98	1	2	regulation of wound healing, spreading of	BP	1	MTOR	up_VCAV_EC
GO:1903691	0.264	0.98	1	2	positive regulation of wound healing, spreading of epidermal cells	BP	1	MTOR	up_VCAV_EC
GO:0006704	0.264	0.974	1	3	glucocorticoid biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0010039	0.264	0.97	1	4	response to iron ion	BP	1	HIF1A	up_VCAV_EC
GO:0031946	0.264	0.974	1	3	regulation of glucocorticoid	BP	1	BMP2	up_VCAV_EC

GO:0034650	0.264	0.974	1	3	cortisol metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0034651	0.264	0.974	1	3	cortisol biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0090030	0.264	0.974	1	3	regulation of steroid hormone biosynthetic	BP	1	BMP2	up_VCAV_EC
GO:1902645	0.264	0.974	1	3	tertiary alcohol biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:2000064	0.264	0.974	1	3	regulation of cortisol biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0048813	0.264	0.963	1	39	dendrite morphogenesis	BP	1	SEMA3A	up_VPOR_EC
GO:1902905	0.264	0.963	1	72	positive regulation of supramolecular fiber	BP	1	CDC42EP5	up_VFEM_EC
GO:0050900	0.264	0.963	1	89	leukocyte migration	BP	1	CCL24	up_VPUL_EC
GO:0034140	0.264	0.973	1	3	negative regulation of toll-like receptor 3 signaling	BP	1	F2RL1	up_VSAP_EC
GO:0035844	0.264	0.974	1	3	cloaca development	BP	1	WNT11	up_VSAP_EC
GO:0045647	0.264	0.973	1	3	negative regulation of erythrocyte	BP	1	ZFP36L1	up_VSAP_EC
GO:0051583	0.264	0.974	1	3	dopamine uptake involved in synaptic	BP	1	SLC6A4	up_VSAP_EC
GO:0051934	0.264	0.974	1	3	catecholamine uptake involved in synaptic	BP	1	SLC6A4	up_VSAP_EC
GO:0060099	0.264	0.974	1	3	regulation of phagocytosis, engulfment	BP	1	F2RL1	up_VSAP_EC
GO:0060100	0.264	0.974	1	3	positive regulation of phagocytosis, engulfment	BP	1	F2RL1	up_VSAP_EC
GO:0090493	0.264	0.974	1	3	catecholamine uptake	BP	1	SLC6A4	up_VSAP_EC
GO:0090494	0.264	0.974	1	3	dopamine uptake	BP	1	SLC6A4	up_VSAP_EC
GO:0097070	0.264	0.974	1	3	ductus arteriosus closure	BP	1	HPGD	up_VSAP_EC
GO:1905153	0.264	0.974	1	3	regulation of membrane invagination	BP	1	F2RL1	up_VSAP_EC
GO:1905155	0.264	0.974	1	3	positive regulation of membrane invagination	BP	1	F2RL1	up_VSAP_EC
GO:0032740	0.264	0.974	1	3	positive regulation of interleukin-17 production	BP	1	MYD88	up_VSAP_EC
GO:0090091	0.264	0.974	1	3	positive regulation of extracellular matrix	BP	1	DDR2	up_VSAP_EC
GO:1902306	0.264	0.974	1	3	negative regulation of sodium ion	BP	1	OSR1	up_VSAP_EC
GO:0072593	0.264	0.963	1	68	reactive oxygen species metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0060914	0.264067217	0.96493	1	11	heart formation	BP	1	TBX5	up_ACOR_EC
GO:0060039	0.264111682	0.96492	1	11	pericardium development	BP	1	TBX5	up_ACOR_EC
GO:0022610	0.264125677	0.83065	11	326	biological adhesion	BP	1	CDH3,ARHGAP6,DUSP26,SMAD6,ACTN2,ELMO2,FOXC2,LRRC15,VCAM1,NRP1,PRKCD	up_ACOR_EC
GO:1901379	0.264127388	0.96465	1	12	regulation of potassium ion transmembrane	BP	1	ACTN2	up_ACOR_EC
GO:0046854	0.264181913	0.9649	1	11	phosphatidylinositol phosphorylation	BP	1	ENSCAFG00000004331	up_ACOR_EC
GO:0099172	0.264352688	0.96485	1	11	presynapse organization	BP	1	LRP4	up_ACOR_EC
GO:0060045	0.264504663	0.96481	1	11	positive regulation of cardiac muscle cell	BP	1	TBX5	up_ACOR_EC
GO:0061178	0.264715007	0.96448	1	12	regulation of insulin secretion involved in cellular response to	BP	1	NR1H4	up_ACOR_EC

GO:0048856	0.265	0.766	153	1533	anatomical structure development	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,PEX7,PCDH19,HOXA9,SEZ6L,CDON,WNT11,HNF4A,CD274,ACKR3,AXIN2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,RADIL,PPARGC1B,MAB21L1,GJB5,LIMS2,LRIG3,ACACB,DDHD1,IL6R,IRX5,SLIT2,CRIP2,HOXD3,SLC6A4,FGF7,ABL1,EBF2,BTG1,HDAC7,EMP2,DLL1,EPN2,HOXA6,OSR1,MAP3K5,CDC42EP5,FUZ,ADAMTSL4,WARS2,SAV1,KLF15,ANXA4,HPSE,PLXNA4,RILPL2,ANKRD54,CLDN1,CDC42EP2,ZBTB16,TOX,RARG,CCBE1,STAT6,HOXC4,RECK,PATZ1,PLPP3,GTF3C5,AMBRA1,F2RL1,DLX3,GLIS2,MORC3,DDR2,MFN2,ZFP36L1,FXN,PIK3R1,TIAM1,BATF2,OMD,MYC,IRX3,ZEB1,FBXW4,CTNS,TBXA2R,SULF2,SHOX2,EEF2,RTN4RL1,SASH1,HOXC10,POLDIP2,MYD88,LOX,TFE3,LRP4,DPYSL2,GDPD5,DAGLB,FRMD6,CLCN2,E2F4,PRKAB1,SMG9,MCPH1,KIF27,FBXO7,NTN4,LIMD1,CDK9,CD83,NR2F6,KDM2B,FBLN1,ZFP36L2,HPGD,RAF1,PNP,TAF8,NFIB,CYB5D2,CDNF,ZFAND5,ANPEP,PQBP1,TTL,PLEKHA5,QARS,ARHGAP12,ACVRL1,TPRA1,VANGL1,HTRA2,FLOT1,PPP3CB,NCK1,BGLAP,ULK1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,OGN,TRADD,PIR,LBH,KEAP1,LATS2	up_VSAP_EC
GO:0023051	0.265	0.772	97	954	regulation of signaling	BP	1	FZD1,SEZ6L,CDON,WNT11,HNF4A,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,SLC8B1,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,ABL1,HDAC7,EMP2,DLL1,EPN2,SESN1,MAP3K5,PDGFD,C1QTNF2,HPSE,ANKRD54,CCBE1,RECK,KLHL24,PLPP3,F2RL1,RAB11B,GLIS2,PDK2,MFN2,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,SULF2,SHOX2,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,PASK,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,KCNB1,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,PRMT2,FBLN1,IGFBP6,RAF1,MAPKBP1,CYBA,ZNF205,STX4,PSD4,KCNC4,QARS,ARHGAP12,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,HMOX1,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0048585	0.265	0.799	27	475	negative regulation of response to stimulus	BP	1	SLC35F6,DCN,PRNP,VASN,FBN1,BGN,KANK2,CHID1,AKT1S1,CHRDL1,CLSTN1,TMEM161A,ASPN,THY1,GLI3,PARK7,CDH2,LOXL3,SPRED1,RAB7B,A2M,GLIS2,FBH1,GREM1,NPHP4,FOXO3,RGMA	down_VCAV_EC
GO:0022604	0.265	0.825	13	122	regulation of cell morphogenesis	BP	1	KIT,IFRD1,RELN,RAB11A,ARAP3,NEDD9,PPP3CA,PDZD8,FES,RAPGEF2,FMNL3,ENSCAFG00000002015,ZMYM2	up_VCAV_EC
GO:0048608	0.265	0.824	13	129	reproductive structure development	BP	1	PCDH12,KIT,PDGFB,CHD7,TIPARP,EIF2B2,GATA3,MDFI,ARID4B,PTGS2,HIF1A,ATRX,VASH1	up_VCAV_EC
GO:0009615	0.265	0.836	10	83	response to virus	BP	1	MX1,TLR3,ISG15,F2RL1,BNIP3,PTPN22,PARP9,CCL5,DDIT4,SERINC3	up_ACOR_VSMC
GO:0007611	0.265	0.853	7	54	learning or memory	BP	1	FGF13,HRH1,LRRN4,POMK,APP,PSEN1,CLN8	up_ACOR_VSMC
GO:0035556	0.265	0.863	6	845	intracellular signal transduction	BP	1	LYN,IGF1R,PDPN,USP28,ASPN,NEDD4	down_ACOR_EC
GO:0060401	0.265	0.87	5	42	cytosolic calcium ion transport	BP	1	PDE4D,CHD7,APLNR,PLCG2,MCU	up_VCAV_EC
GO:0034622	0.265	0.869	5	421	cellular protein-containing complex assembly	BP	1	MZT1,RSL24D1,RPL10L,TWF1,SRP54	up_VPOR_EC
GO:0051588	0.265	0.884	4	28	regulation of neurotransmitter	BP	1	FBXL20,PSEN1,KCNC4,PREPL	up_ACOR_VSMC
GO:0007269	0.265	0.883	4	34	neurotransmitter secretion	BP	1	MEF2C,SNCAIP,SNAP23,STX11	up_VCAV_EC
GO:0099643	0.265	0.883	4	34	signal release from synapse	BP	1	MEF2C,SNCAIP,SNAP23,STX11	up_VCAV_EC
GO:0048659	0.265	0.898	3	36	smooth muscle cell proliferation	BP	1	PDGFRB,BMPR1A,CLSTN1	down_VCAV_EC
GO:0042116	0.265	0.902	3	18	macrophage activation	BP	1	TLR1,PRKCE,APP	up_ACOR_VSMC
GO:0070482	0.265	0.897	3	75	response to oxygen levels	BP	1	ANGPT4,CRYAB,ADAM17	up_AFEM_EC
GO:0023056	0.265	0.9	3	462	positive regulation of signaling	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0016477	0.265	0.899	3	426	cell migration	BP	1	HOXA7,SIX1,TIAM1	up_VFEM_EC

GO:0050819	0.265	0.928	2	12	negative regulation of coagulation	BP	1	TFPI,ANXA5	down_ACOR_VSMC
GO:0006694	0.265	0.922	2	42	steroid biosynthetic process	BP	1	LEP,SDR42E1	up_AFEM_EC
GO:0030073	0.265	0.922	2	42	insulin secretion	BP	1	LEP,CCL5	up_AFEM_EC
GO:0008334	0.265	0.928	2	12	histone mRNA metabolic process	BP	1	TENT2,DCP2	up_VCAV_EC
GO:0007626	0.265	0.963	1	53	locomotory behavior	BP	1	SPG11	down_ACOR_EC
GO:0033500	0.265	0.963	1	64	carbohydrate homeostasis	BP	1	STX4	down_ACOR_EC
GO:0042593	0.265	0.963	1	64	glucose homeostasis	BP	1	STX4	down_ACOR_EC
GO:2001236	0.265	0.963	1	59	regulation of extrinsic apoptotic signaling	BP	1	STX4	down_ACOR_EC
GO:0048263	0.265	0.97	1	4	determination of dorsal identity	BP	1	GREM1	down_ACOR_VSMC
GO:0006878	0.265	0.967	1	6	cellular copper ion homeostasis	BP	1	ATOX1	down_VCAV_EC
GO:0045776	0.265	0.967	1	6	negative regulation of blood pressure	BP	1	RNPEP	down_VCAV_EC
GO:0045947	0.265	0.967	1	6	negative regulation of translational initiation	BP	1	EIF4EBP1	down_VCAV_EC
GO:0048665	0.265	0.967	1	6	neuron fate specification	BP	1	GLI3	down_VCAV_EC
GO:0006071	0.265	0.968	1	5	glycerol metabolic process	BP	1	TPI1	down_VSAP_EC
GO:0061042	0.265	0.968	1	5	vascular wound healing	BP	1	SERPINE1	down_VSAP_EC
GO:0002675	0.265	0.973	1	3	positive regulation of acute inflammatory	BP	1	PARK7	up_ACOR_VSMC
GO:0009650	0.265	0.973	1	3	UV protection	BP	1	MFAP4	up_ACOR_VSMC
GO:0018243	0.265	0.973	1	3	protein O-linked glycosylation via	BP	1	GALNT3	up_ACOR_VSMC
GO:0023021	0.265	0.973	1	3	termination of signal transduction	BP	1	SMPD1	up_ACOR_VSMC
GO:0033700	0.265	0.973	1	3	phospholipid efflux	BP	1	ABCA1	up_ACOR_VSMC
GO:0034140	0.265	0.973	1	3	negative regulation of toll-like receptor 3 signaling	BP	1	F2RL1	up_ACOR_VSMC
GO:0097527	0.265	0.973	1	3	necroptotic signaling pathway	BP	1	TLR3	up_ACOR_VSMC
GO:0071345	0.265	0.965	1	210	cellular response to cytokine stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:1903532	0.265	0.963	1	78	positive regulation of secretion by cell	BP	1	NR1H4	up_APUL_EC
GO:0062033	0.265	0.97	1	4	positive regulation of mitotic sister chromatid	BP	1	SMC5	up_VCAV_EC
GO:0048021	0.265	0.973	1	3	regulation of melanin biosynthetic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0061502	0.265	0.973	1	3	early endosome to recycling endosome	BP	1	DNAJC13	up_VCAV_EC
GO:1900376	0.265	0.973	1	3	regulation of secondary metabolite biosynthetic	BP	1	RAPGEF2	up_VCAV_EC
GO:0010508	0.265	0.963	1	38	positive regulation of autophagy	BP	1	MTDH	up_VPOR_EC
GO:0045667	0.265	0.963	1	38	regulation of osteoblast differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0050678	0.265	0.963	1	117	regulation of epithelial cell proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:0006561	0.265	0.973	1	3	proline biosynthetic process	BP	1	ENSCAFG00000016140	up_VSAP_EC
GO:0032627	0.265	0.973	1	3	interleukin-23 production	BP	1	MYD88	up_VSAP_EC
GO:0032667	0.265	0.973	1	3	regulation of interleukin-23 production	BP	1	MYD88	up_VSAP_EC
GO:0034145	0.265	0.973	1	3	positive regulation of toll-like receptor 4 signaling	BP	1	F2RL1	up_VSAP_EC
GO:0046641	0.265	0.973	1	3	positive regulation of alpha-beta T cell	BP	1	TGFBR2	up_VSAP_EC
GO:0055129	0.265	0.973	1	3	L-proline biosynthetic process	BP	1	ENSCAFG00000016140	up_VSAP_EC
GO:0097384	0.265	0.973	1	3	cellular lipid biosynthetic process	BP	1	PEX7	up_VSAP_EC
GO:1900165	0.265	0.973	1	3	negative regulation of interleukin-6 secretion	BP	1	C5AR2	up_VSAP_EC
GO:1901525	0.265	0.973	1	3	negative regulation of mitophagy	BP	1	HTRA2	up_VSAP_EC

GO:1901569	0.265	0.973	1	3	fatty acid derivative catabolic process	BP	1	ABHD16A	up_VSAP_EC
GO:0001505	0.265	0.963	1	69	regulation of neurotransmitter levels	BP	1	CAV1	up_VSAP_VSMC
GO:0032024	0.265176292	0.96435	1	12	positive regulation of insulin secretion	BP	1	NR1H4	up_ACOR_EC
GO:0090277	0.265176292	0.96435	1	12	positive regulation of peptide hormone	BP	1	NR1H4	up_ACOR_EC
GO:0072376	0.265450856	0.96454	1	11	protein activation cascade	BP	1	C7	up_ACOR_EC
GO:0034405	0.265465949	0.96454	1	11	response to fluid shear stress	BP	1	SMAD6	up_ACOR_EC
GO:0007095	0.265590761	0.9645	1	11	mitotic G2 DNA damage checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0071495	0.266	0.806	21	365	cellular response to endogenous stimulus	BP	1	SMAD9,LRP1,PRNP,VASN,FBN1,ADCY6,KANK2,COL6A1,ENSCAFG00000014978,CHRDL1,AKT2,NR3C1,ASPN,PARK7,ZFP36L1,FUT8,RAB31,SHC1,FBH1,GREM1,RGMA	down_VCAV_EC
GO:0045787	0.266	0.827	12	117	positive regulation of cell cycle	BP	1	PDGFB,EDN1,RAB11A,GDPD5,PROX1,UHRF2,THOC1,SMC5,RAD21,CUL4A,ATRX,TMOD3	up_VCAV_EC
GO:0051495	0.266	0.835	10	82	positive regulation of cytoskeleton organization	BP	1	SYNPO2L,ACTN2,SYNPO2,F2RL1,JMY,NRP1,EVL,PRKCE,EDN1,WASL	up_ACOR_VSMC
GO:0000003	0.266	0.837	9	295	reproduction	BP	1	HOXA9,IRX5,LEP,THRB,OVOL1,AVPR1A,RECK,SPATA6,TNC	up_AFEM_EC
GO:0048511	0.266	0.845	8	72	rhythmic process	BP	1	PPARG,PROX1,ENSCAFG00000010596,TIMELESS,TOP1,CREB1,NR1D2,KDM5A	up_VCAV_EC
GO:0010950	0.266	0.869	5	44	positive regulation of endopeptidase activity	BP	1	HMGB1,PRELID1,PDCD2,CYCS,AIFM1	down_ACOR_VSMC
GO:0001667	0.266	0.867	5	146	ameboidal-type cell migration	BP	1	ANGPT4,GREM1,TBXA2R,FAP,ADAM17	up_AFEM_EC
GO:0007010	0.266	0.868	5	441	cytoskeleton organization	BP	1	MZT1,HOOK3,ARHGEF2,GCC2,TWF1	up_VPOR_EC
GO:0042157	0.266	0.881	4	51	lipoprotein metabolic process	BP	1	CLIP3,LCAT,PIGS,WDR45	down_VCAV_EC
GO:0030301	0.266	0.884	4	27	cholesterol transport	BP	1	LEP,LCAT,ABCA1,SCP2	up_ACOR_VSMC
GO:0015918	0.266	0.884	4	27	sterol transport	BP	1	LEP,LCAT,ABCA1,SCP2	up_ACOR_VSMC
GO:0006081	0.266	0.884	4	27	cellular aldehyde metabolic process	BP	1	ALDH3B1,DHRS4,PNPO,ALDH9A1	up_VSAP_EC
GO:1903901	0.266	0.902	3	19	negative regulation of viral life cycle	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0070265	0.266	0.902	3	19	necrotic cell death	BP	1	MAP3K5,RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0032768	0.266	0.927	2	12	regulation of monooxygenase activity	BP	1	CAV1,NUS1	down_ACOR_VSMC
GO:0071825	0.266	0.927	2	12	protein-lipid complex subunit organization	BP	1	ACSL3,LIPC	down_ACOR_VSMC
GO:0071827	0.266	0.927	2	12	plasma lipoprotein particle organization	BP	1	ACSL3,LIPC	down_ACOR_VSMC
GO:0030858	0.266	0.925	2	17	positive regulation of epithelial cell	BP	1	SERPINE1,CTNNB1	down_VSAP_EC
GO:0048546	0.266	0.925	2	16	digestive tract morphogenesis	BP	1	HIF1A,CTNNB1	down_VSAP_EC
GO:0000902	0.266	0.923	2	266	cell morphogenesis	BP	1	ARHGEF26,SLITRK5	up_APUL_EC
GO:0002067	0.266	0.927	2	12	glandular epithelial cell differentiation	BP	1	BMP2,PROX1	up_VCAV_EC
GO:0030029	0.266	0.922	2	239	actin filament-based process	BP	1	CDC42EP5,MTSS1	up_VFEM_EC
GO:0044249	0.266	1	1	1851	cellular biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0009109	0.266	0.967	1	6	coenzyme catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0010742	0.266	0.967	1	6	macrophage derived foam cell differentiation	BP	1	SOAT1	down_VCAV_EC
GO:0048368	0.266	0.967	1	6	lateral mesoderm development	BP	1	BMPR1A	down_VCAV_EC
GO:0050774	0.266	0.967	1	6	negative regulation of dendrite morphogenesis	BP	1	TLX2	down_VCAV_EC
GO:0090077	0.266	0.967	1	6	foam cell differentiation	BP	1	SOAT1	down_VCAV_EC
GO:0007423	0.266	0.964	1	155	sensory organ development	BP	1	CITED2	down_VPOR_EC
GO:0006026	0.266	0.968	1	5	aminoglycan catabolic process	BP	1	CEMIP2	down_VSAP_EC
GO:0043922	0.266	0.968	1	5	negative regulation by host of viral transcription	BP	1	REST	down_VSAP_EC

GO:0150077	0.266	0.973	1	3	regulation of neuroinflammatory	BP	1	APP	up_ACOR_VSMC
GO:1903978	0.266	0.973	1	3	regulation of microglial cell activation	BP	1	APP	up_ACOR_VSMC
GO:1904796	0.266	0.973	1	3	regulation of core promoter binding	BP	1	PSEN1	up_ACOR_VSMC
GO:0006298	0.266	0.964	1	13	mismatch repair	BP	1	AXIN2	up_AFEM_EC
GO:0097150	0.266	0.964	1	13	neuronal stem cell population maintenance	BP	1	DLL1	up_AFEM_EC
GO:0001660	0.266	0.973	1	3	fever generation	BP	1	PTGS2	up_VCAV_EC
GO:0051415	0.266	0.973	1	3	microtubule nucleation by interphase microtubule organizing center	BP	1	MZT1	up_VCAV_EC
GO:0051418	0.266	0.973	1	3	microtubule nucleation by microtubule organizing	BP	1	MZT1	up_VCAV_EC
GO:0010906	0.266	0.962	1	38	regulation of glucose metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0051348	0.266	0.963	1	90	negative regulation of transferase activity	BP	1	FLRT3	up_VPUL_EC
GO:0001977	0.266	0.973	1	3	renal system process involved in regulation of	BP	1	EMP2	up_VSAP_EC
GO:0003093	0.266	0.973	1	3	regulation of glomerular filtration	BP	1	EMP2	up_VSAP_EC
GO:0003175	0.266	0.973	1	3	tricuspid valve development	BP	1	TGFBR2	up_VSAP_EC
GO:0006432	0.266	0.973	1	3	phenylalanyl-tRNA aminoacylation	BP	1	FARS2	up_VSAP_EC
GO:0006662	0.266	0.973	1	3	glycerol ether metabolic process	BP	1	PEX7	up_VSAP_EC
GO:0018243	0.266	0.973	1	3	protein O-linked glycosylation via	BP	1	GALNT11	up_VSAP_EC
GO:0034393	0.266	0.973	1	3	positive regulation of smooth muscle cell	BP	1	MFN2	up_VSAP_EC
GO:0036037	0.266	0.973	1	3	CD8-positive, alpha-beta T cell activation	BP	1	CD274	up_VSAP_EC
GO:0046485	0.266	0.973	1	3	ether lipid metabolic process	BP	1	PEX7	up_VSAP_EC
GO:0060842	0.266	0.973	1	3	arterial endothelial cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0061343	0.266	0.973	1	3	cell adhesion involved in heart morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:1903912	0.266	0.973	1	3	negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation	BP	1	NCK1	up_VSAP_EC
GO:2000726	0.266	0.973	1	3	negative regulation of cardiac muscle cell	BP	1	DLL1	up_VSAP_EC
GO:2001185	0.266	0.973	1	3	regulation of CD8-positive, alpha-beta T cell	BP	1	CD274	up_VSAP_EC
GO:0045617	0.266	0.973	1	3	negative regulation of keratinocyte	BP	1	HOXA7	up_VSAP_EC
GO:0032607	0.266096475	0.96436	1	11	interferon-alpha production	BP	1	MAVS	up_ACOR_EC
GO:2000008	0.266349074	0.96402	1	12	regulation of protein localization to cell surface	BP	1	ACTN2	up_ACOR_EC
GO:0048468	0.267	0.779	59	553	cell development	BP	1	EXPH5,SH3TC2,ACTN2,LEP,EPYC,HTR2B,SHROOM3,FEZ1,ITM2C,BMP4,FGFR2,GJA1,ATRX,SEC24B,WASF3,LATS2,PDE5A,CITED2,ZNF365,TMEM108,FGF18,ARHGEF26,NEBL,F2RL1,NRP1,GPM6A,ULK2,UNC5B,SMARCD3,SPINT2,SLITRK5,MARF1,FZD3,AFF4,FRS2,RND1,DAG1,APP,PSEN1,CHD7,SPINK2,SIPA1L1,FOSL2,SSH3,EDN1,ARID5B,ASAP1,DMC1,JAM3,B2M,DISC1,ATXN10,FEZ2,WASL,DOCK5,BVES,RREB1,CRKL,MYOZ2	up_ACOR_VSMC
GO:0060284	0.267	0.803	23	212	regulation of cell development	BP	1	HOXA11,THRB,CDON,AXIN2,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,FBLN1,CYB5D2,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC
GO:0031669	0.267	0.858	6	72	cellular response to nutrient levels	BP	1	ASNS,HSPA5,SESN2,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0009410	0.267	0.883	4	27	response to xenobiotic stimulus	BP	1	HNF4A,ABAT,NCEH1,DDIT4	up_VSAP_EC
GO:0072088	0.267	0.897	3	36	nephron epithelium morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0021536	0.267	0.9	3	21	diencephalon development	BP	1	PTCHD1,BMP2,CREB1	up_VCAV_EC

GO:0051310	0.267	0.9	3	22	metaphase plate congression	BP	1	RAB11A,CENPC,ZW10	up_VCAV_EC
GO:0010941	0.267	0.899	3	524	regulation of cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0045934	0.267	0.924	2	407	negative regulation of nucleobase-containing compound metabolic	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:2000679	0.267	0.967	1	6	positive regulation of transcription regulatory region DNA binding	BP	1	PARK7	down_VCAV_EC
GO:1903649	0.267	0.968	1	5	regulation of cytoplasmic transport	BP	1	MSN	down_VSAP_EC
GO:0035791	0.267	0.968	1	5	platelet-derived growth factor receptor-beta	BP	1	PTPN2	down_VSAP_EC
GO:0048268	0.267	0.968	1	5	clathrin coat assembly	BP	1	CLTC	down_VSAP_EC
GO:0002070	0.267	0.973	1	3	epithelial cell maturation	BP	1	GJA1	up_ACOR_VSMC
GO:0006930	0.267	0.973	1	3	substrate-dependent cell migration, cell extension	BP	1	NRP1	up_ACOR_VSMC
GO:0061299	0.267	0.973	1	3	retina vasculature morphogenesis in camera-	BP	1	NRP1	up_ACOR_VSMC
GO:1900121	0.267	0.973	1	3	negative regulation of receptor binding	BP	1	B2M	up_ACOR_VSMC
GO:0035082	0.267	0.964	1	13	axoneme assembly	BP	1	DNAL1	up_AFEM_EC
GO:0045581	0.267	0.964	1	13	negative regulation of T cell differentiation	BP	1	CYLD	up_AFEM_EC
GO:0072077	0.267	0.964	1	13	renal vesicle morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:0072273	0.267	0.964	1	13	metanephric nephron morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:1902476	0.267	0.964	1	13	chloride transmembrane transport	BP	1	CLIC4	up_AFEM_EC
GO:0022411	0.267	0.963	1	130	cellular component disassembly	BP	1	TAOK1	up_AORT_EC
GO:0001944	0.267	0.965	1	263	vasculature development	BP	1	WNT7A	up_AORT_VSMC
GO:0002757	0.267	0.963	1	78	immune response-activating signal	BP	1	NR1H4	up_APUL_EC
GO:0030198	0.267	0.962	1	81	extracellular matrix organization	BP	1	NPNT	up_APUL_EC
GO:0043087	0.267	0.962	1	83	regulation of GTPase activity	BP	1	NTRK2	up_APUL_EC
GO:0002544	0.267	0.973	1	3	chronic inflammatory response	BP	1	TNFAIP3	up_VCAV_EC
GO:0071847	0.267	0.973	1	3	TNFSF11-mediated signaling pathway	BP	1	TJP2	up_VCAV_EC
GO:0006207	0.267	0.973	1	3	'de novo' pyrimidine nucleobase biosynthetic	BP	1	MTOR	up_VCAV_EC
GO:0019856	0.267	0.973	1	3	pyrimidine nucleobase biosynthetic process	BP	1	MTOR	up_VCAV_EC
GO:2001015	0.267	0.973	1	3	negative regulation of skeletal muscle cell	BP	1	EPHB1	up_VCAV_EC
GO:0032271	0.267	0.962	1	73	regulation of protein polymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0032504	0.267	0.963	1	152	multicellular organism reproduction	BP	1	SLIT2	up_VPUL_VSMC
GO:0048609	0.267	0.963	1	152	multicellular organismal reproductive process	BP	1	SLIT2	up_VPUL_VSMC
GO:0000973	0.267	0.973	1	3	posttranscriptional tethering of RNA polymerase II gene DNA at	BP	1	NUP98	up_VSAP_EC
GO:0002710	0.267	0.973	1	3	negative regulation of T cell mediated immunity	BP	1	PPP3CB	up_VSAP_EC
GO:0003140	0.267	0.973	1	3	determination of left/right asymmetry in	BP	1	CITED2	up_VSAP_EC
GO:0009134	0.267	0.973	1	3	nucleoside diphosphate catabolic process	BP	1	ENTPD3	up_VSAP_EC
GO:0009235	0.267	0.973	1	3	cobalamin metabolic process	BP	1	CLYBL	up_VSAP_EC
GO:0034374	0.267	0.973	1	3	low-density lipoprotein particle remodeling	BP	1	LIPC	up_VSAP_EC
GO:0035926	0.267	0.973	1	3	chemokine (C-C motif) ligand 2 secretion	BP	1	F2RL1	up_VSAP_EC
GO:0042402	0.267	0.973	1	3	cellular biogenic amine catabolic process	BP	1	IDO2	up_VSAP_EC
GO:0046835	0.267	0.973	1	3	carbohydrate phosphorylation	BP	1	TKFC	up_VSAP_EC

GO:0003214	0.267	0.973	1	3	cardiac left ventricle morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0060437	0.267	0.973	1	3	lung growth	BP	1	FGF7	up_VSAP_EC
GO:0070384	0.267	0.973	1	3	Harderian gland development	BP	1	RARG	up_VSAP_EC
GO:0080154	0.267	0.973	1	3	regulation of fertilization	BP	1	CFAP69	up_VSAP_EC
GO:0032930	0.267	0.973	1	3	positive regulation of superoxide anion	BP	1	F2RL1	up_VSAP_EC
GO:0034379	0.267	0.973	1	3	very-low-density lipoprotein particle	BP	1	SOAT1	up_VSAP_EC
GO:0032103	0.267	0.962	1	69	positive regulation of response to external	BP	1	TLR2	up_VSAP_VSMC
GO:2000027	0.267	0.962	1	72	regulation of animal organ morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:0045667	0.267041238	0.92131	2	38	regulation of osteoblast differentiation	BP	1	SMAD6,CLSTN1	up_ACOR_EC
GO:0050921	0.267179106	0.92117	2	39	positive regulation of chemotaxis	BP	1	RARRES2,NRP1	up_ACOR_EC
GO:0019222	0.268	0.763	170	1934	regulation of metabolic process	BP	1	ELK3,ACSL3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,MCM7,ILF3,DDX39A,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,MED17,U2AF2,PSMD3,SLC29A1,MTDH,HEY1,PPP1R15B,SF1,PARPBP,SRRT,CTDNEP1,NAB2,SLC35C2,RAN,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,EDC4,AURKB,NONO,HNRNPL,CDKN2C,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,CDK4,SMARCC1,RNASEH2B,PLK3,PCNA,DHX33,HOXA7,SMG9,ARG2,SF3B4,UHRF1,CKS2,PDCD2,HOXC10,RNF152,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PRCP,TFRC,PPARD,RAP2C,YBX3,HNRNPF,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,IQGAP1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,ELOVL6,RBM14,RBM17,RAD23A,NOLC1,CDC20,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,KNL1,ENSCAFG00000015189,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5	down_ACOR_VSMC
GO:0030097	0.268	0.797	27	244	hemopoiesis	BP	1	TMEM176B,TMEM176A,PLCG2,LEP,CD83,RASSF2,BMP4,FGFR2,CITED2,ISG15,FAM210B,P4HTM,CDKN2B,F2RL1,CLSTN1,PTPN22,CHD2,APP,PSEN1,CHD7,RTKN2,JAM3,B2M,CNOT4,ENSCAFG00000003530,IL18R1,BVES	up_ACOR_VSMC
GO:0019752	0.268	0.811	17	283	carboxylic acid metabolic process	BP	1	GPAM,AKT2,ACAA1,ME3,UROS,THNSL2,PEX5,PARK7,ENSCAFG00000002977,HPDL,ACSS2,RDH10,CRTAP,LONP2,GLS2,BCKDHB,ACAT1	down_VCAV_EC
GO:0050896	0.268	0.84	12	2346	response to stimulus	BP	1	EYA1,MAP2K6,MME,AVPR1A,ENSCAFG00000018194,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,ADCY3	up_VFEM_EC
GO:0061458	0.268	0.832	10	131	reproductive system development	BP	1	SULF1,PTPN11,TMED2,PTGS2,HIF1A,CTNNB1,INHBA,SIX4,SPINK2,RTCB	down_VSAP_EC
GO:0009165	0.268	0.849	7	104	nucleotide biosynthetic process	BP	1	GPAM,ADCY6,ATP5MC1,ADK,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0055002	0.268	0.859	6	45	striated muscle cell development	BP	1	ACTN2,BMP4,NEBL,EDN1,BVES,MYOZ2	up_ACOR_VSMC
GO:0050767	0.268	0.855	6	184	regulation of neurogenesis	BP	1	IRX3,DLL1,PLXNA4,THRB,CAMK2A,KANK1	up_AFEM_EC
GO:0048771	0.268	0.88	4	43	tissue remodeling	BP	1	HIF1A,CTNNB1,TFRC,P3H4	down_VSAP_EC
GO:0045638	0.268	0.881	4	33	negative regulation of myeloid cell	BP	1	HOXB8,ITPKB,CUL4A,TJP2	up_VCAV_EC
GO:0043242	0.268	0.9	3	21	negative regulation of protein complex	BP	1	CAPG,LIMA1,ARHGEF2	down_ACOR_VSMC
GO:0042592	0.268	0.899	3	522	homeostatic process	BP	1	HOXA3,NR1H4,NEO1	up_VPUL_EC
GO:0002028	0.268	0.901	3	19	regulation of sodium ion transport	BP	1	OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0043550	0.268	0.923	2	21	regulation of lipid kinase activity	BP	1	PDGFRB,ENSCAFG00000014978	down_VCAV_EC
GO:0050688	0.268	0.923	2	20	regulation of defense response to virus	BP	1	RNF216,MAVS	down_VCAV_EC

GO:0021884	0.268	0.928	2	10	forebrain neuron development	BP	1	FGFR2,NRP1	up_ACOR_VSMC
GO:0051383	0.268	0.926	2	12	kinetochore organization	BP	1	CENPC,SENP6	up_VCAV_EC
GO:0014888	0.268	0.927	2	11	striated muscle adaptation	BP	1	MEF2C,PPP3CA	up_VCAV_EC
GO:0030324	0.268	0.962	1	64	lung development	BP	1	PDPN	down_ACOR_EC
GO:0070304	0.268	0.962	1	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	LYN	down_ACOR_EC
GO:0045981	0.268	0.967	1	6	positive regulation of nucleotide metabolic	BP	1	PARK7	down_VCAV_EC
GO:1900544	0.268	0.967	1	6	positive regulation of purine nucleotide	BP	1	PARK7	down_VCAV_EC
GO:1902231	0.268	0.967	1	6	positive regulation of intrinsic apoptotic signaling pathway in	BP	1	FBH1	down_VCAV_EC
GO:0009893	0.268	0.979	1	995	positive regulation of metabolic process	BP	1	GATA5	down_VFEM_VSMC
GO:0002827	0.268	0.968	1	5	positive regulation of T-helper 1 type immune	BP	1	SOCS5	down_VSAP_EC
GO:0002689	0.268	0.968	1	5	negative regulation of leukocyte chemotaxis	BP	1	MMP28	down_VSAP_EC
GO:0048313	0.268	0.968	1	5	Golgi inheritance	BP	1	PLK3	down_VSAP_EC
GO:1901626	0.268	0.968	1	5	regulation of postsynaptic membrane organization	BP	1	APOE	down_VSAP_EC
GO:1904925	0.268	0.968	1	5	positive regulation of autophagy of mitochondrion in	BP	1	CDC37	down_VSAP_EC
GO:0000098	0.268	0.973	1	3	sulfur amino acid catabolic process	BP	1	PCYOX1	up_ACOR_VSMC
GO:0046641	0.268	0.973	1	3	positive regulation of alpha-beta T cell	BP	1	PTPN22	up_ACOR_VSMC
GO:0070633	0.268	0.973	1	3	transepithelial transport	BP	1	ITPR1	up_ACOR_VSMC
GO:0007606	0.268	0.963	1	13	sensory perception of chemical stimulus	BP	1	REEP2	up_AFEM_EC
GO:0016242	0.268	0.963	1	13	negative regulation of macroautophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0017145	0.268	0.963	1	13	stem cell division	BP	1	LBH	up_AFEM_EC
GO:0001961	0.268	0.963	1	13	positive regulation of cytokine-mediated	BP	1	ADAM17	up_AFEM_EC
GO:0033687	0.268	0.963	1	13	osteoblast proliferation	BP	1	GREM1	up_AFEM_EC
GO:0038084	0.268	0.963	1	13	vascular endothelial growth factor signaling	BP	1	DLL1	up_AFEM_EC
GO:0060740	0.268	0.963	1	13	prostate gland epithelium morphogenesis	BP	1	TNC	up_AFEM_EC
GO:0072202	0.268	0.963	1	13	cell differentiation involved in metanephros	BP	1	GREM1	up_AFEM_EC
GO:0007276	0.268	0.963	1	130	gamete generation	BP	1	HOXA9	up_AORT_EC
GO:0048608	0.268	0.963	1	129	reproductive structure development	BP	1	HOXA9	up_AORT_EC
GO:0008202	0.268	0.962	1	80	steroid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0032886	0.268	0.962	1	81	regulation of microtubule-based process	BP	1	TUBB4A	up_APUL_EC
GO:0043434	0.268	0.962	1	80	response to peptide hormone	BP	1	NR1H4	up_APUL_EC
GO:0001675	0.268	0.97	1	4	acrosome assembly	BP	1	NECTIN2	up_VCAV_EC
GO:1905097	0.268	0.973	1	3	regulation of guanyl-nucleotide exchange	BP	1	STMN1	up_VCAV_EC
GO:0007498	0.268	0.962	1	38	mesoderm development	BP	1	ACVR2A	up_VPOR_EC
GO:0032092	0.268	0.962	1	38	positive regulation of protein binding	BP	1	HOXA3	up_VPOR_EC
GO:0048871	0.268	0.963	1	120	multicellular organismal homeostasis	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048812	0.268	0.963	1	151	neuron projection morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0000447	0.268	0.973	1	3	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-	BP	1	RCL1	up_VSAP_EC

GO:0000459	0.268	0.973	1	3	exonucleolytic trimming involved in rRNA	BP	1	EXOSC7	up_VSAP_EC
GO:0000467	0.268	0.973	1	3	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	EXOSC7	up_VSAP_EC
GO:0002138	0.268	0.973	1	3	retinoic acid biosynthetic process	BP	1	DHRS9	up_VSAP_EC
GO:0006152	0.268	0.973	1	3	purine nucleoside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0006706	0.268	0.973	1	3	steroid catabolic process	BP	1	HSD17B14	up_VSAP_EC
GO:0007271	0.268	0.973	1	3	synaptic transmission, cholinergic	BP	1	CHRM1	up_VSAP_EC
GO:0007603	0.268	0.973	1	3	phototransduction, visible light	BP	1	CHRM1	up_VSAP_EC
GO:0009240	0.268	0.973	1	3	isopentenyl diphosphate biosynthetic process	BP	1	MVK	up_VSAP_EC
GO:0009396	0.268	0.973	1	3	folic acid-containing compound biosynthetic	BP	1	ENSCAFG00000013986	up_VSAP_EC
GO:0010510	0.268	0.973	1	3	regulation of acetyl-CoA biosynthetic process from pyruvate	BP	1	PDK2	up_VSAP_EC
GO:0016078	0.268	0.973	1	3	tRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0016102	0.268	0.973	1	3	diterpenoid biosynthetic process	BP	1	DHRS9	up_VSAP_EC
GO:0016114	0.268	0.973	1	3	terpenoid biosynthetic process	BP	1	DHRS9	up_VSAP_EC
GO:0019287	0.268	0.973	1	3	isopentenyl diphosphate biosynthetic process, mevalonate pathway	BP	1	MVK	up_VSAP_EC
GO:0019323	0.268	0.973	1	3	pentose catabolic process	BP	1	DHDH	up_VSAP_EC
GO:0019388	0.268	0.973	1	3	galactose catabolic process	BP	1	GALK1	up_VSAP_EC
GO:0021978	0.268	0.973	1	3	telencephalon regionalization	BP	1	EMX2	up_VSAP_EC
GO:0031295	0.268	0.973	1	3	T cell costimulation	BP	1	CD274	up_VSAP_EC
GO:0031640	0.268	0.973	1	3	killing of cells of other organism	BP	1	F2RL1	up_VSAP_EC
GO:0032056	0.268	0.973	1	3	positive regulation of translation in response to	BP	1	NCK1	up_VSAP_EC
GO:0032511	0.268	0.973	1	3	late endosome to vacuole transport via multivesicular body	BP	1	VPS36	up_VSAP_EC
GO:0033129	0.268	0.973	1	3	positive regulation of histone phosphorylation	BP	1	CDK9	up_VSAP_EC
GO:0033216	0.268	0.973	1	3	ferric iron import	BP	1	STEAP3	up_VSAP_EC
GO:0034382	0.268	0.973	1	3	chylomicron remnant clearance	BP	1	LMF1	up_VSAP_EC
GO:0035025	0.268	0.973	1	3	positive regulation of Rho protein signal	BP	1	F2RL1	up_VSAP_EC
GO:0039533	0.268	0.973	1	3	regulation of MDA-5 signaling pathway	BP	1	TKFC	up_VSAP_EC
GO:0039534	0.268	0.973	1	3	negative regulation of MDA-5 signaling pathway	BP	1	TKFC	up_VSAP_EC
GO:0042220	0.268	0.973	1	3	response to cocaine	BP	1	ABAT	up_VSAP_EC
GO:0042430	0.268	0.973	1	3	indole-containing compound metabolic	BP	1	IDO2	up_VSAP_EC
GO:0042537	0.268	0.973	1	3	benzene-containing compound metabolic	BP	1	IDO2	up_VSAP_EC
GO:0042762	0.268	0.973	1	3	regulation of sulfur metabolic process	BP	1	PDK2	up_VSAP_EC
GO:0043328	0.268	0.973	1	3	protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular	BP	1	VPS36	up_VSAP_EC
GO:0043633	0.268	0.973	1	3	polyadenylation-dependent RNA catabolic	BP	1	EXOSC7	up_VSAP_EC
GO:0043634	0.268	0.973	1	3	polyadenylation-dependent ncRNA	BP	1	EXOSC7	up_VSAP_EC
GO:0044364	0.268	0.973	1	3	disruption of cells of other organism	BP	1	F2RL1	up_VSAP_EC

GO:0044857	0.268	0.973	1	3	plasma membrane raft organization	BP	1	FLOT1	up_VSAP_EC
GO:0045759	0.268	0.973	1	3	negative regulation of action potential	BP	1	KCNE3	up_VSAP_EC
GO:0046007	0.268	0.973	1	3	negative regulation of activated T cell	BP	1	CD274	up_VSAP_EC
GO:0046130	0.268	0.973	1	3	purine ribonucleoside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0046348	0.268	0.973	1	3	amino sugar catabolic process	BP	1	GNPDA1	up_VSAP_EC
GO:0046490	0.268	0.973	1	3	isopentenyl diphosphate metabolic process	BP	1	MVK	up_VSAP_EC
GO:0050812	0.268	0.973	1	3	regulation of acyl-CoA biosynthetic process	BP	1	PDK2	up_VSAP_EC
GO:0051004	0.268	0.973	1	3	regulation of lipoprotein lipase activity	BP	1	LMF1	up_VSAP_EC
GO:0051580	0.268	0.973	1	3	regulation of neurotransmitter uptake	BP	1	FLOT1	up_VSAP_EC
GO:0051955	0.268	0.973	1	3	regulation of amino acid transport	BP	1	OSR1	up_VSAP_EC
GO:0060028	0.268	0.973	1	3	convergent extension involved in axis elongation	BP	1	WNT11	up_VSAP_EC
GO:0060352	0.268	0.973	1	3	cell adhesion molecule production	BP	1	FLOT1	up_VSAP_EC
GO:0061101	0.268	0.973	1	3	neuroendocrine cell differentiation	BP	1	WNT11	up_VSAP_EC
GO:0070813	0.268	0.973	1	3	hydrogen sulfide metabolic process	BP	1	MPST	up_VSAP_EC
GO:0071029	0.268	0.973	1	3	nuclear ncRNA surveillance	BP	1	EXOSC7	up_VSAP_EC
GO:0071035	0.268	0.973	1	3	nuclear polyadenylation-dependent rRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0071038	0.268	0.973	1	3	nuclear polyadenylation-dependent tRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0071046	0.268	0.973	1	3	nuclear polyadenylation-dependent ncRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0071830	0.268	0.973	1	3	triglyceride-rich lipoprotein particle	BP	1	LMF1	up_VSAP_EC
GO:0072526	0.268	0.973	1	3	pyridine-containing compound catabolic	BP	1	PNP	up_VSAP_EC
GO:0090037	0.268	0.973	1	3	positive regulation of protein kinase C signaling	BP	1	WNT11	up_VSAP_EC
GO:0090503	0.268	0.973	1	3	RNA phosphodiester bond hydrolysis, exonucleolytic	BP	1	EXOSC7	up_VSAP_EC
GO:0097011	0.268	0.973	1	3	cellular response to granulocyte macrophage colony-stimulating factor	BP	1	ZFP36L2	up_VSAP_EC
GO:0097012	0.268	0.973	1	3	response to granulocyte macrophage colony-stimulating factor	BP	1	ZFP36L2	up_VSAP_EC
GO:0097283	0.268	0.973	1	3	keratinocyte apoptotic process	BP	1	ZFP36L1	up_VSAP_EC
GO:1902172	0.268	0.973	1	3	regulation of keratinocyte apoptotic process	BP	1	ZFP36L1	up_VSAP_EC
GO:1903044	0.268	0.973	1	3	protein localization to membrane raft	BP	1	FLOT1	up_VSAP_EC
GO:1903817	0.268	0.973	1	3	negative regulation of voltage-gated potassium	BP	1	KCNE3	up_VSAP_EC
GO:1903898	0.268	0.973	1	3	negative regulation of PERK-mediated unfolded protein response	BP	1	NCK1	up_VSAP_EC
GO:1904672	0.268	0.973	1	3	regulation of somatic stem cell population	BP	1	LBH	up_VSAP_EC
GO:2000271	0.268	0.973	1	3	positive regulation of fibroblast apoptotic	BP	1	BTG1	up_VSAP_EC
GO:2001269	0.268	0.973	1	3	positive regulation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	HTRA2	up_VSAP_EC
GO:0006107	0.268	0.973	1	3	oxaloacetate metabolic process	BP	1	GOT1	up_VSAP_EC
GO:0009435	0.268	0.973	1	3	NAD biosynthetic process	BP	1	PNP	up_VSAP_EC
GO:0019627	0.268	0.973	1	3	urea metabolic process	BP	1	ASS1	up_VSAP_EC
GO:0044854	0.268	0.973	1	3	plasma membrane raft assembly	BP	1	FLOT1	up_VSAP_EC

GO:0070571	0.268	0.973	1	3	negative regulation of neuron projection	BP	1	RTN4RL1	up_VSAP_EC
GO:0071609	0.268	0.973	1	3	chemokine (C-C motif) ligand 5 production	BP	1	MAVS	up_VSAP_EC
GO:0071649	0.268	0.973	1	3	regulation of chemokine (C-C motif) ligand 5	BP	1	MAVS	up_VSAP_EC
GO:0071895	0.268	0.973	1	3	odontoblast differentiation	BP	1	DLX3	up_VSAP_EC
GO:1903530	0.268172449	0.85539	6	165	regulation of secretion by cell	BP	1	NR1H4,KCNB1,FZD5,NOD2,PTGER4,MAVS	up_ACOR_EC
GO:0061458	0.268375405	0.86494	5	131	reproductive system development	BP	1	GATA4,SOX9,FZD5,LHX9,DLX3	up_ACOR_EC
GO:0040018	0.268510831	0.96367	1	11	positive regulation of multicellular organism	BP	1	PLS1	up_ACOR_EC
GO:0071705	0.26876489	0.80897	18	582	nitrogen compound transport	BP	1	SH3TC2,NR1H4,AQP1,KCNB1,EDEM2,FZD5,NOD2,PTGER4,PREB,SLC25A42,MAVS,CHMP4B,VPS16,ABCB9,AZIN2,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0010646	0.269	0.768	96	945	regulation of cell communication	BP	1	FZD1,SEZ6L,CDON,WNT11,HNF4A,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,SLC8B1,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,ABL1,HDAC7,EMP2,DLL1,EPN2,SESN1,MAP3K5,PDGFD,C1QTNF2,HPSE,ANKRD54,CCBE1,RECK,KLHL24,PLPP3,F2RL1,GLIS2,PDK2,MFN2,TRAF7,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,SULF2,SHOX2,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,PASK,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,KCNB1,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,PRMT2,FBLN1,IGFBP6,RAF1,MAPKBP1,CYBA,ZNF205,STX4,PSD4,KCNC4,QARS,ARHGAP12,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,HMOX1,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0051173	0.269	0.77	89	874	positive regulation of nitrogen compound metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,HOXA9,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PPARGC1B,IL6R,CRADD,HOXD3,CDH1,FGF7,ABL1,EMP2,DLL1,OSR1,MAP3K5,PDGFD,KLF15,C1QTNF2,ZBTB16,RARG,CCBE1,STAT6,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,ICE1,ZFP36L1,TRAF7,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,EEF2,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,PHF1,NPAS2,RNF166,RPUSD4,CDK9,PRMT2,OSBPL7,ZFP36L2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,EIF3D,ACVRL1,UBQLN2,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,SOAT1	up_VSAP_EC
GO:0043065	0.269	0.81	17	188	positive regulation of apoptotic process	BP	1	MAP3K11,MEF2C,ATF3,TNFAIP8,BMP2,PAK2,SH3GLB1,NCK1,RAPGEF2,BCL10,CTNNA1,HMGB1,PMAIP1,RIPK1,ITGA6,SKIL,ALDH1A3	up_VCAV_EC
GO:0006813	0.269	0.869	5	37	potassium ion transport	BP	1	ACTN2,KCNE3,AKAP6,KCNJ4,KCNC4	up_ACOR_VSMC
GO:0034620	0.269	0.868	5	38	cellular response to unfolded protein	BP	1	TM7SF3,HERPUD1,WFS1,DZIP3,STC2	up_ACOR_VSMC
GO:0048813	0.269	0.868	5	39	dendrite morphogenesis	BP	1	EPHB1,RELN,PPP3CA,PREX2,RAPGEF2	up_VCAV_EC
GO:0030518	0.269	0.879	4	42	intracellular steroid hormone receptor	BP	1	SMARCA4,UBA5,YWHAH,KDM3A	down_VSAP_EC
GO:0042476	0.269	0.896	3	36	odontogenesis	BP	1	BMPR1A,ASPN,GLI3	down_VCAV_EC
GO:0043500	0.269	0.899	3	21	muscle adaptation	BP	1	MEF2C,EDN1,PPP3CA	up_VCAV_EC
GO:0032526	0.269	0.9	3	19	response to retinoic acid	BP	1	OSR1,RARG,HTRA2	up_VSAP_EC
GO:0009890	0.269	0.897	3	420	negative regulation of biosynthetic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0010771	0.269	0.922	2	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	THY1,TLX2	down_VCAV_EC
GO:0070228	0.269	0.922	2	20	regulation of lymphocyte apoptotic process	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0051641	0.269	0.93	2	858	cellular localization	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0030101	0.269	0.926	2	12	natural killer cell activation	BP	1	RAB27A,ELF4	up_VCAV_EC

GO:0032647	0.269	0.928	2	10	regulation of interferon-alpha production	BP	1	TLR4,TLR3	up_VCAV_EC
GO:0034248	0.269	0.92	2	125	regulation of cellular amide metabolic process	BP	1	PUM3,EIF5	up_VPOR_EC
GO:0016482	0.269	0.962	1	63	cytosolic transport	BP	1	MYO1D	down_ACOR_EC
GO:0043371	0.269	0.966	1	6	negative regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0050996	0.269	0.966	1	6	positive regulation of lipid catabolic process	BP	1	AKT2	down_VCAV_EC
GO:0051444	0.269	0.966	1	6	negative regulation of ubiquitin-protein	BP	1	PARK7	down_VCAV_EC
GO:0060831	0.269	0.966	1	6	smoothened signaling pathway involved in dorsal/ventral neural tube	BP	1	GLI3	down_VCAV_EC
GO:0060841	0.269	0.966	1	6	venous blood vessel development	BP	1	SEMA3C	down_VCAV_EC
GO:0044248	0.269	0.973	1	691	cellular catabolic process	BP	1	USP12	down_VFEM_EC
GO:0040031	0.269	0.967	1	5	snRNA modification	BP	1	MRPL1	down_VSAP_EC
GO:0071971	0.269	0.967	1	5	extracellular exosome assembly	BP	1	SDC4	down_VSAP_EC
GO:1903551	0.269	0.967	1	5	regulation of extracellular exosome assembly	BP	1	SDC4	down_VSAP_EC
GO:0072075	0.269	0.967	1	5	metanephric mesenchyme	BP	1	SIX4	down_VSAP_EC
GO:0038189	0.269	0.973	1	3	neuropilin signaling pathway	BP	1	NRP1	up_ACOR_VSMC
GO:0045350	0.269	0.973	1	3	interferon-beta biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0045357	0.269	0.973	1	3	regulation of interferon-beta biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0060174	0.269	0.972	1	3	limb bud formation	BP	1	FGFR2	up_ACOR_VSMC
GO:0032720	0.269	0.963	1	13	negative regulation of tumor necrosis factor	BP	1	BPI	up_AFEM_EC
GO:0032873	0.269	0.963	1	13	negative regulation of stress-activated MAPK	BP	1	CYLD	up_AFEM_EC
GO:0045843	0.269	0.963	1	13	negative regulation of striated muscle tissue	BP	1	DLL1	up_AFEM_EC
GO:0060571	0.269	0.963	1	13	morphogenesis of an epithelial fold	BP	1	LUZP1	up_AFEM_EC
GO:0060972	0.269	0.963	1	13	left/right pattern formation	BP	1	DLL1	up_AFEM_EC
GO:0070229	0.269	0.963	1	13	negative regulation of lymphocyte apoptotic	BP	1	GPAM	up_AFEM_EC
GO:0070232	0.269	0.963	1	13	regulation of T cell apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0070303	0.269	0.963	1	13	negative regulation of stress-activated protein kinase signaling cascade	BP	1	CYLD	up_AFEM_EC
GO:0070528	0.269	0.963	1	13	protein kinase C signaling	BP	1	FIBIN	up_AFEM_EC
GO:1905209	0.269	0.963	1	13	positive regulation of cardiocyte differentiation	BP	1	GREM1	up_AFEM_EC
GO:0016055	0.269	0.962	1	134	Wnt signaling pathway	BP	1	DKK2	up_AORT_EC
GO:0198738	0.269	0.962	1	134	cell-cell signaling by wnt	BP	1	DKK2	up_AORT_EC
GO:0044092	0.269	0.965	1	270	negative regulation of molecular function	BP	1	ESR1	up_AORT_VSMC
GO:0032959	0.269	0.972	1	3	inositol trisphosphate biosynthetic process	BP	1	PLCG2	up_VCAV_EC
GO:0034499	0.269	0.972	1	3	late endosome to Golgi transport	BP	1	GCC2	up_VCAV_EC
GO:0050910	0.269	0.972	1	3	detection of mechanical stimulus involved in sensory perception of	BP	1	KIT	up_VCAV_EC
GO:0097343	0.269	0.972	1	3	ripoptosome assembly	BP	1	RIPK1	up_VCAV_EC
GO:1901026	0.269	0.972	1	3	ripoptosome assembly involved in necroptotic	BP	1	RIPK1	up_VCAV_EC
GO:1900748	0.269	0.973	1	3	positive regulation of vascular endothelial growth factor signaling	BP	1	JCAD	up_VCAV_EC

GO:1901030	0.269	0.969	1	4	positive regulation of mitochondrial outer membrane permeabilization involved	BP	1	SH3GLB1	up_VCAV_EC
GO:0032640	0.269	0.962	1	39	tumor necrosis factor production	BP	1	ARHGEF2	up_VPOR_EC
GO:0072524	0.269	0.962	1	37	pyridine-containing compound metabolic	BP	1	FBP1	up_VPOR_EC
GO:0060541	0.269	0.962	1	73	respiratory system development	BP	1	SIX1	up_VFEM_EC
GO:0016049	0.269	0.962	1	124	cell growth	BP	1	FBP1	up_VFEM_VSMC
GO:0051056	0.269	0.962	1	87	regulation of small GTPase mediated signal	BP	1	ARHGEF2	up_VPUL_EC
GO:0061138	0.269	0.962	1	73	morphogenesis of a branching epithelium	BP	1	HOXA11	up_VSAP_VSMC
GO:0006810	0.27	0.764	125	1244	transport	BP	1	EXPH5,SH3TC2,FGF13,RHOT1,TLR1,DNAJC6,ACTN2,PLCG2,LEP,SLC26A7,KCNE3,CDC7,HTR2B,TCAF1,USP6NL,MBP,FBXL20,FERMT1,BMP4,SYT16,LCAT,TPC3,EVI5L,TM7SF3,ABCA1,GJA1,SCARB2,SEC24B,ATXN2,CD274,NIPAL3,SARAF,SLC2A5,STX11,GPR155,PTPN3,TMEM108,CLCN3,MICU2,IFT43,ITPR1,KLHL20,ANKRD1,F2RL1,HRH2,DAPK1,APOL6,BNIP3,SLC17A5,CACNB3,AKAP6,CDKN1A,LRRC8C,ABCA4,NRP1,PTPN22,LRPAP1,DMPK,TCN2,OS9,ATP7A,SCP2,KCNJ4,OSBPL1A,SLCO1A2,PRKCE,MYO1B,SCG5,APP,PSEN1,PCSK6,SGSM2,SYNJ2BP,CHD7,PIK3C3,MFSD9,LAMP2,JUP,CCL5,CLN8,ENSCAFG00000001846,ATP6V0E1,RAB11B,EDN1,DYNC1I2,SLC25A20,GTF2A1L,AKTIP,KCNC4,NOD2,LMTK2,B2M,AP2B1,PLIN2,FXYD1,SCAMP5,SCRN2,SAR1B,HERPUD1,TXNDC5,CFI,SUN1,VPS26A,INPP5K,FAF2,RAB5C,PREPL,PFKL,WFS1,AZIN2,RPAIN,ATP2C1,SLC25A12,NDUFA4L2,NAIF1,DYNC1I1,PARK7,SLC8A1,SLC2A12,STC2,ENSCAFG00000013536,BVES,LMF1,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0019439	0.27	0.81	17	150	aromatic compound catabolic process	BP	1	AXIN2,GDA,TENT5C,EXOSC7,PYM1,DFFB,ZFP36L1,GALK1,ENTPD3,SMG9,SAMD4B,ZFP36L2,PNP,TNRC6C,HMOX1,DDIT4,IDO2	up_VSAP_EC
GO:0120035	0.27	0.83	10	160	regulation of plasma membrane bounded cell projection organization	BP	1	PRNP,TRPV2,THY1,TLX2,UST,PRKCSH,EVI5L,RAC2,RGMA,BRSK1	down_VCAV_EC
GO:0050657	0.27	0.857	6	51	nucleic acid transport	BP	1	DDX39A,RAN,NUP62,NUP188,DDX39B,MRPL18	down_ACOR_VSMC
GO:0050658	0.27	0.857	6	51	RNA transport	BP	1	DDX39A,RAN,NUP62,NUP188,DDX39B,MRPL18	down_ACOR_VSMC
GO:0051236	0.27	0.857	6	51	establishment of RNA localization	BP	1	DDX39A,RAN,NUP62,NUP188,DDX39B,MRPL18	down_ACOR_VSMC
GO:0021761	0.27	0.881	4	27	limbic system development	BP	1	FGF13,FGFR2,TMEM108,NRP1	up_ACOR_VSMC
GO:0008219	0.27	0.881	4	611	cell death	BP	1	EYA1,MAP2K6,SIX1,CYP26B1	up_VFEM_EC
GO:0009892	0.27	0.902	3	835	negative regulation of metabolic process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0002028	0.27	0.899	3	19	regulation of sodium ion transport	BP	1	PTPN3,DMPK,FXYD1	up_ACOR_VSMC
GO:0009308	0.27	0.922	2	20	amine metabolic process	BP	1	PARK7,NAPEPLD	down_VCAV_EC
GO:0010648	0.27	0.922	2	407	negative regulation of cell communication	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0030323	0.27	0.961	1	65	respiratory tube development	BP	1	PDPN	down_ACOR_EC
GO:0000727	0.27	0.969	1	4	double-strand break repair via break-induced	BP	1	GINS4	down_ACOR_VSMC
GO:2001046	0.27	0.969	1	4	positive regulation of integrin-mediated	BP	1	EMP2	down_ACOR_VSMC
GO:0007015	0.27	0.962	1	144	actin filament organization	BP	1	FSCN1	down_AFEM_EC
GO:1901576	0.27	1	1	1877	organic substance biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0009143	0.27	0.966	1	6	nucleoside triphosphate catabolic process	BP	1	ENTPD3	down_VCAV_EC
GO:0032890	0.27	0.966	1	6	regulation of organic acid transport	BP	1	AKT2	down_VCAV_EC
GO:0048484	0.27	0.966	1	6	enteric nervous system development	BP	1	TLX2	down_VCAV_EC

GO:0071549	0.27	0.966	1	6	cellular response to dexamethasone stimulus	BP	1	NR3C1	down_VCAV_EC
GO:0006596	0.27	0.972	1	3	polyamine biosynthetic process	BP	1	AZIN2	up_ACOR_VSMC
GO:0009446	0.27	0.972	1	3	putrescine biosynthetic process	BP	1	AZIN2	up_ACOR_VSMC
GO:0033387	0.27	0.972	1	3	putrescine biosynthetic process from ornithine	BP	1	AZIN2	up_ACOR_VSMC
GO:0036500	0.27	0.972	1	3	ATF6-mediated unfolded protein response	BP	1	WFS1	up_ACOR_VSMC
GO:0071947	0.27	0.972	1	3	protein deubiquitination involved in ubiquitin-dependent protein	BP	1	ZRANB1	up_ACOR_VSMC
GO:1990523	0.27	0.972	1	3	bone regeneration	BP	1	LGR6	up_ACOR_VSMC
GO:0009649	0.27	0.963	1	13	entrainment of circadian clock	BP	1	CRY2	up_AFEM_EC
GO:0071675	0.27	0.963	1	13	regulation of mononuclear cell	BP	1	CMKLR1	up_AFEM_EC
GO:0006875	0.27	0.962	1	129	cellular metal ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0048534	0.27	0.965	1	262	hematopoietic or lymphoid organ	BP	1	HOXA9	up_AORT_VSMC
GO:0016042	0.27	0.962	1	80	lipid catabolic process	BP	1	PLCL1	up_APUL_EC
GO:0048638	0.27	0.961	1	82	regulation of developmental growth	BP	1	TBX5	up_APUL_EC
GO:0022604	0.27	0.962	1	122	regulation of cell morphogenesis	BP	1	BAMBI	up_VPOR_VSMC
GO:0060562	0.27	0.962	1	120	epithelial tube morphogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0061564	0.27	0.962	1	119	axon development	BP	1	CHL1	up_VPOR_VSMC
GO:0034762	0.27	0.962	1	122	regulation of transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0120031	0.27	0.963	1	154	plasma membrane bounded cell projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0051099	0.27	0.961	1	70	positive regulation of binding	BP	1	CAV1	up_VSAP_VSMC
GO:0071560	0.27	0.962	1	72	cellular response to transforming growth	BP	1	CAV1	up_VSAP_VSMC
GO:0090092	0.27	0.961	1	72	regulation of transmembrane receptor protein serine/threonine	BP	1	CAV1	up_VSAP_VSMC
GO:0030514	0.27012121	0.96293	1	12	negative regulation of BMP signaling pathway	BP	1	SMAD6	up_ACOR_EC
GO:0010634	0.270258067	0.89374	3	68	positive regulation of epithelial cell migration	BP	1	SOX9,FOXC2,NRP1	up_ACOR_EC
GO:0001523	0.270309493	0.96287	1	12	retinoid metabolic process	BP	1	RARRES2	up_ACOR_EC
GO:0090189	0.270368939	0.96286	1	12	regulation of branching involved in ureteric bud	BP	1	SOX9	up_ACOR_EC
GO:0006913	0.271	0.819	13	124	nucleocytoplasmic transport	BP	1	DDX39A,NEDD4,POLA2,HSPA9,RAN,AAAS,ENSCAFG00000011598,IPO4,NUP62,NUP188,DMAP1,DDX39B,RBM14	down_ACOR_VSMC
GO:0051169	0.271	0.819	13	124	nuclear transport	BP	1	DDX39A,NEDD4,POLA2,HSPA9,RAN,AAAS,ENSCAFG00000011598,IPO4,NUP62,NUP188,DMAP1,DDX39B,RBM14	down_ACOR_VSMC
GO:0046486	0.271	0.823	12	102	glycerolipid metabolic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,PIGN,PIGS,PIGG,CRLS1,SERINC3,SERINC1,INPP5K,LMF1	up_ACOR_VSMC
GO:0006897	0.271	0.829	10	158	endocytosis	BP	1	SNX18,LRP1,CLIP3,ANXA11,LRPAP1,CLTB,CYBA,RAB31,GREM1,PACSIN3	down_VCAV_EC
GO:0032535	0.271	0.83	10	128	regulation of cellular component size	BP	1	LRRC8A,IFRD1,WDR1,MSN,ACTR3,TWF1,PLEKHG2,CLCN3,CAPG,NRP1	down_VSAP_EC
GO:0062012	0.271	0.83	10	100	regulation of small molecule metabolic	BP	1	CDA,PDGFB,FAM3C,BMP2,PROX1,ENSCAFG00000010596,PTGS2,NOS2,PMAIP1,HIF1A	up_VCAV_EC
GO:0009141	0.271	0.84	8	110	nucleoside triphosphate metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5,CMPK1	down_VSAP_EC
GO:0009888	0.271	0.856	6	545	tissue development	BP	1	BARX1,PTK7,HOXA3,SEMA3A,ASPN,ACVR2A	up_VPOR_EC
GO:0048863	0.271	0.864	5	70	stem cell differentiation	BP	1	BMPR1A,SEMA3C,A2M,RDH10,GREM1	down_VCAV_EC
GO:0071901	0.271	0.867	5	37	negative regulation of protein serine/threonine	BP	1	BMP4,LATS2,CDKN1A,SMPD1,INPP5K	up_ACOR_VSMC
GO:0006334	0.271	0.866	5	45	nucleosome assembly	BP	1	NASP,HIST1H1A,ASF1A,ATRX,HP1BP3	up_VCAV_EC
GO:0015850	0.271	0.867	5	37	organic hydroxy compound transport	BP	1	LIPC,SLC6A4,ABCB11,LCAT,SOAT1	up_VSAP_EC
GO:0051100	0.271	0.877	4	53	negative regulation of binding	BP	1	CLSTN1,LRPAP1,PARK7,FBH1	down_VCAV_EC

GO:1903555	0.271	0.895	3	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	BPI,CYBA,MAVS	down_VCAV_EC
GO:2000144	0.271	0.925	2	12	positive regulation of DNA-templated transcription,	BP	1	FOSL1,PSMC1	down_ACOR_VSMC
GO:0045595	0.271	0.923	2	469	regulation of cell differentiation	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0014812	0.271	0.921	2	21	muscle cell migration	BP	1	PDGFRB,BMPR1A	down_VCAV_EC
GO:0043069	0.271	0.92	2	262	negative regulation of programmed cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0007186	0.271	0.919	2	124	G protein-coupled receptor signaling	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:1901137	0.271	0.92	2	232	carbohydrate derivative biosynthetic process	BP	1	ADCY3,CHST7	up_VFEM_EC
GO:0040011	0.271	0.923	2	505	locomotion	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0051057	0.271	0.926	2	11	positive regulation of small GTPase mediated signal transduction	BP	1	CDON,F2RL1	up_VSAP_EC
GO:0043583	0.271	0.961	1	59	ear development	BP	1	HOXA1	down_ACOR_EC
GO:0006882	0.271	0.966	1	6	cellular zinc ion homeostasis	BP	1	SLC39A6	down_VCAV_EC
GO:0045061	0.271	0.966	1	6	thymic T cell selection	BP	1	GLI3	down_VCAV_EC
GO:0048679	0.271	0.966	1	6	regulation of axon regeneration	BP	1	RGMA	down_VCAV_EC
GO:0055069	0.271	0.966	1	6	zinc ion homeostasis	BP	1	SLC39A6	down_VCAV_EC
GO:0085029	0.271	0.966	1	6	extracellular matrix assembly	BP	1	LOX	down_VCAV_EC
GO:0098869	0.271	0.966	1	6	cellular oxidant detoxification	BP	1	PARK7	down_VCAV_EC
GO:0035641	0.271	0.967	1	5	locomotory exploration behavior	BP	1	APOE	down_VSAP_EC
GO:0034375	0.271	0.967	1	5	high-density lipoprotein particle remodeling	BP	1	APOE	down_VSAP_EC
GO:0060644	0.271	0.967	1	5	mammary gland epithelial cell differentiation	BP	1	HIF1A	down_VSAP_EC
GO:0042535	0.271	0.972	1	3	positive regulation of tumor necrosis factor biosynthetic process	BP	1	TLR1	up_ACOR_VSMC
GO:0045141	0.271	0.972	1	3	meiotic telomere clustering	BP	1	SUN1	up_ACOR_VSMC
GO:0051386	0.271	0.972	1	3	regulation of neurotrophin TRK	BP	1	TMEM108	up_ACOR_VSMC
GO:0090220	0.271	0.972	1	3	chromosome localization to nuclear envelope involved in homologous chromosome segregation	BP	1	SUN1	up_ACOR_VSMC
GO:2000465	0.271	0.972	1	3	regulation of glycogen (starch) synthase activity	BP	1	INPP5K	up_ACOR_VSMC
GO:0007250	0.271	0.972	1	3	activation of NF-kappaB-inducing kinase activity	BP	1	MAP3K7	up_ACOR_VSMC
GO:0099010	0.271	0.972	1	3	modification of postsynaptic structure	BP	1	WASF3	up_ACOR_VSMC
GO:0031341	0.271	0.963	1	13	regulation of cell killing	BP	1	LEP	up_AFEM_EC
GO:0061217	0.271	0.963	1	13	regulation of mesonephros	BP	1	GREM1	up_AFEM_EC
GO:0097734	0.271	0.962	1	13	extracellular exosome biogenesis	BP	1	RAB7A	up_AFEM_EC
GO:1990182	0.271	0.962	1	13	exosomal secretion	BP	1	RAB7A	up_AFEM_EC
GO:0097190	0.271	0.963	1	217	apoptotic signaling pathway	BP	1	EYA1	up_AFEM_VSMC
GO:0061458	0.271	0.962	1	131	reproductive system development	BP	1	HOXA9	up_AORT_EC
GO:0060341	0.271	0.964	1	255	regulation of cellular localization	BP	1	WNT7A	up_AORT_VSMC
GO:0051056	0.271	0.961	1	87	regulation of small GTPase mediated signal	BP	1	ARHGEF26	up_APUL_EC
GO:0006686	0.271	0.969	1	4	sphingomyelin biosynthetic process	BP	1	SPTLC2	up_VCAV_EC
GO:0043970	0.271	0.969	1	4	histone H3-K9 acetylation	BP	1	GATA3	up_VCAV_EC
GO:0071871	0.271	0.972	1	3	response to epinephrine	BP	1	PDE4D	up_VCAV_EC

GO:0071872	0.271	0.972	1	3	cellular response to epinephrine stimulus	BP	1	PDE4D	up_VCAV_EC
GO:2000615	0.271	0.969	1	4	regulation of histone H3-K9 acetylation	BP	1	GATA3	up_VCAV_EC
GO:0008212	0.271	0.972	1	3	mineralocorticoid metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0010172	0.271	0.972	1	3	embryonic body morphogenesis	BP	1	CDON	up_VCAV_EC
GO:0019896	0.271	0.972	1	3	axonal transport of mitochondrion	BP	1	HIF1A	up_VCAV_EC
GO:0030252	0.271	0.972	1	3	growth hormone secretion	BP	1	CHD7	up_VCAV_EC
GO:0032341	0.271	0.972	1	3	aldosterone metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0032344	0.271	0.972	1	3	regulation of aldosterone metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0043624	0.271	0.961	1	39	cellular protein complex disassembly	BP	1	ARHGEF2	up_VPOR_EC
GO:2001234	0.271	0.961	1	75	negative regulation of apoptotic signaling	BP	1	EYA1	up_VFEM_EC
GO:0070371	0.271	0.961	1	91	ERK1 and ERK2 cascade	BP	1	CCL24	up_VPUL_EC
GO:0030031	0.271	0.962	1	155	cell projection assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0035115	0.271168458	0.96262	1	12	embryonic forelimb morphogenesis	BP	1	TBX5	up_ACOR_EC
GO:2000058	0.271533671	0.89299	3	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	PIAS1,CLU,RNF114	up_ACOR_EC
GO:0060669	0.271619172	0.96249	1	12	embryonic placenta morphogenesis	BP	1	FZD5	up_ACOR_EC
GO:0050877	0.271721236	0.85287	6	164	nervous system process	BP	1	BRSK1,AQP1,PDE4A,INSYN1,USP53,MAPK8IP2	up_ACOR_EC
GO:0071985	0.271794948	0.96244	1	12	multivesicular body sorting pathway	BP	1	ABCB9	up_ACOR_EC
GO:0060260	0.271811599	0.96243	1	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	CLSTN1	up_ACOR_EC
GO:0012501	0.272	0.778	49	561	programmed cell death	BP	1	PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,MAP3K11,STK10,MEF2C,ATF3,GATA3,TNFAIP8,FIGNL1,PELI1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,ENSCAFG00000010596,MADD,PAK2,THOC1,SH3GLB1,TLR3,NCK1,CASP10,EXOC5,PTGS2,RAPGEF2,ENSCAFG00000005099,PLCG2,BCL10,USP28,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ATP2A1,ARHGEF2	up_VCAV_EC
GO:0046907	0.272	0.79	30	536	intracellular transport	BP	1	SNX18,PRNP,TMEM230,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,MICALL2,SNUPN,SSR2,SCP2,CLTB,SSR3,PEX5,GLI3,PARK7,YIF1A,IFT57,MAVS,TOM1,MGARP,RAB7B,SEC61B,HM13,ARHGAP1,EVI5L,LONP2,RAC2,ANKRD54,SEC61A1	down_VCAV_EC
GO:0051338	0.272	0.808	17	288	regulation of transferase activity	BP	1	PDGFRB,DCN,PRNP,BGN,LMO4,ENSCAFG00000014978,AKT1S1,CSPG4,ASPN,THY1,PARK7,SASH1,SPRED1,MAPRE3,DDR2,SHC1,GREM1	down_VCAV_EC
GO:0071216	0.272	0.848	7	61	cellular response to biotic stimulus	BP	1	IRAK1,SMC1A,MTDH,PPP1R15B,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0007179	0.272	0.864	5	57	transforming growth factor beta receptor	BP	1	HSPA5,SNX25,TGFBR1,ADAM17,STRAP	down_VSAP_EC
GO:0002768	0.272	0.866	5	37	immune response-regulating cell surface receptor signaling	BP	1	PLCG2,ELF1,PTPN22,PSEN1,DUSP22	up_ACOR_VSMC
GO:0051253	0.272	0.894	3	359	negative regulation of RNA metabolic process	BP	1	HOXA7,ELK3,NEDD4	down_ACOR_EC
GO:0009653	0.272	0.9	3	773	anatomical structure morphogenesis	BP	1	HOXC10,HOXA9,DUSP2	up_AORT_EC
GO:0038066	0.272	0.898	3	19	p38MAPK cascade	BP	1	MAP3K5,ZFP36L1,SASH1	up_VSAP_EC
GO:0034661	0.272	0.924	2	12	ncRNA catabolic process	BP	1	DIS3,EXOSC5	down_ACOR_VSMC
GO:0006023	0.272	0.922	2	17	aminoglycan biosynthetic process	BP	1	CHSY1,EXT1	down_VSAP_EC
GO:0048641	0.272	0.922	2	16	regulation of skeletal muscle tissue	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0048771	0.272	0.919	2	43	tissue remodeling	BP	1	LEP,GREM1	up_AFEM_EC

GO:1901698	0.272	0.92	2	266	response to nitrogen compound	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0098659	0.272	0.924	2	13	inorganic cation import across plasma membrane	BP	1	SLC39A8,KCNJ3	up_VCAV_EC
GO:0099587	0.272	0.924	2	13	inorganic ion import across plasma membrane	BP	1	SLC39A8,KCNJ3	up_VCAV_EC
GO:0010639	0.272	0.918	2	128	negative regulation of organelle organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0023057	0.272	0.922	2	409	negative regulation of signaling	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0006415	0.272	0.968	1	4	translational termination	BP	1	EIF5A	down_ACOR_VSMC
GO:0032787	0.272	0.962	1	144	monocarboxylic acid metabolic process	BP	1	ETFA	down_AFEM_EC
GO:0071417	0.272	0.962	1	142	cellular response to organonitrogen	BP	1	GABPA	down_AFEM_EC
GO:0010984	0.272	0.965	1	6	regulation of lipoprotein particle clearance	BP	1	LRPAP1	down_VCAV_EC
GO:0015844	0.272	0.965	1	6	monoamine transport	BP	1	PARK7	down_VCAV_EC
GO:0034143	0.272	0.966	1	6	regulation of toll-like receptor 4 signaling	BP	1	RAB7B	down_VCAV_EC
GO:0034497	0.272	0.965	1	6	protein localization to phagophore assembly site	BP	1	WDR45	down_VCAV_EC
GO:0043496	0.272	0.965	1	6	regulation of protein homodimerization activity	BP	1	PARK7	down_VCAV_EC
GO:0097286	0.272	0.965	1	6	iron ion import	BP	1	ARHGAP1	down_VCAV_EC
GO:1901071	0.272	0.965	1	6	glucosamine-containing compound metabolic	BP	1	CHID1	down_VCAV_EC
GO:1905214	0.272	0.965	1	6	regulation of RNA binding	BP	1	LARP6	down_VCAV_EC
GO:1905216	0.272	0.965	1	6	positive regulation of RNA binding	BP	1	LARP6	down_VCAV_EC
GO:0030539	0.272	0.967	1	5	male genitalia development	BP	1	CTNNB1	down_VSAP_EC
GO:0045217	0.272	0.972	1	3	cell-cell junction maintenance	BP	1	F2RL1	up_ACOR_VSMC
GO:0048014	0.272	0.972	1	3	Tie signaling pathway	BP	1	ANGPT1	up_ACOR_VSMC
GO:0060013	0.272	0.972	1	3	righting reflex	BP	1	GLRB	up_ACOR_VSMC
GO:0060052	0.272	0.972	1	3	neurofilament cytoskeleton organization	BP	1	CLN8	up_ACOR_VSMC
GO:0071622	0.272	0.962	1	13	regulation of granulocyte chemotaxis	BP	1	CMKLR1	up_AFEM_EC
GO:0043207	0.272	0.963	1	216	response to external biotic stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0051707	0.272	0.963	1	216	response to other organism	BP	1	TLR2	up_AFEM_VSMC
GO:0072358	0.272	0.964	1	268	cardiovascular system development	BP	1	WNT7A	up_AORT_VSMC
GO:0002764	0.272	0.961	1	80	immune response-regulating signaling	BP	1	NR1H4	up_APUL_EC
GO:0015711	0.272	0.961	1	81	organic anion transport	BP	1	NTRK2	up_APUL_EC
GO:0052548	0.272	0.961	1	80	regulation of endopeptidase activity	BP	1	PCSK1N	up_APUL_EC
GO:0044093	0.272	0.967	1	437	positive regulation of molecular function	BP	1	HOXA3	up_APUL_VSMC
GO:0002903	0.272	0.968	1	4	negative regulation of B cell apoptotic process	BP	1	BCL10	up_VCAV_EC
GO:0019367	0.272	0.967	1	5	fatty acid elongation, saturated fatty acid	BP	1	ELOVL7	up_VCAV_EC
GO:0019368	0.272	0.967	1	5	fatty acid elongation, unsaturated fatty acid	BP	1	ELOVL7	up_VCAV_EC
GO:0034626	0.272	0.967	1	5	fatty acid elongation, polyunsaturated fatty acid	BP	1	ELOVL7	up_VCAV_EC
GO:0035338	0.272	0.967	1	5	long-chain fatty-acyl-CoA biosynthetic process	BP	1	ELOVL7	up_VCAV_EC
GO:0090073	0.272	0.968	1	4	positive regulation of protein homodimerization	BP	1	MEF2C	up_VCAV_EC
GO:0034092	0.272	0.972	1	3	negative regulation of maintenance of sister chromatid cohesion	BP	1	ATRX	up_VCAV_EC
GO:0034183	0.272	0.972	1	3	negative regulation of maintenance of mitotic sister chromatid cohesion	BP	1	ATRX	up_VCAV_EC
GO:0034625	0.272	0.967	1	5	fatty acid elongation, monounsaturated fatty	BP	1	ELOVL7	up_VCAV_EC

GO:0045875	0.272	0.972	1	3	negative regulation of sister chromatid cohesion	BP	1	ATRX	up_VCAV_EC
GO:1902170	0.272	0.972	1	3	cellular response to reactive nitrogen species	BP	1	GUCY1B1	up_VCAV_EC
GO:0022412	0.272	0.961	1	76	cellular process involved in reproduction in multicellular organism	BP	1	CYP26B1	up_VFEM_EC
GO:0050878	0.272	0.961	1	75	regulation of body fluid levels	BP	1	CYP26B1	up_VFEM_EC
GO:0021987	0.27216886	0.91886	2	37	cerebral cortex development	BP	1	DIXDC1,NRP1	up_ACOR_EC
GO:0060674	0.272170162	0.96233	1	12	placenta blood vessel development	BP	1	FZD5	up_ACOR_EC
GO:0071384	0.27224408	0.96231	1	12	cellular response to corticosteroid stimulus	BP	1	AQP1	up_ACOR_EC
GO:0071385	0.27224408	0.96231	1	12	cellular response to glucocorticoid stimulus	BP	1	AQP1	up_ACOR_EC
GO:0032768	0.272783493	0.96215	1	12	regulation of monooxygenase activity	BP	1	CDH3	up_ACOR_EC
GO:0045444	0.273	0.83	10	84	fat cell differentiation	BP	1	SMAD6,LEP,FNDC5,PPARGC1A,PLAC8B,BNIP3,LRRC8C,CCDC3,DKKL1,ARID5B	up_ACOR_VSMC
GO:0043900	0.273	0.845	7	104	regulation of multi-organism process	BP	1	SYDE1,TRIM8,RNF216,B4GALT1,SASH1,CYBA,MAVS	down_VCAV_EC
GO:0050657	0.273	0.855	6	51	nucleic acid transport	BP	1	IWS1,QKI,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0050658	0.273	0.855	6	51	RNA transport	BP	1	IWS1,QKI,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0051236	0.273	0.855	6	51	establishment of RNA localization	BP	1	IWS1,QKI,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0035265	0.273	0.876	4	54	organ growth	BP	1	THBS3,BMPR1A,EVC,DDR2	down_VCAV_EC
GO:0046173	0.273	0.898	3	19	polyol biosynthetic process	BP	1	GOT1,PPIP5K1,PCBD1	up_VSAP_EC
GO:0002444	0.273	0.921	2	18	myeloid leukocyte mediated immunity	BP	1	WDR1,LYN	down_VSAP_EC
GO:0110111	0.273	0.921	2	17	negative regulation of animal organ	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0034341	0.273	0.918	2	43	response to interferon-gamma	BP	1	RAB20,CCL5	up_AFEM_EC
GO:0042098	0.273	0.918	2	43	T cell proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0097696	0.273	0.918	2	43	STAT cascade	BP	1	LEP,LRRC15	up_AFEM_EC
GO:0009966	0.273	0.929	2	868	regulation of signal transduction	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0007628	0.273	0.925	2	11	adult walking behavior	BP	1	CHD7,SPTBN4	up_VCAV_EC
GO:0031327	0.273	0.921	2	412	negative regulation of cellular biosynthetic	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:0009607	0.273	0.919	2	232	response to biotic stimulus	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0071216	0.273	0.961	1	61	cellular response to biotic stimulus	BP	1	LYN	down_ACOR_EC
GO:0046070	0.273	0.968	1	4	dGTP metabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0060394	0.273	0.965	1	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	GREM1	down_VCAV_EC
GO:0002715	0.273	0.966	1	5	regulation of natural killer cell mediated immunity	BP	1	PVR	down_VSAP_EC
GO:0042269	0.273	0.966	1	5	regulation of natural killer cell mediated cytotoxicity	BP	1	PVR	down_VSAP_EC
GO:0060122	0.273	0.966	1	5	inner ear receptor cell stereocilium organization	BP	1	SDC4	down_VSAP_EC
GO:0071677	0.273	0.966	1	5	positive regulation of mononuclear cell	BP	1	SERPINE1	down_VSAP_EC
GO:0090026	0.273	0.966	1	5	positive regulation of monocyte chemotaxis	BP	1	SERPINE1	down_VSAP_EC
GO:0030728	0.273	0.966	1	5	ovulation	BP	1	INHBA	down_VSAP_EC
GO:0021869	0.273	0.972	1	3	forebrain ventricular zone progenitor cell division	BP	1	FGFR2	up_ACOR_VSMC
GO:0060385	0.273	0.972	1	3	axonogenesis involved in innervation	BP	1	NRP1	up_ACOR_VSMC
GO:2000121	0.273	0.972	1	3	regulation of removal of superoxide radicals	BP	1	PARK7	up_ACOR_VSMC
GO:0043604	0.273	0.964	1	288	amide biosynthetic process	BP	1	ARG2	up_AORT_VSMC
GO:0010842	0.273	0.968	1	4	retina layer formation	BP	1	TSPAN12	up_VCAV_EC

GO:0002029	0.273	0.968	1	4	desensitization of G protein-coupled receptor signaling pathway	BP	1	APLNR	up_VCAV_EC
GO:0002717	0.273	0.968	1	4	positive regulation of natural killer cell	BP	1	NECTIN2	up_VCAV_EC
GO:0022401	0.273	0.968	1	4	negative adaptation of signaling pathway	BP	1	APLNR	up_VCAV_EC
GO:0045954	0.273	0.968	1	4	positive regulation of natural killer cell	BP	1	NECTIN2	up_VCAV_EC
GO:1903897	0.273	0.966	1	5	regulation of PERK-mediated unfolded	BP	1	NCK1	up_VCAV_EC
GO:0051896	0.273	0.96	1	39	regulation of protein kinase B signaling	BP	1	MTDH	up_VPOR_EC
GO:0055123	0.273	0.96	1	40	digestive system development	BP	1	BARX1	up_VPOR_EC
GO:1901615	0.273	0.961	1	128	organic hydroxy compound metabolic	BP	1	CYP26B1	up_VPOR_VSMC
GO:0090287	0.273	0.961	1	91	regulation of cellular response to growth factor	BP	1	NEO1	up_VPUL_EC
GO:0031346	0.273	0.961	1	73	positive regulation of cell projection organization	BP	1	SHOX2	up_VSAP_VSMC
GO:0072079	0.273444148	0.96195	1	12	nephron tubule formation	BP	1	SOX9	up_ACOR_EC
GO:0050819	0.273952682	0.9618	1	12	negative regulation of coagulation	BP	1	PRKCD	up_ACOR_EC
GO:0097205	0.273975451	0.9618	1	12	renal filtration	BP	1	AQP1	up_ACOR_EC
GO:0006082	0.274	0.789	29	305	organic acid metabolic process	BP	1	SCD,SREBF1,ACLY,ENSCAFG00000016095,BCAT1,VARS,INSIG1,CAV1,XYLT1,PFAS,ARG2,BRCA1,ELOVL1,FARSA,SUCLG1,PPARD,AADAT,GSTO1,ELOVL6,SGPL1,RARS,PRPS1,CTH,PDHA1,GGH,LIPC,PGD,CTPS1,ACADL	down_ACOR_VSMC
GO:0007420	0.274	0.816	13	169	brain development	BP	1	HSPA5,PTPN11,AARS,HOOK3,HIF1A,UBA6,UCHL5,CTNNB1,GSK3B,EXT1,DISC1,INHBA,NRP1	down_VSAP_EC
GO:0007600	0.274	0.834	9	73	sensory perception	BP	1	MBP,COCH,GLRB,USP53,ABCA4,POMK,CHD7,CLN8,WFS1	up_ACOR_VSMC
GO:0071248	0.274	0.877	4	35	cellular response to metal ion	BP	1	MEF2C,TJP1,ITPKB,CREB1	up_VCAV_EC
GO:1904019	0.274	0.896	3	22	epithelial cell apoptotic process	BP	1	TNFAIP3,GATA3,EXOC5	up_VCAV_EC
GO:2000108	0.274	0.924	2	12	positive regulation of leukocyte apoptotic	BP	1	PRELID1,PIK3CD	down_ACOR_VSMC
GO:0043242	0.274	0.92	2	21	negative regulation of protein complex	BP	1	CLEC16A,PLEKHH2	down_VCAV_EC
GO:1903533	0.274	0.92	2	21	regulation of protein targeting	BP	1	PRNP,AKT2	down_VCAV_EC
GO:0033865	0.274	0.918	2	43	nucleoside bisphosphate metabolic process	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0033875	0.274	0.918	2	43	ribonucleoside bisphosphate metabolic	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0034032	0.274	0.918	2	43	purine nucleoside bisphosphate metabolic	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0050793	0.274	0.925	2	731	regulation of developmental process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0009058	0.274	1	1	1910	biosynthetic process	BP	1	GATA5	down_AFEM_VSMC
GO:0007339	0.274	0.965	1	6	binding of sperm to zona pellucida	BP	1	B4GALT1	down_VCAV_EC
GO:0035036	0.274	0.965	1	6	sperm-egg recognition	BP	1	B4GALT1	down_VCAV_EC
GO:0043567	0.274	0.965	1	6	regulation of insulin-like growth factor receptor	BP	1	IGFBP6	down_VCAV_EC
GO:0060676	0.274	0.965	1	6	ureteric bud formation	BP	1	GREM1	down_VCAV_EC
GO:0001553	0.274	0.966	1	5	luteinization	BP	1	INHBA	down_VSAP_EC
GO:0006206	0.274	0.966	1	5	pyrimidine nucleobase metabolic process	BP	1	CMPK1	down_VSAP_EC
GO:0032060	0.274	0.965	1	6	bleb assembly	BP	1	ANLN	down_VSAP_EC
GO:0072643	0.274	0.966	1	5	interferon-gamma secretion	BP	1	NR1H4	down_VSAP_EC
GO:0006435	0.274	0.971	1	3	threonyl-tRNA aminoacylation	BP	1	TARSL2	up_ACOR_VSMC
GO:0006685	0.274	0.971	1	3	sphingomyelin catabolic process	BP	1	SMPD1	up_ACOR_VSMC
GO:0036480	0.274	0.971	1	3	neuron intrinsic apoptotic signaling pathway in response to oxidative	BP	1	PARK7	up_ACOR_VSMC

GO:0060080	0.274	0.971	1	3	inhibitory postsynaptic potential	BP	1	INSYN1	up_ACOR_VSMC
GO:1903376	0.274	0.971	1	3	regulation of oxidative stress-induced neuron intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:0045088	0.274	0.96	1	81	regulation of innate immune response	BP	1	NR1H4	up_APUL_EC
GO:1900273	0.274	0.971	1	3	positive regulation of long-term synaptic	BP	1	RELN	up_VCAV_EC
GO:1901341	0.274	0.971	1	3	positive regulation of store-operated calcium	BP	1	PLCG2	up_VCAV_EC
GO:0006610	0.274	0.971	1	3	ribosomal protein import into nucleus	BP	1	IPO11	up_VCAV_EC
GO:0032237	0.274	0.971	1	3	activation of store-operated calcium channel	BP	1	PLCG2	up_VCAV_EC
GO:0090219	0.274	0.968	1	4	negative regulation of lipid kinase activity	BP	1	PPP2R5A	up_VCAV_EC
GO:0090343	0.274	0.968	1	4	positive regulation of cell aging	BP	1	ARG2	up_VCAV_EC
GO:2000774	0.274	0.968	1	4	positive regulation of cellular senescence	BP	1	ARG2	up_VCAV_EC
GO:0002694	0.274	0.961	1	126	regulation of leukocyte activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006936	0.274	0.96	1	74	muscle contraction	BP	1	MAP2K6	up_VFEM_EC
GO:0051146	0.274	0.96	1	76	striated muscle cell differentiation	BP	1	CYP26B1	up_VFEM_EC
GO:0002253	0.274	0.96	1	92	activation of immune response	BP	1	NR1H4	up_VPUL_EC
GO:0035690	0.274	0.96	1	91	cellular response to drug	BP	1	ARHGEF2	up_VPUL_EC
GO:0050891	0.274220409	0.96172	1	12	multicellular organismal water homeostasis	BP	1	AQP1	up_ACOR_EC
GO:0030162	0.274400976	0.84305	7	202	regulation of proteolysis	BP	1	PCSK1N,EDEM2,IFI6,CST3,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0051648	0.27450469	0.8912	3	69	vesicle localization	BP	1	CDH3,DYNC1I1,PREB	up_ACOR_EC
GO:0007548	0.274998551	0.89094	3	68	sex differentiation	BP	1	GATA4,SOX9,LHX9	up_ACOR_EC
GO:0006629	0.275	0.78	40	382	lipid metabolic process	BP	1	PIP5K1B,PLCG2,LEP,PLCL1,HTR2B,PRKAA2,LCAT,CHPT1,FAXDC2,ABCA1,PPARGC1A,LPL,PIGN,PIGS,UGCG,PLPP2,PIGG,ACAD11,GGPS1,LIPE,CYP2J2,SCP2,ORMDL3,SMPD1,CCDC3,PRKCE,CRLS1,DKKL1,APP,CLN8,EDN1,HPGD,SERINC3,NEU3,SERINC1,CFI,INPP5K,ENSCAFG00000029553,ELOVL7,LMF1	up_ACOR_VSMC
GO:0019752	0.275	0.791	27	283	carboxylic acid metabolic process	BP	1	SCD,SREBF1,ACLY,ENSCAFG00000016095,BCAT1,VARS,INSIG1,CAV1,PFAS,ARG2,BRCA1,ELOVL1,FARSA,SUCLG1,PPARD,AADAT,GSTO1,ELOVL6,SGPL1,RARS,CTH,PDHA1,GGH,LIPC,PGD,CTPS1,ACADL	down_ACOR_VSMC
GO:2000147	0.275	0.802	19	169	positive regulation of cell motility	BP	1	VEGFD,LGR6,BMP4,SH3RF2,SASH1,FGF18,F2RL1,NRP1,PRKCE,APP,SEMA6D,CCL5,DDR2,EDN1,FAM107A,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0044282	0.275	0.844	7	89	small molecule catabolic process	BP	1	TPI1,ALDH1L2,SESN2,CEMIP2,ENTPD4,APOE,GALE	down_VSAP_EC
GO:0010675	0.275	0.854	6	46	regulation of cellular carbohydrate metabolic	BP	1	ACACB,C1QTNF2,PDK2,PASK,NCOA2,DDIT4	up_VSAP_EC
GO:0006665	0.275	0.863	5	48	sphingolipid metabolic process	BP	1	KIT,SERINC5,SPTLC2,SAMD8,CREM	up_VCAV_EC
GO:0001738	0.275	0.878	4	27	morphogenesis of a polarized epithelium	BP	1	MLLT3,SEC24B,ZNRF3,FZD3	up_ACOR_VSMC
GO:0031623	0.275	0.893	3	31	receptor internalization	BP	1	VEGFA,TFRC,LRRTM2	down_VSAP_EC
GO:0008037	0.275	0.895	3	22	cell recognition	BP	1	NECTIN2,CD200,PEAR1	up_VCAV_EC
GO:0022613	0.275	0.918	2	208	ribonucleoprotein complex biogenesis	BP	1	RPSA,WDR12	down_ACOR_EC
GO:0120163	0.275	0.92	2	17	negative regulation of cold-induced	BP	1	PLCL1,DDIT3	down_VSAP_EC
GO:0003203	0.275	0.924	2	11	endocardial cushion morphogenesis	BP	1	GATA5,TBX20	up_ACOR_VSMC
GO:0061036	0.275	0.924	2	11	positive regulation of cartilage development	BP	1	BMP4,FGF18	up_ACOR_VSMC
GO:0032651	0.275	0.923	2	13	regulation of interleukin-1 beta production	BP	1	TNFAIP3,ARG2	up_VCAV_EC
GO:0045843	0.275	0.922	2	13	negative regulation of striated muscle tissue	BP	1	EPHB1,BMP2	up_VCAV_EC

GO:2000036	0.275	0.923	2	12	regulation of stem cell population maintenance	BP	1	KDM3A,ZC3H13	up_VCAV_EC
GO:2000108	0.275	0.923	2	12	positive regulation of leukocyte apoptotic	BP	1	MEF2C,RAPGEF2	up_VCAV_EC
GO:0009896	0.275	0.917	2	127	positive regulation of catabolic process	BP	1	MTDH,ABHD5	up_VPOR_EC
GO:0003382	0.275	0.924	2	11	epithelial cell morphogenesis	BP	1	RILPL2,FRMD6	up_VSAP_EC
GO:0060633	0.275	0.968	1	4	negative regulation of transcription initiation from RNA polymerase II	BP	1	HMGB1	down_ACOR_VSMC
GO:2000143	0.275	0.968	1	4	negative regulation of DNA-templated	BP	1	HMGB1	down_ACOR_VSMC
GO:0006995	0.275	0.965	1	6	cellular response to nitrogen starvation	BP	1	GABARAP	down_VCAV_EC
GO:0043562	0.275	0.965	1	6	cellular response to nitrogen levels	BP	1	GABARAP	down_VCAV_EC
GO:0010523	0.275	0.965	1	6	negative regulation of calcium ion transport into	BP	1	CALM1	down_VSAP_EC
GO:0034656	0.275	0.965	1	6	nucleobase-containing small molecule catabolic	BP	1	ENTPD4	down_VSAP_EC
GO:0043455	0.275	0.966	1	5	regulation of secondary metabolic process	BP	1	PGAM1	down_VSAP_EC
GO:0060513	0.275	0.966	1	5	prostatic bud formation	BP	1	SULF1	down_VSAP_EC
GO:0002455	0.275	0.971	1	3	humoral immune response mediated by circulating	BP	1	C1S	up_ACOR_VSMC
GO:0090315	0.275	0.971	1	3	negative regulation of protein targeting to	BP	1	INPP5K	up_ACOR_VSMC
GO:0030810	0.275	0.971	1	3	positive regulation of nucleotide biosynthetic	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0032808	0.275	0.971	1	3	lacrimal gland development	BP	1	FGFR2	up_ACOR_VSMC
GO:0042640	0.275	0.971	1	3	anagen	BP	1	FERMT1	up_ACOR_VSMC
GO:0048843	0.275	0.971	1	3	negative regulation of axon extension involved in axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0051884	0.275	0.971	1	3	regulation of timing of anagen	BP	1	FERMT1	up_ACOR_VSMC
GO:1900373	0.275	0.971	1	3	positive regulation of purine nucleotide	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0019752	0.275	0.963	1	283	carboxylic acid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0097202	0.275	0.968	1	4	activation of cysteine-type endopeptidase activity	BP	1	CASP8	up_VCAV_EC
GO:1901723	0.275	0.968	1	4	negative regulation of cell proliferation involved in kidney development	BP	1	GATA3	up_VCAV_EC
GO:0010694	0.275	0.971	1	3	positive regulation of alkaline phosphatase	BP	1	MEF2C	up_VCAV_EC
GO:0090520	0.275	0.968	1	4	sphingolipid mediated signaling pathway	BP	1	SPNS3	up_VCAV_EC
GO:0030036	0.275	0.962	1	223	actin cytoskeleton organization	BP	1	LIMK1	up_VCAV_VSMC
GO:2000146	0.275	0.96	1	92	negative regulation of cell motility	BP	1	TBX5	up_VPUL_EC
GO:0048565	0.2752276	0.91727	2	38	digestive tract development	BP	1	GATA4,RARRES2	up_ACOR_EC
GO:0045893	0.276	0.777	43	413	positive regulation of transcription, DNA-templated	BP	1	HOXA11,FZD1,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,ZBTB16,RARG,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,NPAS2,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:0030855	0.276	0.803	18	183	epithelial cell differentiation	BP	1	FLNB,HNRNPH3,CAV1,CDK1,NF2,EZH2,GREM1,PCNA,HOXA7,E2F8,B4GALT1,RAP2C,PLK4,IQGAP1,HOXB5,EZR,GLI1,ANXA7	down_ACOR_VSMC
GO:1902533	0.276	0.806	16	271	positive regulation of intracellular signal transduction	BP	1	NOTCH2,PDGFRB,DCN,GLIPR2,CSPG4,PARK7,MYDGF,SASH1,CLEC16A,ARL2BP,CDH2,GSDME,SPRED1,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0006914	0.276	0.807	16	141	autophagy	BP	1	LEP,HTR2B,FEZ1,PRKAA2,TP53INP1,GABARAPL1,DAPK1,BNIP3,ULK2,PSEN1,PIK3C3,LAMP2,ATG16L2,FEZ2,SH3BP4,ZFYVE1	up_ACOR_VSMC
GO:0061919	0.276	0.807	16	141	process utilizing autophagic mechanism	BP	1	LEP,HTR2B,FEZ1,PRKAA2,TP53INP1,GABARAPL1,DAPK1,BNIP3,ULK2,PSEN1,PIK3C3,LAMP2,ATG16L2,FEZ2,SH3BP4,ZFYVE1	up_ACOR_VSMC

GO:0051222	0.276	0.82	12	103	positive regulation of protein transport	BP	1	CD274,ARHGEF5,CDH1,ABL1,IL17RC,F2RL1,ICE1,PIK3R1,KCNB1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0070997	0.276	0.823	11	93	neuron death	BP	1	PPARGC1A,USP53,EGLN1,NRP1,UNC5B,APP,PSEN1,CCL5,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0031344	0.276	0.825	10	161	regulation of cell projection organization	BP	1	PRNP,TRPV2,THY1,TLX2,UST,PRKCSH,EVI5L,RAC2,RGMA,BRSK1	down_VCAV_EC
GO:0006457	0.276	0.837	8	77	protein folding	BP	1	SLC29A1,HSPA9,PPIE,FKBP11,PPIH,CCT4,TBCC,PPIB	down_ACOR_VSMC
GO:0031667	0.276	0.837	8	102	response to nutrient levels	BP	1	ASNS,HSPA5,SESN2,APOE,DDIT3,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0043900	0.276	0.837	8	104	regulation of multi-organism process	BP	1	P4HB,SMARCA4,CNOT7,APOE,REST,RAD23A,INHBA,SPINK2	down_VSAP_EC
GO:0019058	0.276	0.844	7	64	viral life cycle	BP	1	ILF3,SLC29A1,CAV1,TRIM35,SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0051239	0.276	0.855	6	859	regulation of multicellular organismal process	BP	1	ACVRL1,LYN,PDPN,HOXA7,SULF1,ASPN	down_ACOR_EC
GO:1903828	0.276	0.863	5	38	negative regulation of cellular protein	BP	1	ACTN2,FERMT1,OS9,INPP5K,PARK7	up_ACOR_VSMC
GO:0048568	0.276	0.86	5	148	embryonic organ development	BP	1	TBX15,IRX5,HOXA7,DLL1,HOXA6	up_AFEM_EC
GO:0007009	0.276	0.878	4	27	plasma membrane organization	BP	1	SH3TC2,AR,ASAP1,WASL	up_ACOR_VSMC
GO:0042129	0.276	0.876	4	35	regulation of T cell proliferation	BP	1	PELI1,ARG2,NCK1,HMGB1	up_VCAV_EC
GO:0021675	0.276	0.877	4	29	nerve development	BP	1	HOXD3,PLXNA4,SULF2,CITED2	up_VSAP_EC
GO:0090303	0.276	0.897	3	18	positive regulation of wound healing	BP	1	ENPP4,PRKCE,RREB1	up_ACOR_VSMC
GO:0048762	0.276	0.89	3	77	mesenchymal cell differentiation	BP	1	TMEM100,GREM1,AXIN2	up_AFEM_EC
GO:0099175	0.276	0.919	2	21	regulation of postsynapse organization	BP	1	PRNP,CDH2	down_VCAV_EC
GO:0071242	0.276	0.924	2	11	cellular response to ammonium ion	BP	1	AGRN,GNAQ	up_ACOR_VSMC
GO:0010256	0.276	0.916	2	129	endomembrane system organization	BP	1	HOOK3,GCC2	up_VPOR_EC
GO:0031102	0.276	0.923	2	11	neuron projection regeneration	BP	1	RTN4RL1,MAP2K2	up_VSAP_EC
GO:1902914	0.276	0.923	2	11	regulation of protein polyubiquitination	BP	1	SASH1,FBXO4	up_VSAP_EC
GO:2001233	0.276	0.961	1	149	regulation of apoptotic signaling pathway	BP	1	IVNS1ABP	down_AFEM_EC
GO:0006139	0.276	1	1	1909	nucleobase-containing compound metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0018195	0.276	0.964	1	6	peptidyl-arginine modification	BP	1	PARK7	down_VCAV_EC
GO:0003161	0.276	0.964	1	6	cardiac conduction system development	BP	1	BMPR1A	down_VCAV_EC
GO:1903827	0.276	0.961	1	164	regulation of cellular protein localization	BP	1	RAB11B	down_VPOR_EC
GO:0045064	0.276	0.966	1	5	T-helper 2 cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0072347	0.276	0.966	1	5	response to anesthetic	BP	1	HOMER1	down_VSAP_EC
GO:0010359	0.276	0.971	1	3	regulation of anion channel activity	BP	1	TCAF1	up_ACOR_VSMC
GO:1901298	0.276	0.971	1	3	regulation of hydrogen peroxide-mediated	BP	1	PARK7	up_ACOR_VSMC
GO:1901299	0.276	0.971	1	3	negative regulation of hydrogen peroxide-mediated programmed	BP	1	PARK7	up_ACOR_VSMC
GO:0006325	0.276	0.962	1	234	chromatin organization	BP	1	EYA1	up_AFEM_VSMC
GO:0032880	0.276	0.963	1	266	regulation of protein localization	BP	1	ARG2	up_AORT_VSMC
GO:0033629	0.276	0.968	1	4	negative regulation of cell adhesion mediated by	BP	1	SWAP70	up_VCAV_EC
GO:1900037	0.276	0.968	1	4	regulation of cellular response to hypoxia	BP	1	CD34	up_VCAV_EC
GO:1900038	0.276	0.968	1	4	negative regulation of cellular response to	BP	1	CD34	up_VCAV_EC
GO:1901660	0.276	0.971	1	3	calcium ion export	BP	1	ATP2B1	up_VCAV_EC
GO:0071706	0.276	0.96	1	40	tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	up_VPOR_EC
GO:1990823	0.276	0.96	1	39	response to leukemia inhibitory factor	BP	1	GNPNAT1	up_VPOR_EC
GO:1990830	0.276	0.96	1	39	cellular response to leukemia inhibitory factor	BP	1	GNPNAT1	up_VPOR_EC

GO:0045637	0.276	0.96	1	73	regulation of myeloid cell differentiation	BP	1	HOXA9	up_VSAP_VSMC
GO:0043067	0.277	0.777	42	479	regulation of programmed cell death	BP	1	PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,MAP3K11,STK10,MEF2C,ATF3,GATA3,TNFAIP8,FIGNL1,PELI1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,MADD,PAK2,SH3GLB1,NCK1,CASP10,PTGS2,RAPGEF2,PLCG2,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0051656	0.277	0.814	13	129	establishment of organelle localization	BP	1	ZW10,CENPA,RAN,BIRC5,KIF22,CDCA8,PREB,NDC80,NUP62,TRAK1,ENSCAFG00000005299,EZR,CEP83	down_ACOR_VSMC
GO:0002221	0.277	0.852	6	46	pattern recognition receptor signaling	BP	1	TLR1,TLR3,F2RL1,PTPN22,PRKCE,NOD2	up_ACOR_VSMC
GO:0042445	0.277	0.853	6	46	hormone metabolic process	BP	1	LEP,ERO1B,DKKL1,SCG5,PCSK6,STC2	up_ACOR_VSMC
GO:0002758	0.277	0.852	6	46	innate immune response-activating signal	BP	1	TLR1,TLR3,F2RL1,PTPN22,PRKCE,NOD2	up_ACOR_VSMC
GO:0007272	0.277	0.876	4	31	ensheathment of neurons	BP	1	MALL,EIF2B2,SERINC5,MTOR	up_VCAV_EC
GO:0008366	0.277	0.876	4	31	axon ensheathment	BP	1	MALL,EIF2B2,SERINC5,MTOR	up_VCAV_EC
GO:0097190	0.277	0.917	2	217	apoptotic signaling pathway	BP	1	USP28,STX4	down_ACOR_EC
GO:0046782	0.277	0.92	2	17	regulation of viral transcription	BP	1	SMARCA4,REST	down_VSAP_EC
GO:1901701	0.277	0.917	2	271	cellular response to oxygen-containing	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:1901031	0.277	0.922	2	12	regulation of response to reactive oxygen species	BP	1	GCH1,RIPK1	up_VCAV_EC
GO:0035630	0.277	0.967	1	4	bone mineralization involved in bone	BP	1	GREM1	down_ACOR_VSMC
GO:0060316	0.277	0.967	1	4	positive regulation of ryanodine-sensitive calcium-release channel	BP	1	GSTO1	down_ACOR_VSMC
GO:0060390	0.277	0.964	1	6	regulation of SMAD protein signal	BP	1	BMPR1A	down_VCAV_EC
GO:0046823	0.277	0.964	1	6	negative regulation of nucleocytoplasmic	BP	1	PARK7	down_VCAV_EC
GO:1901385	0.277	0.964	1	6	regulation of voltage-gated calcium channel	BP	1	CACNB3	down_VCAV_EC
GO:0001840	0.277	0.965	1	5	neural plate development	BP	1	CTNNB1	down_VSAP_EC
GO:0072520	0.277	0.965	1	5	seminiferous tubule development	BP	1	SPINK2	down_VSAP_EC
GO:1901186	0.277	0.965	1	5	positive regulation of ERBB signaling pathway	BP	1	ADAM17	down_VSAP_EC
GO:0009143	0.277	0.964	1	6	nucleoside triphosphate catabolic process	BP	1	ENPP1	down_VSAP_EC
GO:0014831	0.277	0.971	1	3	gastro-intestinal system smooth muscle	BP	1	HTR2B	up_ACOR_VSMC
GO:0001955	0.277	0.971	1	3	blood vessel maturation	BP	1	RECK	up_ACOR_VSMC
GO:0061626	0.277	0.971	1	3	pharyngeal arch artery morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0030099	0.277	0.96	1	133	myeloid cell differentiation	BP	1	HOXA9	up_AORT_EC
GO:0052547	0.277	0.959	1	82	regulation of peptidase activity	BP	1	PCSK1N	up_APUL_EC
GO:0017015	0.277	0.959	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	ASPN	up_VPOR_EC
GO:0051262	0.277	0.959	1	40	protein tetramerization	BP	1	FBP1	up_VPOR_EC
GO:1903844	0.277	0.959	1	40	regulation of cellular response to transforming growth factor beta	BP	1	ASPN	up_VPOR_EC
GO:0060348	0.277	0.959	1	78	bone development	BP	1	CYP26B1	up_VFEM_EC
GO:0010256	0.277	0.96	1	129	endomembrane system organization	BP	1	ATP8B4	up_VFEM_VSMC
GO:0060485	0.277	0.96	1	93	mesenchyme development	BP	1	TBX5	up_VPUL_EC
GO:0009395	0.277032227	0.96089	1	12	phospholipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0046425	0.277108338	0.91626	2	39	regulation of JAK-STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:0061045	0.27727322	0.96081	1	12	negative regulation of wound healing	BP	1	PRKCD	up_ACOR_EC

GO:0045861	0.277396501	0.88942	3	71	negative regulation of proteolysis	BP	1	PCSK1N,IFI6,CST3	up_ACOR_EC
GO:0071622	0.277481864	0.9605	1	13	regulation of granulocyte chemotaxis	BP	1	RARRES2	up_ACOR_EC
GO:0010556	0.278	0.76	102	1137	regulation of macromolecule biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,PPP1R15B,SRRT,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,HMGN1,CCT4,SIX4,NECAB3,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:1901699	0.278	0.823	10	164	cellular response to nitrogen compound	BP	1	LRP1,PRNP,ADCY6,COL6A1,ENSCAFG00000014978,AKT2,ZFP36L1,MAVS,RAB31,SHC1	down_VCAV_EC
GO:0009165	0.278	0.835	8	104	nucleotide biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC,PAPSS1,CMPK1	down_VSAP_EC
GO:0006812	0.278	0.84	7	222	cation transport	BP	1	KCNC4,ATP6V1B2,CAMK2A,FXYD1,ATP6V0B,NIPAL1,DMPK	up_AFEM_EC
GO:0050870	0.278	0.862	5	42	positive regulation of T cell activation	BP	1	HMGB1,CAV1,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0002521	0.278	0.858	5	149	leukocyte differentiation	BP	1	LEP,HOXA7,DLL1,CYLD,EVI2B	up_AFEM_EC
GO:0051606	0.278	0.875	4	33	detection of stimulus	BP	1	EPHB1,KIT,MMP24,P2RX2	up_VCAV_EC
GO:0032268	0.278	0.877	4	778	regulation of cellular protein metabolic process	BP	1	CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0001570	0.278	0.891	3	37	vasculogenesis	BP	1	PDGFRB,ZFP36L1,SPRED1	down_VCAV_EC
GO:0008637	0.278	0.891	3	35	apoptotic mitochondrial changes	BP	1	BNIP3,FAM162A,SH3GLB1	down_VSAP_EC
GO:1903038	0.278	0.892	3	30	negative regulation of leukocyte cell-cell	BP	1	SOCS5,PTPN2,SDC4	down_VSAP_EC
GO:2000379	0.278	0.894	3	20	positive regulation of reactive oxygen species	BP	1	F2RL1,CDKN1A,PARK7	up_ACOR_VSMC
GO:0032496	0.278	0.889	3	77	response to lipopolysaccharide	BP	1	CD40,TBXA2R,ADAM17	up_AFEM_EC
GO:0050790	0.278	0.893	3	532	regulation of catalytic activity	BP	1	CCL24,PTGER2,FLRT3	up_VPUL_EC
GO:2000379	0.278	0.918	2	20	positive regulation of reactive oxygen species	BP	1	PARK7,CYBA	down_VCAV_EC
GO:0042592	0.278	0.92	2	522	homeostatic process	BP	1	CITED2,RAB11B	down_VPOR_EC
GO:0006471	0.278	0.919	2	17	protein ADP-ribosylation	BP	1	PUM3,ARF4	down_VSAP_EC
GO:0009593	0.278	0.922	2	11	detection of chemical stimulus	BP	1	TLR1,NOD2	up_ACOR_VSMC
GO:0035239	0.278	0.917	2	299	tube morphogenesis	BP	1	HOXA3,CCL24	up_VPUL_EC
GO:0010623	0.278	0.967	1	4	programmed cell death involved in cell	BP	1	CASP2	down_ACOR_VSMC
GO:0009394	0.278	0.964	1	6	2'-deoxyribonucleotide metabolic process	BP	1	ADK	down_VCAV_EC
GO:0019692	0.278	0.964	1	6	deoxyribose phosphate metabolic process	BP	1	ADK	down_VCAV_EC
GO:0045623	0.278	0.965	1	5	negative regulation of T-helper cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0006699	0.278	0.965	1	5	bile acid biosynthetic process	BP	1	NR1H4	down_VSAP_EC
GO:0043603	0.278	0.964	1	372	cellular amide metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_VSMC
GO:0002475	0.278	0.97	1	3	antigen processing and presentation via MHC	BP	1	B2M	up_ACOR_VSMC
GO:0060613	0.278	0.97	1	3	fat pad development	BP	1	ARID5B	up_ACOR_VSMC
GO:0060297	0.278	0.971	1	3	regulation of sarcomere organization	BP	1	EDN1	up_ACOR_VSMC
GO:0050865	0.278	0.96	1	135	regulation of cell activation	BP	1	BPI	up_AORT_EC

GO:0006816	0.278	0.959	1	84	calcium ion transport	BP	1	HOXA3	up_APUL_EC
GO:1901653	0.278	0.959	1	84	cellular response to peptide	BP	1	NR1H4	up_APUL_EC
GO:0048870	0.278	0.965	1	451	cell motility	BP	1	TBX5	up_APUL_VSMC
GO:0051674	0.278	0.965	1	451	localization of cell	BP	1	TBX5	up_APUL_VSMC
GO:0045429	0.278	0.967	1	4	positive regulation of nitric oxide biosynthetic	BP	1	TLR4	up_VCAV_EC
GO:1904407	0.278	0.967	1	4	positive regulation of nitric oxide metabolic	BP	1	TLR4	up_VCAV_EC
GO:0032147	0.278	0.959	1	77	activation of protein kinase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0002683	0.278	0.96	1	126	negative regulation of immune system process	BP	1	HOXA9	up_VFEM_VSMC
GO:0007268	0.278	0.96	1	130	chemical synaptic transmission	BP	1	NETO1	up_VFEM_VSMC
GO:0098916	0.278	0.96	1	130	anterograde trans-synaptic signaling	BP	1	NETO1	up_VFEM_VSMC
GO:0120039	0.278	0.96	1	158	plasma membrane bounded cell projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0071559	0.278	0.959	1	75	response to transforming growth factor beta	BP	1	CAV1	up_VSAP_VSMC
GO:0097352	0.278109259	0.96056	1	12	autophagosome maturation	BP	1	VPS16	up_ACOR_EC
GO:0045071	0.278435368	0.96046	1	12	negative regulation of viral genome replication	BP	1	MAVS	up_ACOR_EC
GO:1903362	0.278556756	0.87091	4	100	regulation of cellular protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0043624	0.278589851	0.91552	2	39	cellular protein complex disassembly	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0001754	0.278605205	0.96041	1	12	eye photoreceptor cell differentiation	BP	1	SOX9	up_ACOR_EC
GO:0018193	0.278856663	0.81542	12	368	peptidyl-amino acid modification	BP	1	NR1H4,PLCL1,PHF20,PIAS1,DCLK2,LRP4,AGBL5,RIOX2,STK32C,NRP1,PRKCD,PYGO2	up_ACOR_EC
GO:0072604	0.278950457	0.96031	1	12	interleukin-6 secretion	BP	1	MAVS	up_ACOR_EC
GO:0043062	0.2789695	0.87066	4	99	extracellular structure organization	BP	1	FMOD,ADAMTSL2,FOXC2,MFAP4	up_ACOR_EC
GO:0043269	0.279	0.812	13	135	regulation of ion transport	BP	1	ATP8A1,PDGFB,RELN,PDE4D,MEF2C,CHD7,STC1,APLNR,KCNJ3,KCNJ2,PLCG2,SPTBN4,RIPK1	up_VCAV_EC
GO:0040017	0.279	0.819	11	180	positive regulation of locomotion	BP	1	PDGFRB,GLIPR2,RHOD,AKT2,SYDE1,SEMA3C,THY1,SASH1,TWIST2,DDR2,RAC2	down_VCAV_EC
GO:0045664	0.279	0.828	9	144	regulation of neuron differentiation	BP	1	TRPV2,THY1,TLX2,GLI3,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0007051	0.279	0.836	8	70	spindle organization	BP	1	PLK2,RAB11A,MZT1,STMN1,SENP6,ATRX,HAUS3,FBXO5	up_VCAV_EC
GO:0002685	0.279	0.843	7	55	regulation of leukocyte migration	BP	1	HOXA7,C5AR2,SLC8B1,SLIT2,F2RL1,MYD88,ZNF580	up_VSAP_EC
GO:0001649	0.279	0.85	6	54	osteoblast differentiation	BP	1	MEF2C,FIGNL1,BMP2,JAG1,ASF1A,FBXO5	up_VCAV_EC
GO:0051252	0.279	0.855	6	1051	regulation of RNA metabolic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0008645	0.279	0.862	5	37	hexose transmembrane transport	BP	1	LEP,SLC2A5,EDN1,INPP5K,SLC2A12	up_ACOR_VSMC
GO:0015749	0.279	0.862	5	37	monosaccharide transmembrane transport	BP	1	LEP,SLC2A5,EDN1,INPP5K,SLC2A12	up_ACOR_VSMC
GO:0034219	0.279	0.862	5	37	carbohydrate transmembrane transport	BP	1	LEP,SLC2A5,EDN1,INPP5K,SLC2A12	up_ACOR_VSMC
GO:0006405	0.279	0.862	5	39	RNA export from nucleus	BP	1	IWS1,HHEX,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0042472	0.279	0.876	4	27	inner ear morphogenesis	BP	1	FGFR2,SEC24B,FZD3,CHD7	up_ACOR_VSMC
GO:0051051	0.279	0.871	4	112	negative regulation of transport	BP	1	LEP,CRY2,CRYAB,RAB7A	up_AFEM_EC
GO:0001959	0.279	0.875	4	33	regulation of cytokine-mediated signaling	BP	1	NLRC5,OTUD4,CNOT7,LSM14A	up_VCAV_EC
GO:0045069	0.279	0.893	3	22	regulation of viral genome replication	BP	1	ILF3,RAD23A,PPIH	down_ACOR_VSMC
GO:0021545	0.279	0.893	3	21	cranial nerve development	BP	1	HOXA3,NAV2,SIX4	down_ACOR_VSMC
GO:0032663	0.279	0.894	3	19	regulation of interleukin-2 production	BP	1	ABL1,HDAC7,CD83	up_VSAP_EC
GO:0007507	0.279	0.916	2	194	heart development	BP	1	ACVRL1,NRP2	down_ACOR_EC
GO:0010464	0.279	0.917	2	21	regulation of mesenchymal cell	BP	1	BMPR1A,CLSTN1	down_VCAV_EC

GO:0032387	0.279	0.917	2	20	negative regulation of intracellular transport	BP	1	PARK7,ARHGAP1	down_VCAV_EC
GO:0070536	0.279	0.923	2	10	protein K63-linked deubiquitination	BP	1	ZRANB1,USP20	up_ACOR_VSMC
GO:2000677	0.279	0.921	2	12	regulation of transcription regulatory region DNA	BP	1	GATA3,NSD1	up_VCAV_EC
GO:0048608	0.279	0.914	2	129	reproductive structure development	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0046854	0.279	0.922	2	11	phosphatidylinositol phosphorylation	BP	1	PIK3R1,ZFYVE21	up_VSAP_EC
GO:0099172	0.279	0.922	2	11	presynapse organization	BP	1	FZD1,LRP4	up_VSAP_EC
GO:0001505	0.279	0.958	1	69	regulation of neurotransmitter levels	BP	1	STX4	down_ACOR_EC
GO:0035107	0.279	0.959	1	60	appendage morphogenesis	BP	1	SULF1	down_ACOR_EC
GO:0035108	0.279	0.959	1	60	limb morphogenesis	BP	1	SULF1	down_ACOR_EC
GO:0019222	0.279	1	1	1934	regulation of metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0002437	0.279	0.964	1	6	inflammatory response to antigenic stimulus	BP	1	PARK7	down_VCAV_EC
GO:0030575	0.279	0.965	1	5	nuclear body organization	BP	1	ZPR1	down_VSAP_EC
GO:0002347	0.279	0.963	1	6	response to tumor cell	BP	1	PVR	down_VSAP_EC
GO:0043584	0.279	0.965	1	5	nose development	BP	1	SIX4	down_VSAP_EC
GO:0140131	0.279	0.965	1	5	positive regulation of lymphocyte chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:1903587	0.279	0.965	1	5	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	JCAD	down_VSAP_EC
GO:0002371	0.279	0.97	1	3	dendritic cell cytokine production	BP	1	TLR3	up_ACOR_VSMC
GO:0060594	0.279	0.97	1	3	mammary gland specification	BP	1	FGFR2	up_ACOR_VSMC
GO:0072578	0.279	0.97	1	3	neurotransmitter-gated ion channel clustering	BP	1	GLRB	up_ACOR_VSMC
GO:2000601	0.279	0.97	1	3	positive regulation of Arp2/3 complex-mediated actin nucleation	BP	1	WASL	up_ACOR_VSMC
GO:0007417	0.279	0.961	1	235	central nervous system development	BP	1	HOXC10	up_AFEM_VSMC
GO:0033365	0.279	0.962	1	276	protein localization to organelle	BP	1	ESR1	up_AORT_VSMC
GO:0002829	0.279	0.967	1	4	negative regulation of type 2 immune response	BP	1	ARG2	up_VCAV_EC
GO:1902176	0.279	0.967	1	4	negative regulation of oxidative stress-induced intrinsic apoptotic	BP	1	HIF1A	up_VCAV_EC
GO:2001241	0.279	0.967	1	4	positive regulation of extrinsic apoptotic signaling pathway in	BP	1	CTNNA1	up_VCAV_EC
GO:0046425	0.279	0.958	1	39	regulation of JAK-STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:0050921	0.279	0.959	1	39	positive regulation of chemotaxis	BP	1	C3AR1	up_VPOR_EC
GO:0007276	0.279	0.959	1	130	gamete generation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0099537	0.279	0.959	1	131	trans-synaptic signaling	BP	1	NETO1	up_VFEM_VSMC
GO:0051258	0.279	0.959	1	94	protein polymerization	BP	1	CCL24	up_VPUL_EC
GO:0120035	0.279	0.96	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	SLIT2	up_VPUL_VSMC
GO:2001235	0.279	0.959	1	69	positive regulation of apoptotic signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0010817	0.279609806	0.87018	4	102	regulation of hormone levels	BP	1	NR1H4,PCSK1N,AQP1,KCNB1	up_ACOR_EC
GO:0010942	0.28	0.799	18	200	positive regulation of cell death	BP	1	MAP3K11,MEF2C,ATF3,TLR4,TNFAIP8,BMP2,PAK2,SH3GLB1,NCK1,RAPGEF2,BCL10,CTNNA1,HMGB1,PMAIP1,RIPK1,ITGA6,SKIL,ALDH1A3	up_VCAV_EC
GO:0006753	0.28	0.811	13	211	nucleoside phosphate metabolic process	BP	1	GPAM,ADCY6,H6PD,NT5C2,ENTPD3,PGLS,ATP5MC1,UQCR10,ADK,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC

GO:0010817	0.28	0.816	12	102	regulation of hormone levels	BP	1	HNF4A,SLC8B1,HSD17B8,RAB11B,RETSAT,PASK,KCNB1,DHRS9,RAF1,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0016485	0.28	0.848	6	73	protein processing	BP	1	MYH9,SERPINE1,PRKACB,ENSCAFG00000005575,PGK1,A2M	down_VSAP_EC
GO:0043123	0.28	0.85	6	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	HTR2B,TLR3,F2RL1,PRKCE,NOD2,MAP3K7	up_ACOR_VSMC
GO:0002573	0.28	0.858	5	71	myeloid leukocyte differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,ZFP36L1	down_VCAV_EC
GO:0009605	0.28	0.874	4	538	response to external stimulus	BP	1	LYN,PDPN,NRP2,STX4	down_ACOR_EC
GO:0032784	0.28	0.893	3	21	regulation of DNA-templated transcription,	BP	1	EZH2,DDX39B,SUPT16H	down_ACOR_VSMC
GO:0034121	0.28	0.893	3	22	regulation of toll-like receptor signaling	BP	1	HMGB1,CAV1,CACTIN	down_ACOR_VSMC
GO:0038066	0.28	0.894	3	19	p38MAPK cascade	BP	1	LEP,SASH1,PTPN22	up_ACOR_VSMC
GO:0060348	0.28	0.888	3	78	bone development	BP	1	XYLT1,GREM1,AXIN2	up_AFEM_EC
GO:0002690	0.28	0.891	3	26	positive regulation of leukocyte chemotaxis	BP	1	CXCL8,SWAP70,HMGB1	up_VCAV_EC
GO:0035567	0.28	0.894	3	19	non-canonical Wnt signaling pathway	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0030224	0.28	0.917	2	18	monocyte differentiation	BP	1	VEGFA,MYH9	down_VSAP_EC
GO:1903131	0.28	0.917	2	18	mononuclear cell differentiation	BP	1	VEGFA,MYH9	down_VSAP_EC
GO:0048286	0.28	0.922	2	11	lung alveolus development	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0060291	0.28	0.921	2	11	long-term synaptic potentiation	BP	1	APP,FAM107A	up_ACOR_VSMC
GO:0050731	0.28	0.914	2	44	positive regulation of peptidyl-tyrosine	BP	1	GREM1,ADAM17	up_AFEM_EC
GO:0007276	0.28	0.914	2	130	gamete generation	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0009628	0.28	0.916	2	302	response to abiotic stimulus	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0002684	0.28	0.915	2	239	positive regulation of immune system process	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0032103	0.28	0.958	1	69	positive regulation of response to external	BP	1	STX4	down_ACOR_EC
GO:0060159	0.28	0.967	1	4	regulation of dopamine receptor signaling	BP	1	PRMT5	down_ACOR_VSMC
GO:0060161	0.28	0.967	1	4	positive regulation of dopamine receptor	BP	1	PRMT5	down_ACOR_VSMC
GO:0061218	0.28	0.967	1	4	negative regulation of mesonephros	BP	1	GREM1	down_ACOR_VSMC
GO:0006012	0.28	0.963	1	6	galactose metabolic process	BP	1	B4GALT1	down_VCAV_EC
GO:0043517	0.28	0.963	1	6	positive regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	SPRED1	down_VCAV_EC
GO:0046949	0.28	0.963	1	6	fatty-acyl-CoA biosynthetic process	BP	1	ACAT1	down_VCAV_EC
GO:2001267	0.28	0.963	1	6	regulation of cysteine-type endopeptidase activity involved in	BP	1	PARK7	down_VCAV_EC
GO:0030335	0.28	0.96	1	165	positive regulation of cell migration	BP	1	HDAC7	down_VPOR_EC
GO:0045624	0.28	0.965	1	5	positive regulation of T-helper cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0036499	0.28	0.963	1	6	PERK-mediated unfolded protein response	BP	1	PTPN2	down_VSAP_EC
GO:1901524	0.28	0.965	1	5	regulation of mitophagy	BP	1	CDC37	down_VSAP_EC
GO:0010172	0.28	0.97	1	3	embryonic body morphogenesis	BP	1	DAG1	up_ACOR_VSMC
GO:0032105	0.28	0.97	1	3	negative regulation of response to extracellular	BP	1	LEP	up_ACOR_VSMC
GO:0032108	0.28	0.97	1	3	negative regulation of response to nutrient	BP	1	LEP	up_ACOR_VSMC
GO:0034499	0.28	0.97	1	3	late endosome to Golgi transport	BP	1	SGSM2	up_ACOR_VSMC
GO:0030334	0.28	0.962	1	267	regulation of cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0043543	0.28	0.958	1	84	protein acylation	BP	1	ZDHHC16	up_APUL_EC
GO:0032310	0.28	0.97	1	3	prostaglandin secretion	BP	1	NOS2	up_VCAV_EC

GO:0097368	0.28	0.97	1	3	establishment of Sertoli cell barrier	BP	1	ARID4B	up_VCAV_EC
GO:0098917	0.28	0.97	1	3	retrograde trans-synaptic signaling	BP	1	GUCY1A1	up_VCAV_EC
GO:0009164	0.28	0.964	1	5	nucleoside catabolic process	BP	1	CDA	up_VCAV_EC
GO:0042454	0.28	0.964	1	5	ribonucleoside catabolic process	BP	1	CDA	up_VCAV_EC
GO:0045834	0.28	0.958	1	41	positive regulation of lipid metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0023061	0.28	0.959	1	95	signal release	BP	1	NR1H4	up_VPUL_EC
GO:0050808	0.28	0.959	1	93	synapse organization	BP	1	FLRT3	up_VPUL_EC
GO:0031344	0.28	0.959	1	161	regulation of cell projection organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0048858	0.28	0.96	1	159	cell projection morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0050727	0.28	0.958	1	74	regulation of inflammatory response	BP	1	TLR2	up_VSAP_VSMC
GO:0060795	0.280184782	0.95993	1	12	cell fate commitment involved in formation of	BP	1	FOXC2	up_ACOR_EC
GO:0060337	0.280230521	0.95992	1	12	type I interferon signaling pathway	BP	1	MAVS	up_ACOR_EC
GO:0071357	0.280230521	0.95992	1	12	cellular response to type I interferon	BP	1	MAVS	up_ACOR_EC
GO:0033059	0.280288412	0.9599	1	12	cellular pigmentation	BP	1	CDH3	up_ACOR_EC
GO:0043269	0.280338425	0.85665	5	135	regulation of ion transport	BP	1	KCNB1,ACTN2,MAPK8IP2,PRKCD,PM20D1	up_ACOR_EC
GO:0071236	0.280415392	0.9146	2	39	cellular response to antibiotic	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:0071300	0.280588884	0.95981	1	12	cellular response to retinoic acid	BP	1	AQP1	up_ACOR_EC
GO:0043462	0.280609683	0.95955	1	13	regulation of ATPase activity	BP	1	DYNC1I1	up_ACOR_EC
GO:0051050	0.281	0.792	22	235	positive regulation of transport	BP	1	HCLS1,SELE,ATP8A1,PDGFB,TMEM173,RELN,FERMT1,STC1,GATA3,EDN1,APLNR,RAB27A,PPP3CA,ABCA1,SH3GLB1,HIST1H1A,PLCG2,CTDSPL2,CREB1,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0043410	0.281	0.827	9	144	positive regulation of MAPK cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,CSPG4,MYDGF,SASH1,CDH2,GSDME,SHC1	down_VCAV_EC
GO:1903037	0.281	0.834	8	65	regulation of leukocyte cell-cell adhesion	BP	1	LEP,CD83,BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0051924	0.281	0.849	6	53	regulation of calcium ion transport	BP	1	HOXA3,CAV1,SLC30A1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0002699	0.281	0.85	6	46	positive regulation of immune effector process	BP	1	TP53BP1,F2RL1,PTPN22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051099	0.281	0.857	5	70	positive regulation of binding	BP	1	LRP1,LARP6,PLCL1,PARK7,MAPRE3	down_VCAV_EC
GO:0010810	0.281	0.858	5	60	regulation of cell-substrate adhesion	BP	1	VEGFA,SERPINE1,ENSCAFG00000002015,GSK3B,NRP1	down_VSAP_EC
GO:1901566	0.281	0.873	4	598	organonitrogen compound biosynthetic	BP	1	RPSA,CSGALNACT1,ACSL3,TNRC6B	down_ACOR_EC
GO:0035050	0.281	0.874	4	28	embryonic heart tube development	BP	1	GJA1,CITED2,TBX20,PSEN1	up_ACOR_VSMC
GO:0051592	0.281	0.873	4	33	response to calcium ion	BP	1	MEF2C,PPP3CA,TJP1,ITPKB	up_VCAV_EC
GO:0055092	0.281	0.874	4	28	sterol homeostasis	BP	1	HNF4A,LIPC,LCAT,SOAT1	up_VSAP_EC
GO:0008037	0.281	0.892	3	22	cell recognition	BP	1	B4GALT1,JMJD6,CCT4	down_ACOR_VSMC
GO:0008203	0.281	0.889	3	37	cholesterol metabolic process	BP	1	LCAT,CYB5R3,SOAT1	down_VCAV_EC
GO:0072028	0.281	0.889	3	37	nephron morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0090559	0.281	0.893	3	20	regulation of membrane permeability	BP	1	RHOT1,BNIP3,NAIF1	up_ACOR_VSMC
GO:0071260	0.281	0.893	3	19	cellular response to mechanical stimulus	BP	1	WNT11,MAP3K14,CRADD	up_VSAP_EC
GO:0002695	0.281	0.914	2	44	negative regulation of leukocyte activation	BP	1	BPI,CYLD	up_AFEM_EC
GO:0042790	0.281	0.921	2	11	nucleolar large rRNA transcription by RNA	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0051353	0.281	0.919	2	13	positive regulation of oxidoreductase activity	BP	1	EDN1,GCH1	up_VCAV_EC
GO:0072376	0.281	0.921	2	11	protein activation cascade	BP	1	PRCP,KLKB1	up_VCAV_EC

GO:1901836	0.281	0.921	2	11	regulation of transcription of nucleolar large rRNA by RNA polymerase I	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0006875	0.281	0.913	2	129	cellular metal ion homeostasis	BP	1	C3AR1,ENSCAFG00000005494	up_VPOR_EC
GO:0009890	0.281	0.917	2	420	negative regulation of biosynthetic process	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:0022603	0.281	0.916	2	301	regulation of anatomical structure morphogenesis	BP	1	TBX5,CCL24	up_VPUL_EC
GO:0072006	0.281	0.958	1	59	nephron development	BP	1	SULF1	down_ACOR_EC
GO:0001833	0.281	0.966	1	4	inner cell mass cell proliferation	BP	1	GINS4	down_ACOR_VSMC
GO:0033483	0.281	0.966	1	4	gas homeostasis	BP	1	CAV1	down_ACOR_VSMC
GO:0051354	0.281	0.966	1	4	negative regulation of oxidoreductase activity	BP	1	CAV1	down_ACOR_VSMC
GO:0046483	0.281	1	1	1948	heterocycle metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0071624	0.281	0.963	1	6	positive regulation of granulocyte chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0090023	0.281	0.963	1	6	positive regulation of neutrophil chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0030154	0.281	0.977	1	1040	cell differentiation	BP	1	GATA5	down_VFEM_VSMC
GO:0032959	0.281	0.97	1	3	inositol trisphosphate biosynthetic process	BP	1	PLCG2	up_ACOR_VSMC
GO:0034092	0.281	0.97	1	3	negative regulation of maintenance of sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0034183	0.281	0.97	1	3	negative regulation of maintenance of mitotic sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0045875	0.281	0.97	1	3	negative regulation of sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0070424	0.281	0.97	1	3	regulation of nucleotide-binding oligomerization domain containing	BP	1	PTPN22	up_ACOR_VSMC
GO:0070432	0.281	0.97	1	3	regulation of nucleotide-binding oligomerization domain containing 2	BP	1	PTPN22	up_ACOR_VSMC
GO:0048666	0.281	0.961	1	258	neuron development	BP	1	WNT7A	up_AORT_VSMC
GO:0060839	0.281	0.966	1	4	endothelial cell fate commitment	BP	1	PROX1	up_VCAV_EC
GO:0072148	0.281	0.966	1	4	epithelial cell fate commitment	BP	1	PROX1	up_VCAV_EC
GO:0009206	0.281	0.958	1	39	purine ribonucleoside triphosphate biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0048762	0.281	0.958	1	77	mesenchymal cell differentiation	BP	1	TIAM1	up_VFEM_EC
GO:0048667	0.281	0.959	1	140	cell morphogenesis involved in neuron	BP	1	SHOX2	up_VFEM_VSMC
GO:0048705	0.281	0.958	1	95	skeletal system morphogenesis	BP	1	HOXA3	up_VPUL_EC
GO:0006936	0.281	0.958	1	74	muscle contraction	BP	1	CAV1	up_VSAP_VSMC
GO:0035561	0.281300133	0.95959	1	12	regulation of chromatin binding	BP	1	PYGO2	up_ACOR_EC
GO:0048333	0.28156146	0.95951	1	12	mesodermal cell differentiation	BP	1	FOXC2	up_ACOR_EC
GO:0071526	0.281689508	0.95947	1	12	semaphorin-plexin signaling pathway	BP	1	NRP1	up_ACOR_EC
GO:0060602	0.281752992	0.95946	1	12	branch elongation of an epithelium	BP	1	SOX9	up_ACOR_EC
GO:0120033	0.281914912	0.95941	1	12	negative regulation of plasma membrane bounded cell projection	BP	1	PRKCD	up_ACOR_EC
GO:0030149	0.281954351	0.95939	1	12	sphingolipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0046466	0.281954351	0.95939	1	12	membrane lipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0060255	0.282	0.862	6	1782	regulation of macromolecule metabolic	BP	1	EYA1,HOXA10,HOXA9,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051346	0.282	0.886	3	78	negative regulation of hydrolase activity	BP	1	CRYAB,MYO1D,RECK	up_AFEM_EC
GO:0045582	0.282	0.891	3	22	positive regulation of T cell differentiation	BP	1	IL7R,GATA3,ITPKB	up_VCAV_EC
GO:0042102	0.282	0.892	3	19	positive regulation of T cell proliferation	BP	1	PNP,NCK1,TGFBR2	up_VSAP_EC

GO:0055013	0.282	0.917	2	17	cardiac muscle cell development	BP	1	FHL2,NEXN	down_VSAP_EC
GO:0045736	0.282	0.921	2	11	negative regulation of cyclin-dependent protein serine/threonine kinase	BP	1	LATS2,CDKN1A	up_ACOR_VSMC
GO:0060572	0.282	0.921	2	11	morphogenesis of an epithelial bud	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:1904030	0.282	0.921	2	11	negative regulation of cyclin-dependent protein	BP	1	LATS2,CDKN1A	up_ACOR_VSMC
GO:0044092	0.282	0.915	2	270	negative regulation of molecular function	BP	1	NR1H4,PCSK1N	up_APUL_EC
GO:0002720	0.282	0.919	2	13	positive regulation of cytokine production involved in immune	BP	1	TLR4,GATA3	up_VCAV_EC
GO:0018279	0.282	0.918	2	14	protein N-linked glycosylation via	BP	1	ST6GAL1,ST3GAL6	up_VCAV_EC
GO:0042130	0.282	0.919	2	13	negative regulation of T cell proliferation	BP	1	PELI1,ARG2	up_VCAV_EC
GO:1905209	0.282	0.919	2	13	positive regulation of cardiocyte differentiation	BP	1	MEF2C,EDN1	up_VCAV_EC
GO:0050922	0.282	0.92	2	11	negative regulation of chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0050730	0.282	0.958	1	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	LYN	down_ACOR_EC
GO:0034470	0.282	0.959	1	154	ncRNA processing	BP	1	TSEN15	down_AFEM_EC
GO:0006725	0.282	1	1	1956	cellular aromatic compound metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0003264	0.282	0.964	1	5	regulation of cardioblast proliferation	BP	1	CTNNB1	down_VSAP_EC
GO:0071404	0.282	0.964	1	5	cellular response to low-density lipoprotein	BP	1	SOCS5	down_VSAP_EC
GO:0003266	0.282	0.964	1	5	regulation of secondary heart field cardioblast	BP	1	CTNNB1	down_VSAP_EC
GO:0002577	0.282	0.97	1	3	regulation of antigen processing and	BP	1	TAPBPL	up_ACOR_VSMC
GO:0009617	0.282	0.958	1	133	response to bacterium	BP	1	BPI	up_AORT_EC
GO:0031330	0.282	0.958	1	85	negative regulation of cellular catabolic process	BP	1	LZTS1	up_APUL_EC
GO:0009445	0.282	0.966	1	4	putrescine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0072106	0.282	0.966	1	4	regulation of ureteric bud formation	BP	1	GATA3	up_VCAV_EC
GO:0072107	0.282	0.966	1	4	positive regulation of ureteric bud formation	BP	1	GATA3	up_VCAV_EC
GO:1905278	0.282	0.966	1	4	positive regulation of epithelial tube formation	BP	1	GATA3	up_VCAV_EC
GO:0097435	0.282	0.96	1	230	supramolecular fiber organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0030518	0.282	0.957	1	42	intracellular steroid hormone receptor	BP	1	RNF6	up_VPOR_EC
GO:2000241	0.282	0.958	1	40	regulation of reproductive process	BP	1	SEMA3A	up_VPOR_EC
GO:0003007	0.282	0.958	1	94	heart morphogenesis	BP	1	TBX5	up_VPUL_EC
GO:0055074	0.282	0.958	1	95	calcium ion homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0042326	0.282	0.959	1	163	negative regulation of phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0090066	0.282	0.959	1	162	regulation of anatomical structure size	BP	1	SLIT2	up_VPUL_VSMC
GO:0042158	0.282118751	0.91367	2	40	lipoprotein biosynthetic process	BP	1	PORCN,PIGS	up_ACOR_EC
GO:0007275	0.282126976	0.77632	40	1370	multicellular organism development	BP	1	SH3TC2,CPAMD8,CDH3,NR1H4,TMOD1,GATA4,BRSK1,TBX18,SOX9,PTH1R,NDRG2,AQP1,ENSCAFG00000004331,FZD5,SEMA6D,DIXDC1,PDLIM3,RGMA,LHX9,SMAD6,ACTN2,ESM1,PAK3,DLX3,TNFRSF19,PTGER4,ARHGDIB,DCLK2,ADAMTSL2,MAPK8IP2,FOXC2,TBX5,LRP4,CLSTN1,C23H3orf58,RARRES2,NRP1,PYGO2,DBNDD2,EFEMP1	up_ACOR_EC
GO:0034762	0.283	0.807	14	122	regulation of transmembrane transport	BP	1	AMIGO1,ABL1,KCNE3,OSR1,CLIC5,KLF15,C1QTNF2,KLHL24,PIK3R1,AZIN2,KCNB1,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0006913	0.283	0.81	13	124	nucleocytoplasmic transport	BP	1	HCLS1,MX2,TMEM173,IWS1,FERMT1,PPP3CA,HHEX,THOC1,APOD,CTDSPL2,SMG7,NUP133,IPO11	up_VCAV_EC

GO:0051169	0.283	0.81	13	124	nuclear transport	BP	1	HCLS1,MX2,TMEM173,IWS1,FERMT1,PPP3CA,HHEX,THOC1,APOD,CTDSPL2,SMG7,NUP133,IPO11	up_VCAV_EC
GO:0002237	0.283	0.822	10	85	response to molecule of bacterial origin	BP	1	TLR1,PLCG2,ABCA1,PTGIR,SASH1,ANKRD1,PRKCE,NOD2,B2M,TNFRSF11B	up_ACOR_VSMC
GO:0048534	0.283	0.83	8	262	hematopoietic or lymphoid organ	BP	1	HOXA9,LEP,HOXA7,DLL1,NFE2L1,CYLD,EVI2B,BVES	up_AFEM_EC
GO:0044085	0.283	0.844	7	1076	cellular component biogenesis	BP	1	ACVRL1,IGF1R,SPG11,RPSA,ACSL3,WDR12,STX4	down_ACOR_EC
GO:1901293	0.283	0.837	7	106	nucleoside phosphate biosynthetic process	BP	1	GPAM,ADCY6,ATP5MC1,ADK,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0010468	0.283	0.846	7	1270	regulation of gene expression	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,CYP26B1	up_VFEM_EC
GO:0008150	0.283	1	6	5646	biological_process	BP	1	TGFBI,AK5,GATA5,TGFBR1,MEIS2,ENSCAFG00000028814	down_VSAP_VSMC
GO:0043270	0.283	0.847	6	56	positive regulation of ion transport	BP	1	ATP8A1,PDGFB,RELN,STC1,APLNR,PLCG2	up_VCAV_EC
GO:0032680	0.283	0.859	5	36	regulation of tumor necrosis factor production	BP	1	TLR1,LEP,TLR3,PTPN22,NOD2	up_ACOR_VSMC
GO:0031214	0.283	0.858	5	45	biomineral tissue development	BP	1	MEF2C,BMP2,BMP2K,HIF1A,FBXO5	up_VCAV_EC
GO:0022404	0.283	0.873	4	28	molting cycle process	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0022405	0.283	0.873	4	28	hair cycle process	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0001942	0.283	0.873	4	28	hair follicle development	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0001889	0.283	0.891	3	22	liver development	BP	1	EZH2,E2F8,GLI1	down_ACOR_VSMC
GO:0009791	0.283	0.888	3	38	post-embryonic development	BP	1	NDN,FBN1,SEMA3C	down_VCAV_EC
GO:0002705	0.283	0.889	3	31	positive regulation of leukocyte mediated	BP	1	FAM49B,PVR,TFRC	down_VSAP_EC
GO:1903725	0.283	0.889	3	30	regulation of phospholipid metabolic process	BP	1	NR1H4,LYN,SH3GLB1	down_VSAP_EC
GO:0048477	0.283	0.892	3	19	oogenesis	BP	1	PDE5A,MARF1,DMC1	up_ACOR_VSMC
GO:0006650	0.283	0.886	3	78	glycerophospholipid metabolic process	BP	1	GPAM,NAPEPLD,AGPAT2	up_AFEM_EC
GO:0032233	0.283	0.891	3	21	positive regulation of actin filament bundle	BP	1	ARHGEF15,MTOR,SWAP70	up_VCAV_EC
GO:1901137	0.283	0.914	2	232	carbohydrate derivative biosynthetic process	BP	1	CSGALNACT1,TNRC6B	down_ACOR_EC
GO:0071526	0.283	0.919	2	12	semaphorin-plexin signaling pathway	BP	1	ARHGDIA,RAC1	down_ACOR_VSMC
GO:0010596	0.283	0.915	2	21	negative regulation of endothelial cell migration	BP	1	DCN,SPRED1	down_VCAV_EC
GO:0032623	0.283	0.915	2	21	interleukin-2 production	BP	1	GPAM,PRNP	down_VCAV_EC
GO:0032760	0.283	0.915	2	22	positive regulation of tumor necrosis factor	BP	1	CYBA,MAVS	down_VCAV_EC
GO:1903557	0.283	0.915	2	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	CYBA,MAVS	down_VCAV_EC
GO:0030042	0.283	0.916	2	17	actin filament depolymerization	BP	1	WDR1,CAPG	down_VSAP_EC
GO:0030834	0.283	0.916	2	17	regulation of actin filament depolymerization	BP	1	WDR1,CAPG	down_VSAP_EC
GO:0031663	0.283	0.917	2	17	lipopolysaccharide-mediated signaling	BP	1	MTDH,LYN	down_VSAP_EC
GO:0009994	0.283	0.92	2	11	oocyte differentiation	BP	1	PDE5A,DMC1	up_ACOR_VSMC
GO:0050691	0.283	0.92	2	11	regulation of defense response to virus by host	BP	1	PTPN22,PARP9	up_ACOR_VSMC
GO:0046474	0.283	0.913	2	44	glycerophospholipid biosynthetic process	BP	1	GPAM,AGPAT2	up_AFEM_EC
GO:0009967	0.283	0.917	2	435	positive regulation of signal transduction	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0032370	0.283	0.918	2	13	positive regulation of lipid transport	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0045913	0.283	0.918	2	15	positive regulation of carbohydrate metabolic	BP	1	PDGFB,PMAIP1	up_VCAV_EC
GO:0007268	0.283	0.913	2	130	chemical synaptic transmission	BP	1	HTR7,SV2C	up_VPOR_EC
GO:0098916	0.283	0.913	2	130	anterograde trans-synaptic signaling	BP	1	HTR7,SV2C	up_VPOR_EC
GO:0045824	0.283	0.92	2	11	negative regulation of innate immune response	BP	1	TRAFD1,NLRX1	up_VSAP_EC
GO:0022617	0.283	0.92	2	11	extracellular matrix disassembly	BP	1	DDR2,FLOT1	up_VSAP_EC

GO:0045165	0.283	0.957	1	65	cell fate commitment	BP	1	PDPN	down_ACOR_EC
GO:0030502	0.283	0.966	1	4	negative regulation of bone mineralization	BP	1	GREM1	down_ACOR_VSMC
GO:0065008	0.283	0.977	1	1056	regulation of biological quality	BP	1	JUP	down_VFEM_VSMC
GO:0007289	0.283	0.964	1	5	spermatid nucleus differentiation	BP	1	KDM3A	down_VSAP_EC
GO:0010694	0.283	0.969	1	3	positive regulation of alkaline phosphatase	BP	1	NPNT	up_ACOR_VSMC
GO:0048714	0.283	0.969	1	3	positive regulation of oligodendrocyte	BP	1	ZNF365	up_ACOR_VSMC
GO:0060600	0.283	0.969	1	3	dichotomous subdivision of an epithelial terminal	BP	1	NRP1	up_ACOR_VSMC
GO:0060666	0.283	0.969	1	3	dichotomous subdivision of terminal units involved in salivary gland	BP	1	NRP1	up_ACOR_VSMC
GO:1905097	0.283	0.969	1	3	regulation of guanyl-nucleotide exchange	BP	1	CCPG1	up_ACOR_VSMC
GO:0060421	0.283	0.959	1	14	positive regulation of heart growth	BP	1	ACACB	up_AFEM_EC
GO:0010506	0.283	0.958	1	86	regulation of autophagy	BP	1	LZTS1	up_APUL_EC
GO:0045444	0.283	0.958	1	84	fat cell differentiation	BP	1	WIF1	up_APUL_EC
GO:0051047	0.283	0.957	1	84	positive regulation of secretion	BP	1	NR1H4	up_APUL_EC
GO:0030502	0.283	0.966	1	4	negative regulation of bone mineralization	BP	1	HIF1A	up_VCAV_EC
GO:0032691	0.283	0.966	1	4	negative regulation of interleukin-1 beta	BP	1	TNFAIP3	up_VCAV_EC
GO:1904502	0.283	0.969	1	3	regulation of lipophagy	BP	1	SPTLC2	up_VCAV_EC
GO:1904504	0.283	0.969	1	3	positive regulation of lipophagy	BP	1	SPTLC2	up_VCAV_EC
GO:0099536	0.283	0.958	1	133	synaptic signaling	BP	1	NETO1	up_VFEM_VSMC
GO:0032870	0.283	0.959	1	162	cellular response to hormone stimulus	BP	1	SLIT2	up_VPUL_VSMC
GO:0030100	0.283	0.957	1	70	regulation of endocytosis	BP	1	CAV1	up_VSAP_VSMC
GO:0019637	0.283551601	0.81522	11	342	organophosphate metabolic process	BP	1	NR1H4,NMNAT2,ENSCAFG00000004331,CFI,GUCY1B1,CHPT1,PIGS,AK7,ALDOC,AGPAT2,PRKCD	up_ACOR_EC
GO:0035295	0.284	0.773	38	356	tube development	BP	1	VEGFD,SMAD6,LEP,GATA5,GATA4,ANGPT1,SHROOM3,BMP4,FGFR2,GJA1,ATRX,TLR3,SEC24B,CITED2,SPINT1,SASH1,LMO4,FGF18,EGLN1,CLSTN1,NRP1,NPNT,SPINT2,TBX20,TBX5,FZD3,DAG1,PSEN1,SYNJ2BP,CHD7,JUP,SPINK2,EDN1,HPGD,JAM3,WDR48,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0060322	0.284	0.79	22	193	head development	BP	1	FGF13,BMP4,FGFR2,ATRX,SEC24B,ZNF365,TMEM108,NDRG2,ATRN,NRP1,SLITRK5,FZD3,FRS2,POMK,APP,PSEN1,SEMA6D,CHD7,ARID5B,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0050767	0.284	0.792	20	184	regulation of neurogenesis	BP	1	THRB,CDON,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,CYB5D2,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC
GO:0051272	0.284	0.795	19	170	positive regulation of cellular component movement	BP	1	VEGFD,LGR6,BMP4,SH3RF2,SASH1,FGF18,F2RL1,NRP1,PRKCE,APP,SEMA6D,CCL5,DDR2,EDN1,FAM107A,DOCK5,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0043068	0.284	0.798	17	190	positive regulation of programmed cell death	BP	1	MAP3K11,MEF2C,ATF3,TNFAIP8,BMP2,PAK2,SH3GLB1,NCK1,RAPGEF2,BCL10,CTNNA1,HMGB1,PMAIP1,RIPK1,ITGA6,SKIL,ALDH1A3	up_VCAV_EC
GO:0071214	0.284	0.817	11	93	cellular response to abiotic stimulus	BP	1	WNT11,MAP3K14,CRADD,OSR1,DDB2,TNKS1BP1,RAB11B,ZFP36L1,PIK3R1,SLC12A6,FBXO4	up_VSAP_EC
GO:0104004	0.284	0.817	11	93	cellular response to environmental stimulus	BP	1	WNT11,MAP3K14,CRADD,OSR1,DDB2,TNKS1BP1,RAB11B,ZFP36L1,PIK3R1,SLC12A6,FBXO4	up_VSAP_EC
GO:0006906	0.284	0.847	6	55	vesicle fusion	BP	1	SNAP23,CAV2,STX11,TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0070588	0.284	0.869	4	54	calcium ion transmembrane transport	BP	1	PRNP,CACNB3,THY1,CYBA	down_VCAV_EC
GO:0034198	0.284	0.872	4	27	cellular response to amino acid starvation	BP	1	CDKN1A,SESN3,SESN1,BMT2	up_ACOR_VSMC

GO:1990928	0.284	0.872	4	27	response to amino acid starvation	BP	1	CDKN1A,SESN3,SESN1,BMT2	up_ACOR_VSMC
GO:0007044	0.284	0.872	4	27	cell-substrate junction assembly	BP	1	ACTN2,NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0070665	0.284	0.888	3	31	positive regulation of leukocyte proliferation	BP	1	TFRC,LYN,CDKN1A	down_VSAP_EC
GO:1905477	0.284	0.888	3	32	positive regulation of protein localization to	BP	1	MYO1C,KIF5B,SH3GLB1	down_VSAP_EC
GO:0035567	0.284	0.891	3	19	non-canonical Wnt signaling pathway	BP	1	MLLT3,ZNRF3,FZD3	up_ACOR_VSMC
GO:0045010	0.284	0.891	3	19	actin nucleation	BP	1	JMY,EVL,WASL	up_ACOR_VSMC
GO:0070534	0.284	0.892	3	19	protein K63-linked ubiquitination	BP	1	SASH1,PTPN22,NOD2	up_ACOR_VSMC
GO:0043408	0.284	0.913	2	211	regulation of MAPK cascade	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0035924	0.284	0.915	2	21	cellular response to vascular endothelial growth factor stimulus	BP	1	PDGFRB,DCN	down_VCAV_EC
GO:0008152	0.284	1	2	3714	metabolic process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0048522	0.284	0.934	2	1484	positive regulation of cellular process	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0040036	0.284	0.92	2	11	regulation of fibroblast growth factor receptor	BP	1	GATA3,PRKD2	up_VCAV_EC
GO:0071300	0.284	0.919	2	12	cellular response to retinoic acid	BP	1	YES1,ABCA1	up_VCAV_EC
GO:0072604	0.284	0.919	2	12	interleukin-6 secretion	BP	1	HMGB1,NOS2	up_VCAV_EC
GO:0032269	0.284	0.914	2	306	negative regulation of cellular protein metabolic	BP	1	PTGER2,FLRT3	up_VPUL_EC
GO:0034097	0.284	0.913	2	238	response to cytokine	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:1904018	0.284	0.957	1	69	positive regulation of vasculature development	BP	1	ACVRL1	down_ACOR_EC
GO:0002949	0.284	0.966	1	4	tRNA threonylcarbamoyladenosine modification	BP	1	OSGEP	down_ACOR_VSMC
GO:0032700	0.284	0.966	1	4	negative regulation of interleukin-17 production	BP	1	ARG2	down_ACOR_VSMC
GO:0038166	0.284	0.966	1	4	angiotensin-activated signaling pathway	BP	1	CAV1	down_ACOR_VSMC
GO:0060033	0.284	0.965	1	4	anatomical structure regression	BP	1	GLI1	down_ACOR_VSMC
GO:1901228	0.284	0.965	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GREM1	down_ACOR_VSMC
GO:0031324	0.284	0.969	1	735	negative regulation of cellular metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0065009	0.284	0.969	1	735	regulation of molecular function	BP	1	PLCL1	down_VFEM_EC
GO:0060314	0.284	0.962	1	6	regulation of ryanodine-sensitive calcium-release	BP	1	CALM1	down_VSAP_EC
GO:1990253	0.284	0.963	1	5	cellular response to leucine starvation	BP	1	SESN2	down_VSAP_EC
GO:0007616	0.284	0.963	1	5	long-term memory	BP	1	APOE	down_VSAP_EC
GO:0070816	0.284	0.963	1	5	phosphorylation of RNA polymerase II C-terminal	BP	1	GTF2H1	down_VSAP_EC
GO:0032237	0.284	0.969	1	3	activation of store-operated calcium channel	BP	1	PLCG2	up_ACOR_VSMC
GO:1901341	0.284	0.969	1	3	positive regulation of store-operated calcium	BP	1	PLCG2	up_ACOR_VSMC
GO:0070266	0.284	0.958	1	14	necroptotic process	BP	1	CYLD	up_AFEM_EC
GO:0030336	0.284	0.957	1	86	negative regulation of cell migration	BP	1	TBX5	up_APUL_EC
GO:0070372	0.284	0.957	1	85	regulation of ERK1 and ERK2 cascade	BP	1	NPNT	up_APUL_EC
GO:0043252	0.284	0.965	1	4	sodium-independent organic anion transport	BP	1	SLCO3A1	up_VCAV_EC
GO:0048703	0.284	0.966	1	4	embryonic viscerocranium morphogenesis	BP	1	MEF2C	up_VCAV_EC
GO:0060633	0.284	0.965	1	4	negative regulation of transcription initiation from RNA polymerase II	BP	1	HMGB1	up_VCAV_EC
GO:2000143	0.284	0.965	1	4	negative regulation of DNA-templated	BP	1	HMGB1	up_VCAV_EC

GO:0007052	0.284	0.957	1	42	mitotic spindle organization	BP	1	MZT1	up_VPOR_EC
GO:0043087	0.284	0.957	1	83	regulation of GTPase activity	BP	1	TIAM1	up_VFEM_EC
GO:0043393	0.284	0.957	1	77	regulation of protein binding	BP	1	TIAM1	up_VFEM_EC
GO:0016053	0.284	0.957	1	97	organic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0046394	0.284	0.957	1	97	carboxylic acid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0070838	0.284	0.957	1	96	divalent metal ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0045453	0.284117948	0.95873	1	12	bone resorption	BP	1	PTH1R	up_ACOR_EC
GO:0070979	0.284256661	0.95842	1	13	protein K11-linked ubiquitination	BP	1	UBE2H	up_ACOR_EC
GO:2000241	0.284605006	0.9124	2	40	regulation of reproductive process	BP	1	SOX9,ARHGDIB	up_ACOR_EC
GO:0055023	0.284814376	0.95851	1	12	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0048585	0.285	0.766	50	475	negative regulation of response to stimulus	BP	1	SMAD6,LEP,LBH,HTR2B,RASSF2,PRKAA2,MLLT3,FERMT1,BMP4,TP53BP1,ELF1,CASTOR1,LATS2,ZNRF3,AR,PTGIR,NDRG2,ITPR1,F2RL1,DAPK1,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,OS9,UNC5B,SMPD1,APLP1,TBX20,SESN3,SH3RF1,CCDC3,RGS2,DAG1,PSEN1,SYNJ2BP,WWC2,DUSP22,SESN1,OXR1,DUSP26,LRRC4,DDIT4,HERPUD1,INPP5K,BMT2,WFS1,SH3BP4,PARK7	up_ACOR_VSMC
GO:1901699	0.285	0.795	18	164	cellular response to nitrogen compound	BP	1	SLIT2,CDH1,GOT1,CHRM1,MAP3K5,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,CASTOR1,PQBP1,FLOT1,NCK1,MAVS,BGLAP	up_VSAP_EC
GO:0045597	0.285	0.801	15	253	positive regulation of cell differentiation	BP	1	GLIPR2,BMPR1A,TRPV2,NUMBL,CLSTN1,SEMA3C,GLI3,ZFP36L1,RAB7B,DDR2,GREM1,NAPEPLD,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0010817	0.285	0.82	10	102	regulation of hormone levels	BP	1	CHD7,TIPARP,GATA3,EDN1,SNAP23,BMP2,CREB1,MCU,HIF1A,ALDH1A3	up_VCAV_EC
GO:0043405	0.285	0.825	9	85	regulation of MAP kinase activity	BP	1	KIT,MAP3K11,PDGFB,TLR4,EDN1,BMP2,MADD,RIPK1,PDGFD	up_VCAV_EC
GO:0010033	0.285	0.832	8	772	response to organic substance	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0007611	0.285	0.846	6	54	learning or memory	BP	1	PLK2,ATP8A1,RELN,MEF2C,CREB1,HIF1A	up_VCAV_EC
GO:0019439	0.285	0.853	5	150	aromatic compound catabolic process	BP	1	TENT5C,MOXD1,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0006813	0.285	0.858	5	37	potassium ion transport	BP	1	AMIGO1,KCNE3,KLHL24,KCNB1,KCNC4	up_VSAP_EC
GO:0050777	0.285	0.871	4	28	negative regulation of immune response	BP	1	TRAFD1,STAT6,NLRX1,PPP3CB	up_VSAP_EC
GO:0048167	0.285	0.871	4	28	regulation of synaptic plasticity	BP	1	FAM107A,ABL1,KCNB1,STX4	up_VSAP_EC
GO:0019915	0.285	0.89	3	22	lipid storage	BP	1	SREBF2,CAV1,ABHD5	down_ACOR_VSMC
GO:0042552	0.285	0.888	3	30	myelination	BP	1	ILK,ZPR1,CTNNB1	down_VSAP_EC
GO:0046513	0.285	0.891	3	19	ceramide biosynthetic process	BP	1	CERS4,ENSCAFG00000000071,B3GALT4	up_VSAP_EC
GO:0014068	0.285	0.914	2	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	DCN,MYDGF	down_VCAV_EC
GO:0032647	0.285	0.92	2	10	regulation of interferon-alpha production	BP	1	TLR3,PTPN22	up_ACOR_VSMC
GO:0032653	0.285	0.919	2	11	regulation of interleukin-10 production	BP	1	CD83,CD274	up_ACOR_VSMC
GO:0061458	0.285	0.912	2	131	reproductive system development	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0099537	0.285	0.912	2	131	trans-synaptic signaling	BP	1	HTR7,SV2C	up_VPOR_EC
GO:0048255	0.285	0.919	2	11	mRNA stabilization	BP	1	AXIN2,TENT5C	up_VSAP_EC
GO:1902042	0.285	0.919	2	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	RAF1,HMOX1	up_VSAP_EC
GO:0042634	0.285	0.919	2	11	regulation of hair cycle	BP	1	HPSE,TRADD	up_VSAP_EC
GO:0046328	0.285	0.957	1	61	regulation of JNK cascade	BP	1	IGF1R	down_ACOR_EC
GO:0120031	0.285	0.958	1	154	plasma membrane bounded cell projection	BP	1	FSCN1	down_AFEM_EC

GO:0071380	0.285	0.961	1	7	cellular response to prostaglandin E stimulus	BP	1	ADCY6	down_VCAV_EC
GO:0044085	0.285	0.976	1	1076	cellular component biogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0003339	0.285	0.963	1	5	regulation of mesenchymal to epithelial transition involved in	BP	1	CTNNB1	down_VSAP_EC
GO:0019369	0.285	0.963	1	5	arachidonic acid metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0045124	0.285	0.963	1	5	regulation of bone resorption	BP	1	TFRC	down_VSAP_EC
GO:0048251	0.285	0.969	1	3	elastic fiber assembly	BP	1	MFAP4	up_ACOR_VSMC
GO:0060916	0.285	0.969	1	3	mesenchymal cell proliferation involved in	BP	1	FGFR2	up_ACOR_VSMC
GO:0010660	0.285	0.958	1	14	regulation of muscle cell apoptotic process	BP	1	CAMK2A	up_AFEM_EC
GO:0030837	0.285	0.958	1	14	negative regulation of actin filament	BP	1	KANK1	up_AFEM_EC
GO:0060512	0.285	0.958	1	14	prostate gland morphogenesis	BP	1	TNC	up_AFEM_EC
GO:0072087	0.285	0.958	1	14	renal vesicle development	BP	1	GREM1	up_AFEM_EC
GO:0098661	0.285	0.958	1	14	inorganic anion transmembrane transport	BP	1	CLIC4	up_AFEM_EC
GO:0002237	0.285	0.957	1	85	response to molecule of bacterial origin	BP	1	NR1H4	up_APUL_EC
GO:0060332	0.285	0.969	1	3	positive regulation of response to interferon-	BP	1	NLRC5	up_VCAV_EC
GO:0060335	0.285	0.969	1	3	positive regulation of interferon-gamma-mediated signaling	BP	1	NLRC5	up_VCAV_EC
GO:0030212	0.285	0.965	1	4	hyaluronan metabolic process	BP	1	PDGFB	up_VCAV_EC
GO:0031392	0.285	0.969	1	3	regulation of prostaglandin	BP	1	PTGS2	up_VCAV_EC
GO:0071346	0.285	0.957	1	41	cellular response to interferon-gamma	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:1904892	0.285	0.956	1	40	regulation of STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:0051056	0.285	0.957	1	87	regulation of small GTPase mediated signal	BP	1	TIAM1	up_VFEM_EC
GO:0050769	0.285	0.957	1	95	positive regulation of neurogenesis	BP	1	ARHGEF2	up_VPUL_EC
GO:0043254	0.285	0.958	1	164	regulation of protein complex assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0050877	0.285	0.958	1	164	nervous system process	BP	1	LRRN4	up_VPUL_VSMC
GO:0014065	0.285726068	0.91189	2	39	phosphatidylinositol 3-kinase signaling	BP	1	SOX9,C23H3orf58	up_ACOR_EC
GO:0051090	0.285824173	0.85284	5	134	regulation of DNA-binding transcription factor	BP	1	NR1H4,NOD2,MAVS,CLSTN1,CLU	up_ACOR_EC
GO:0031324	0.286	0.759	65	735	negative regulation of cellular metabolic process	BP	1	EDNRB,HCLS1,PPP2R5A,CDA,TNFAIP3,TNIP1,PDGFB,CD34,PDE4D,MEF2C,ATF3,DLL4,RAPGEF1,WWP1,TLR4,GATA3,EDN1,HOXB8,SOX18,PPP3CA,FAM3C,MTOR,TENT2,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,SH3BP5,ENC1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,HMBOX1,PAK2,THOC1,SWAP70,SMARCA4,APOD,NCK1,TIMELESS,PTGS2,RAPGEF2,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,BLM,RAD17,MTA2,KDM5A,HIF1A,KDM3A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,IVNS1ABP,FKBP15,ELK3	up_VCAV_EC
GO:0006807	0.286	0.884	6	3221	nitrogen compound metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0065008	0.286	0.85	6	1056	regulation of biological quality	BP	1	HOXC10,MAP2K6,AVPR1A,SIX1,CYP26B1,CDC42EP5	up_VFEM_EC
GO:0009913	0.286	0.846	6	47	epidermal cell differentiation	BP	1	HOXA7,DLL1,SAV1,ZFP36L1,KEAP1,LATS2	up_VSAP_EC
GO:0042180	0.286	0.855	5	61	cellular ketone metabolic process	BP	1	NR1H4,TRIB3,PTGS2,SLC45A3,REST	down_VSAP_EC
GO:0071383	0.286	0.855	5	58	cellular response to steroid hormone stimulus	BP	1	SMARCA4,UBA5,REST,YWHAH,KDM3A	down_VSAP_EC
GO:0019079	0.286	0.87	4	29	viral genome replication	BP	1	MX1,ISG15,ATG16L2,INPP5K	up_ACOR_VSMC
GO:0051153	0.286	0.871	4	28	regulation of striated muscle cell differentiation	BP	1	BMP4,DMPK,FRS2,EDN1	up_ACOR_VSMC

GO:0001843	0.286	0.886	3	38	neural tube closure	BP	1	SDC4,LMO4,IFT57	down_VCAV_EC
GO:0001934	0.286	0.913	2	274	positive regulation of protein phosphorylation	BP	1	NPNT,NTRK2	up_APUL_EC
GO:0023014	0.286	0.912	2	248	signal transduction by protein phosphorylation	BP	1	MAP2K6,CDC42EP5	up_VFEM_EC
GO:0036475	0.286	0.919	2	11	neuron death in response to oxidative stress	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:1903203	0.286	0.919	2	11	regulation of oxidative stress-induced neuron	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:0035493	0.286	0.919	2	11	SNARE complex assembly	BP	1	STX4,VPS11	up_VSAP_EC
GO:0008284	0.286	0.912	2	238	positive regulation of cell proliferation	BP	1	MAB21L1,SHOX2	up_VSAP_VSMC
GO:0045089	0.286	0.956	1	70	positive regulation of innate immune response	BP	1	LYN	down_ACOR_EC
GO:0003256	0.286	0.965	1	4	regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell	BP	1	GREM1	down_ACOR_VSMC
GO:0071051	0.286	0.965	1	4	polyadenylation-dependent snoRNA 3'-end	BP	1	EXOSC5	down_ACOR_VSMC
GO:0018065	0.286	0.965	1	4	protein-cofactor linkage	BP	1	CTH	down_ACOR_VSMC
GO:0045006	0.286	0.965	1	4	DNA deamination	BP	1	EXOSC5	down_ACOR_VSMC
GO:0030031	0.286	0.957	1	155	cell projection assembly	BP	1	FSCN1	down_AFEM_EC
GO:0060627	0.286	0.958	1	165	regulation of vesicle-mediated transport	BP	1	RAB11B	down_VPOR_EC
GO:2000147	0.286	0.958	1	169	positive regulation of cell motility	BP	1	HDAC7	down_VPOR_EC
GO:0048642	0.286	0.963	1	5	negative regulation of skeletal muscle tissue	BP	1	SIX4	down_VSAP_EC
GO:0090128	0.286	0.963	1	5	regulation of synapse maturation	BP	1	DISC1	down_VSAP_EC
GO:0006591	0.286	0.963	1	5	ornithine metabolic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0021824	0.286	0.969	1	3	cerebral cortex tangential migration using cell-axon interactions	BP	1	NRP1	up_ACOR_VSMC
GO:0021828	0.286	0.969	1	3	gonadotrophin-releasing hormone neuronal migration to the	BP	1	NRP1	up_ACOR_VSMC
GO:0021856	0.286	0.969	1	3	hypothalamic tangential migration using cell-axon interactions	BP	1	NRP1	up_ACOR_VSMC
GO:0021886	0.286	0.969	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	up_ACOR_VSMC
GO:0021888	0.286	0.969	1	3	hypothalamus gonadotrophin-releasing hormone neuron	BP	1	NRP1	up_ACOR_VSMC
GO:0021979	0.286	0.969	1	3	hypothalamus cell differentiation	BP	1	NRP1	up_ACOR_VSMC
GO:0030299	0.286	0.968	1	3	intestinal cholesterol absorption	BP	1	LEP	up_ACOR_VSMC
GO:0035290	0.286	0.969	1	3	trunk segmentation	BP	1	NRP1	up_ACOR_VSMC
GO:0036484	0.286	0.969	1	3	trunk neural crest cell migration	BP	1	NRP1	up_ACOR_VSMC
GO:0036486	0.286	0.969	1	3	ventral trunk neural crest cell migration	BP	1	NRP1	up_ACOR_VSMC
GO:0097490	0.286	0.969	1	3	sympathetic neuron projection extension	BP	1	NRP1	up_ACOR_VSMC
GO:0097491	0.286	0.969	1	3	sympathetic neuron projection guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0098856	0.286	0.968	1	3	intestinal lipid absorption	BP	1	LEP	up_ACOR_VSMC
GO:1901166	0.286	0.969	1	3	neural crest cell migration involved in autonomic nervous system	BP	1	NRP1	up_ACOR_VSMC
GO:1903375	0.286	0.969	1	3	facioacoustic ganglion development	BP	1	NRP1	up_ACOR_VSMC
GO:0010955	0.286	0.958	1	14	negative regulation of protein processing	BP	1	GAS1	up_AFEM_EC
GO:0030204	0.286	0.958	1	14	chondroitin sulfate metabolic process	BP	1	XYLT1	up_AFEM_EC
GO:0032613	0.286	0.958	1	14	interleukin-10 production	BP	1	DLL1	up_AFEM_EC

GO:0032722	0.286	0.958	1	14	positive regulation of chemokine production	BP	1	ADAM17	up_AFEM_EC
GO:0050994	0.286	0.958	1	14	regulation of lipid catabolic process	BP	1	ACACB	up_AFEM_EC
GO:0051445	0.286	0.958	1	14	regulation of meiotic cell cycle	BP	1	OVOL1	up_AFEM_EC
GO:0072528	0.286	0.958	1	14	pyrimidine-containing compound biosynthetic	BP	1	GPAM	up_AFEM_EC
GO:1903318	0.286	0.958	1	14	negative regulation of protein maturation	BP	1	GAS1	up_AFEM_EC
GO:2000243	0.286	0.958	1	14	positive regulation of reproductive process	BP	1	OVOL1	up_AFEM_EC
GO:0002520	0.286	0.96	1	279	immune system development	BP	1	HOXA9	up_AORT_VSMC
GO:0021681	0.286	0.965	1	4	cerebellar granular layer development	BP	1	PROX1	up_VCAV_EC
GO:0002643	0.286	0.963	1	5	regulation of tolerance induction	BP	1	HMGB1	up_VCAV_EC
GO:0006027	0.286	0.965	1	4	glycosaminoglycan catabolic process	BP	1	LYVE1	up_VCAV_EC
GO:0042033	0.286	0.965	1	4	chemokine biosynthetic process	BP	1	TLR3	up_VCAV_EC
GO:0045073	0.286	0.965	1	4	regulation of chemokine biosynthetic process	BP	1	TLR3	up_VCAV_EC
GO:0045080	0.286	0.965	1	4	positive regulation of chemokine biosynthetic	BP	1	TLR3	up_VCAV_EC
GO:0050755	0.286	0.965	1	4	chemokine metabolic process	BP	1	TLR3	up_VCAV_EC
GO:0007417	0.286	0.959	1	235	central nervous system development	BP	1	SLITRK5	up_VCAV_VSMC
GO:0048638	0.286	0.956	1	82	regulation of developmental growth	BP	1	SIX1	up_VFEM_EC
GO:0007264	0.286	0.958	1	164	small GTPase mediated signal transduction	BP	1	SLIT2	up_VPUL_VSMC
GO:0048562	0.286126135	0.86589	4	102	embryonic organ morphogenesis	BP	1	SOX9,FZD5,FOXC2,EFEMP1	up_ACOR_EC
GO:0032984	0.286619355	0.8839	3	70	protein-containing complex disassembly	BP	1	TMOD1,ACTN2,VPS16	up_ACOR_EC
GO:0051353	0.286963285	0.95758	1	13	positive regulation of oxidoreductase activity	BP	1	CDH3	up_ACOR_EC
GO:0008150	0.287	0.858	26	5646	biological_process	BP	1	HOXC10,TBX15,EYA1,HOXA9,TOX,MAP2K6,MME,ENOX1,AVPR1A,HOXA10,TRIM9,HOXB7,HOXA7,ENSCAFG00000018194,SIX1,YBX3,MAB21L1,TIAM1,RADIL,RASD2,CYP26B1,CDC42EP5,MTSS1,CA9,ADCY3,CHST7	up_VFEM_EC
GO:0001817	0.287	0.79	20	182	regulation of cytokine production	BP	1	TLR1,PLCG2,LEP,CD83,HTR2B,MBP,FERMT1,ELF1,TLR3,ISG15,CD274,NDRG2,F2RL1,PTPN22,NOD2,B2M,SCAMP5,MAP3K7,PARK7,IL18R1	up_ACOR_VSMC
GO:0061458	0.287	0.806	13	131	reproductive system development	BP	1	PCDH12,KIT,PDGFB,CHD7,TIPARP,EIF2B2,GATA3,MDFI,ARID4B,PTGS2,HIF1A,ATRX,VASH1	up_VCAV_EC
GO:0050789	0.287	0.849	10	3295	regulation of biological process	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,NETO1,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:1903708	0.287	0.83	8	65	positive regulation of hemopoiesis	BP	1	PPARGC1B,ANKRD54,ZBTB16,TOX,ZFP36L1,CD83,PNP,TGFBR2	up_VSAP_EC
GO:0048523	0.287	0.844	7	1399	negative regulation of cellular process	BP	1	NR1H4,TBX5,BPI,TUBB4A,PCSK1N,LZTS1,NTRK2	up_APUL_EC
GO:0006611	0.287	0.845	6	51	protein export from nucleus	BP	1	IWS1,HHEX,THOC1,CTDSPL2,SMG7,NUP133	up_VCAV_EC
GO:0002065	0.287	0.856	5	37	columnar/cuboidal epithelial cell	BP	1	GATA5,GATA4,BMP4,FGFR2,SEC24B	up_ACOR_VSMC
GO:0051241	0.287	0.867	4	336	negative regulation of multicellular organismal	BP	1	HOOK3,SEMA3A,ASPN,RNF6	up_VPOR_EC
GO:0006304	0.287	0.888	3	22	DNA modification	BP	1	EZH2,EXOSC5,MIS18A	down_ACOR_VSMC
GO:0070509	0.287	0.913	2	21	calcium ion import	BP	1	PRNP,TRPV2	down_VCAV_EC
GO:0046907	0.287	0.916	2	536	intracellular transport	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:1903793	0.287	0.918	2	11	positive regulation of anion transport	BP	1	TCAF1,PSEN1	up_ACOR_VSMC
GO:0007167	0.287	0.912	2	274	enzyme linked receptor protein signaling pathway	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0140112	0.287	0.915	2	15	extracellular vesicle biogenesis	BP	1	RAB11A,RAB27A	up_VCAV_EC
GO:0032881	0.287	0.918	2	11	regulation of polysaccharide metabolic	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0032885	0.287	0.918	2	11	regulation of polysaccharide	BP	1	C1QTNF2,PASK	up_VSAP_EC

GO:0070670	0.287	0.918	2	11	response to interleukin-4	BP	1	STAT6,KEAP1	up_VSAP_EC
GO:0071353	0.287	0.918	2	11	cellular response to interleukin-4	BP	1	STAT6,KEAP1	up_VSAP_EC
GO:2001275	0.287	0.918	2	11	positive regulation of glucose import in response to insulin	BP	1	KLF15,PIK3R1	up_VSAP_EC
GO:0006991	0.287	0.965	1	4	response to sterol depletion	BP	1	INSIG1	down_ACOR_VSMC
GO:0032933	0.287	0.965	1	4	SREBP signaling pathway	BP	1	INSIG1	down_ACOR_VSMC
GO:0051292	0.287	0.965	1	4	nuclear pore complex assembly	BP	1	NDC1	down_ACOR_VSMC
GO:0071501	0.287	0.965	1	4	cellular response to sterol depletion	BP	1	INSIG1	down_ACOR_VSMC
GO:0051272	0.287	0.957	1	170	positive regulation of cellular component	BP	1	HDAC7	down_VPOR_EC
GO:0010605	0.287	0.968	1	745	negative regulation of macromolecule metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0006700	0.287	0.963	1	5	C21-steroid hormone biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0055062	0.287	0.963	1	5	phosphate ion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0072505	0.287	0.963	1	5	divalent inorganic anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0072506	0.287	0.963	1	5	trivalent inorganic anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:0032310	0.287	0.968	1	3	prostaglandin secretion	BP	1	LEP	up_ACOR_VSMC
GO:0036091	0.287	0.968	1	3	positive regulation of transcription from RNA polymerase II promoter in response to oxidative	BP	1	CHD6	up_ACOR_VSMC
GO:1900273	0.287	0.968	1	3	positive regulation of long-term synaptic	BP	1	APP	up_ACOR_VSMC
GO:0006220	0.287	0.957	1	14	pyrimidine nucleotide metabolic process	BP	1	GPAM	up_AFEM_EC
GO:0001953	0.287	0.957	1	14	negative regulation of cell-matrix adhesion	BP	1	HOXA7	up_AFEM_EC
GO:0002090	0.287	0.957	1	14	regulation of receptor internalization	BP	1	GREM1	up_AFEM_EC
GO:0035384	0.287	0.957	1	14	thioester biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0048635	0.287	0.958	1	14	negative regulation of muscle organ	BP	1	DLL1	up_AFEM_EC
GO:0071616	0.287	0.957	1	14	acyl-CoA biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:1901862	0.287	0.957	1	14	negative regulation of muscle tissue	BP	1	DLL1	up_AFEM_EC
GO:1902742	0.287	0.957	1	14	apoptotic process involved in development	BP	1	CRYAB	up_AFEM_EC
GO:1903556	0.287	0.957	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	BPI	up_AFEM_EC
GO:0032940	0.287	0.958	1	231	secretion by cell	BP	1	TLR2	up_AFEM_VSMC
GO:0014850	0.287	0.965	1	4	response to muscle activity	BP	1	HIF1A	up_VCAV_EC
GO:0060159	0.287	0.965	1	4	regulation of dopamine receptor signaling	BP	1	CAV2	up_VCAV_EC
GO:0060161	0.287	0.965	1	4	positive regulation of dopamine receptor	BP	1	CAV2	up_VCAV_EC
GO:0060729	0.287	0.965	1	4	intestinal epithelial structure maintenance	BP	1	TLR4	up_VCAV_EC
GO:0009145	0.287	0.956	1	40	purine nucleoside triphosphate biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0072511	0.287	0.956	1	97	divalent inorganic cation transport	BP	1	HOXA3	up_VPUL_EC
GO:1901699	0.287	0.957	1	164	cellular response to nitrogen compound	BP	1	SLIT2	up_VPUL_VSMC
GO:0070482	0.287	0.956	1	75	response to oxygen levels	BP	1	CAV1	up_VSAP_VSMC
GO:0018108	0.287	0.956	1	79	peptidyl-tyrosine phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0034330	0.287	0.956	1	80	cell junction organization	BP	1	CAV1	up_VSAP_VSMC
GO:1904892	0.287188537	0.91107	2	40	regulation of STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:0051216	0.287743247	0.88321	3	70	cartilage development	BP	1	SOX9,PTH1R,EFEMP1	up_ACOR_EC

GO:0045089	0.287796726	0.88318	3	70	positive regulation of innate immune response	BP	1	NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0017015	0.287963084	0.91067	2	40	regulation of transforming growth factor beta receptor signaling	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:1903844	0.287963084	0.91067	2	40	regulation of cellular response to transforming growth factor beta	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:1902680	0.288	0.767	43	415	positive regulation of RNA biosynthetic process	BP	1	HOXA11,FZD1,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,ZBTB16,RARG,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,NPAS2,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:1903508	0.288	0.767	43	415	positive regulation of nucleic acid-templated transcription	BP	1	HOXA11,FZD1,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,ZBTB16,RARG,F2RL1,ICE1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,NPAS2,CDK9,PRMT2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:0040017	0.288	0.79	20	180	positive regulation of locomotion	BP	1	VEGFD,LGR6,BMP4,SH3RF2,SASH1,FGF18,F2RL1,NRP1,PRKCE,APP,SEMA6D,CCL5,DDR2,EDN1,FAM107A,DOCK5,BVES,RREB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0050673	0.288	0.8	15	135	epithelial cell proliferation	BP	1	VEGFD,LEP,HTR2B,FERMT1,BMP4,FGFR2,CDKN2B,LIMS2,FRS2,PSEN1,TGFBR1,SYNJ2BP,SERPINB5,WDR48,RREB1	up_ACOR_VSMC
GO:0010720	0.288	0.806	13	110	positive regulation of cell development	BP	1	BMP4,PDE5A,ZNF365,NRP1,SMARCD3,FZD3,APP,PSEN1,EDN1,DISC1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0033674	0.288	0.812	11	144	positive regulation of kinase activity	BP	1	VEGFA,PTPN11,TNIK,ADAM17,MAGED1,LYN,MMD,VLDLR,SH3GLB1,PAK2,MADD	down_VSAP_EC
GO:0015672	0.288	0.822	9	89	monovalent inorganic cation transport	BP	1	NNT,NEDD4,CAV1,NKAIN1,CDK2,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:1903008	0.288	0.845	6	47	organelle disassembly	BP	1	RETREG1,AMBRA1,MFN2,FBXO7,HTRA2,FUNDC2	up_VSAP_EC
GO:0044281	0.288	0.869	4	622	small molecule metabolic process	BP	1	MME,CYP26B1,ADCY3,CHST7	up_VFEM_EC
GO:0007565	0.288	0.887	3	23	female pregnancy	BP	1	ACSL4,PPARD,EMP2	down_ACOR_VSMC
GO:0051893	0.288	0.889	3	20	regulation of focal adhesion assembly	BP	1	NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0090109	0.288	0.889	3	20	regulation of cell-substrate junction	BP	1	NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0001889	0.288	0.888	3	22	liver development	BP	1	TNFAIP3,HHEX,PROX1	up_VCAV_EC
GO:0010522	0.288	0.887	3	24	regulation of calcium ion transport into cytosol	BP	1	PDE4D,CHD7,APLNR	up_VCAV_EC
GO:0055086	0.288	0.911	2	237	nucleobase-containing small molecule metabolic	BP	1	CSGALNACT1,TNRC6B	down_ACOR_EC
GO:0034766	0.288	0.913	2	19	negative regulation of ion transmembrane transport	BP	1	REM1,CALM1	down_VSAP_EC
GO:0044764	0.288	0.918	2	11	multi-organism cellular process	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0016331	0.288	0.956	1	66	morphogenesis of embryonic epithelium	BP	1	SULF1	down_ACOR_EC
GO:0002323	0.288	0.965	1	4	natural killer cell activation involved in	BP	1	CORO1A	down_ACOR_VSMC
GO:0010715	0.288	0.964	1	4	regulation of extracellular matrix disassembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0043320	0.288	0.965	1	4	natural killer cell degranulation	BP	1	CORO1A	down_ACOR_VSMC
GO:0007413	0.288	0.962	1	5	axonal fasciculation	BP	1	NRP1	down_VSAP_EC
GO:0106030	0.288	0.962	1	5	neuron projection fasciculation	BP	1	NRP1	down_VSAP_EC
GO:0045719	0.288	0.968	1	3	negative regulation of glycogen biosynthetic	BP	1	INPP5K	up_ACOR_VSMC
GO:0060332	0.288	0.968	1	3	positive regulation of response to interferon-	BP	1	PARP9	up_ACOR_VSMC
GO:0060335	0.288	0.968	1	3	positive regulation of interferon-gamma-mediated signaling	BP	1	PARP9	up_ACOR_VSMC
GO:0070874	0.288	0.968	1	3	negative regulation of glycogen metabolic	BP	1	INPP5K	up_ACOR_VSMC
GO:0098917	0.288	0.968	1	3	retrograde trans-synaptic signaling	BP	1	DAG1	up_ACOR_VSMC

GO:0060359	0.288	0.957	1	14	response to ammonium ion	BP	1	CHRM2	up_AFEM_EC
GO:0090184	0.288	0.957	1	14	positive regulation of kidney development	BP	1	GREM1	up_AFEM_EC
GO:1902108	0.288	0.957	1	14	regulation of mitochondrial membrane permeability involved in	BP	1	CAMK2A	up_AFEM_EC
GO:0051050	0.288	0.958	1	235	positive regulation of transport	BP	1	TLR2	up_AFEM_VSMC
GO:0080135	0.288	0.958	1	240	regulation of cellular response to stress	BP	1	EYA1	up_AFEM_VSMC
GO:0039530	0.288	0.964	1	4	MDA-5 signaling pathway	BP	1	RIOK3	up_VCAV_EC
GO:0060766	0.288	0.968	1	3	negative regulation of androgen receptor	BP	1	SMARCA4	up_VCAV_EC
GO:0016567	0.288	0.958	1	232	protein ubiquitination	BP	1	LIMK1	up_VCAV_VSMC
GO:0072089	0.288	0.955	1	43	stem cell proliferation	BP	1	ARHGEF2	up_VPOR_EC
GO:0016570	0.288	0.956	1	143	histone modification	BP	1	EYA1	up_VFEM_VSMC
GO:0051052	0.288	0.956	1	145	regulation of DNA metabolic process	BP	1	EYA1	up_VFEM_VSMC
GO:0006790	0.288	0.956	1	99	sulfur compound metabolic process	BP	1	ENSCAFG00000028814	up_VPUL_EC
GO:0043434	0.288	0.956	1	80	response to peptide hormone	BP	1	CAV1	up_VSAP_VSMC
GO:0016571	0.288118526	0.91066	2	39	histone methylation	BP	1	NR1H4,PYGO2	up_ACOR_EC
GO:0048583	0.289	0.778	29	1095	regulation of response to stimulus	BP	1	CMKLR1,LEP,LBH,CRY2,GAS1,CD40,DLL1,F3,PLXNA4,MLLT11,LMCD1,TMEM100,PLAGL2,GREM1,FAM53B,GREM2,CLEC16A,CYLD,POSTN,LRRC15,RECK,LGR6,RAB7A,AXIN2,NAPEPLD,CCL5,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0048872	0.289	0.821	9	85	homeostasis of number of cells	BP	1	HMGB1,HSPA9,PRMT1,EZH2,HMGB2,CORO1A,BAP1,JMJD6,PIK3CD	down_ACOR_VSMC
GO:0015850	0.289	0.855	5	37	organic hydroxy compound transport	BP	1	LEP,LCAT,ABCA1,SCP2,PARK7	up_ACOR_VSMC
GO:2000177	0.289	0.87	4	26	regulation of neural precursor cell	BP	1	LIMS2,SMARCD3,FZD3,DISC1	up_ACOR_VSMC
GO:0002687	0.289	0.867	4	36	positive regulation of leukocyte migration	BP	1	SELP,CXCL8,SWAP70,HMGB1	up_VCAV_EC
GO:0023051	0.289	0.892	3	954	regulation of signaling	BP	1	HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0009798	0.289	0.885	3	31	axis specification	BP	1	TMED2,CTNNB1,DDIT3	down_VSAP_EC
GO:0031529	0.289	0.888	3	20	ruffle organization	BP	1	ARHGEF26,EVL,INPP5K	up_ACOR_VSMC
GO:0032330	0.289	0.888	3	20	regulation of chondrocyte differentiation	BP	1	BMP4,LNPK,FGF18	up_ACOR_VSMC
GO:0014812	0.289	0.888	3	21	muscle cell migration	BP	1	DOCK4,PDGFB,MEF2C	up_VCAV_EC
GO:1902042	0.289	0.917	2	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	DAPK1,PARK7	up_ACOR_VSMC
GO:0002711	0.289	0.915	2	14	positive regulation of T cell mediated immunity	BP	1	GATA3,NECTIN2	up_VCAV_EC
GO:0009112	0.289	0.915	2	14	nucleobase metabolic process	BP	1	MTOR,ACPP	up_VCAV_EC
GO:0034508	0.289	0.914	2	15	centromere complex assembly	BP	1	CENPC,SENP6	up_VCAV_EC
GO:0010605	0.289	0.919	2	745	negative regulation of macromolecule metabolic	BP	1	LIMK1,GATA5	up_VCAV_VSMC
GO:0045736	0.289	0.917	2	11	negative regulation of cyclin-dependent protein serine/threonine kinase	BP	1	FBXO7,LATS2	up_VSAP_EC
GO:1904030	0.289	0.917	2	11	negative regulation of cyclin-dependent protein	BP	1	FBXO7,LATS2	up_VSAP_EC
GO:0035176	0.289	0.917	2	11	social behavior	BP	1	SLC6A4,PPP3CB	up_VSAP_EC
GO:0051703	0.289	0.917	2	11	intraspecies interaction between organisms	BP	1	SLC6A4,PPP3CB	up_VSAP_EC
GO:0030705	0.289	0.956	1	56	cytoskeleton-dependent intracellular transport	BP	1	SPG11	down_ACOR_EC
GO:0035148	0.289	0.955	1	66	tube formation	BP	1	HOXA1	down_ACOR_EC
GO:0032377	0.289	0.964	1	4	regulation of intracellular lipid transport	BP	1	NUS1	down_ACOR_VSMC
GO:0032380	0.289	0.964	1	4	regulation of intracellular sterol transport	BP	1	NUS1	down_ACOR_VSMC

GO:0032383	0.289	0.964	1	4	regulation of intracellular cholesterol transport	BP	1	NUS1	down_ACOR_VSMC
GO:0060136	0.289	0.964	1	4	embryonic process involved in female	BP	1	ACSL4	down_ACOR_VSMC
GO:0051716	0.289	1	1	2001	cellular response to stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0007350	0.289	0.96	1	7	blastoderm segmentation	BP	1	PCSK6	down_VCAV_EC
GO:0010587	0.289	0.962	1	5	miRNA catabolic process	BP	1	SND1	down_VSAP_EC
GO:0032230	0.289	0.962	1	5	positive regulation of synaptic transmission,	BP	1	KIF5B	down_VSAP_EC
GO:0030252	0.289	0.968	1	3	growth hormone secretion	BP	1	CHD7	up_ACOR_VSMC
GO:0031294	0.289	0.964	1	4	lymphocyte costimulation	BP	1	CD274	up_ACOR_VSMC
GO:0070098	0.289	0.957	1	14	chemokine-mediated signaling pathway	BP	1	CCL5	up_AFEM_EC
GO:0097178	0.289	0.957	1	14	ruffle assembly	BP	1	KANK1	up_AFEM_EC
GO:0009607	0.289	0.958	1	232	response to biotic stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0048711	0.289	0.964	1	4	positive regulation of astrocyte differentiation	BP	1	BMP2	up_VCAV_EC
GO:0003071	0.289	0.962	1	5	renal system process involved in regulation of systemic arterial blood	BP	1	PDGFB	up_VCAV_EC
GO:0090045	0.289	0.964	1	4	positive regulation of deacetylase activity	BP	1	PRKD2	up_VCAV_EC
GO:0010715	0.289	0.964	1	4	regulation of extracellular matrix disassembly	BP	1	FSCN1	up_VCAV_EC
GO:0050927	0.289	0.962	1	5	positive regulation of positive chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:0060149	0.289	0.964	1	4	negative regulation of posttranscriptional gene	BP	1	PPP3CA	up_VCAV_EC
GO:0060965	0.289	0.964	1	4	negative regulation of gene silencing by miRNA	BP	1	PPP3CA	up_VCAV_EC
GO:0060967	0.289	0.964	1	4	negative regulation of gene silencing by RNA	BP	1	PPP3CA	up_VCAV_EC
GO:1903799	0.289	0.964	1	4	negative regulation of production of miRNAs involved in gene silencing	BP	1	PPP3CA	up_VCAV_EC
GO:0051050	0.289	0.958	1	235	positive regulation of transport	BP	1	CA2	up_VCAV_VSMC
GO:0008154	0.289	0.955	1	81	actin polymerization or depolymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0030099	0.289	0.956	1	133	myeloid cell differentiation	BP	1	HOXA9	up_VFEM_VSMC
GO:0031503	0.289	0.955	1	79	protein-containing complex localization	BP	1	NETO1	up_VSAP_VSMC
GO:0031113	0.289306032	0.95684	1	13	regulation of microtubule polymerization	BP	1	TUBB4A	up_ACOR_EC
GO:0006505	0.289327891	0.95683	1	13	GPI anchor metabolic process	BP	1	PIGS	up_ACOR_EC
GO:0006506	0.289327891	0.95683	1	13	GPI anchor biosynthetic process	BP	1	PIGS	up_ACOR_EC
GO:0019748	0.289403981	0.95681	1	13	secondary metabolic process	BP	1	CDH3	up_ACOR_EC
GO:0016101	0.289722688	0.9567	1	13	diterpenoid metabolic process	BP	1	RARRES2	up_ACOR_EC
GO:1901890	0.289908133	0.95664	1	13	positive regulation of cell junction assembly	BP	1	NRP1	up_ACOR_EC
GO:0061217	0.289979788	0.95662	1	13	regulation of mesonephros	BP	1	SOX9	up_ACOR_EC
GO:0010647	0.29	0.762	48	460	positive regulation of cell communication	BP	1	CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,LIMS2,IL6R,CRADD,ABL1,EMP2,DLL1,EPN2,MAP3K5,PDGFD,C1QTNF2,HPSE,CCBE1,F2RL1,TRAF7,PIK3R1,RBCK1,FAM53B,SULF2,SHOX2,SASH1,CREBRF,MYD88,S100A4,TSPAN5,ENSCAFG00000011993,RAF1,CYBA,ZNF205,STX4,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,CITED2,BAG4,TRADD,DEDD2	up_VSAP_EC
GO:0051129	0.29	0.785	21	221	negative regulation of cellular component organization	BP	1	ARHGEF15,IFRD1,ARHGAP28,TMOD1,PPP3CA,RIOK3,STMN1,SWAP70,APOD,RAPGEF2,TAOK1,HMGB1,RAD21,ZW10,KDM5A,KDM3A,ATRX,DCP2,TMOD3,ARHGEF2,FBXO5	up_VCAV_EC
GO:0048608	0.29	0.804	13	129	reproductive structure development	BP	1	SLC29A1,SF1,DHCR24,E2F8,PPARD,FOSL1,PLK4,HMGB2,SGPL1,ASPM,HOXA9,RTCB,SIX4	down_ACOR_VSMC

GO:0090287	0.29	0.84	6	91	regulation of cellular response to growth factor	BP	1	DCN,VASN,FBN1,CHRDL1,ASPN,GREM1	down_VCAV_EC
GO:0021953	0.29	0.843	6	49	central nervous system neuron differentiation	BP	1	EPHB1,DLL4,GDPD5,PROX1,RAPGEF2,SPTBN4	up_VCAV_EC
GO:0071356	0.29	0.842	6	57	cellular response to tumor necrosis factor	BP	1	CXCL8,GATA3,RIPK1,ENSCAFG00000002015,ARHGEF2,TJP2	up_VCAV_EC
GO:0008643	0.29	0.853	5	45	carbohydrate transport	BP	1	SLC35A3,EDN1,YES1,RSC1A1,SLC2A3	up_VCAV_EC
GO:0002819	0.29	0.865	4	44	regulation of adaptive immune response	BP	1	SOCS5,FAM49B,PVR,TFRC	down_VSAP_EC
GO:0046660	0.29	0.868	4	28	female sex differentiation	BP	1	CHD7,ARID5B,DMC1,LHX9	up_ACOR_VSMC
GO:0048583	0.29	0.873	4	1095	regulation of response to stimulus	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0014065	0.29	0.883	3	39	phosphatidylinositol 3-kinase signaling	BP	1	DCN,ZFP36L1,MYDGF	down_VCAV_EC
GO:0014013	0.29	0.888	3	19	regulation of gliogenesis	BP	1	ZNF365,APP,CRKL	up_ACOR_VSMC
GO:0007159	0.29	0.882	3	79	leukocyte cell-cell adhesion	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0010959	0.29	0.881	3	79	regulation of metal ion transport	BP	1	CAMK2A,FXYD1,DMPK	up_AFEM_EC
GO:0048589	0.29	0.91	2	188	developmental growth	BP	1	SPG11,NRP2	down_ACOR_EC
GO:0061024	0.29	0.91	2	215	membrane organization	BP	1	SPG11,STX4	down_ACOR_EC
GO:0045648	0.29	0.915	2	13	positive regulation of erythrocyte	BP	1	PRMT1,HMGB2	down_ACOR_VSMC
GO:0060976	0.29	0.912	2	22	coronary vasculature development	BP	1	PDGFRB,SPRED1	down_VCAV_EC
GO:0006357	0.29	0.914	2	547	regulation of transcription by RNA polymerase II	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0002066	0.29	0.913	2	17	columnar/cuboidal epithelial cell	BP	1	HIF1A,KLF5	down_VSAP_EC
GO:0001958	0.29	0.917	2	11	endochondral ossification	BP	1	BMP4,FGF18	up_ACOR_VSMC
GO:0036075	0.29	0.917	2	11	replacement ossification	BP	1	BMP4,FGF18	up_ACOR_VSMC
GO:0045893	0.29	0.913	2	413	positive regulation of transcription, DNA-	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0032715	0.29	0.917	2	11	negative regulation of interleukin-6 production	BP	1	C5AR2,NLRX1	up_VSAP_EC
GO:0043300	0.29	0.917	2	11	regulation of leukocyte degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0007039	0.29	0.959	1	7	protein catabolic process in the vacuole	BP	1	LRP1	down_VCAV_EC
GO:0044703	0.29	0.956	1	172	multi-organism reproductive process	BP	1	CITED2	down_VPOR_EC
GO:0043653	0.29	0.96	1	6	mitochondrial fragmentation involved in	BP	1	BNIP3	down_VSAP_EC
GO:1901135	0.29	0.96	1	390	carbohydrate derivative metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:1990791	0.29	0.968	1	3	dorsal root ganglion development	BP	1	NRP1	up_ACOR_VSMC
GO:2000145	0.29	0.959	1	279	regulation of cell motility	BP	1	WNT7A	up_AORT_VSMC
GO:0016236	0.29	0.955	1	88	macroautophagy	BP	1	LZTS1	up_APUL_EC
GO:0045595	0.29	0.962	1	469	regulation of cell differentiation	BP	1	TBX5	up_APUL_VSMC
GO:2000659	0.29	0.964	1	4	regulation of interleukin-1-mediated signaling	BP	1	OTUD4	up_VCAV_EC
GO:0010243	0.29	0.957	1	238	response to organonitrogen	BP	1	CA2	up_VCAV_VSMC
GO:0050865	0.29	0.956	1	135	regulation of cell activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0002696	0.29	0.955	1	80	positive regulation of leukocyte activation	BP	1	TOX	up_VFEM_EC
GO:0097191	0.29	0.955	1	79	extrinsic apoptotic signaling pathway	BP	1	EYA1	up_VFEM_EC
GO:0016569	0.29	0.956	1	144	covalent chromatin modification	BP	1	EYA1	up_VFEM_VSMC
GO:0051271	0.29	0.955	1	98	negative regulation of cellular component	BP	1	TBX5	up_VPUL_EC
GO:0046486	0.290158218	0.8632	4	102	glycerolipid metabolic process	BP	1	NR1H4,ENSCAFG00000004331,PIGS,AGPAT2	up_ACOR_EC
GO:0046718	0.290842433	0.95635	1	13	viral entry into host cell	BP	1	TRIM8	up_ACOR_EC
GO:0038084	0.29085803	0.95634	1	13	vascular endothelial growth factor signaling	BP	1	NRP1	up_ACOR_EC

GO:0006464	0.291	0.744	117	1162	cellular protein modification process	BP	1	FGF13,ADRA1B,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MBP,ZRANB1,LIPT2,B3GALNT2,SKP2,PRKAA2,BMP4,B3GNT7,FGFR2,CCDC126,ABCA1,ATRX,TLR3,SH3RF2,LATS2,PIGN,PDE5A,PIGS,ISG15,SASH1,FGF18,NDRG2,TMX3,CDKN2B,USP53,GRK7,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,ERO1B,DAPK1,MAGT1,EGLN1,SUMF1,NCEH1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,OS9,STT3B,SMPD1,FUT11,UBE2H,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,FRS2,RNF19A,LYPLAL1,DAG1,FUT8,POMK,PARP9,APP,PSEN1,SYNJ2BP,SHPRH,PIK3C3,CCL5,DDR2,PSKH1,DUSP22,EDN1,OXR1,RNF141,PHF20,AKTIP,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PRKAG3,SH3RF3,EOGT,DCUN1D4,RNF181,USP20,HERPUD1,RPRD1B,MAP3K7,INPP5K,CNOT4,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,ENSCAFG00000029553,PARK7,ZDHHC21,LMF1,CRKL,CDKL2	up_ACOR_VSMC
GO:0036211	0.291	0.744	117	1162	protein modification process	BP	1	FGF13,ADRA1B,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MBP,ZRANB1,LIPT2,B3GALNT2,SKP2,PRKAA2,BMP4,B3GNT7,FGFR2,CCDC126,ABCA1,ATRX,TLR3,SH3RF2,LATS2,PIGN,PDE5A,PIGS,ISG15,SASH1,FGF18,NDRG2,TMX3,CDKN2B,USP53,GRK7,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,ERO1B,DAPK1,MAGT1,EGLN1,SUMF1,NCEH1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,OS9,STT3B,SMPD1,FUT11,UBE2H,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,FRS2,RNF19A,LYPLAL1,DAG1,FUT8,POMK,PARP9,APP,PSEN1,SYNJ2BP,SHPRH,PIK3C3,CCL5,DDR2,PSKH1,DUSP22,EDN1,OXR1,RNF141,PHF20,AKTIP,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PRKAG3,SH3RF3,EOGT,DCUN1D4,RNF181,USP20,HERPUD1,RPRD1B,MAP3K7,INPP5K,CNOT4,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,ENSCAFG00000029553,PARK7,ZDHHC21,LMF1,CRKL,CDKL2	up_ACOR_VSMC
GO:0006996	0.291	0.746	114	1301	organelle organization	BP	1	PLK2,TEK,HCLS1,KIT,ARHGEF15,ENSCAFG00000007112,ATP8A1,MX2,AMOT,PDGFB,BAIAP2L1,RELN,IWS1,MEF2C,CHD7,GATA3,EDN1,RAB11A,RALB,RAB27A,PSME4,ARHGAP28,TMOD1,FIGNL1,NASP,MTSS1,NECTIN2,MTOR,HOOK3,SNAP23,HHEX,CAV2,SLK,CEP68,CNOT6,PDZD8,ABCA1,NCKAP1,MZT1,PROX1,UHRF2,IQGAP2,ENSCAFG00000010224,EPB41,ELMO1,ARID4B,STMN1,FLNB,SNX2,HMBOX1,BAZ1A,PAK2,PRKD2,SH3GLB1,SWAP70,SMARCA4,CENPC,NCK1,ESCO1,EXOC5,FES,NSD1,MRRF,HIST1H1A,TOP1,CREB1,SENP6,PAN3,GCC2,TAOK1,CTNNA1,CNOT7,FMNL3,STX11,SMG7,VPS54,ASF1A,HMGB1,TBC1D1,PMAIP1,ARPC5L,BLM,NUP133,SMC5,LSM14A,RAD21,DNAJC13,ARHGDIB,ZW10,KDM5A,HIF1A,KDM3A,ARHGAP26,ALS2,IQUB,ATRX,HAUS3,HIST2H2AC,HP1BP3,GAS2L3,DCP2,TNFAIP1,ATP2A1,SPATA6,TMOD3,RABGAP1,TET2,ARHGEF2,FSCN1,FBXO5,USP6NL,ZMYM2,SASS6,GINS4	up_VCAV_EC
GO:0006796	0.291	0.748	95	938	phosphate-containing compound metabolic process	BP	1	FGF13,ADRA1B,SMAD6,PIP5K1B,PLCG2,LEP,PLCL1,MAP3K8,MID1,CDC7,HTR2B,RASSF2,MBP,PRKAA2,BMP4,LCAT,CHPT1,FGFR2,TLR3,SH3RF2,PPARGC1A,LATS2,PIGN,PDE5A,PIGS,PLPP2,AR,SASH1,LMO4,PFKM,FGF18,NDRG2,CDKN2B,ADCY6,PPIP5K1,GRK7,PIGG,F2RL1,FAM129A,CAMK2D,DAPK1,NCEH1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,MARF1,CRLS1,FRS2,DAG1,ENSCAFG00000018611,PPP1R26,PARP9,APP,PSEN1,SYNJ2BP,PIK3C3,CCL5,DDR2,CLN8,PSKH1,DUSP22,EDN1,ALDOC,AKTIP,DUSP26,NOD2,LRRC4,ENTPD3,LMTK2,PRKAG3,DDIT4,SH3RF3,SERINC3,SERINC1,CFI,RPRD1B,MAP3K7,INPP5K,PFKL,NT5C2,ENSCAFG00000029553,NMNAT1,PARK7,ELOVL7,GPATCH2,ZFYVE1,CRKL,CDKL2	up_ACOR_VSMC

GO:0036503	0.291	0.843	6	47	ERAD pathway	BP	1	OS9,STT3B,HERPUD1,FAF2,WFS1,DZIP3	up_ACOR_VSMC
GO:0072524	0.291	0.853	5	37	pyridine-containing compound metabolic	BP	1	NADK,GALK1,PNPO,PNP,DDIT4	up_VSAP_EC
GO:0035270	0.291	0.866	4	35	endocrine system development	BP	1	GATA3,BMP2,HHEX,CREB1	up_VCAV_EC
GO:0009308	0.291	0.887	3	20	amine metabolic process	BP	1	MOXD1,AZIN2,PARK7	up_ACOR_VSMC
GO:0019748	0.291	0.915	2	13	secondary metabolic process	BP	1	GSTO1,CTH	down_ACOR_VSMC
GO:0031113	0.291	0.914	2	13	regulation of microtubule polymerization	BP	1	STMN1,RAC1	down_ACOR_VSMC
GO:0036475	0.291	0.916	2	11	neuron death in response to oxidative stress	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0003382	0.291	0.917	2	11	epithelial cell morphogenesis	BP	1	ARHGEF26,SPINT2	up_ACOR_VSMC
GO:1903203	0.291	0.916	2	11	regulation of oxidative stress-induced neuron	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:2001169	0.291	0.916	2	11	regulation of ATP biosynthetic process	BP	1	PPARGC1A,DDIT4	up_ACOR_VSMC
GO:0031113	0.291	0.915	2	13	regulation of microtubule polymerization	BP	1	STMN1,FES	up_VCAV_EC
GO:0040019	0.291	0.915	2	12	positive regulation of embryonic development	BP	1	AMOT,GATA3	up_VCAV_EC
GO:0071396	0.291	0.909	2	134	cellular response to lipid	BP	1	MTDH,RNF6	up_VPOR_EC
GO:0099536	0.291	0.909	2	133	synaptic signaling	BP	1	HTR7,SV2C	up_VPOR_EC
GO:1902680	0.291	0.912	2	415	positive regulation of RNA biosynthetic process	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:1903508	0.291	0.912	2	415	positive regulation of nucleic acid-templated	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0070646	0.291	0.955	1	63	protein modification by small protein removal	BP	1	USP28	down_ACOR_EC
GO:2000641	0.291	0.964	1	4	regulation of early endosome to late	BP	1	EZR	down_ACOR_VSMC
GO:2001198	0.291	0.964	1	4	regulation of dendritic cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:1901360	0.291	1	1	2016	organic cyclic compound metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0031958	0.291	0.962	1	5	corticosteroid receptor signaling pathway	BP	1	YWHAH	down_VSAP_EC
GO:0042921	0.291	0.962	1	5	glucocorticoid receptor signaling pathway	BP	1	YWHAH	down_VSAP_EC
GO:0072109	0.291	0.96	1	6	glomerular mesangium development	BP	1	ACTA2	down_VSAP_EC
GO:0001826	0.291	0.967	1	3	inner cell mass cell differentiation	BP	1	LATS2	up_ACOR_VSMC
GO:0045794	0.291	0.967	1	3	negative regulation of cell volume	BP	1	CLCN3	up_ACOR_VSMC
GO:0043410	0.291	0.956	1	144	positive regulation of MAPK cascade	BP	1	TAOK1	up_AORT_EC
GO:0000902	0.291	0.958	1	266	cell morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:1901701	0.291	0.958	1	271	cellular response to oxygen-containing	BP	1	ESR1	up_AORT_VSMC
GO:0035809	0.291	0.964	1	4	regulation of urine volume	BP	1	EDN1	up_VCAV_EC
GO:0035810	0.291	0.964	1	4	positive regulation of urine volume	BP	1	EDN1	up_VCAV_EC
GO:0033690	0.291	0.964	1	4	positive regulation of osteoblast proliferation	BP	1	BMP2	up_VCAV_EC
GO:0045743	0.291	0.967	1	3	positive regulation of fibroblast growth factor receptor signaling	BP	1	PRKD2	up_VCAV_EC
GO:0035023	0.291	0.954	1	46	regulation of Rho protein signal transduction	BP	1	ARHGEF2	up_VPOR_EC
GO:0003018	0.291	0.955	1	42	vascular process in circulatory system	BP	1	HTR7	up_VPOR_EC
GO:0071241	0.291	0.954	1	42	cellular response to inorganic substance	BP	1	FBP1	up_VPOR_EC
GO:0016042	0.291	0.955	1	80	lipid catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0051054	0.291	0.955	1	81	positive regulation of DNA metabolic process	BP	1	EYA1	up_VFEM_EC
GO:0032990	0.291	0.956	1	167	cell part morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0060828	0.291	0.955	1	82	regulation of canonical Wnt signaling pathway	BP	1	CAV1	up_VSAP_VSMC

GO:1903532	0.291	0.955	1	78	positive regulation of secretion by cell	BP	1	TLR2	up_VSAP_VSMC
GO:0070647	0.292	0.77	33	311	protein modification by small protein conjugation or removal	BP	1	PCGF5,ZRANB1,SKP2,SH3RF2,ISG15,SASH1,USP53,KLHL20,MARCH5,PTPN22,OS9,UBE2H,SH3RF1,RNF24,PRKCE,RNF19A,PSEN1,SHPRH,RNF141,NOD2,FAM107A,SH3RF3,DCUN1D4,RNF181,USP20,HERPUD1,CNOT4,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,PARK7	up_ACOR_VSMC
GO:0008152	0.292	0.863	9	3714	metabolic process	BP	1	CST3,HDAC7,CITED2,GSTP1,RAB11B,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:1903532	0.292	0.825	8	78	positive regulation of secretion by cell	BP	1	FERMT1,GATA3,EDN1,RAB27A,CREB1,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0034765	0.292	0.831	7	91	regulation of ion transmembrane transport	BP	1	REM1,WDR1,LYN,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0019953	0.292	0.848	5	152	sexual reproduction	BP	1	HOXA9,LEP,THRB,OVOL1,SPATA6	up_AFEM_EC
GO:1902806	0.292	0.866	4	33	regulation of cell cycle G1/S phase transition	BP	1	CASP2,EZH2,GLI1,MTBP	down_ACOR_VSMC
GO:0051494	0.292	0.864	4	44	negative regulation of cytoskeleton organization	BP	1	ARHGEF2,TWF1,CAPG,MID1	down_VSAP_EC
GO:0007062	0.292	0.867	4	29	sister chromatid cohesion	BP	1	ESCO1,SMC5,RAD21,ATRX	up_VCAV_EC
GO:0072527	0.292	0.885	3	23	pyrimidine-containing compound metabolic	BP	1	TK1,DCK,CTPS1	down_ACOR_VSMC
GO:0007062	0.292	0.884	3	29	sister chromatid cohesion	BP	1	NAA10,CTNNB1,PDS5B	down_VSAP_EC
GO:0006915	0.292	0.885	3	550	apoptotic process	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0001906	0.292	0.911	2	20	cell killing	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0021846	0.292	0.916	2	11	cell proliferation in forebrain	BP	1	FGFR2,DISC1	up_ACOR_VSMC
GO:0003333	0.292	0.915	2	12	amino acid transmembrane transport	BP	1	LRRC8D,SLC38A1	up_VCAV_EC
GO:0061036	0.292	0.916	2	11	positive regulation of cartilage development	BP	1	HOXA11,ZBTB16	up_VSAP_EC
GO:0019725	0.292	0.909	2	245	cellular homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0051099	0.292	0.954	1	70	positive regulation of binding	BP	1	HOXA3	down_ACOR_EC
GO:0046185	0.292	0.963	1	4	aldehyde catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0015693	0.292	0.963	1	4	magnesium ion transport	BP	1	NIPA2	down_ACOR_VSMC
GO:0048563	0.292	0.963	1	4	post-embryonic animal organ morphogenesis	BP	1	HMGN1	down_ACOR_VSMC
GO:0002009	0.292	0.956	1	177	morphogenesis of an epithelium	BP	1	CITED2	down_VPOR_EC
GO:0031649	0.292	0.961	1	5	heat generation	BP	1	PTGS2	down_VSAP_EC
GO:0050926	0.292	0.96	1	6	regulation of positive chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0051094	0.292	0.96	1	388	positive regulation of developmental process	BP	1	GATA5	down_VSAP_VSMC
GO:0033087	0.292	0.967	1	3	negative regulation of immature T cell	BP	1	BMP4	up_ACOR_VSMC
GO:0033088	0.292	0.967	1	3	negative regulation of immature T cell	BP	1	BMP4	up_ACOR_VSMC
GO:0043436	0.292	0.958	1	303	oxoacid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0030029	0.292	0.957	1	239	actin filament-based process	BP	1	LIMK1	up_VCAV_VSMC
GO:0009201	0.292	0.954	1	41	ribonucleoside triphosphate biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0008202	0.292	0.955	1	80	steroid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0034655	0.292	0.955	1	135	nucleobase-containing compound catabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0110053	0.292	0.955	1	98	regulation of actin filament organization	BP	1	CCL24	up_VPUL_EC
GO:0046777	0.292	0.954	1	86	protein autophosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0043393	0.292	0.954	1	77	regulation of protein binding	BP	1	CAV1	up_VSAP_VSMC
GO:0043900	0.292508351	0.86159	4	104	regulation of multi-organism process	BP	1	TRIM8,ARHGDIB,MAVS,CHMP4B	up_ACOR_EC
GO:0015849	0.293	0.832	7	56	organic acid transport	BP	1	LEP,SLC17A5,PSEN1,CLN8,PLIN2,CFI,SLC25A12	up_ACOR_VSMC
GO:0046942	0.293	0.832	7	56	carboxylic acid transport	BP	1	LEP,SLC17A5,PSEN1,CLN8,PLIN2,CFI,SLC25A12	up_ACOR_VSMC

GO:0032504	0.293	0.848	5	152	multicellular organism reproduction	BP	1	HOXA9,THRB,OVOL1,AVPR1A,SPATA6	up_AFEM_EC
GO:0048609	0.293	0.848	5	152	multicellular organismal reproductive process	BP	1	HOXA9,THRB,OVOL1,AVPR1A,SPATA6	up_AFEM_EC
GO:0046785	0.293	0.885	3	23	microtubule polymerization	BP	1	FBXO5,STMN1,RAC1	down_ACOR_VSMC
GO:1902652	0.293	0.882	3	38	secondary alcohol metabolic process	BP	1	LCAT,CYB5R3,SOAT1	down_VCAV_EC
GO:0007431	0.293	0.886	3	19	salivary gland development	BP	1	FGFR2,NRP1,DAG1	up_ACOR_VSMC
GO:0006094	0.293	0.884	3	24	gluconeogenesis	BP	1	ATF3,FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0035272	0.293	0.885	3	21	exocrine system development	BP	1	NTN4,IGSF3,BTBD7	up_VCAV_EC
GO:0048708	0.293	0.885	3	20	astrocyte differentiation	BP	1	ABL1,DLL1,PLPP3	up_VSAP_EC
GO:0070232	0.293	0.914	2	13	regulation of T cell apoptotic process	BP	1	PRELID1,ARG2	down_ACOR_VSMC
GO:0006692	0.293	0.915	2	11	prostanoid metabolic process	BP	1	EDN1,HPGD	up_ACOR_VSMC
GO:0006693	0.293	0.915	2	11	prostaglandin metabolic process	BP	1	EDN1,HPGD	up_ACOR_VSMC
GO:0070528	0.293	0.914	2	13	protein kinase C signaling	BP	1	PDGFB,AKAP12	up_VCAV_EC
GO:0042558	0.293	0.915	2	11	pteridine-containing compound metabolic	BP	1	ENSCAFG00000013986,PCBD1	up_VSAP_EC
GO:0052548	0.293	0.954	1	80	regulation of endopeptidase activity	BP	1	LYN	down_ACOR_EC
GO:0000097	0.293	0.963	1	4	sulfur amino acid biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0006555	0.293	0.963	1	4	methionine metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0009086	0.293	0.963	1	4	methionine biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0051186	0.293	0.955	1	159	cofactor metabolic process	BP	1	SUCLG2	down_AFEM_EC
GO:0008038	0.293	0.958	1	7	neuron recognition	BP	1	NDN	down_VCAV_EC
GO:0031664	0.293	0.958	1	7	regulation of lipopolysaccharide-	BP	1	SASH1	down_VCAV_EC
GO:0032717	0.293	0.959	1	7	negative regulation of interleukin-8 production	BP	1	BPI	down_VCAV_EC
GO:0043086	0.293	0.955	1	170	negative regulation of catalytic activity	BP	1	CST3	down_VPOR_EC
GO:0048583	0.293	0.975	1	1095	regulation of response to stimulus	BP	1	GATA5	down_VFEM_VSMC
GO:0002684	0.293	0.957	1	239	positive regulation of immune system process	BP	1	TLR2	up_AFEM_VSMC
GO:0006082	0.293	0.958	1	305	organic acid metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0009416	0.293	0.954	1	88	response to light stimulus	BP	1	HOXA1	up_APUL_EC
GO:0006525	0.293	0.963	1	4	arginine metabolic process	BP	1	ARG2	up_VCAV_EC
GO:0006413	0.293	0.954	1	42	translational initiation	BP	1	EIF5	up_VPOR_EC
GO:0007411	0.293	0.954	1	45	axon guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0048771	0.293	0.954	1	43	tissue remodeling	BP	1	HOXA3	up_VPOR_EC
GO:0097485	0.293	0.954	1	45	neuron projection guidance	BP	1	SEMA3A	up_VPOR_EC
GO:0009152	0.293	0.954	1	80	purine ribonucleotide biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0062012	0.293	0.954	1	100	regulation of small molecule metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0098542	0.293	0.954	1	100	defense response to other organism	BP	1	NR1H4	up_VPUL_EC
GO:0050772	0.29330947	0.95555	1	13	positive regulation of axonogenesis	BP	1	NRP1	up_ACOR_EC
GO:0030865	0.29367952	0.95543	1	13	cortical cytoskeleton organization	BP	1	PLS1	up_ACOR_EC
GO:0055123	0.293767149	0.90765	2	40	digestive system development	BP	1	GATA4,RARRES2	up_ACOR_EC
GO:0030104	0.293887466	0.95537	1	13	water homeostasis	BP	1	AQP1	up_ACOR_EC
GO:0030900	0.29396571	0.86067	4	101	forebrain development	BP	1	AQP1,DIXDC1,DCLK2,NRP1	up_ACOR_EC

GO:0002376	0.294	0.753	64	622	immune system process	BP	1	HOXA7,HOXA9,CD274,MAP3K14,ARHGEF5,C5AR2,ENPP2,SLC8B1,PPARGC1B,TBC1D10C,SLIT2,CRIP2,ABL1,EMP2,DLL1,IL17RC,CTSS,TRAFD1,TNFSF13,ANKRD54,CDC42EP2,HSD3B7,ZBTB16,TOX,RARG,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,RBCK1,BATF2,PLA2G6,MYC,ZEB1,EEF2,MYD88,TFE3,CFD,FBXO7,NLRX1,TKFC,CD83,RNF216,ZFP36L2,RAF1,PNP,ZNF580,CYBA,STX4,PQBP1,UNC93B1,FLOT1,PPP3CB,NCK1,MAVS,IRAK1BP1,HMOX1,MAP2K2,TGFBR2,CITED2,JCHAIN,PIR,DDIT4	up_VSAP_EC
GO:0007015	0.294	0.793	16	144	actin filament organization	BP	1	WNT11,FAM107A,ARHGEF5,PPARGC1B,SLIT2,ABL1,EMP2,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,WIPF1,MYO1B,ARHGAP12,NCK1,BAG4	up_VSAP_EC
GO:0016331	0.294	0.824	8	66	morphogenesis of embryonic epithelium	BP	1	FZD1,ABL1,OSR1,FUZ,RARG,IRX3,KDM2B,CITED2	up_VSAP_EC
GO:0090174	0.294	0.839	6	56	organelle membrane fusion	BP	1	SNAP23,CAV2,STX11,TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0048870	0.294	0.849	5	451	cell motility	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:0051674	0.294	0.849	5	451	localization of cell	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:1902117	0.294	0.864	4	32	positive regulation of organelle assembly	BP	1	FSCN1,SDC1,NUP62,PLK4	down_ACOR_VSMC
GO:0001704	0.294	0.863	4	43	formation of primary germ layer	BP	1	ITGA2,CTNNB1,INHBA,COL12A1	down_VSAP_EC
GO:0032527	0.294	0.91	2	19	protein exit from endoplasmic reticulum	BP	1	HM13,SEL1L	down_VSAP_EC
GO:0043551	0.294	0.911	2	17	regulation of phosphatidylinositol 3-	BP	1	LYN,SH3GLB1	down_VSAP_EC
GO:0003254	0.294	0.914	2	12	regulation of membrane depolarization	BP	1	GJA1,PTPN3	up_ACOR_VSMC
GO:0033687	0.294	0.913	2	13	osteoblast proliferation	BP	1	FIGNL1,BMP2	up_VCAV_EC
GO:0045597	0.294	0.908	2	253	positive regulation of cell differentiation	BP	1	TOX,CYP26B1	up_VFEM_EC
GO:0010594	0.294	0.954	1	71	regulation of endothelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0042113	0.294	0.954	1	64	B cell activation	BP	1	LYN	down_ACOR_EC
GO:1904779	0.294	0.963	1	4	regulation of protein localization to	BP	1	NUP62	down_ACOR_VSMC
GO:0120035	0.294	0.955	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	FSCN1	down_AFEM_EC
GO:0006188	0.294	0.958	1	7	IMP biosynthetic process	BP	1	AMPD2	down_VCAV_EC
GO:0007588	0.294	0.958	1	7	excretion	BP	1	KIRREL1	down_VCAV_EC
GO:0021511	0.294	0.958	1	7	spinal cord patterning	BP	1	GLI3	down_VCAV_EC
GO:0001525	0.294	0.955	1	173	angiogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0033572	0.294	0.961	1	5	transferrin transport	BP	1	TFRC	down_VSAP_EC
GO:0021648	0.294	0.967	1	3	vestibulocochlear nerve morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0008284	0.294	0.956	1	238	positive regulation of cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0030097	0.294	0.956	1	244	hemopoiesis	BP	1	HOXA9	up_AFEM_VSMC
GO:1905114	0.294	0.955	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	DKK2	up_AORT_EC
GO:0051403	0.294	0.954	1	89	stress-activated MAPK cascade	BP	1	MAPK10	up_APUL_EC
GO:0050872	0.294	0.963	1	4	white fat cell differentiation	BP	1	PPARG	up_VCAV_EC
GO:0051547	0.294	0.963	1	4	regulation of keratinocyte migration	BP	1	MTOR	up_VCAV_EC
GO:0051549	0.294	0.963	1	4	positive regulation of keratinocyte migration	BP	1	MTOR	up_VCAV_EC
GO:0007259	0.294	0.953	1	42	JAK-STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:0051053	0.294	0.954	1	45	negative regulation of DNA metabolic process	BP	1	CXHXorf57	up_VPOR_EC
GO:0072657	0.294	0.955	1	144	protein localization to membrane	BP	1	LHFPL4	up_VPOR_VSMC

GO:0051495	0.294	0.954	1	82	positive regulation of cytoskeleton organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0007517	0.294	0.954	1	100	muscle organ development	BP	1	TBX5	up_VPUL_EC
GO:0007420	0.294	0.955	1	169	brain development	BP	1	SLIT2	up_VPUL_VSMC
GO:0018212	0.294	0.954	1	81	peptidyl-tyrosine modification	BP	1	CAV1	up_VSAP_VSMC
GO:0015833	0.294155382	0.79177	16	521	peptide transport	BP	1	SH3TC2,NR1H4,AQP1,KCNB1,EDEM2,FZD5,NOD2,PTGER4,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0071675	0.294385566	0.9552	1	13	regulation of mononuclear cell	BP	1	RARRES2	up_ACOR_EC
GO:0033687	0.294517335	0.95516	1	13	osteoblast proliferation	BP	1	FIGNL1	up_ACOR_EC
GO:0097178	0.294986292	0.95477	1	14	ruffle assembly	BP	1	ARHGEF26	up_ACOR_EC
GO:0007507	0.295	0.785	19	194	heart development	BP	1	CALCRL,ADAMTS9,PDGFB,MEF2C,CHD7,DLL4,GATA3,EDN1,APLNR,SOX18,MTOR,BMP2,HHEX,PROX1,ENSCAFG00000010596,JAG1,CREB1,HIF1A,LUZP1	up_VCAV_EC
GO:0040017	0.295	0.799	13	180	positive regulation of locomotion	BP	1	ARHGEF2,VEGFA,HSPA5,SERPINE1,SPARC,JCAD,MYO1C,PIK3C2A,HIF1A,ADAM17,PTP4A1,LYN,NRP1	down_VSAP_EC
GO:0045444	0.295	0.812	10	84	fat cell differentiation	BP	1	NAPEPLD,EBF2,SAV1,ARL4A,ZBTB16,ALDH6A1,ZFP36L1,ZADH2,ZFP36L2,TAF8	up_VSAP_EC
GO:0006403	0.295	0.83	7	64	RNA localization	BP	1	IWS1,QKI,HHEX,THOC1,SMG7,NUP133,DCP2	up_VCAV_EC
GO:0070588	0.295	0.839	6	54	calcium ion transmembrane transport	BP	1	PDE4D,CHD7,APLNR,SLC25A25,PLCG2,MCU	up_VCAV_EC
GO:0032273	0.295	0.85	5	44	positive regulation of protein polymerization	BP	1	RAC1,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:1903039	0.295	0.85	5	43	positive regulation of leukocyte cell-cell	BP	1	HMGB1,CAV1,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0006796	0.295	0.854	5	938	phosphate-containing compound metabolic	BP	1	NR1H4,MAPK10,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0010906	0.295	0.851	5	38	regulation of glucose metabolic process	BP	1	ACACB,C1QTNF2,PDK2,PASK,NCOA2	up_VSAP_EC
GO:0042273	0.295	0.863	4	35	ribosomal large subunit biogenesis	BP	1	NOC2L,DDX28,RSL1D1,ENSCAFG00000015189	down_ACOR_VSMC
GO:0071322	0.295	0.865	4	29	cellular response to carbohydrate stimulus	BP	1	PRKAA2,SLC2A5,PRKCE,RAB11B	up_ACOR_VSMC
GO:0030148	0.295	0.865	4	28	sphingolipid biosynthetic process	BP	1	CERS4,ENSCAFG00000000071,HACD4,B3GALT4	up_VSAP_EC
GO:0045446	0.295	0.881	3	32	endothelial cell differentiation	BP	1	MSN,CTNNB1,PLOD3	down_VSAP_EC
GO:0045600	0.295	0.884	3	21	positive regulation of fat cell differentiation	BP	1	FNDC5,CCDC3,DKKL1	up_ACOR_VSMC
GO:1902105	0.295	0.879	3	80	regulation of leukocyte differentiation	BP	1	HOXA7,CYLD,EVI2B	up_AFEM_EC
GO:0034754	0.295	0.883	3	24	cellular hormone metabolic process	BP	1	TIPARP,BMP2,ALDH1A3	up_VCAV_EC
GO:0048870	0.295	0.881	3	451	cell motility	BP	1	HOXA7,SIX1,TIAM1	up_VFEM_EC
GO:0051674	0.295	0.881	3	451	localization of cell	BP	1	HOXA7,SIX1,TIAM1	up_VFEM_EC
GO:0016239	0.295	0.884	3	20	positive regulation of macroautophagy	BP	1	MFN2,PIP4K2B,HMOX1	up_VSAP_EC
GO:0044093	0.295	0.881	3	437	positive regulation of molecular function	BP	1	STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:1901890	0.295	0.913	2	13	positive regulation of cell junction assembly	BP	1	CAV1,RAC1	down_ACOR_VSMC
GO:0009880	0.295	0.909	2	22	embryonic pattern specification	BP	1	PCSK6,ZBTB16	down_VCAV_EC
GO:0006911	0.295	0.914	2	11	phagocytosis, engulfment	BP	1	ABCA1,F2RL1	up_ACOR_VSMC
GO:0008347	0.295	0.915	2	11	glial cell migration	BP	1	SUN1,CRKL	up_ACOR_VSMC
GO:0006414	0.295	0.912	2	15	translational elongation	BP	1	SECISBP2L,DPH5	up_VCAV_EC
GO:1901890	0.295	0.913	2	13	positive regulation of cell junction assembly	BP	1	TEK,ENSCAFG00000002015	up_VCAV_EC
GO:0048667	0.295	0.907	2	140	cell morphogenesis involved in neuron	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0051090	0.295	0.906	2	134	regulation of DNA-binding transcription factor	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0003203	0.295	0.914	2	11	endocardial cushion morphogenesis	BP	1	ACVRL1,TGFBR2	up_VSAP_EC

GO:1900101	0.295	0.914	2	11	regulation of endoplasmic reticulum unfolded protein response	BP	1	PIK3R1,NCK1	up_VSAP_EC
GO:0048666	0.295	0.908	2	258	neuron development	BP	1	IRX5,SHOX2	up_VSAP_VSMC
GO:0018095	0.295	0.963	1	4	protein polyglutamylation	BP	1	TTLL1	down_ACOR_VSMC
GO:0001976	0.295	0.963	1	4	neurological system process involved in regulation of systemic	BP	1	NAV2	down_ACOR_VSMC
GO:0032077	0.295	0.963	1	4	positive regulation of deoxyribonuclease	BP	1	PCNA	down_ACOR_VSMC
GO:0060294	0.295	0.963	1	4	cilium movement involved in cell motility	BP	1	TTLL1	down_ACOR_VSMC
GO:0030001	0.295	0.955	1	172	metal ion transport	BP	1	RAB11B	down_VPOR_EC
GO:0051640	0.295	0.955	1	174	organelle localization	BP	1	RAB11B	down_VPOR_EC
GO:0034097	0.295	0.956	1	238	response to cytokine	BP	1	TLR2	up_AFEM_VSMC
GO:0010216	0.295	0.966	1	3	maintenance of DNA methylation	BP	1	UHRF2	up_VCAV_EC
GO:0031279	0.295	0.963	1	4	regulation of cyclase activity	BP	1	NOS2	up_VCAV_EC
GO:0038089	0.295	0.962	1	4	positive regulation of cell migration by vascular endothelial growth factor	BP	1	PRKD2	up_VCAV_EC
GO:0045672	0.295	0.963	1	4	positive regulation of osteoclast differentiation	BP	1	CREB1	up_VCAV_EC
GO:0048505	0.295	0.963	1	4	regulation of timing of cell differentiation	BP	1	GDPD5	up_VCAV_EC
GO:0002684	0.295	0.956	1	239	positive regulation of immune system process	BP	1	C6	up_VCAV_VSMC
GO:0009855	0.295	0.953	1	42	determination of bilateral symmetry	BP	1	ACVR2A	up_VPOR_EC
GO:0022612	0.295	0.953	1	44	gland morphogenesis	BP	1	SEMA3A	up_VPOR_EC
GO:0030218	0.295	0.953	1	42	erythrocyte differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0071396	0.295	0.954	1	134	cellular response to lipid	BP	1	CYP26B1	up_VPOR_VSMC
GO:1901214	0.295	0.954	1	81	regulation of neuron death	BP	1	SIX1	up_VFEM_EC
GO:0040013	0.295	0.954	1	100	negative regulation of locomotion	BP	1	TBX5	up_VPUL_EC
GO:0030001	0.295	0.955	1	172	metal ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0007159	0.295	0.953	1	79	leukocyte cell-cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0002696	0.295	0.953	1	80	positive regulation of leukocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:0045047	0.295367147	0.95464	1	14	protein targeting to ER	BP	1	CHMP4B	up_ACOR_EC
GO:0072599	0.295367147	0.95464	1	14	establishment of protein localization to endoplasmic reticulum	BP	1	CHMP4B	up_ACOR_EC
GO:0048566	0.295674047	0.95478	1	13	embryonic digestive tract development	BP	1	RARRES2	up_ACOR_EC
GO:0006468	0.296	0.753	56	544	protein phosphorylation	BP	1	FZD1,CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,OSR1,MAP3K5,CDC42EP5,PDGFD,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,F2RL1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,PIK3R1,MYC,RTN4RL1,SASH1,MYD88,LRP4,PASK,STK16,FBXO7,CDK9,FBLN1,ZFP36L2,RAF1,QARS,ACVRL1,FLOT1,PPP3CB,NCK1,MAVS,ULK1,MAP2K2,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0002790	0.296	0.799	13	133	peptide secretion	BP	1	GBP5,FERMT1,CHD7,TLR4,GATA3,EDN1,ARG2,ABCA1,CD200,HMGB1,NOS2,MCU,HIF1A	up_VCAV_EC
GO:0019318	0.296	0.817	9	75	hexose metabolic process	BP	1	ACACB,C1QTNF2,PDK2,GALK2,GALK1,PASK,KHK,PC,NCOA2	up_VSAP_EC
GO:0009612	0.296	0.839	6	47	response to mechanical stimulus	BP	1	TLR3,USP53,ANKRD1,BNIP3,JUP,SLC8A1	up_ACOR_VSMC
GO:0050921	0.296	0.85	5	39	positive regulation of chemotaxis	BP	1	VEGFD,FGF18,F2RL1,NRP1,CCL5	up_ACOR_VSMC
GO:0010646	0.296	0.853	5	945	regulation of cell communication	BP	1	NR1H4,PLCL1,ARHGEF26,NPNT,NTRK2	up_APUL_EC

GO:0046661	0.296	0.861	4	45	male sex differentiation	BP	1	CTNNB1,INHBA,SIX4,SPINK2	down_VSAP_EC
GO:2001056	0.296	0.862	4	38	positive regulation of cysteine-type	BP	1	CASP8,BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:1901888	0.296	0.864	4	29	regulation of cell junction assembly	BP	1	FAM107A,ABL1,ACVRL1,FLOT1	up_VSAP_EC
GO:0043154	0.296	0.883	3	23	negative regulation of cysteine-type endopeptidase activity	BP	1	BIRC5,DHCR24,ENSCAFG00000005299	down_ACOR_VSMC
GO:0016042	0.296	0.878	3	80	lipid catabolic process	BP	1	LEP,RAB7A,ACACB	up_AFEM_EC
GO:0002696	0.296	0.878	3	80	positive regulation of leukocyte activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0006357	0.296	0.883	3	547	regulation of transcription by RNA polymerase II	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0006928	0.296	0.911	2	557	movement of cell or subcellular component	BP	1	HDAC7,HSD3B7	down_VPOR_EC
GO:0000387	0.296	0.909	2	19	spliceosomal snRNP assembly	BP	1	PRPF3,STRAP	down_VSAP_EC
GO:0022617	0.296	0.914	2	11	extracellular matrix disassembly	BP	1	DDR2,KIF9	up_ACOR_VSMC
GO:1902305	0.296	0.913	2	12	regulation of sodium ion transmembrane transport	BP	1	PTPN3,FXYD1	up_ACOR_VSMC
GO:0055023	0.296	0.913	2	12	positive regulation of cardiac muscle tissue	BP	1	MEF2C,EDN1	up_VCAV_EC
GO:0009967	0.296	0.91	2	435	positive regulation of signal transduction	BP	1	BAMBI,ANKRD6	up_VPOR_VSMC
GO:0043066	0.296	0.907	2	253	negative regulation of apoptotic process	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0009605	0.296	0.912	2	538	response to external stimulus	BP	1	IL22RA1,SLIT2	up_VPUL_VSMC
GO:0048545	0.296	0.953	1	68	response to steroid hormone	BP	1	NEDD4	down_ACOR_EC
GO:0050727	0.296	0.953	1	74	regulation of inflammatory response	BP	1	LYN	down_ACOR_EC
GO:0007288	0.296	0.962	1	4	sperm axoneme assembly	BP	1	TTLL1	down_ACOR_VSMC
GO:0006573	0.296	0.962	1	4	valine metabolic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0010766	0.296	0.962	1	4	negative regulation of sodium ion transport	BP	1	NEDD4	down_ACOR_VSMC
GO:0019320	0.296	0.962	1	4	hexose catabolic process	BP	1	GALE	down_ACOR_VSMC
GO:0031344	0.296	0.954	1	161	regulation of cell projection organization	BP	1	FSCN1	down_AFEM_EC
GO:0000289	0.296	0.958	1	7	nuclear-transcribed mRNA poly(A) tail shortening	BP	1	SAMD4B	down_VCAV_EC
GO:0009190	0.296	0.957	1	8	cyclic nucleotide biosynthetic process	BP	1	ADCY6	down_VCAV_EC
GO:0043114	0.296	0.957	1	7	regulation of vascular permeability	BP	1	CLSTN1	down_VCAV_EC
GO:0052652	0.296	0.957	1	8	cyclic purine nucleotide metabolic process	BP	1	ADCY6	down_VCAV_EC
GO:1902175	0.296	0.957	1	7	regulation of oxidative stress-induced intrinsic apoptotic signaling	BP	1	PARK7	down_VCAV_EC
GO:0051573	0.296	0.96	1	5	negative regulation of histone H3-K9	BP	1	KDM3A	down_VSAP_EC
GO:0010984	0.296	0.959	1	6	regulation of lipoprotein particle clearance	BP	1	NR1H4	down_VSAP_EC
GO:0097286	0.296	0.959	1	6	iron ion import	BP	1	TFRC	down_VSAP_EC
GO:2000810	0.296	0.96	1	5	regulation of bicellular tight junction assembly	BP	1	MYO1C	down_VSAP_EC
GO:0070831	0.296	0.966	1	3	basement membrane assembly	BP	1	DAG1	up_ACOR_VSMC
GO:0072697	0.296	0.962	1	4	protein localization to cell cortex	BP	1	EPB41	up_VCAV_EC
GO:0098662	0.296	0.954	1	131	inorganic cation transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0030073	0.296203495	0.90624	2	42	insulin secretion	BP	1	NR1H4,KCNB1	up_ACOR_EC
GO:0048339	0.296284744	0.95459	1	13	paraxial mesoderm development	BP	1	FOXC2	up_ACOR_EC
GO:0098659	0.296510038	0.95451	1	13	inorganic cation import across plasma membrane	BP	1	SLC9A9	up_ACOR_EC
GO:0099587	0.296510038	0.95451	1	13	inorganic ion import across plasma membrane	BP	1	SLC9A9	up_ACOR_EC
GO:0007215	0.296566196	0.95449	1	13	glutamate receptor signaling pathway	BP	1	MAPK8IP2	up_ACOR_EC

GO:0007606	0.29657907	0.95449	1	13	sensory perception of chemical stimulus	BP	1	PDE4A	up_ACOR_EC
GO:1905209	0.29672547	0.95444	1	13	positive regulation of cardiocyte differentiation	BP	1	TBX5	up_ACOR_EC
GO:1902905	0.296909993	0.87751	3	72	positive regulation of supramolecular fiber	BP	1	SYNPO2,ACTN2,NRP1	up_ACOR_EC
GO:0003006	0.297	0.798	13	180	developmental process involved in reproduction	BP	1	SULF1,CELF1,PTPN11,TMED2,PTGS2,HIF1A,CTNNB1,CDYL,INHBA,SIX4,SPINK2,RTCB,KDM3A	down_VSAP_EC
GO:0065007	0.297	0.846	10	3499	biological regulation	BP	1	HOXC10,DKK2,ENSCAFG00000005494,HOXA9,LNPEP,ERC1,TAOK1,BPI,CTNNAL1,GPR155	up_AORT_EC
GO:0072522	0.297	0.815	9	91	purine-containing compound biosynthetic	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,NOS2,HIF1A	up_VCAV_EC
GO:0000082	0.297	0.83	7	57	G1/S transition of mitotic cell cycle	BP	1	SKP2,NACC2,LATS2,CDKN1A,CRLF3,FAM107A,KLF11	up_ACOR_VSMC
GO:0050789	0.297	0.878	6	3295	regulation of biological process	BP	1	HOXC10,TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0022900	0.297	0.838	6	46	electron transport chain	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,SLC25A12,NDUFS2,NDUFV1	up_VSAP_EC
GO:0097553	0.297	0.863	4	32	calcium ion transmembrane import	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0042775	0.297	0.864	4	28	mitochondrial ATP synthesis coupled	BP	1	COQ9,ENSCAFG00000004260,NDUFS2,NDUFV1	up_VSAP_EC
GO:0030216	0.297	0.863	4	29	keratinocyte differentiation	BP	1	HOXA7,SAV1,ZFP36L1,LATS2	up_VSAP_EC
GO:0009607	0.297	0.878	3	232	response to biotic stimulus	BP	1	OAS3,MTDH,NAALADL2	up_VPOR_EC
GO:0032879	0.297	0.885	3	767	regulation of localization	BP	1	HOXA3,NKX2-5,C3AR1	up_VPOR_VSMC
GO:0006739	0.297	0.912	2	13	NADP metabolic process	BP	1	NNT,PGD	down_ACOR_VSMC
GO:0030104	0.297	0.912	2	13	water homeostasis	BP	1	STMN1,ANXA7	down_ACOR_VSMC
GO:0009187	0.297	0.914	2	10	cyclic nucleotide metabolic process	BP	1	PDE5A,ADCY6	up_ACOR_VSMC
GO:0043401	0.297	0.906	2	46	steroid hormone mediated signaling	BP	1	LBH,CRY2	up_AFEM_EC
GO:0051248	0.297	0.908	2	316	negative regulation of protein metabolic process	BP	1	PTGER2,FLRT3	up_VPUL_EC
GO:1903524	0.297	0.913	2	11	positive regulation of blood circulation	BP	1	F2RL1,TBXA2R	up_VSAP_EC
GO:0050890	0.297	0.953	1	67	cognition	BP	1	HOXA1	down_ACOR_EC
GO:0015780	0.297	0.962	1	4	nucleotide-sugar transmembrane transport	BP	1	SLC35C2	down_ACOR_VSMC
GO:0032471	0.297	0.962	1	4	negative regulation of endoplasmic reticulum calcium ion concentration	BP	1	THADA	down_ACOR_VSMC
GO:0070200	0.297	0.962	1	4	establishment of protein localization to telomere	BP	1	CCT4	down_ACOR_VSMC
GO:0001963	0.297	0.957	1	7	synaptic transmission, dopaminergic	BP	1	PARK7	down_VCAV_EC
GO:0015682	0.297	0.957	1	7	ferric iron transport	BP	1	ARHGAP1	down_VCAV_EC
GO:0072512	0.297	0.957	1	7	trivalent inorganic cation transport	BP	1	ARHGAP1	down_VCAV_EC
GO:1900746	0.297	0.957	1	7	regulation of vascular endothelial growth factor	BP	1	DCN	down_VCAV_EC
GO:1902547	0.297	0.957	1	7	regulation of cellular response to vascular endothelial growth factor	BP	1	DCN	down_VCAV_EC
GO:2000727	0.297	0.957	1	7	positive regulation of cardiac muscle cell	BP	1	GREM1	down_VCAV_EC
GO:0001711	0.297	0.96	1	5	endodermal cell fate commitment	BP	1	CTNNB1	down_VSAP_EC
GO:0010954	0.297	0.958	1	6	positive regulation of protein processing	BP	1	MYH9	down_VSAP_EC
GO:1903319	0.297	0.958	1	6	positive regulation of protein maturation	BP	1	MYH9	down_VSAP_EC
GO:0033601	0.297	0.966	1	3	positive regulation of mammary gland epithelial	BP	1	RREB1	up_ACOR_VSMC
GO:0010155	0.297	0.962	1	4	regulation of proton transport	BP	1	PARK7	up_ACOR_VSMC
GO:0030242	0.297	0.966	1	3	autophagy of peroxisome	BP	1	PIK3C3	up_ACOR_VSMC
GO:1902307	0.297	0.962	1	4	positive regulation of sodium ion	BP	1	FXYD1	up_ACOR_VSMC
GO:0044772	0.297	0.954	1	144	mitotic cell cycle phase transition	BP	1	TAOK1	up_AORT_EC

GO:0051049	0.297	0.96	1	479	regulation of transport	BP	1	HOXA3	up_APUL_VSMC
GO:0009635	0.297	0.962	1	4	response to herbicide	BP	1	MAPK13	up_VCAV_EC
GO:0014883	0.297	0.962	1	4	transition between fast and slow fiber	BP	1	PPP3CA	up_VCAV_EC
GO:0017085	0.297	0.962	1	4	response to insecticide	BP	1	MAPK13	up_VCAV_EC
GO:1902074	0.297	0.962	1	4	response to salt	BP	1	MAPK13	up_VCAV_EC
GO:1902075	0.297	0.962	1	4	cellular response to salt	BP	1	MAPK13	up_VCAV_EC
GO:1903935	0.297	0.962	1	4	response to sodium arsenite	BP	1	MAPK13	up_VCAV_EC
GO:1903936	0.297	0.962	1	4	cellular response to sodium arsenite	BP	1	MAPK13	up_VCAV_EC
GO:0034349	0.297	0.962	1	4	glial cell apoptotic process	BP	1	PRKCH	up_VCAV_EC
GO:0071073	0.297	0.962	1	4	positive regulation of phospholipid biosynthetic	BP	1	ADGRF5	up_VCAV_EC
GO:0019216	0.297	0.953	1	101	regulation of lipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0050708	0.297	0.953	1	101	regulation of protein secretion	BP	1	NR1H4	up_VPUL_EC
GO:0014070	0.297	0.954	1	172	response to organic cyclic compound	BP	1	SLIT2	up_VPUL_VSMC
GO:0032101	0.297	0.954	1	173	regulation of response to external stimulus	BP	1	SLIT2	up_VPUL_VSMC
GO:0097191	0.297	0.953	1	79	extrinsic apoptotic signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0007249	0.297278849	0.87731	3	71	I-kappaB kinase/NF-kappaB signaling	BP	1	NR1H4,NOD2,TNFRSF19	up_ACOR_EC
GO:0009409	0.297454011	0.9542	1	13	response to cold	BP	1	PCSK1N	up_ACOR_EC
GO:0072077	0.297795129	0.95409	1	13	renal vesicle morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0072273	0.297795129	0.95409	1	13	metanephric nephron morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0002720	0.297906306	0.95405	1	13	positive regulation of cytokine production involved in immune	BP	1	FZD5	up_ACOR_EC
GO:0043949	0.297960775	0.95403	1	13	regulation of cAMP-mediated signaling	BP	1	PDE4A	up_ACOR_EC
GO:0098771	0.298	0.786	17	180	inorganic ion homeostasis	BP	1	EDNRB,CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0045859	0.298	0.796	13	219	regulation of protein kinase activity	BP	1	DCN,PRNP,BGN,AKT1S1,CSPG4,ASPN,THY1,PARK7,SASH1,SPRED1,MAPRE3,DDR2,SHC1	down_VCAV_EC
GO:0032990	0.298	0.808	10	167	cell part morphogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,POLDIP2,THY1,TLX2,GLI3,UST,BRSK1	down_VCAV_EC
GO:0045927	0.298	0.828	7	61	positive regulation of growth	BP	1	MEF2C,CHD7,EDN1,RAB11A,PROX1,CREB1,SPTBN4	up_VCAV_EC
GO:0008406	0.298	0.829	7	57	gonad development	BP	1	HOXA11,HOXA9,IRX5,SLIT2,OSR1,PATZ1,CITED2	up_VSAP_EC
GO:0045137	0.298	0.829	7	57	development of primary sexual characteristics	BP	1	HOXA11,HOXA9,IRX5,SLIT2,OSR1,PATZ1,CITED2	up_VSAP_EC
GO:0010508	0.298	0.849	5	38	positive regulation of autophagy	BP	1	PLEKHF1,MFN2,FBXO7,PIP4K2B,HMOX1	up_VSAP_EC
GO:1905952	0.298	0.862	4	33	regulation of lipid localization	BP	1	SREBF2,PRELID1,ABHD5,NUS1	down_ACOR_VSMC
GO:0051492	0.298	0.863	4	28	regulation of stress fiber assembly	BP	1	ARHGAP28,NRP1,EVL,INPP5K	up_ACOR_VSMC
GO:0044344	0.298	0.862	4	33	cellular response to fibroblast growth factor	BP	1	CXCL8,DLL4,GATA3,PRKD2	up_VCAV_EC
GO:0071774	0.298	0.862	4	33	response to fibroblast growth factor	BP	1	CXCL8,DLL4,GATA3,PRKD2	up_VCAV_EC
GO:1903036	0.298	0.883	3	19	positive regulation of response to wounding	BP	1	ENPP4,PRKCE,RREB1	up_ACOR_VSMC
GO:0051123	0.298	0.911	2	14	RNA polymerase II preinitiation complex	BP	1	HMGB1,PSMC1	down_ACOR_VSMC
GO:0097178	0.298	0.911	2	14	ruffle assembly	BP	1	CAV1,RAC1	down_ACOR_VSMC
GO:0060389	0.298	0.908	2	21	pathway-restricted SMAD protein phosphorylation	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0034394	0.298	0.908	2	19	protein localization to cell surface	BP	1	CTNNB1,TAX1BP3	down_VSAP_EC
GO:0010517	0.298	0.913	2	11	regulation of phospholipase activity	BP	1	HTR2B,FGFR2	up_ACOR_VSMC
GO:0021799	0.298	0.913	2	11	cerebral cortex radially oriented cell migration	BP	1	DISC1,SUN1	up_ACOR_VSMC

GO:0008360	0.298	0.905	2	46	regulation of cell shape	BP	1	BVES,CDC42EP5	up_AFEM_EC
GO:0002090	0.298	0.911	2	14	regulation of receptor internalization	BP	1	SELE,PLCG2	up_VCAV_EC
GO:0032607	0.298	0.913	2	11	interferon-alpha production	BP	1	TLR4,TLR3	up_VCAV_EC
GO:0000902	0.298	0.906	2	266	cell morphogenesis	BP	1	RADIL,CDC42EP5	up_VFEM_EC
GO:0009887	0.298	0.907	2	314	animal organ morphogenesis	BP	1	TBX5,HOXA3	up_VPUL_EC
GO:0035303	0.298	0.952	1	65	regulation of dephosphorylation	BP	1	MYO1D	down_ACOR_EC
GO:1902033	0.298	0.962	1	4	regulation of hematopoietic stem cell	BP	1	PDCD2	down_ACOR_VSMC
GO:0010888	0.298	0.962	1	4	negative regulation of lipid storage	BP	1	ABHD5	down_ACOR_VSMC
GO:0031118	0.298	0.962	1	4	rRNA pseudouridine synthesis	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0032816	0.298	0.962	1	4	positive regulation of natural killer cell	BP	1	TOX	down_ACOR_VSMC
GO:0048384	0.298	0.962	1	4	retinoic acid receptor signaling pathway	BP	1	EZH2	down_ACOR_VSMC
GO:0048385	0.298	0.962	1	4	regulation of retinoic acid receptor signaling	BP	1	EZH2	down_ACOR_VSMC
GO:0071941	0.298	0.962	1	4	nitrogen cycle metabolic process	BP	1	ARG2	down_ACOR_VSMC
GO:0006517	0.298	0.957	1	7	protein deglycosylation	BP	1	PARK7	down_VCAV_EC
GO:0090335	0.298	0.957	1	7	regulation of brown fat cell differentiation	BP	1	NAPEPLD	down_VCAV_EC
GO:0000729	0.298	0.96	1	5	DNA double-strand break processing	BP	1	RBBP8	down_VSAP_EC
GO:0035330	0.298	0.959	1	5	regulation of hippo signaling	BP	1	WWC3	down_VSAP_EC
GO:0045773	0.298	0.958	1	6	positive regulation of axon extension	BP	1	NRP1	down_VSAP_EC
GO:0060753	0.298	0.962	1	4	regulation of mast cell chemotaxis	BP	1	VEGFD	up_ACOR_VSMC
GO:0021955	0.298	0.954	1	15	central nervous system neuron axonogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0031589	0.298	0.953	1	93	cell-substrate adhesion	BP	1	NPNT	up_APUL_EC
GO:0090287	0.298	0.952	1	91	regulation of cellular response to growth factor	BP	1	NPNT	up_APUL_EC
GO:0003221	0.298	0.966	1	3	right ventricular cardiac muscle tissue	BP	1	CHD7	up_VCAV_EC
GO:0045618	0.298	0.962	1	4	positive regulation of keratinocyte	BP	1	PRKCH	up_VCAV_EC
GO:0030097	0.298	0.955	1	244	hemopoiesis	BP	1	LRRC17	up_VCAV_VSMC
GO:0034341	0.298	0.952	1	43	response to interferon-gamma	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0050731	0.298	0.952	1	44	positive regulation of peptidyl-tyrosine	BP	1	ARHGEF2	up_VPOR_EC
GO:0032787	0.298	0.953	1	144	monocarboxylic acid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0043269	0.298	0.953	1	135	regulation of ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0010817	0.298	0.953	1	102	regulation of hormone levels	BP	1	NR1H4	up_VPUL_EC
GO:1904292	0.298253303	0.95394	1	13	regulation of ERAD pathway	BP	1	EDEM2	up_ACOR_EC
GO:1904353	0.298478984	0.95386	1	13	regulation of telomere capping	BP	1	PKIB	up_ACOR_EC
GO:0002064	0.298632637	0.87647	3	71	epithelial cell development	BP	1	TMOD1,FOXC2,ARHGEF26	up_ACOR_EC
GO:0016572	0.298655826	0.95381	1	13	histone phosphorylation	BP	1	PRKCD	up_ACOR_EC

GO:0006796	0.299	0.74	95	938	phosphate-containing compound metabolic process	BP	1	FZD1,NAPEPLD,CDON,WNT11,ACSM3,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,EEF2K,IL6R,SLIT2,NADK,FGF7,ABL1,EMP2,OSR1,MAP3K5,CDC42EP5,INPP5E,PDGFD,C1QTNF2,CNPPD1,COQ9,NDUFS1,ENSCAFG00000004260,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,PHKA2,PPIP5K1,MORC3,DDR2,PDK2,ZFP36L1,TRAF7,FXN,GALK1,PIK3R1,ENTPD3,PLA2G6,MYC,PIK3IP1,CTNS,TMEM225B,RTN4RL1,SASH1,MYD88,NDUFS2,LRP4,PASK,NT5C2,STK16,NCEH1,FBXO7,MOCOS,LCAT,LIMD1,ACSS2,TKFC,CDK9,FBLN1,MVK,PNPO,DCAKD,ZFP36L2,ENSCAFG00000013366,RAF1,PNP,ZFYVE21,QARS,ACVRL1,IDH1,FLOT1,PLPP5,PPP3CB,NCK1,NDUFV1,MAVS,ULK1,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0010629	0.299	0.755	46	502	negative regulation of gene expression	BP	1	EDNRB,HCLS1,PDGFB,MOV10,MEF2C,FERMT1,TIPARP,DLL4,WWP1,GATA3,EDN1,HOXB8,SOX18,PPP3CA,TENT2,BMP2,HMG20A,HHEX,CREM,TUT7,CNOT6,ENC1,PROX1,UHRF2,MDFI,HMBOX1,SMARCA4,NCK1,TIMELESS,TCERG1,CREB1,BASP1,PAN3,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,MTA2,KDM5A,HIF1A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,ELK3	up_VCAV_EC
GO:0023052	0.299	0.798	15	1602	signaling	BP	1	C3AR1,BARX1,HTR7,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,SV2C,PDE1C,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:1901342	0.299	0.797	13	114	regulation of vasculature development	BP	1	ENPP2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,CCBE1,TBXA2R,SASH1,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:1901360	0.299	0.813	12	2016	organic cyclic compound metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,CSGALNACT1,WDR12,TNRC6B,NEDD4	down_ACOR_EC
GO:0050878	0.299	0.82	8	75	regulation of body fluid levels	BP	1	TFPI,TFPI2,CAV1,STMN1,ITGB3,EMP2,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0007283	0.299	0.826	7	91	spermatogenesis	BP	1	CELF1,PHC2,CCNYL1,CDYL,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0048706	0.299	0.836	6	59	embryonic skeletal system development	BP	1	HOXB7,MEF2C,HOXB8,MDFI,HOXB5,ZEB1	up_VCAV_EC
GO:0001952	0.299	0.861	4	34	regulation of cell-matrix adhesion	BP	1	GREM1,HOXA7,RAC1,EMP2	down_ACOR_VSMC
GO:0032640	0.299	0.878	3	39	tumor necrosis factor production	BP	1	BPI,CYBA,MAVS	down_VCAV_EC
GO:0060349	0.299	0.878	3	38	bone morphogenesis	BP	1	NAB2,THBS3,GLI3	down_VCAV_EC
GO:0051893	0.299	0.882	3	20	regulation of focal adhesion assembly	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0090109	0.299	0.882	3	20	regulation of cell-substrate junction	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0000122	0.299	0.905	2	218	negative regulation of transcription by RNA polymerase II	BP	1	HOXA7,NEDD4	down_ACOR_EC
GO:0032940	0.299	0.905	2	231	secretion by cell	BP	1	LYN,STX4	down_ACOR_EC
GO:1902186	0.299	0.91	2	13	regulation of viral release from host cell	BP	1	TRIM35,SMC3	down_ACOR_VSMC
GO:0010675	0.299	0.904	2	46	regulation of cellular carbohydrate metabolic	BP	1	LEP,ACACB	up_AFEM_EC
GO:0031333	0.299	0.904	2	46	negative regulation of protein complex assembly	BP	1	CRYAB,KANK1	up_AFEM_EC
GO:0042445	0.299	0.904	2	46	hormone metabolic process	BP	1	LEP,GCNT4	up_AFEM_EC
GO:0045944	0.299	0.906	2	287	positive regulation of transcription by RNA polymerase II	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0044093	0.299	0.909	2	437	positive regulation of molecular function	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0006606	0.299	0.952	1	67	protein import into nucleus	BP	1	IPO7	down_ACOR_EC
GO:0006309	0.299	0.962	1	4	apoptotic DNA fragmentation	BP	1	AIFM1	down_ACOR_VSMC
GO:0042996	0.299	0.962	1	4	regulation of Golgi to plasma membrane	BP	1	ACSL3	down_ACOR_VSMC
GO:0045540	0.299	0.961	1	4	regulation of cholesterol biosynthetic process	BP	1	SREBF1	down_ACOR_VSMC

GO:0045899	0.299	0.961	1	4	positive regulation of RNA polymerase II transcriptional	BP	1	PSMC1	down_ACOR_VSMC
GO:0106118	0.299	0.961	1	4	regulation of sterol biosynthetic process	BP	1	SREBF1	down_ACOR_VSMC
GO:1902187	0.299	0.961	1	4	negative regulation of viral release from host cell	BP	1	TRIM35	down_ACOR_VSMC
GO:0009084	0.299	0.957	1	7	glutamine family amino acid biosynthetic process	BP	1	GLS2	down_VCAV_EC
GO:0033006	0.299	0.957	1	7	regulation of mast cell activation involved in	BP	1	RAC2	down_VCAV_EC
GO:0043304	0.299	0.957	1	7	regulation of mast cell degranulation	BP	1	RAC2	down_VCAV_EC
GO:0055089	0.299	0.956	1	7	fatty acid homeostasis	BP	1	GPAM	down_VCAV_EC
GO:1903205	0.299	0.957	1	7	regulation of hydrogen peroxide-induced cell	BP	1	PARK7	down_VCAV_EC
GO:2001038	0.299	0.957	1	7	regulation of cellular response to drug	BP	1	PARK7	down_VCAV_EC
GO:0098609	0.299	0.953	1	181	cell-cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0032268	0.299	0.965	1	778	regulation of cellular protein metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0070168	0.299	0.958	1	6	negative regulation of biomineral tissue	BP	1	HIF1A	down_VSAP_EC
GO:0070257	0.299	0.962	1	4	positive regulation of mucus secretion	BP	1	PRKCE	up_ACOR_VSMC
GO:0060079	0.299	0.953	1	15	excitatory postsynaptic potential	BP	1	DMPK	up_AFEM_EC
GO:0061462	0.299	0.953	1	15	protein localization to lysosome	BP	1	RAB7A	up_AFEM_EC
GO:0055065	0.299	0.953	1	145	metal ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0055078	0.299	0.962	1	4	sodium ion homeostasis	BP	1	EDN1	up_VCAV_EC
GO:0090009	0.299	0.961	1	4	primitive streak formation	BP	1	HHEX	up_VCAV_EC
GO:0042559	0.299	0.958	1	6	pteridine-containing compound biosynthetic	BP	1	GCH1	up_VCAV_EC
GO:0055015	0.299	0.959	1	5	ventricular cardiac muscle cell development	BP	1	PROX1	up_VCAV_EC
GO:0070831	0.299	0.965	1	3	basement membrane assembly	BP	1	LAMC2	up_VCAV_EC
GO:0050867	0.299	0.952	1	83	positive regulation of cell activation	BP	1	TOX	up_VFEM_EC
GO:0046486	0.299	0.952	1	102	glycerolipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0048562	0.299	0.952	1	102	embryonic organ morphogenesis	BP	1	HOXA3	up_VPUL_EC
GO:0006469	0.299	0.952	1	78	negative regulation of protein kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0015711	0.299	0.952	1	81	organic anion transport	BP	1	SLC16A12	up_VSAP_VSMC
GO:1901653	0.299	0.952	1	84	cellular response to peptide	BP	1	CAV1	up_VSAP_VSMC
GO:0032370	0.299096433	0.95366	1	13	positive regulation of lipid transport	BP	1	PRKCD	up_ACOR_EC
GO:0016242	0.299182171	0.95363	1	13	negative regulation of macroautophagy	BP	1	CHMP4B	up_ACOR_EC
GO:0071470	0.299203885	0.95362	1	13	cellular response to osmotic stress	BP	1	AQP1	up_ACOR_EC
GO:0071840	0.299677343	0.75404	58	2059	cellular component organization or biogenesis	BP	1	CNTNAP4,SH3TC2,MYOZ2,FMOD,NR1H4,TMOD1,BRSK1,TRPS1,KCTD12,PKIB,CALY,SOX9,RHOU,ARHGAP6,PHF20,ATG16L2,AQP1,SYNPO2,KCNB1,FZD5,IFI6,DIXDC1,PDLIM3,RGMA,SMAD6,PLS1,ACTN2,ZMYND8,ARHGAP28,ESM1,PAK3,PTGER4,ARHGDIB,ELMO2,PREB,DCLK2,ADAMTSL2,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,LRRC4,CLU,CHMP4B,TP53INP2,VPS16,RIOX2,NRP1,AZIN2,ARHGEF26,PRKCD,PYGO2,DBNDD2,ENSCAFG00000010493,MFAP4,TUBB4A	up_ACOR_EC
GO:0043085	0.3	0.765	30	323	positive regulation of catalytic activity	BP	1	HMGB1,IRAK1,HNRNPD,UBE2S,SLC29A1,PRELID1,RFC2,RFC5,RFC3,AURKB,ABHD5,EZH2,GREM1,MAP3K20,RFC4,NEK2,PCNA,CKS2,PDCD2,YWHAB,CYCS,EMP2,HMGB2,CLSPN,CDC20,AIFM1,NUS1,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC

GO:0070848	0.3	0.777	21	193	response to growth factor	BP	1	FZD1,SLIT2,FGF7,ABL1,DLL1,EPN2,CCBE1,ZFP36L1,GAS1,ZEB1,SULF2,LRP4,STK16,ZFP36L2,HPGD,RAF1,ACVRL1,HTRA2,TGFBR2,CITED2,BAG4	up_VSAP_EC
GO:0050803	0.3	0.827	7	55	regulation of synapse structure or activity	BP	1	EGLN1,DMPK,SLITRK5,DAG1,APP,LRRC4,DISC1	up_ACOR_VSMC
GO:0050807	0.3	0.827	7	55	regulation of synapse organization	BP	1	EGLN1,DMPK,SLITRK5,DAG1,APP,LRRC4,DISC1	up_ACOR_VSMC
GO:0010876	0.3	0.833	6	92	lipid localization	BP	1	AKT2,LCAT,SCP2,OSBPL10,ENSCAFG00000017708,SOAT1	down_VCAV_EC
GO:0045321	0.3	0.832	6	191	leukocyte activation	BP	1	LEP,CD40,DLL1,BPI,GPAM,CYLD	up_AFEM_EC
GO:0072009	0.3	0.836	6	48	nephron epithelium development	BP	1	HOXA11,WNT11,DLL1,OSR1,KLF15,IRX3	up_VSAP_EC
GO:0010952	0.3	0.846	5	46	positive regulation of peptidase activity	BP	1	HMGB1,PRELID1,PDCD2,CYCS,AIFM1	down_ACOR_VSMC
GO:0090304	0.3	0.861	5	1694	nucleic acid metabolic process	BP	1	IVNS1ABP,DARS,SRSF6,GABPA,TSEN15	down_AFEM_EC
GO:0051701	0.3	0.846	5	45	interaction with host	BP	1	CXCL8,TNIP1,GUCY1A1,NECTIN2,THOC1	up_VCAV_EC
GO:0045833	0.3	0.861	4	29	negative regulation of lipid metabolic process	BP	1	INSIG2,ACACB,ENSCAFG00000000071,PIK3IP1	up_VSAP_EC
GO:0002456	0.3	0.88	3	23	T cell mediated immunity	BP	1	HMGB1,FAM49B,EMP2	down_ACOR_VSMC
GO:0052548	0.3	0.875	3	80	regulation of endopeptidase activity	BP	1	CRYAB,F3,RECK	up_AFEM_EC
GO:0045582	0.3	0.906	2	22	positive regulation of T cell differentiation	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:0002028	0.3	0.907	2	19	regulation of sodium ion transport	BP	1	NKAIN1,YWHAH	down_VSAP_EC
GO:0048878	0.3	0.906	2	283	chemical homeostasis	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0001953	0.3	0.91	2	14	negative regulation of cell-matrix adhesion	BP	1	APOD,JAG1	up_VCAV_EC
GO:0009617	0.3	0.904	2	133	response to bacterium	BP	1	MTDH,NAALADL2	up_VPOR_EC
GO:0003205	0.3	0.952	1	67	cardiac chamber development	BP	1	NRP2	down_ACOR_EC
GO:0045666	0.3	0.952	1	68	positive regulation of neuron differentiation	BP	1	LYN	down_ACOR_EC
GO:0052547	0.3	0.952	1	82	regulation of peptidase activity	BP	1	LYN	down_ACOR_EC
GO:1904814	0.3	0.961	1	4	regulation of protein localization to	BP	1	CCT4	down_ACOR_VSMC
GO:0048207	0.3	0.961	1	4	vesicle targeting, rough ER to cis-Golgi	BP	1	PREB	down_ACOR_VSMC
GO:0048208	0.3	0.961	1	4	COPII vesicle coating	BP	1	PREB	down_ACOR_VSMC
GO:0090520	0.3	0.961	1	4	sphingolipid mediated signaling pathway	BP	1	EZR	down_ACOR_VSMC
GO:2000288	0.3	0.961	1	4	positive regulation of myoblast proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0007264	0.3	0.953	1	164	small GTPase mediated signal transduction	BP	1	GPSM2	down_AFEM_EC
GO:0048557	0.3	0.956	1	7	embryonic digestive tract morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0061061	0.3	0.953	1	179	muscle structure development	BP	1	CITED2	down_VPOR_EC
GO:0048869	0.3	0.973	1	1119	cellular developmental process	BP	1	GATA5	down_VFEM_VSMC
GO:0050858	0.3	0.957	1	6	negative regulation of antigen receptor-mediated signaling	BP	1	PTPN2	down_VSAP_EC
GO:0050860	0.3	0.957	1	6	negative regulation of T cell receptor signaling	BP	1	PTPN2	down_VSAP_EC
GO:0051451	0.3	0.957	1	6	myoblast migration	BP	1	SIX4	down_VSAP_EC
GO:0003221	0.3	0.965	1	3	right ventricular cardiac muscle tissue	BP	1	CHD7	up_ACOR_VSMC
GO:0021559	0.3	0.965	1	3	trigeminal nerve development	BP	1	NRP1	up_ACOR_VSMC
GO:0021636	0.3	0.965	1	3	trigeminal nerve morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0021637	0.3	0.965	1	3	trigeminal nerve structural organization	BP	1	NRP1	up_ACOR_VSMC
GO:0021785	0.3	0.965	1	3	branchiomotor neuron axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1902287	0.3	0.965	1	3	semaphorin-plexin signaling pathway involved in axon guidance	BP	1	NRP1	up_ACOR_VSMC

GO:0003338	0.3	0.953	1	15	metanephros morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:0046622	0.3	0.953	1	15	positive regulation of organ growth	BP	1	ACACB	up_AFEM_EC
GO:0031349	0.3	0.952	1	90	positive regulation of defense response	BP	1	NR1H4	up_APUL_EC
GO:0051240	0.3	0.959	1	489	positive regulation of multicellular organismal	BP	1	TBX5	up_APUL_VSMC
GO:0071624	0.3	0.957	1	6	positive regulation of granulocyte chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:0090023	0.3	0.957	1	6	positive regulation of neutrophil chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:2000481	0.3	0.965	1	3	positive regulation of cAMP-dependent protein	BP	1	RAPGEF2	up_VCAV_EC
GO:0035089	0.3	0.959	1	5	establishment of apical/basal cell polarity	BP	1	FSCN1	up_VCAV_EC
GO:0046085	0.3	0.959	1	5	adenosine metabolic process	BP	1	ACPP	up_VCAV_EC
GO:2001053	0.3	0.961	1	4	regulation of mesenchymal cell	BP	1	HIF1A	up_VCAV_EC
GO:0045216	0.3	0.952	1	44	cell-cell junction organization	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0090288	0.3	0.952	1	44	negative regulation of cellular response to growth factor stimulus	BP	1	ASPN	up_VPOR_EC
GO:0097696	0.3	0.951	1	43	STAT cascade	BP	1	ASPN	up_VPOR_EC
GO:0048812	0.3	0.953	1	151	neuron projection morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0035051	0.30063834	0.90395	2	41	cardiocyte differentiation	BP	1	ACTN2,TBX5	up_ACOR_EC
GO:0006749	0.300647556	0.9529	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	up_ACOR_EC
GO:0045843	0.30067398	0.95314	1	13	negative regulation of striated muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0032720	0.300735875	0.95311	1	13	negative regulation of tumor necrosis factor	BP	1	NR1H4	up_ACOR_EC
GO:0023056	0.301	0.752	48	462	positive regulation of signaling	BP	1	CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,LIMS2,IL6R,CRADD,ABL1,EMP2,DLL1,EPN2,MAP3K5,PDGFD,C1QTNF2,HPSE,CCBE1,F2RL1,TRAF7,PIK3R1,RBCK1,FAM53B,SULF2,SHOX2,SASH1,CREBRF,MYD88,S100A4,TSPAN5,ENSCAFG00000011993,RAF1,CYBA,ZNF205,STX4,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,CITED2,BAG4,TRADD,DEDD2	up_VSAP_EC
GO:0098660	0.301	0.806	10	141	inorganic ion transmembrane transport	BP	1	SLC39A7,ERO1A,REM1,NDUFA4L2,LYN,DDIT3,CLCN3,HTT,CALM1,YWHAH	down_VSAP_EC
GO:0010506	0.301	0.808	10	86	regulation of autophagy	BP	1	PLEKHF1,TPCN2,MFN2,POLDIP2,FBXO7,PIP4K2B,UBQLN2,HTRA2,HMOX1,NPRL3	up_VSAP_EC
GO:0010921	0.301	0.836	6	46	regulation of phosphatase activity	BP	1	SH3RF2,NPNT,MARF1,PPP1R26,GPATCH2,ZFYVE1	up_ACOR_VSMC
GO:0051224	0.301	0.835	6	47	negative regulation of protein transport	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1,BAG4	up_VSAP_EC
GO:1904950	0.301	0.835	6	47	negative regulation of establishment of protein localization	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1,BAG4	up_VSAP_EC
GO:0014065	0.301	0.846	5	39	phosphatidylinositol 3-kinase signaling	BP	1	PDGFD,F2RL1,ZFP36L1,PIK3R1,PIK3IP1	up_VSAP_EC
GO:0031333	0.301	0.858	4	46	negative regulation of protein complex assembly	BP	1	CRYAB,TWF1,GSK3B,CAPG	down_VSAP_EC
GO:0007498	0.301	0.877	3	38	mesoderm development	BP	1	BMPR1A,TLX2,ZFP36L1	down_VCAV_EC
GO:0060606	0.301	0.877	3	39	tube closure	BP	1	SDC4,LMO4,IFT57	down_VCAV_EC
GO:0048469	0.301	0.877	3	31	cell maturation	BP	1	HIF1A,CTNNB1,BTK	down_VSAP_EC
GO:2000514	0.301	0.91	2	13	regulation of CD4-positive, alpha-beta T cell	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0010629	0.301	0.908	2	502	negative regulation of gene expression	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0055024	0.301	0.906	2	22	regulation of cardiac muscle tissue	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0009581	0.301	0.907	2	18	detection of external stimulus	BP	1	GNAQ,RDH11	down_VSAP_EC
GO:0009582	0.301	0.907	2	18	detection of abiotic stimulus	BP	1	GNAQ,RDH11	down_VSAP_EC
GO:1904705	0.301	0.909	2	14	regulation of vascular smooth muscle cell	BP	1	PDGFB,MEF2C	up_VCAV_EC

GO:1990874	0.301	0.909	2	14	vascular smooth muscle cell proliferation	BP	1	PDGFB,MEF2C	up_VCAV_EC
GO:0008283	0.301	0.909	2	545	cell proliferation	BP	1	HOXA3,TBX5	up_VPUL_VSMC
GO:0045926	0.301	0.951	1	72	negative regulation of growth	BP	1	ACVRL1	down_ACOR_EC
GO:0033313	0.301	0.961	1	4	meiotic cell cycle checkpoint	BP	1	TTK	down_ACOR_VSMC
GO:0032616	0.301	0.961	1	4	interleukin-13 production	BP	1	ARG2	down_ACOR_VSMC
GO:0032656	0.301	0.961	1	4	regulation of interleukin-13 production	BP	1	ARG2	down_ACOR_VSMC
GO:0090042	0.301	0.961	1	4	tubulin deacetylation	BP	1	TADA2A	down_ACOR_VSMC
GO:0090043	0.301	0.961	1	4	regulation of tubulin deacetylation	BP	1	TADA2A	down_ACOR_VSMC
GO:0001504	0.301	0.956	1	7	neurotransmitter uptake	BP	1	PARK7	down_VCAV_EC
GO:0002823	0.301	0.956	1	7	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	LOXL3	down_VCAV_EC
GO:0002820	0.301	0.956	1	7	negative regulation of adaptive immune	BP	1	LOXL3	down_VCAV_EC
GO:1904707	0.301	0.956	1	7	positive regulation of vascular smooth muscle	BP	1	BMPR1A	down_VCAV_EC
GO:2000778	0.301	0.956	1	7	positive regulation of interleukin-6 secretion	BP	1	MAVS	down_VCAV_EC
GO:0040017	0.301	0.953	1	180	positive regulation of locomotion	BP	1	HDAC7	down_VPOR_EC
GO:0042159	0.301	0.957	1	6	lipoprotein catabolic process	BP	1	APOE	down_VSAP_EC
GO:0045061	0.301	0.957	1	6	thymic T cell selection	BP	1	PTPN2	down_VSAP_EC
GO:1901385	0.301	0.957	1	6	regulation of voltage-gated calcium channel	BP	1	REM1	down_VSAP_EC
GO:0006012	0.301	0.957	1	6	galactose metabolic process	BP	1	GALE	down_VSAP_EC
GO:0034143	0.301	0.957	1	6	regulation of toll-like receptor 4 signaling	BP	1	LYN	down_VSAP_EC
GO:0006384	0.301	0.961	1	4	transcription initiation from RNA polymerase III	BP	1	GTF3C1	up_ACOR_VSMC
GO:0021575	0.301	0.953	1	15	hindbrain morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:0021587	0.301	0.953	1	15	cerebellum morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:0070371	0.301	0.951	1	91	ERK1 and ERK2 cascade	BP	1	NPNT	up_APUL_EC
GO:2000146	0.301	0.952	1	92	negative regulation of cell motility	BP	1	TBX5	up_APUL_EC
GO:0042693	0.301	0.961	1	4	muscle cell fate commitment	BP	1	MEF2C	up_VCAV_EC
GO:0032483	0.301	0.965	1	3	regulation of Rab protein signal transduction	BP	1	MADD	up_VCAV_EC
GO:0070857	0.301	0.961	1	4	regulation of bile acid biosynthetic process	BP	1	PROX1	up_VCAV_EC
GO:1904251	0.301	0.961	1	4	regulation of bile acid metabolic process	BP	1	PROX1	up_VCAV_EC
GO:0019725	0.301	0.954	1	245	cellular homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0009799	0.301	0.951	1	43	specification of symmetry	BP	1	ACVR2A	up_VPOR_EC
GO:0050673	0.301	0.952	1	135	epithelial cell proliferation	BP	1	EYA1	up_VFEM_VSMC
GO:1905114	0.301	0.952	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	NETO1	up_VFEM_VSMC
GO:0003018	0.30146185	0.90344	2	42	vascular process in circulatory system	BP	1	FOXC2,CLSTN1	up_ACOR_EC
GO:0071241	0.301824857	0.90325	2	42	cellular response to inorganic substance	BP	1	AQP1,GUCY1B1	up_ACOR_EC
GO:0001974	0.301982759	0.9527	1	13	blood vessel remodeling	BP	1	FOXC2	up_ACOR_EC
GO:0010629	0.302	0.79	14	502	negative regulation of gene expression	BP	1	LEP,CRY2,GAS1,HOXA7,CRYAB,LMCD1,THRB,GREM1,TENT5C,NR3C1,AXIN2,ACACB,CTIF,SAMD4B	up_AFEM_EC
GO:0043900	0.302	0.798	12	104	regulation of multi-organism process	BP	1	F2RL1,CFAP69,SASH1,MYD88,NLRX1,TKFC,PC,RNF216,MAPKBP1,CYBA,PQBP1,MAVS	up_VSAP_EC

GO:0002697	0.302	0.807	10	85	regulation of immune effector process	BP	1	LEP,TP53BP1,TLR3,F2RL1,PTPN22,PARP9,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0001936	0.302	0.835	6	49	regulation of endothelial cell proliferation	BP	1	VEGFD,LEP,HTR2B,BMP4,TGFBR1,SYNJ2BP	up_ACOR_VSMC
GO:0032944	0.302	0.834	6	48	regulation of mononuclear cell	BP	1	LEP,BMP4,PDE5A,CD274,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0050670	0.302	0.834	6	48	regulation of lymphocyte proliferation	BP	1	LEP,BMP4,PDE5A,CD274,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0055001	0.302	0.834	6	47	muscle cell development	BP	1	ACTN2,BMP4,NEBL,EDN1,BVES,MYOZ2	up_ACOR_VSMC
GO:0007600	0.302	0.842	5	73	sensory perception	BP	1	NDN,LUM,ENSCAFG00000017708,RDH10,THRB	down_VCAV_EC
GO:0044249	0.302	0.861	5	1851	cellular biosynthetic process	BP	1	HDAC7,CITED2,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:0010608	0.302	0.841	5	154	posttranscriptional regulation of gene	BP	1	PRR16,TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0120031	0.302	0.841	5	154	plasma membrane bounded cell projection	BP	1	CYLD,DNAL1,SPATA6,CDC42EP5,KANK1	up_AFEM_EC
GO:0098656	0.302	0.845	5	42	anion transmembrane transport	BP	1	LRRC8D,SLC35A3,SLC38A1,LRRC8C,RIPK1	up_VCAV_EC
GO:0007229	0.302	0.86	4	32	integrin-mediated signaling pathway	BP	1	ITGB3,EMP2,PHACTR4,ITGA2	down_ACOR_VSMC
GO:0060537	0.302	0.855	4	117	muscle tissue development	BP	1	DLL1,GREM1,BVES,PPARGC1A	up_AFEM_EC
GO:1904589	0.302	0.859	4	33	regulation of protein import	BP	1	HCLS1,TMEM173,FERMT1,APOD	up_VCAV_EC
GO:1901700	0.302	0.877	3	364	response to oxygen-containing compound	BP	1	LYN,IGF1R,STX4	down_ACOR_EC
GO:0007272	0.302	0.877	3	31	ensheathment of neurons	BP	1	ILK,ZPR1,CTNNB1	down_VSAP_EC
GO:0008366	0.302	0.877	3	31	axon ensheathment	BP	1	ILK,ZPR1,CTNNB1	down_VSAP_EC
GO:0030521	0.302	0.881	3	19	androgen receptor signaling pathway	BP	1	MED14,AR,PARK7	up_ACOR_VSMC
GO:0034599	0.302	0.874	3	81	cellular response to oxidative stress	BP	1	NFE2L1,PPARGC1A,SOD1	up_AFEM_EC
GO:0010771	0.302	0.88	3	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	IFRD1,PPP3CA,RAPGEF2	up_VCAV_EC
GO:0043620	0.302	0.879	3	24	regulation of DNA-templated transcription in	BP	1	ATF3,NCK1,HIF1A	up_VCAV_EC
GO:0021545	0.302	0.88	3	21	cranial nerve development	BP	1	HOXD3,PLXNA4,CITED2	up_VSAP_EC
GO:0019915	0.302	0.905	2	22	lipid storage	BP	1	ENSCAFG00000017708,SOAT1	down_VCAV_EC
GO:0033077	0.302	0.905	2	22	T cell differentiation in thymus	BP	1	GLI3,ZFP36L1	down_VCAV_EC
GO:0034121	0.302	0.905	2	22	regulation of toll-like receptor signaling	BP	1	CYBA,RAB7B	down_VCAV_EC
GO:0045685	0.302	0.911	2	11	regulation of glial cell differentiation	BP	1	ZNF365,APP	up_ACOR_VSMC
GO:0007266	0.302	0.951	1	64	Rho protein signal transduction	BP	1	PDPN	down_ACOR_EC
GO:0034329	0.302	0.951	1	60	cell junction assembly	BP	1	ACVRL1	down_ACOR_EC
GO:0032536	0.302	0.961	1	4	regulation of cell projection size	BP	1	EZR	down_ACOR_VSMC
GO:0036315	0.302	0.961	1	4	cellular response to sterol	BP	1	INSIG1	down_ACOR_VSMC
GO:0060900	0.302	0.961	1	4	embryonic camera-type eye formation	BP	1	PHACTR4	down_ACOR_VSMC
GO:0010592	0.302	0.956	1	7	positive regulation of lamellipodium assembly	BP	1	RAC2	down_VCAV_EC
GO:0042554	0.302	0.956	1	7	superoxide anion generation	BP	1	CYBA	down_VCAV_EC
GO:0045622	0.302	0.956	1	7	regulation of T-helper cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0048569	0.302	0.956	1	7	post-embryonic animal organ development	BP	1	FBN1	down_VCAV_EC
GO:0030155	0.302	0.953	1	180	regulation of cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0050774	0.302	0.957	1	6	negative regulation of dendrite morphogenesis	BP	1	YWHAH	down_VSAP_EC
GO:0021854	0.302	0.957	1	6	hypothalamus development	BP	1	NRP1	down_VSAP_EC
GO:0072413	0.302	0.957	1	6	signal transduction involved in mitotic cell	BP	1	CDKN1A	down_VSAP_EC
GO:1902402	0.302	0.957	1	6	signal transduction involved in mitotic DNA	BP	1	CDKN1A	down_VSAP_EC

GO:1902403	0.302	0.957	1	6	signal transduction involved in mitotic DNA	BP	1	CDKN1A	down_VSAP_EC
GO:1903069	0.302	0.957	1	6	regulation of ER-associated ubiquitin-dependent protein	BP	1	USP14	down_VSAP_EC
GO:0002836	0.302	0.961	1	4	positive regulation of response to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0002839	0.302	0.961	1	4	positive regulation of immune response to	BP	1	CD274	up_ACOR_VSMC
GO:0006801	0.302	0.952	1	15	superoxide metabolic process	BP	1	SOD1	up_AFEM_EC
GO:0030516	0.302	0.952	1	15	regulation of axon extension	BP	1	PLXNA4	up_AFEM_EC
GO:0045620	0.302	0.952	1	15	negative regulation of lymphocyte	BP	1	CYLD	up_AFEM_EC
GO:0050795	0.302	0.952	1	15	regulation of behavior	BP	1	HTR1D	up_AFEM_EC
GO:0071277	0.302	0.952	1	15	cellular response to calcium ion	BP	1	CPNE7	up_AFEM_EC
GO:0048666	0.302	0.954	1	258	neuron development	BP	1	IRX5	up_AFEM_VSMC
GO:0003007	0.302	0.951	1	94	heart morphogenesis	BP	1	TBX5	up_APUL_EC
GO:0033623	0.302	0.961	1	4	regulation of integrin activation	BP	1	SELP	up_VCAV_EC
GO:0009260	0.302	0.951	1	83	ribonucleotide biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0046390	0.302	0.951	1	83	ribose phosphate biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0072507	0.302	0.951	1	103	divalent inorganic cation homeostasis	BP	1	HOXA3	up_VPUL_EC
GO:0055080	0.302	0.953	1	176	cation homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0014910	0.302067522	0.95267	1	13	regulation of smooth muscle cell migration	BP	1	SEMA6D	up_ACOR_EC
GO:2001259	0.302168254	0.95264	1	13	positive regulation of cation channel activity	BP	1	ACTN2	up_ACOR_EC
GO:0035249	0.302493716	0.95253	1	13	synaptic transmission, glutamatergic	BP	1	MAPK8IP2	up_ACOR_EC
GO:0045214	0.302541054	0.95251	1	13	sarcomere organization	BP	1	ACTN2	up_ACOR_EC
GO:0090169	0.302689978	0.95246	1	13	regulation of spindle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:1902476	0.302754501	0.95244	1	13	chloride transmembrane transport	BP	1	CLIC3	up_ACOR_EC
GO:0098660	0.302928977	0.84061	5	141	inorganic ion transmembrane transport	BP	1	CLIC3,KCNB1,ACTN2,SLC9A9,PM20D1	up_ACOR_EC
GO:0016310	0.303	0.743	66	641	phosphorylation	BP	1	FGF13,ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,CDC7,HTR2B,RASSF2,MBP,PRKAA2,BMP4,FGFR2,TLR3,SH3RF2,LATS2,PDE5A,AR,SASH1,LMO4,FGF18,NDRG2,CDKN2B,GRK7,F2RL1,FAM129A,CAMK2D,DAPK1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,DAG1,PARP9,APP,PSEN1,SYNJ2BP,PIK3C3,CCL5,DDR2,PSKH1,DUSP22,EDN1,ALDOC,AKTIP,DUSP26,NOD2,LRRC4,LMTK2,PRKAG3,DDIT4,SH3RF3,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,CRKL,CDKL2	up_ACOR_VSMC
GO:0000122	0.303	0.775	21	218	negative regulation of transcription by RNA polymerase II	BP	1	HMGB1,SREBF1,CBX5,SREBF2,NEDD4,MTDH,CAV1,TIMELESS,AURKB,EZH2,PLK3,HOXA7,UHRF1,NOC2L,PPARD,SUV39H1,DMAP1,CDK2,EZR,ERF,TCERG1	down_ACOR_VSMC
GO:0006811	0.303	0.778	19	330	ion transport	BP	1	PRNP,FOLR2,FXYD1,TRPV2,AKT2,SCP2,SLC39A6,CACNB3,ATP5MC1,THY1,ATP6V0C,PARK7,SLC17A9,SCARA5,TPC3,CYBA,ARHGAP1,CLIC4,PACSIN3	down_VCAV_EC
GO:0032504	0.303	0.783	17	152	multicellular organism reproduction	BP	1	PRDX4,BMP4,ATRX,PDE5A,CITED2,CTSB,CREBRF,MARF1,AFF4,DKKL1,APP,SPINK2,HPGD,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0048609	0.303	0.783	17	152	multicellular organismal reproductive process	BP	1	PRDX4,BMP4,ATRX,PDE5A,CITED2,CTSB,CREBRF,MARF1,AFF4,DKKL1,APP,SPINK2,HPGD,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0051249	0.303	0.801	11	107	regulation of lymphocyte activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,MMP14,HMGB3,ARG2,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0019538	0.303	0.815	10	1713	protein metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,RPSA,SULF1,CSGALNACT1,ASPN,NEDD4	down_ACOR_EC
GO:0099536	0.303	0.805	10	133	synaptic signaling	BP	1	KIF5B,HTR7,PLCL1,CDH11,CTNNB1,APOE,GSK3B,KPNA1,LRRTM2,USP14	down_VSAP_EC

GO:0006793	0.303	0.848	5	948	phosphorus metabolic process	BP	1	NR1H4,MAPK10,PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0023051	0.303	0.848	5	954	regulation of signaling	BP	1	NR1H4,PLCL1,ARHGEF26,NPNT,NTRK2	up_APUL_EC
GO:0006836	0.303	0.844	5	47	neurotransmitter transport	BP	1	MEF2C,EDN1,SNCAIP,SNAP23,STX11	up_VCAV_EC
GO:0001838	0.303	0.856	4	56	embryonic epithelial tube formation	BP	1	SDC4,LMO4,IFT57,GREM1	down_VCAV_EC
GO:0002792	0.303	0.86	4	29	negative regulation of peptide secretion	BP	1	LEP,F2RL1,PTPN22,PFKL	up_ACOR_VSMC
GO:1900076	0.303	0.86	4	29	regulation of cellular response to insulin	BP	1	KLF15,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:1901184	0.303	0.88	3	20	regulation of ERBB signaling pathway	BP	1	SH3TC2,APP,PSEN1	up_ACOR_VSMC
GO:0015711	0.303	0.874	3	81	organic anion transport	BP	1	LEP,SLC17A5,SLC6A6	up_AFEM_EC
GO:0002698	0.303	0.878	3	25	negative regulation of immune effector process	BP	1	IL7R,RIOK3,THOC1	up_VCAV_EC
GO:0012501	0.303	0.878	3	561	programmed cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:0017145	0.303	0.909	2	13	stem cell division	BP	1	ASPM,ARHGEF2	down_ACOR_VSMC
GO:0008037	0.303	0.905	2	22	cell recognition	BP	1	NDN,B4GALT1	down_VCAV_EC
GO:1905515	0.303	0.905	2	22	non-motile cilium assembly	BP	1	TTC8,IFT57	down_VCAV_EC
GO:2000026	0.303	0.908	2	560	regulation of multicellular organismal development	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0048519	0.303	0.926	2	1554	negative regulation of biological process	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0007606	0.303	0.908	2	13	sensory perception of chemical stimulus	BP	1	NAV2,P2RX2	up_VCAV_EC
GO:0038084	0.303	0.908	2	13	vascular endothelial growth factor signaling	BP	1	PRKD2,JCAD	up_VCAV_EC
GO:0009967	0.303	0.906	2	435	positive regulation of signal transduction	BP	1	NETO1,SHOX2	up_VFEM_VSMC
GO:0033522	0.303	0.91	2	12	histone H2A ubiquitination	BP	1	DDB2,KDM2B	up_VSAP_EC
GO:0045597	0.303	0.904	2	253	positive regulation of cell differentiation	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0030522	0.303	0.95	1	67	intracellular receptor signaling pathway	BP	1	NEDD4	down_ACOR_EC
GO:0032388	0.303	0.951	1	62	positive regulation of intracellular transport	BP	1	NEDD4	down_ACOR_EC
GO:0032055	0.303	0.96	1	4	negative regulation of translation in response to	BP	1	RBM14	down_ACOR_VSMC
GO:0045940	0.303	0.96	1	4	positive regulation of steroid metabolic process	BP	1	SREBF1	down_ACOR_VSMC
GO:0002829	0.303	0.96	1	4	negative regulation of type 2 immune response	BP	1	ARG2	down_ACOR_VSMC
GO:0060681	0.303	0.96	1	4	branch elongation involved in ureteric bud	BP	1	SIX4	down_ACOR_VSMC
GO:0072106	0.303	0.96	1	4	regulation of ureteric bud formation	BP	1	SIX4	down_ACOR_VSMC
GO:0072107	0.303	0.96	1	4	positive regulation of ureteric bud formation	BP	1	SIX4	down_ACOR_VSMC
GO:1905278	0.303	0.96	1	4	positive regulation of epithelial tube formation	BP	1	SIX4	down_ACOR_VSMC
GO:0043254	0.303	0.952	1	164	regulation of protein complex assembly	BP	1	FSCN1	down_AFEM_EC
GO:0033238	0.303	0.955	1	7	regulation of cellular amine metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0045652	0.303	0.955	1	7	regulation of megakaryocyte	BP	1	RAB7B	down_VCAV_EC
GO:0070242	0.303	0.955	1	7	thymocyte apoptotic process	BP	1	GLI3	down_VCAV_EC
GO:1900120	0.303	0.955	1	7	regulation of receptor binding	BP	1	PLCL1	down_VCAV_EC
GO:0000394	0.303	0.956	1	6	RNA splicing, via endonucleolytic cleavage	BP	1	RTCB	down_VSAP_EC
GO:0006388	0.303	0.956	1	6	tRNA splicing, via endonucleolytic cleavage	BP	1	RTCB	down_VSAP_EC
GO:0032793	0.303	0.956	1	6	positive regulation of CREB transcription factor	BP	1	VEGFA	down_VSAP_EC
GO:0009081	0.303	0.956	1	6	branched-chain amino acid metabolic process	BP	1	BCAT1	down_VSAP_EC
GO:0034110	0.303	0.956	1	6	regulation of homotypic cell-cell adhesion	BP	1	LYN	down_VSAP_EC
GO:0072033	0.303	0.958	1	5	renal vesicle formation	BP	1	CTNNB1	down_VSAP_EC

GO:2000197	0.303	0.958	1	5	regulation of ribonucleoprotein	BP	1	IWS1	down_VSAP_EC
GO:2001046	0.303	0.96	1	4	positive regulation of integrin-mediated	BP	1	LIMS2	up_ACOR_VSMC
GO:0006084	0.303	0.952	1	15	acetyl-CoA metabolic process	BP	1	ACACB	up_AFEM_EC
GO:0006111	0.303	0.952	1	15	regulation of gluconeogenesis	BP	1	LEP	up_AFEM_EC
GO:0006509	0.303	0.952	1	15	membrane protein ectodomain proteolysis	BP	1	ADAM17	up_AFEM_EC
GO:0006904	0.303	0.952	1	15	vesicle docking involved in exocytosis	BP	1	CAMK2A	up_AFEM_EC
GO:0030808	0.303	0.952	1	15	regulation of nucleotide biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0031016	0.303	0.952	1	15	pancreas development	BP	1	DLL1	up_AFEM_EC
GO:0032435	0.303	0.952	1	15	negative regulation of proteasomal ubiquitin-dependent protein	BP	1	CLEC16A	up_AFEM_EC
GO:0002260	0.303	0.952	1	15	lymphocyte homeostasis	BP	1	GPAM	up_AFEM_EC
GO:0045022	0.303	0.952	1	15	early endosome to late endosome transport	BP	1	RAB7A	up_AFEM_EC
GO:0002762	0.303	0.952	1	15	negative regulation of myeloid leukocyte	BP	1	HOXA7	up_AFEM_EC
GO:1900371	0.303	0.952	1	15	regulation of purine nucleotide biosynthetic	BP	1	PPARGC1A	up_AFEM_EC
GO:0001568	0.303	0.953	1	252	blood vessel development	BP	1	EYA1	up_AFEM_VSMC
GO:0043517	0.303	0.956	1	6	positive regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	PMAIP1	up_VCAV_EC
GO:0051601	0.303	0.96	1	4	exocyst localization	BP	1	EXOC3L2	up_VCAV_EC
GO:0001525	0.303164291	0.82985	6	173	angiogenesis	BP	1	AQP1,ENSCAFG00000004331,FZD5,ESM1,FOXC2,NRP1	up_ACOR_EC
GO:0001961	0.303225887	0.95228	1	13	positive regulation of cytokine-mediated	BP	1	MAVS	up_ACOR_EC
GO:0015696	0.303393697	0.95197	1	14	ammonium transport	BP	1	AQP1	up_ACOR_EC
GO:0051172	0.303438104	0.77611	20	663	negative regulation of nitrogen compound metabolic process	BP	1	NR1H4,TRPS1,PKIB,SOX9,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,ZMYND8,CST3,PIAS1,FOXC2,LRRC15,CLSTN1,LRRC4,RIOX2,AZIN2,PRKCD,DBNDD2	up_ACOR_EC
GO:0060445	0.303494496	0.95219	1	13	branching involved in salivary gland	BP	1	NRP1	up_ACOR_EC
GO:2000027	0.303718982	0.87325	3	72	regulation of animal organ morphogenesis	BP	1	SOX9,FOXC2,TBX5	up_ACOR_EC
GO:0060740	0.303790874	0.95209	1	13	prostate gland epithelium morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0019220	0.304	0.747	54	525	regulation of phosphate metabolic process	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,DDR2,PDK2,TRAF7,PIK3R1,MYC,PIK3IP1,TMEM225B,RTN4RL1,SASH1,MYD88,LRP4,FBXO7,CDK9,FBLN1,RAF1,QARS,ACVRL1,IDH1,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0051174	0.304	0.747	54	525	regulation of phosphorus metabolic process	BP	1	FZD1,CDON,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,DDR2,PDK2,TRAF7,PIK3R1,MYC,PIK3IP1,TMEM225B,RTN4RL1,SASH1,MYD88,LRP4,FBXO7,CDK9,FBLN1,RAF1,QARS,ACVRL1,IDH1,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0007346	0.304	0.775	20	210	regulation of mitotic cell cycle	BP	1	PLK2,PDGFB,STK10,EDN1,RAB11A,MAP3K3,SLK,ENSCAFG00000010596,PAK2,TAOK1,BLM,SMC5,RAD21,RAD17,CUL4A,ZW10,ATRX,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0061564	0.304	0.79	14	119	axon development	BP	1	EPYC,FEZ1,FGFR2,NRP1,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2	up_ACOR_VSMC
GO:0031175	0.304	0.792	13	224	neuron projection development	BP	1	NDN,SDC4,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,NCDN,UST,PRKCSH,RGMA,BRSK1	down_VCAV_EC

GO:0022618	0.304	0.8	11	111	ribonucleoprotein complex assembly	BP	1	USP4,EDC3,SLC29A1,DDX28,DDX39B,SF3A2,PRMT5,ENSCAFG00000015189,GEMIN7,SF3A1,EIF3M	down_ACOR_VSMC
GO:0010632	0.304	0.801	11	95	regulation of epithelial cell migration	BP	1	BMP4,SASH1,FGF18,NRP1,EVL,PRKCE,SYNJ2BP,JUP,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0044271	0.304	0.825	8	1501	cellular nitrogen compound biosynthetic	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0003012	0.304	0.822	7	90	muscle system process	BP	1	SULF1,TPM4,HTR7,ACTA2,CALM1,MYBPC2,HOMER1	down_VSAP_EC
GO:0007281	0.304	0.842	5	60	germ cell development	BP	1	CELF1,CTNNB1,CDYL,SPINK2,KDM3A	down_VSAP_EC
GO:0050679	0.304	0.842	5	62	positive regulation of epithelial cell proliferation	BP	1	VEGFA,JCAD,TGFBR1,ADAM17,CTNNB1	down_VSAP_EC
GO:1901361	0.304	0.84	5	154	organic cyclic compound catabolic process	BP	1	TENT5C,MOXD1,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:1902531	0.304	0.857	4	536	regulation of intracellular signal transduction	BP	1	LYN,IGF1R,ASPN,NEDD4	down_ACOR_EC
GO:0022409	0.304	0.855	4	56	positive regulation of cell-cell adhesion	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:0045778	0.304	0.857	4	35	positive regulation of ossification	BP	1	MEF2C,BMP2,JAG1,FBXO5	up_VCAV_EC
GO:1903169	0.304	0.858	4	34	regulation of calcium ion transmembrane transport	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0032946	0.304	0.859	4	29	positive regulation of mononuclear cell	BP	1	MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0050671	0.304	0.859	4	29	positive regulation of lymphocyte proliferation	BP	1	MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:2000045	0.304	0.859	4	29	regulation of G1/S transition of mitotic cell	BP	1	FAM107A,CRADD,FBXO7,LSM10	up_VSAP_EC
GO:0010717	0.304	0.875	3	32	regulation of epithelial to mesenchymal transition	BP	1	TGFBR1,CTNNB1,STRAP	down_VSAP_EC
GO:0046324	0.304	0.879	3	20	regulation of glucose import	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0007601	0.304	0.904	2	22	visual perception	BP	1	LUM,RDH10	down_VCAV_EC
GO:0050953	0.304	0.904	2	22	sensory perception of light stimulus	BP	1	LUM,RDH10	down_VCAV_EC
GO:0090630	0.304	0.904	2	23	activation of GTPase activity	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0060039	0.304	0.91	2	11	pericardium development	BP	1	TBX20,TBX5	up_ACOR_VSMC
GO:2000378	0.304	0.909	2	12	negative regulation of reactive oxygen species	BP	1	BNIP3,PARK7	up_ACOR_VSMC
GO:0032989	0.304	0.903	2	292	cellular component morphogenesis	BP	1	ARHGEF26,SLITRK5	up_APUL_EC
GO:0061384	0.304	0.909	2	12	heart trabecula morphogenesis	BP	1	CHD7,DLL4	up_VCAV_EC
GO:0099024	0.304	0.908	2	13	plasma membrane invagination	BP	1	ABCA1,ELMO1	up_VCAV_EC
GO:0007254	0.304	0.95	1	67	JNK cascade	BP	1	IGF1R	down_ACOR_EC
GO:0032496	0.304	0.95	1	77	response to lipopolysaccharide	BP	1	LYN	down_ACOR_EC
GO:0048736	0.304	0.95	1	66	appendage development	BP	1	SULF1	down_ACOR_EC
GO:0060173	0.304	0.95	1	66	limb development	BP	1	SULF1	down_ACOR_EC
GO:0006525	0.304	0.96	1	4	arginine metabolic process	BP	1	ARG2	down_ACOR_VSMC
GO:0072697	0.304	0.96	1	4	protein localization to cell cortex	BP	1	EZR	down_ACOR_VSMC
GO:0080009	0.304	0.96	1	4	mRNA methylation	BP	1	WTAP	down_ACOR_VSMC
GO:0034134	0.304	0.955	1	7	toll-like receptor 2 signaling pathway	BP	1	CYBA	down_VCAV_EC
GO:0003006	0.304	0.952	1	180	developmental process involved in reproduction	BP	1	CITED2	down_VPOR_EC
GO:0035721	0.304	0.956	1	6	intraciliary retrograde transport	BP	1	DYNLL1	down_VSAP_EC
GO:0010640	0.304	0.956	1	6	regulation of platelet-derived growth factor receptor signaling	BP	1	PTPN2	down_VSAP_EC
GO:0071679	0.304	0.958	1	5	commissural neuron axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0051409	0.304	0.96	1	4	response to nitrosative stress	BP	1	PARK7	up_ACOR_VSMC
GO:0019076	0.304	0.952	1	15	viral release from host cell	BP	1	RAB7A	up_AFEM_EC
GO:0030520	0.304	0.952	1	15	intracellular estrogen receptor signaling	BP	1	LBH	up_AFEM_EC

GO:0032371	0.304	0.952	1	15	regulation of sterol transport	BP	1	LEP	up_AFEM_EC
GO:0032374	0.304	0.952	1	15	regulation of cholesterol transport	BP	1	LEP	up_AFEM_EC
GO:0035890	0.304	0.952	1	15	exit from host	BP	1	RAB7A	up_AFEM_EC
GO:0035891	0.304	0.952	1	15	exit from host cell	BP	1	RAB7A	up_AFEM_EC
GO:0052126	0.304	0.952	1	15	movement in host environment	BP	1	RAB7A	up_AFEM_EC
GO:0052192	0.304	0.952	1	15	movement in environment of other organism involved in	BP	1	RAB7A	up_AFEM_EC
GO:0051270	0.304	0.954	1	296	regulation of cellular component movement	BP	1	WNT7A	up_AORT_VSMC
GO:0006486	0.304	0.95	1	91	protein glycosylation	BP	1	GALNT17	up_APUL_EC
GO:0043413	0.304	0.95	1	91	macromolecule glycosylation	BP	1	GALNT17	up_APUL_EC
GO:0051258	0.304	0.95	1	94	protein polymerization	BP	1	TUBB4A	up_APUL_EC
GO:0060485	0.304	0.95	1	93	mesenchyme development	BP	1	TBX5	up_APUL_EC
GO:0003306	0.304	0.96	1	4	Wnt signaling pathway involved in heart	BP	1	BMP2	up_VCAV_EC
GO:0008356	0.304	0.964	1	3	asymmetric cell division	BP	1	ARHGEF2	up_VCAV_EC
GO:1905208	0.304	0.96	1	4	negative regulation of cardiocyte differentiation	BP	1	BMP2	up_VCAV_EC
GO:0031334	0.304	0.95	1	84	positive regulation of protein complex assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0051222	0.304	0.951	1	103	positive regulation of protein transport	BP	1	NR1H4	up_VPUL_EC
GO:1901293	0.304216208	0.85362	4	106	nucleoside phosphate biosynthetic process	BP	1	NMNAT2,GUCY1B1,AK7,ALDOC	up_ACOR_EC
GO:0033555	0.304396342	0.95189	1	13	multicellular organismal response to stress	BP	1	MAPK8IP2	up_ACOR_EC
GO:0048869	0.305	0.732	114	1119	cellular developmental process	BP	1	EXPH5,SH3TC2,VEGFD,TMEM176B,TMEM176A,SMAD6,ACTN2,PLCG2,LEP,LBH,GATA5,GATA4,CD83,CDC7,ANGPT1,EPYC,HTR2B,RASSF2,FNDC5,ZRANB1,SHROOM3,FEZ1,ITM2C,BMP4,LNPK,FGFR2,GJA1,ELF1,ATRX,TRPS1,SEC24B,WASF3,PPARGC1A,LATS2,PDE5A,CITED2,TP53INP1,ISG15,ACSL6,ZNF365,LMO4,TMEM108,FGF18,FAM210B,ARHGEF26,P4HTM,NEBL,CDKN2B,ZMYM2,PLAC8B,ANKRD1,PLEKHB2,F2RL1,CAMK2D,MARCH5,CTSB,BNIP3,CDKN1A,CLSTN1,LRRC8C,NRP1,PTPN22,GPM6A,CHD2,ULK2,DMPK,NPNT,UNC5B,SMARCD3,SPINT2,SLITRK5,TBX20,TPT1,TBX5,CCDC3,MARF1,FZD3,AFF4,DKKL1,FRS2,RND1,DAG1,POMK,APP,LAMA3,PSEN1,TGFBR1,CHD7,SPINK2,SIPA1L1,DDR2,CLN8,FOSL2,SSH3,EDN1,ARID5B,ASAP1,DMC1,PRELP,JAM3,B2M,DISC1,ATXN10,FEZ2,SUN1,CNOT4,WASL,DOCK5,ENSCAFG00000003530,IL18R1,BVES,RREB1,CRKL,MYOZ2	up_ACOR_VSMC
GO:0032940	0.305	0.767	25	231	secretion by cell	BP	1	HNF4A,CD274,C5AR2,SLC8B1,FGF7,ABL1,IL17RC,ANXA4,F2RL1,LMF1,RAB11B,PASK,SCFD2,STEAP3,KCNB1,RAF1,PNP,MAPKBP1,STX4,VPS11,KCNC4,PPP3CB,MAVS,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0097435	0.305	0.771	22	230	supramolecular fiber organization	BP	1	FSCN1,CAPG,SLC29A1,COLGALT1,FBXO5,LIMA1,NF2,STMN1,GREM1,PLK3,RAC1,EMP2,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,ARPC1B,ARHGEF2,SERPINH1,SIX4,KIF24	down_ACOR_VSMC
GO:0072594	0.305	0.785	15	155	establishment of protein localization to organelle	BP	1	SREBF1,NEDD4,TIMM44,POLA2,RAN,ENSCAFG00000011598,TRAM1,IPO4,NUP62,NUP188,TOMM34,SAMM50,DMAP1,PMPCA,CCT4	down_ACOR_VSMC
GO:0016043	0.305	0.809	12	1973	cellular component organization	BP	1	ACVRL1,LYN,IGF1R,SPG11,PDPN,NRP2,RPSA,SULF1,CSGALNACT1,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0001817	0.305	0.798	11	182	regulation of cytokine production	BP	1	GPAM,PRNP,LUM,CHID1,RNF216,PARK7,MAST2,BPI,CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0001701	0.305	0.803	10	134	in utero embryonic development	BP	1	SEC24D,TMED2,HIF1A,ZPR1,CTNNB1,PLOD3,MYO1E,RBBP8,PRMT1,RTCB	down_VSAP_EC
GO:0005996	0.305	0.805	10	85	monosaccharide metabolic process	BP	1	DHDH,ACACB,C1QTNF2,PDK2,GALK2,GALK1,PASK,KHK,PC,NCOA2	up_VSAP_EC
GO:0018105	0.305	0.808	9	116	peptidyl-serine phosphorylation	BP	1	VEGFA,SGK1,BCAR3,ILK,PTGS2,PLCL1,GSK3B,PAK2,CAMK2D	down_VSAP_EC

GO:2000146	0.305	0.83	6	92	negative regulation of cell motility	BP	1	DCN,BMPR1A,RECK,THY1,SPRED1,FOXO3	down_VCAV_EC
GO:0106106	0.305	0.832	6	48	cold-induced thermogenesis	BP	1	PPARGC1B,EBF2,STAT6,MFN2,HOXC10,PRKAB1	up_VSAP_EC
GO:0120161	0.305	0.832	6	48	regulation of cold-induced thermogenesis	BP	1	PPARGC1B,EBF2,STAT6,MFN2,HOXC10,PRKAB1	up_VSAP_EC
GO:0033554	0.305	0.844	5	708	cellular response to stress	BP	1	LYN,IGF1R,USP28,ATRIP,NEDD4	down_ACOR_EC
GO:1901137	0.305	0.873	3	232	carbohydrate derivative biosynthetic process	BP	1	OSTC,FBP1,GNPNAT1	up_VPOR_EC
GO:0007606	0.305	0.908	2	13	sensory perception of chemical stimulus	BP	1	B3GNT2,NAV2	down_ACOR_VSMC
GO:0090559	0.305	0.904	2	20	regulation of membrane permeability	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0032024	0.305	0.909	2	12	positive regulation of insulin secretion	BP	1	TM7SF3,PRKCE	up_ACOR_VSMC
GO:0090277	0.305	0.909	2	12	positive regulation of peptide hormone	BP	1	TM7SF3,PRKCE	up_ACOR_VSMC
GO:0006936	0.305	0.95	1	74	muscle contraction	BP	1	SULF1	down_ACOR_EC
GO:0030889	0.305	0.96	1	4	negative regulation of B cell proliferation	BP	1	MNDA	down_ACOR_VSMC
GO:0071073	0.305	0.96	1	4	positive regulation of phospholipid biosynthetic	BP	1	ACSL3	down_ACOR_VSMC
GO:1900227	0.305	0.96	1	4	positive regulation of NLRP3 inflammasome	BP	1	DHX33	down_ACOR_VSMC
GO:1903827	0.305	0.951	1	164	regulation of cellular protein localization	BP	1	GPSM2	down_AFEM_EC
GO:0009154	0.305	0.955	1	7	purine ribonucleotide catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:1901213	0.305	0.955	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GREM1	down_VCAV_EC
GO:1903427	0.305	0.955	1	7	negative regulation of reactive oxygen species biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:1902667	0.305	0.957	1	5	regulation of axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0007602	0.305	0.96	1	4	phototransduction	BP	1	GNAQ	up_ACOR_VSMC
GO:1902003	0.305	0.96	1	4	regulation of amyloid-beta formation	BP	1	APP	up_ACOR_VSMC
GO:0031952	0.305	0.951	1	15	regulation of protein autophosphorylation	BP	1	GREM1	up_AFEM_EC
GO:0048260	0.305	0.951	1	15	positive regulation of receptor-mediated	BP	1	GREM1	up_AFEM_EC
GO:0051443	0.305	0.951	1	15	positive regulation of ubiquitin-protein	BP	1	DCUN1D3	up_AFEM_EC
GO:2000242	0.305	0.951	1	15	negative regulation of reproductive process	BP	1	OVOL1	up_AFEM_EC
GO:0019953	0.305	0.951	1	152	sexual reproduction	BP	1	HOXA9	up_AORT_EC
GO:0050769	0.305	0.95	1	95	positive regulation of neurogenesis	BP	1	NTRK2	up_APUL_EC
GO:0003211	0.305	0.96	1	4	cardiac ventricle formation	BP	1	MEF2C	up_VCAV_EC
GO:1990440	0.305	0.957	1	5	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP	1	ATF3	up_VCAV_EC
GO:0051259	0.305	0.951	1	140	protein complex oligomerization	BP	1	FBP1	up_VFEM_VSMC
GO:0002791	0.305	0.95	1	104	regulation of peptide secretion	BP	1	NR1H4	up_VPUL_EC
GO:0042493	0.305	0.951	1	178	response to drug	BP	1	SLIT2	up_VPUL_VSMC
GO:0050867	0.305	0.95	1	83	positive regulation of cell activation	BP	1	CAV1	up_VSAP_VSMC
GO:0044703	0.305064964	0.82844	6	172	multi-organism reproductive process	BP	1	SOX9,ARHGDIB,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0043266	0.305204778	0.95136	1	14	regulation of potassium ion transport	BP	1	ACTN2	up_ACOR_EC
GO:0097237	0.305743547	0.90114	2	42	cellular response to toxic substance	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:0032990	0.306	0.776	19	167	cell part morphogenesis	BP	1	EPYC,FEZ1,FGFR2,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,FEZ2,WASL,RREB1	up_ACOR_VSMC

GO:0032869	0.306	0.823	7	57	cellular response to insulin stimulus	BP	1	GOT1,KLF15,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0072522	0.306	0.828	6	91	purine-containing compound biosynthetic	BP	1	ADCY6,ATP5MC1,ADK,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0050878	0.306	0.829	6	75	regulation of body fluid levels	BP	1	SERPINE1,HIF1A,APOE,LYN,SLC7A11,ITGB3	down_VSAP_EC
GO:0003231	0.306	0.831	6	48	cardiac ventricle development	BP	1	FZD1,WNT11,SAV1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0003279	0.306	0.831	6	48	cardiac septum development	BP	1	FZD1,WNT11,SAV1,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0090263	0.306	0.857	4	33	positive regulation of canonical Wnt signaling	BP	1	CTDNEP1,CAV1,ASPM,AMER1	down_ACOR_VSMC
GO:0030509	0.306	0.854	4	47	BMP signaling pathway	BP	1	SULF1,ILK,NEO1,ENSCAFG00000018360	down_VSAP_EC
GO:0006497	0.306	0.874	3	38	protein lipidation	BP	1	CLIP3,PIGS,WDR45	down_VCAV_EC
GO:2001244	0.306	0.875	3	27	positive regulation of intrinsic apoptotic	BP	1	NCK1,PMAIP1,SKIL	up_VCAV_EC
GO:0043331	0.306	0.878	3	20	response to dsRNA	BP	1	PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0032272	0.306	0.905	2	18	negative regulation of protein polymerization	BP	1	TWF1,CAPG	down_VSAP_EC
GO:0035307	0.306	0.904	2	18	positive regulation of protein	BP	1	PPP1R12A,CALM1	down_VSAP_EC
GO:1904427	0.306	0.904	2	18	positive regulation of calcium ion	BP	1	HTT,CALM1	down_VSAP_EC
GO:0051254	0.306	0.905	2	431	positive regulation of RNA metabolic process	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0002757	0.306	0.949	1	78	immune response-activating signal	BP	1	LYN	down_ACOR_EC
GO:0051170	0.306	0.949	1	69	import into nucleus	BP	1	IPO7	down_ACOR_EC
GO:0003334	0.306	0.959	1	4	keratinocyte development	BP	1	FLNB	down_ACOR_VSMC
GO:0007005	0.306	0.951	1	175	mitochondrion organization	BP	1	NDUFA10	down_AFEM_EC
GO:0001710	0.306	0.954	1	7	mesodermal cell fate commitment	BP	1	BMPR1A	down_VCAV_EC
GO:1902018	0.306	0.954	1	7	negative regulation of cilium assembly	BP	1	EVI5L	down_VCAV_EC
GO:0032660	0.306	0.954	1	7	regulation of interleukin-17 production	BP	1	PRNP	down_VCAV_EC
GO:0060487	0.306	0.954	1	7	lung epithelial cell differentiation	BP	1	THRB	down_VCAV_EC
GO:0061307	0.306	0.954	1	7	cardiac neural crest cell differentiation involved in heart development	BP	1	SEMA3C	down_VCAV_EC
GO:0061308	0.306	0.954	1	7	cardiac neural crest cell development involved in heart development	BP	1	SEMA3C	down_VCAV_EC
GO:0034433	0.306	0.96	1	4	steroid esterification	BP	1	LCAT	up_ACOR_VSMC
GO:0034434	0.306	0.96	1	4	sterol esterification	BP	1	LCAT	up_ACOR_VSMC
GO:0034435	0.306	0.96	1	4	cholesterol esterification	BP	1	LCAT	up_ACOR_VSMC
GO:0140112	0.306	0.951	1	15	extracellular vesicle biogenesis	BP	1	RAB7A	up_AFEM_EC
GO:1901616	0.306	0.951	1	15	organic hydroxy compound catabolic	BP	1	MOXD1	up_AFEM_EC
GO:0032504	0.306	0.95	1	152	multicellular organism reproduction	BP	1	HOXA9	up_AORT_EC
GO:0048609	0.306	0.95	1	152	multicellular organismal reproductive process	BP	1	HOXA9	up_AORT_EC
GO:0002253	0.306	0.95	1	92	activation of immune response	BP	1	NR1H4	up_APUL_EC
GO:0006266	0.306	0.959	1	4	DNA ligation	BP	1	HMGB1	up_VCAV_EC
GO:0051151	0.306	0.957	1	5	negative regulation of smooth muscle cell	BP	1	PDGFB	up_VCAV_EC
GO:0072538	0.306	0.96	1	4	T-helper 17 type immune response	BP	1	IL6	up_VCAV_EC
GO:0072539	0.306	0.96	1	4	T-helper 17 cell differentiation	BP	1	IL6	up_VCAV_EC
GO:0034309	0.306	0.959	1	4	primary alcohol biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0035458	0.306	0.957	1	5	cellular response to interferon-beta	BP	1	TMEM173	up_VCAV_EC
GO:0051000	0.306	0.957	1	5	positive regulation of nitric-oxide synthase	BP	1	GCH1	up_VCAV_EC

GO:0090153	0.306	0.957	1	5	regulation of sphingolipid biosynthetic process	BP	1	SAMD8	up_VCAV_EC
GO:1905038	0.306	0.957	1	5	regulation of membrane lipid metabolic process	BP	1	SAMD8	up_VCAV_EC
GO:2000303	0.306	0.957	1	5	regulation of ceramide biosynthetic process	BP	1	SAMD8	up_VCAV_EC
GO:0043401	0.306	0.949	1	46	steroid hormone mediated signaling	BP	1	RNF6	up_VPOR_EC
GO:0045765	0.306	0.95	1	105	regulation of angiogenesis	BP	1	CCL24	up_VPUL_EC
GO:0043405	0.306	0.95	1	85	regulation of MAP kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0001953	0.306040016	0.95107	1	14	negative regulation of cell-matrix adhesion	BP	1	ARHGAP6	up_ACOR_EC
GO:0050789	0.307	0.872	6	3295	regulation of biological process	BP	1	SLITRK5,LIMK1,GATA5,CA2,LRRC17,C6	up_VCAV_VSMC
GO:0030031	0.307	0.838	5	155	cell projection assembly	BP	1	CYLD,DNAL1,SPATA6,CDC42EP5,KANK1	up_AFEM_EC
GO:0098773	0.307	0.857	4	29	skin epidermis development	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0048523	0.307	0.867	4	1399	negative regulation of cellular process	BP	1	TBX5,TMEM176A,TMEM176B,SLIT2	up_VPUL_VSMC
GO:0061008	0.307	0.876	3	23	hepaticobiliary system development	BP	1	EZH2,E2F8,GLI1	down_ACOR_VSMC
GO:0009308	0.307	0.877	3	20	amine metabolic process	BP	1	NAPEPLD,AZIN2,IDO2	up_VSAP_EC
GO:0006749	0.307	0.906	2	14	glutathione metabolic process	BP	1	GSTO1,ENSCAFG00000006478	down_ACOR_VSMC
GO:0072698	0.307	0.906	2	13	protein localization to microtubule cytoskeleton	BP	1	NUP62,TTK	down_ACOR_VSMC
GO:1902110	0.307	0.907	2	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	RHOT1,BNIP3	up_ACOR_VSMC
GO:1902686	0.307	0.907	2	12	mitochondrial outer membrane permeabilization involved	BP	1	RHOT1,BNIP3	up_ACOR_VSMC
GO:0051302	0.307	0.9	2	47	regulation of cell division	BP	1	LBH,DLL1	up_AFEM_EC
GO:0010646	0.307	0.913	2	945	regulation of cell communication	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0042327	0.307	0.902	2	289	positive regulation of phosphorylation	BP	1	NPNT,NTRK2	up_APUL_EC
GO:0031952	0.307	0.905	2	15	regulation of protein autophosphorylation	BP	1	PDGFB,PDGFD	up_VCAV_EC
GO:0060541	0.307	0.949	1	73	respiratory system development	BP	1	PDPN	down_ACOR_EC
GO:0072425	0.307	0.959	1	4	signal transduction involved in G2 DNA	BP	1	DTL	down_ACOR_VSMC
GO:0006266	0.307	0.959	1	4	DNA ligation	BP	1	HMGB1	down_ACOR_VSMC
GO:0051601	0.307	0.959	1	4	exocyst localization	BP	1	STXBP6	down_ACOR_VSMC
GO:1901699	0.307	0.951	1	164	cellular response to nitrogen compound	BP	1	GABPA	down_AFEM_EC
GO:0007218	0.307	0.954	1	7	neuropeptide signaling pathway	BP	1	CRCP	down_VCAV_EC
GO:0010719	0.307	0.954	1	7	negative regulation of epithelial to mesenchymal	BP	1	VASN	down_VCAV_EC
GO:0072015	0.307	0.957	1	5	glomerular visceral epithelial cell	BP	1	MYO1E	down_VSAP_EC
GO:0072310	0.307	0.957	1	5	glomerular epithelial cell development	BP	1	MYO1E	down_VSAP_EC
GO:1903055	0.307	0.955	1	6	positive regulation of extracellular matrix	BP	1	FSCN1	down_VSAP_EC
GO:0036462	0.307	0.959	1	4	TRAIL-activated apoptotic signaling pathway	BP	1	PARK7	up_ACOR_VSMC
GO:0042135	0.307	0.959	1	4	neurotransmitter catabolic process	BP	1	MAOA	up_ACOR_VSMC
GO:0043066	0.307	0.952	1	253	negative regulation of apoptotic process	BP	1	EYA1	up_AFEM_VSMC
GO:0009895	0.307	0.949	1	94	negative regulation of catabolic process	BP	1	LZTS1	up_APUL_EC
GO:0040011	0.307	0.957	1	505	locomotion	BP	1	TBX5	up_APUL_VSMC
GO:0009309	0.307	0.959	1	4	amine biosynthetic process	BP	1	ODC1	up_VCAV_EC
GO:0035860	0.307	0.959	1	4	glial cell-derived neurotrophic factor	BP	1	GATA3	up_VCAV_EC

GO:0042401	0.307	0.959	1	4	cellular biogenic amine biosynthetic process	BP	1	ODC1	up_VCAV_EC
GO:0042636	0.307	0.959	1	4	negative regulation of hair cycle	BP	1	FERMT1	up_VCAV_EC
GO:0051799	0.307	0.959	1	4	negative regulation of hair follicle development	BP	1	FERMT1	up_VCAV_EC
GO:1902644	0.307	0.959	1	4	tertiary alcohol metabolic process	BP	1	BMP2	up_VCAV_EC
GO:2000369	0.307	0.959	1	4	regulation of clathrin-dependent endocytosis	BP	1	BMP2K	up_VCAV_EC
GO:0030336	0.307	0.949	1	86	negative regulation of cell migration	BP	1	HOXA7	up_VFEM_EC
GO:0061061	0.307	0.951	1	179	muscle structure development	BP	1	TBX5	up_VPUL_VSMC
GO:0098771	0.307	0.951	1	180	inorganic ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0007600	0.307106495	0.87108	3	73	sensory perception	BP	1	AQP1,PDE4A,USP53	up_ACOR_EC
GO:0006997	0.307389929	0.90025	2	42	nucleus organization	BP	1	CHMP4B,PYGO2	up_ACOR_EC
GO:0070507	0.307987416	0.87052	3	73	regulation of microtubule cytoskeleton organization	BP	1	DIXDC1,CHMP4B,TUBB4A	up_ACOR_EC
GO:0019438	0.308	0.73	109	1258	aromatic compound biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0048519	0.308	0.754	40	1554	negative regulation of biological process	BP	1	HOXA9,CMKLR1,MT2A,IRX3,HOXC10,LEP,LBH,CRY2,ENSCAFG00000009113,GAS1,ANGPT4,HOXA7,DLL1,CRYAB,BPI,GPAM,LMCD1,TWIST2,THRB,MYO1D,GREM1,OVOL1,TENT5C,GREM2,CLEC16A,CYLD,LRRC15,RECK,NR3C1,TBXA2R,DCUN1D3,RAB7A,AXIN2,ACACB,PPARGC1A,CTIF,FAP,ADAM17,SAMD4B,KANK1	up_AFEM_EC
GO:0016567	0.308	0.765	25	232	protein ubiquitination	BP	1	FAM107A,ABL1,KLHL36,DTX2,DDB2,CISH,KLHL24,KLHDC8B,TRAF7,RBCK1,KBTBD12,RNF24,SASH1,FBXO4,RMND5A,FBXW5,FBXO7,ASB8,RNF166,CDK9,KDM2B,RNF216,CDC26,ZER1,KEAP1	up_VSAP_EC
GO:0044703	0.308	0.774	19	172	multi-organism reproductive process	BP	1	LEP,PRDX4,RECK,BMP4,ATRX,PDE5A,CITED2,GLRB,CTSB,MARF1,AFF4,DKKL1,APP,SPINK2,HPGD,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0030855	0.308	0.788	13	183	epithelial cell differentiation	BP	1	TAGLN2,SERPINE1,ERRFI1,CASP3,PGK1,FLNB,MSN,HIF1A,ACTA2,CTNNB1,PLOD3,KLF5,MYO1E	down_VSAP_EC
GO:0050678	0.308	0.789	13	117	regulation of epithelial cell proliferation	BP	1	VEGFD,LEP,HTR2B,BMP4,FGFR2,CDKN2B,LIMS2,FRS2,TGFBR1,SYNJ2BP,SERPINB5,WDR48,RREB1	up_ACOR_VSMC
GO:0098655	0.308	0.8	10	142	cation transmembrane transport	BP	1	SLC39A7,ERO1A,REM1,NDUFA4L2,LYN,DDIT3,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0010506	0.308	0.807	9	86	regulation of autophagy	BP	1	PLK2,RALB,SPTLC2,MTOR,DEPP1,SH3GLB1,HMGB1,USP13,HIF1A	up_VCAV_EC
GO:0061448	0.308	0.806	9	89	connective tissue development	BP	1	PDGFB,MEF2C,GPR4,STC1,EDN1,BMP2,SLC25A25,HIF1A,ZEB1	up_VCAV_EC
GO:0010508	0.308	0.842	5	38	positive regulation of autophagy	BP	1	PRKAA2,TP53INP1,DAPK1,BNIP3,SH3BP4	up_ACOR_VSMC
GO:0002011	0.308	0.857	4	28	morphogenesis of an epithelial sheet	BP	1	ENSCAFG00000006238,TBX20,DAG1,RREB1	up_ACOR_VSMC
GO:0061564	0.308	0.851	4	119	axon development	BP	1	PLXNA4,NEFH,LRRN2,TNC	up_AFEM_EC
GO:0006112	0.308	0.874	3	30	energy reserve metabolic process	BP	1	ENPP1,PPP1R3C,GSK3B	down_VSAP_EC

GO:0051058	0.308	0.876	3	21	negative regulation of small GTPase mediated signal transduction	BP	1	SLIT2,MFN2,ARHGAP12	up_VSAP_EC
GO:0030199	0.308	0.876	3	21	collagen fibril organization	BP	1	DDR2,LOX,DPT	up_VSAP_EC
GO:0006970	0.308	0.902	2	23	response to osmotic stress	BP	1	ZFP36L1,TSC22D3	down_VCAV_EC
GO:0044070	0.308	0.902	2	22	regulation of anion transport	BP	1	PRNP,AKT2	down_VCAV_EC
GO:2000059	0.308	0.903	2	19	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0048016	0.308	0.903	2	19	inositol phosphate-mediated signaling	BP	1	FHL2,GSK3B	down_VSAP_EC
GO:1903432	0.308	0.903	2	18	regulation of TORC1 signaling	BP	1	SESN2,SEC13	down_VSAP_EC
GO:0051092	0.308	0.9	2	47	positive regulation of NF-kappaB transcription	BP	1	GREM1,CAMK2A	up_AFEM_EC
GO:1902107	0.308	0.9	2	47	positive regulation of leukocyte differentiation	BP	1	CYLD,EVI2B	up_AFEM_EC
GO:0010647	0.308	0.904	2	460	positive regulation of cell communication	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0032268	0.308	0.909	2	778	regulation of cellular protein metabolic process	BP	1	LIMK1,C6	up_VCAV_VSMC
GO:0071318	0.308	0.959	1	4	cellular response to ATP	BP	1	PDXP	down_ACOR_VSMC
GO:0014841	0.308	0.959	1	4	skeletal muscle satellite cell proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0014842	0.308	0.959	1	4	regulation of skeletal muscle satellite cell	BP	1	PPARD	down_ACOR_VSMC
GO:0014856	0.308	0.959	1	4	skeletal muscle cell proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0014857	0.308	0.959	1	4	regulation of skeletal muscle cell proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0051661	0.308	0.959	1	4	maintenance of centrosome location	BP	1	ASPM	down_ACOR_VSMC
GO:0070970	0.308	0.959	1	4	interleukin-2 secretion	BP	1	EZR	down_ACOR_VSMC
GO:1902946	0.308	0.959	1	4	protein localization to early endosome	BP	1	EZR	down_ACOR_VSMC
GO:0003272	0.308	0.954	1	7	endocardial cushion formation	BP	1	BMPR1A	down_VCAV_EC
GO:0070207	0.308	0.954	1	7	protein homotrimerization	BP	1	SCARA5	down_VCAV_EC
GO:0090322	0.308	0.954	1	7	regulation of superoxide metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0000727	0.308	0.959	1	4	double-strand break repair via break-induced	BP	1	CDC7	up_ACOR_VSMC
GO:0003056	0.308	0.963	1	3	regulation of vascular smooth muscle	BP	1	DOCK5	up_ACOR_VSMC
GO:2000009	0.308	0.959	1	4	negative regulation of protein localization to cell	BP	1	ACTN2	up_ACOR_VSMC
GO:0090199	0.308	0.95	1	15	regulation of release of cytochrome c from	BP	1	MLLT11	up_AFEM_EC
GO:0055074	0.308	0.949	1	95	calcium ion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0014841	0.308	0.959	1	4	skeletal muscle satellite cell proliferation	BP	1	EPHB1	up_VCAV_EC
GO:0014842	0.308	0.959	1	4	regulation of skeletal muscle satellite cell	BP	1	EPHB1	up_VCAV_EC
GO:0014856	0.308	0.959	1	4	skeletal muscle cell proliferation	BP	1	EPHB1	up_VCAV_EC
GO:0014857	0.308	0.959	1	4	regulation of skeletal muscle cell proliferation	BP	1	EPHB1	up_VCAV_EC
GO:0032471	0.308	0.959	1	4	negative regulation of endoplasmic reticulum calcium ion concentration	BP	1	ATP2A1	up_VCAV_EC
GO:0043691	0.308	0.959	1	4	reverse cholesterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0055076	0.308	0.949	1	44	transition metal ion homeostasis	BP	1	ENSCAFG00000005494	up_VPOR_EC
GO:2001020	0.308	0.949	1	88	regulation of response to DNA damage stimulus	BP	1	EYA1	up_VFEM_EC
GO:0003006	0.308	0.95	1	180	developmental process involved in reproduction	BP	1	SLIT2	up_VPUL_VSMC
GO:0040017	0.308	0.95	1	180	positive regulation of locomotion	BP	1	SLIT2	up_VPUL_VSMC
GO:0097104	0.308	0.959	1	4	postsynaptic membrane assembly	BP	1	LRP4	up_VSAP_EC

GO:0099068	0.308	0.959	1	4	postsynapse assembly	BP	1	LRP4	up_VSAP_EC
GO:0060041	0.308287306	0.89983	2	41	retina development in camera-type eye	BP	1	SOX9,NRP1	up_ACOR_EC
GO:0090184	0.308341888	0.95028	1	14	positive regulation of kidney development	BP	1	SOX9	up_ACOR_EC
GO:0007259	0.30861262	0.89958	2	42	JAK-STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:0097009	0.308720906	0.95041	1	13	energy homeostasis	BP	1	PM20D1	up_ACOR_EC
GO:0002376	0.309	0.778	17	622	immune system process	BP	1	HOXA9,CMKLR1,LEP,RAB20,HOXA7,CD40,DLL1,CTSS,BPI,GPAM,HCK,NFE2L1,CYLD,EVI2B,BVES,CCL5,ADAM17	up_AFEM_EC
GO:0022407	0.309	0.797	11	96	regulation of cell-cell adhesion	BP	1	CD274,CDH1,ABL1,ZBTB16,CD83,PNP,ASS1,FLOT1,NCK1,TGFBR2,CITED2	up_VSAP_EC
GO:0006790	0.309	0.801	10	99	sulfur compound metabolic process	BP	1	ACLY,HSPA9,XYLT1,MVD,ELOVL1,GSTO1,ELOVL6,ENSCAFG00000006478,CTH,PDHA1	down_ACOR_VSMC
GO:1905114	0.309	0.804	9	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	RECK,CLSTN1,ATP6V0C,GLI3,CDH2,GREM1,NPHP4,FOXO3,CDK14	down_VCAV_EC
GO:0018210	0.309	0.829	6	48	peptidyl-threonine modification	BP	1	OSR1,CAMKK2,TNKS1BP1,GALNT11,ULK1,TGFBR2	up_VSAP_EC
GO:0042445	0.309	0.853	4	46	hormone metabolic process	BP	1	PTPN11,HIF1A,REST,YWHAH	down_VSAP_EC
GO:0006112	0.309	0.855	4	30	energy reserve metabolic process	BP	1	PCDH12,ADGRF5,MTOR,PPP1CB	up_VCAV_EC
GO:0060688	0.309	0.856	4	29	regulation of morphogenesis of a	BP	1	FGF7,ABL1,SHOX2,NTN4	up_VSAP_EC
GO:1901136	0.309	0.872	3	38	carbohydrate derivative catabolic process	BP	1	CHID1,ENSCAFG00000017708,ACAT1	down_VCAV_EC
GO:1903391	0.309	0.875	3	21	regulation of adherens junction organization	BP	1	NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0072676	0.309	0.874	3	25	lymphocyte migration	BP	1	STK10,GATA3,APOD	up_VCAV_EC
GO:0050710	0.309	0.906	2	13	negative regulation of cytokine secretion	BP	1	ARG2,EZR	down_ACOR_VSMC
GO:0030225	0.309	0.906	2	12	macrophage differentiation	BP	1	BMP4,APP	up_ACOR_VSMC
GO:0018196	0.309	0.904	2	15	peptidyl-asparagine modification	BP	1	ST6GAL1,ST3GAL6	up_VCAV_EC
GO:0043069	0.309	0.9	2	262	negative regulation of programmed cell death	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0043587	0.309	0.959	1	4	tongue morphogenesis	BP	1	SIX4	down_ACOR_VSMC
GO:0044241	0.309	0.959	1	4	lipid digestion	BP	1	LIMA1	down_ACOR_VSMC
GO:0044794	0.309	0.959	1	4	positive regulation by host of viral process	BP	1	SMC3	down_ACOR_VSMC
GO:0006397	0.309	0.95	1	168	mRNA processing	BP	1	SRSF6	down_AFEM_EC
GO:0001556	0.309	0.953	1	7	oocyte maturation	BP	1	FOXO3	down_VCAV_EC
GO:0034367	0.309	0.953	1	7	protein-containing complex remodeling	BP	1	LCAT	down_VCAV_EC
GO:0034368	0.309	0.953	1	7	protein-lipid complex remodeling	BP	1	LCAT	down_VCAV_EC
GO:0034369	0.309	0.953	1	7	plasma lipoprotein particle remodeling	BP	1	LCAT	down_VCAV_EC
GO:0071548	0.309	0.954	1	7	response to dexamethasone	BP	1	NR3C1	down_VCAV_EC
GO:1905809	0.309	0.953	1	7	negative regulation of synapse organization	BP	1	PRNP	down_VCAV_EC
GO:0001817	0.309	0.95	1	182	regulation of cytokine production	BP	1	HDAC7	down_VPOR_EC
GO:0070486	0.309	0.954	1	6	leukocyte aggregation	BP	1	MSN	down_VSAP_EC
GO:0042074	0.309	0.959	1	4	cell migration involved in gastrulation	BP	1	AMOT	up_VCAV_EC
GO:0000280	0.309	0.95	1	145	nuclear division	BP	1	CYP26B1	up_VPOR_VSMC
GO:0051091	0.309	0.948	1	87	positive regulation of DNA-binding transcription factor activity	BP	1	TLR2	up_VSAP_VSMC
GO:0006721	0.309067181	0.95003	1	14	terpenoid metabolic process	BP	1	RARRES2	up_ACOR_EC
GO:0042886	0.309277778	0.77897	16	527	amide transport	BP	1	SH3TC2,NR1H4,AQP1,KCNB1,EDEM2,FZD5,NOD2,PTGER4,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC

GO:0090313	0.309358268	0.94993	1	14	regulation of protein targeting to membrane	BP	1	KCNB1	up_ACOR_EC
GO:0006903	0.309420888	0.94991	1	14	vesicle targeting	BP	1	PREB	up_ACOR_EC
GO:0060255	0.31	0.724	156	1782	regulation of macromolecule metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,ILF3,DDX39A,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,MED17,U2AF2,PSMD3,SLC29A1,MTDH,HEY1,PPP1R15B,PARPBP,SRRT,NAB2,SLC35C2,RAN,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,EDC4,AURKB,NONO,HNRNPL,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,CDK4,SMARCC1,RNASEH2B,PLK3,PCNA,DHX33,HOXA7,SMG9,SF3B4,UHRF1,CKS2,PDCD2,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,TFRC,PPARD,RAP2C,YBX3,HNRNPF,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,RBM14,RBM17,RAD23A,NOLC1,CDC20,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,ENSCAFG00000015189,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,DELE1,EXOSC5,CCNB3,MIS18A,HMGN1,CCT4,SIX4,MTBP,NECAB3,SF3A1,MED16,ENSCAFG	down_ACOR_VSMC
GO:0043085	0.31	0.753	34	323	positive regulation of catalytic activity	BP	1	TNNT2,LEP,MAP3K8,HTR2B,RASSF2,USP6NL,MBP,BMP4,EVI5L,FGFR2,PDE5A,PKP4,SASH1,LMO4,FGF18,F2RL1,DAPK1,NPNT,ATP7A,CCNT1,FRS2,PSEN1,SGSM2,CCL5,DDR2,PERP,EDN1,DYNC1I2,DCUN1D4,MAP3K7,DYNC1I1,PARK7,HMBOX1,LMF1	up_ACOR_VSMC
GO:0010468	0.31	0.757	33	1270	regulation of gene expression	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B,TNC	up_AFEM_EC
GO:0045944	0.31	0.756	30	287	positive regulation of transcription by RNA polymerase II	BP	1	THRB,HOXA9,CDON,INSIG2,PPARGC1B,HOXD3,DLL1,OSR1,KLF15,RARG,F2RL1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,NPAS2,CDK9,RAF1,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,CITED2	up_VSAP_EC
GO:0061024	0.31	0.765	23	215	membrane organization	BP	1	SH3TC2,RHOT1,USP6NL,MBP,SYT16,EVI5L,MX1,ABCA1,SEC24B,GLRB,AR,STX11,F2RL1,BNIP3,DMPK,SGSM2,CLN8,LRRC4,ASAP1,SUN1,AZIN2,WASL,NAIF1	up_ACOR_VSMC
GO:0070371	0.31	0.826	6	91	ERK1 and ERK2 cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,ZFP36L1,SPRED1,SHC1	down_VCAV_EC
GO:0050707	0.31	0.839	5	44	regulation of cytokine secretion	BP	1	FERMT1,TLR4,GATA3,ARG2,HMGB1	up_VCAV_EC
GO:0051094	0.31	0.871	3	388	positive regulation of developmental process	BP	1	ACVRL1,LYN,PDPN	down_ACOR_EC
GO:0043087	0.31	0.869	3	83	regulation of GTPase activity	BP	1	RASGEF1B,BVES,CCL5	up_AFEM_EC
GO:0031329	0.31	0.87	3	241	regulation of cellular catabolic process	BP	1	FBP1,MTDH,ABHD5	up_VPOR_EC
GO:0016126	0.31	0.876	3	20	sterol biosynthetic process	BP	1	INSIG2,MVK,CYB5R3	up_VSAP_EC
GO:0016574	0.31	0.875	3	21	histone ubiquitination	BP	1	DDB2,CDK9,KDM2B	up_VSAP_EC
GO:0060443	0.31	0.905	2	13	mammary gland morphogenesis	BP	1	CAV1,B4GALT1	down_ACOR_VSMC
GO:0032648	0.31	0.901	2	23	regulation of interferon-beta production	BP	1	RNF216,MAVS	down_VCAV_EC
GO:0014002	0.31	0.907	2	11	astrocyte development	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0023056	0.31	0.903	2	462	positive regulation of signaling	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0030334	0.31	0.9	2	267	regulation of cell migration	BP	1	HOXA7,TIAM1	up_VFEM_EC
GO:0021517	0.31	0.906	2	12	ventral spinal cord development	BP	1	HOXC10,GDPD5	up_VSAP_EC
GO:0045922	0.31	0.906	2	12	negative regulation of fatty acid metabolic	BP	1	INSIG2,ACACB	up_VSAP_EC

GO:0006287	0.31	0.958	1	4	base-excision repair, gap-filling	BP	1	POLE	down_ACOR_VSMC
GO:1901977	0.31	0.958	1	4	negative regulation of cell cycle checkpoint	BP	1	DDX39B	down_ACOR_VSMC
GO:1903753	0.31	0.958	1	4	negative regulation of p38MAPK cascade	BP	1	EZR	down_ACOR_VSMC
GO:1904396	0.31	0.958	1	4	regulation of neuromuscular junction	BP	1	SIX4	down_ACOR_VSMC
GO:2000002	0.31	0.958	1	4	negative regulation of DNA damage checkpoint	BP	1	DDX39B	down_ACOR_VSMC
GO:0007042	0.31	0.953	1	7	lysosomal lumen acidification	BP	1	ATP6V0C	down_VCAV_EC
GO:0009262	0.31	0.953	1	7	deoxyribonucleotide metabolic process	BP	1	ADK	down_VCAV_EC
GO:0072337	0.31	0.953	1	7	modified amino acid transport	BP	1	FOLR2	down_VCAV_EC
GO:0021516	0.31	0.958	1	4	dorsal spinal cord development	BP	1	LMO4	up_ACOR_VSMC
GO:0050930	0.31	0.958	1	4	induction of positive chemotaxis	BP	1	VEGFD	up_ACOR_VSMC
GO:0061218	0.31	0.958	1	4	negative regulation of mesonephros	BP	1	BMP4	up_ACOR_VSMC
GO:0040012	0.31	0.952	1	303	regulation of locomotion	BP	1	WNT7A	up_AORT_VSMC
GO:0090083	0.31	0.958	1	4	regulation of inclusion body assembly	BP	1	SNCAIP	up_VCAV_EC
GO:0010743	0.31	0.958	1	4	regulation of macrophage derived foam cell	BP	1	PRKCH	up_VCAV_EC
GO:0048535	0.31	0.956	1	5	lymph node development	BP	1	IL7R	up_VCAV_EC
GO:0003056	0.31	0.962	1	3	regulation of vascular smooth muscle	BP	1	DOCK4	up_VCAV_EC
GO:0042796	0.31	0.958	1	4	snRNA transcription by RNA polymerase III	BP	1	ICE1	up_VSAP_EC
GO:0098656	0.310790606	0.89839	2	42	anion transmembrane transport	BP	1	CLIC3,SLC25A42	up_ACOR_EC
GO:0032269	0.311	0.754	32	306	negative regulation of cellular protein metabolic process	BP	1	SMAD6,RASSF2,RECK,PRKAA2,BMP4,SH3RF2,LATS2,ISG15,PTPN3,NDRG2,CST3,F2RL1,FAM129A,DAPK1,CDKN1A,PTPN22,OS9,SMPD1,SH3RF1,PRKCE,DAG1,PSEN1,SYNJ2BP,SPINK2,DUSP22,EDN1,OXR1,DUSP26,LRRC4,INPP5K,PARK7,CRKL	up_ACOR_VSMC
GO:0061458	0.311	0.787	13	131	reproductive system development	BP	1	SLC29A1,SF1,DHCR24,E2F8,PPARD,FOSL1,PLK4,HMGB2,SGPL1,ASPM,HOXA9,RTCB,SIX4	down_ACOR_VSMC
GO:0006417	0.311	0.794	11	109	regulation of translation	BP	1	ILF3,EIF4A3,HNRNPD,PPP1R15B,TRUB2,FASTKD3,EIF5A,NCL,RBM14,NOLC1,PUM3	down_ACOR_VSMC
GO:0050865	0.311	0.798	10	135	regulation of cell activation	BP	1	SOCS5,FAM49B,PTPN2,CTNNB1,TFRC,APOE,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0006402	0.311	0.805	9	77	mRNA catabolic process	BP	1	AXIN2,TENT5C,EXOSC7,PYM1,ZFP36L1,SMG9,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0048518	0.311	0.822	8	1676	positive regulation of biological process	BP	1	NR1H4,TBX5,HOXA3,SLITRK5,WIF1,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0001959	0.311	0.853	4	33	regulation of cytokine-mediated signaling	BP	1	IRAK1,SLC29A1,CAV1,CACTIN	down_ACOR_VSMC
GO:0043270	0.311	0.85	4	56	positive regulation of ion transport	BP	1	FXYD1,TRPV2,THY1,PARK7	down_VCAV_EC
GO:0051716	0.311	0.874	4	2001	cellular response to stimulus	BP	1	CYP1A1,LIMK1,GATA5,CA2	up_VCAV_VSMC
GO:0034446	0.311	0.873	3	23	substrate adhesion-dependent cell spreading	BP	1	TEK,NEDD9,ENSCAFG00000002015	up_VCAV_EC
GO:0061008	0.311	0.873	3	23	hepaticobiliary system development	BP	1	TNFAIP3,HHEX,PROX1	up_VCAV_EC
GO:0032720	0.311	0.905	2	13	negative regulation of tumor necrosis factor	BP	1	ARG2,CACTIN	down_ACOR_VSMC
GO:0055006	0.311	0.902	2	18	cardiac cell development	BP	1	FHL2,NEXN	down_VSAP_EC
GO:0034405	0.311	0.907	2	11	response to fluid shear stress	BP	1	SMAD6,ABCA1	up_ACOR_VSMC
GO:0050856	0.311	0.905	2	12	regulation of T cell receptor signaling	BP	1	ELF1,DUSP22	up_ACOR_VSMC
GO:0098868	0.311	0.907	2	11	bone growth	BP	1	LEP,DDR2	up_ACOR_VSMC
GO:0003230	0.311	0.904	2	14	cardiac atrium development	BP	1	DLL4,PROX1	up_VCAV_EC
GO:0034142	0.311	0.904	2	14	toll-like receptor 4 signaling pathway	BP	1	TLR4,PELI1	up_VCAV_EC
GO:0003209	0.311	0.904	2	14	cardiac atrium morphogenesis	BP	1	DLL4,PROX1	up_VCAV_EC

GO:0046903	0.311	0.899	2	255	secretion	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0045780	0.311	0.958	1	4	positive regulation of bone resorption	BP	1	TFRC	down_ACOR_VSMC
GO:0046852	0.311	0.958	1	4	positive regulation of bone remodeling	BP	1	TFRC	down_ACOR_VSMC
GO:0006089	0.311	0.953	1	7	lactate metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0045596	0.311	0.949	1	186	negative regulation of cell differentiation	BP	1	HDAC7	down_VPOR_EC
GO:0006882	0.311	0.954	1	6	cellular zinc ion homeostasis	BP	1	SLC39A7	down_VSAP_EC
GO:0048484	0.311	0.954	1	6	enteric nervous system development	BP	1	PDS5B	down_VSAP_EC
GO:0055069	0.311	0.954	1	6	zinc ion homeostasis	BP	1	SLC39A7	down_VSAP_EC
GO:1900271	0.311	0.954	1	6	regulation of long-term synaptic potentiation	BP	1	APOE	down_VSAP_EC
GO:0038092	0.311	0.958	1	4	nodal signaling pathway	BP	1	CITED2	up_ACOR_VSMC
GO:0001822	0.311	0.948	1	98	kidney development	BP	1	NPNT	up_APUL_EC
GO:1902237	0.311	0.955	1	5	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	NCK1	up_VCAV_EC
GO:0007204	0.311	0.947	1	46	positive regulation of cytosolic calcium ion	BP	1	C3AR1	up_VPOR_EC
GO:0007596	0.311	0.948	1	47	blood coagulation	BP	1	SLC7A11	up_VPOR_EC
GO:0006164	0.311	0.948	1	86	purine nucleotide biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0120039	0.311	0.949	1	158	plasma membrane bounded cell projection	BP	1	SHOX2	up_VFEM_VSMC
GO:0007178	0.311	0.948	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	NEO1	up_VPUL_EC
GO:0098609	0.311	0.949	1	181	cell-cell adhesion	BP	1	GATA5	up_VPUL_VSMC
GO:0017000	0.311	0.958	1	4	antibiotic biosynthetic process	BP	1	ZNF205	up_VSAP_EC
GO:1902285	0.311	0.958	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	PLXNA4	up_VSAP_EC
GO:0033628	0.311487196	0.94919	1	14	regulation of cell adhesion mediated by integrin	BP	1	FOXC2	up_ACOR_EC
GO:0060993	0.31181746	0.89783	2	42	kidney morphogenesis	BP	1	SOX9,CLSTN1	up_ACOR_EC
GO:0009892	0.312	0.73	85	835	negative regulation of metabolic process	BP	1	SMAD6,LEP,PLCL1,GATA5,HTR2B,RASSF2,RECK,FEZ1,NACC2,PRKAA2,ITM2C,FERMT1,BMP4,PNRC1,FGFR2,TP53BP1,EIF4A2,GJA1,ATRX,TRPS1,SH3RF2,LATS2,TP53INP1,ATXN2,ISG15,AR,PTPN3,NDRG2,CDKN2B,CST3,ZNF174,ANKRD1,F2RL1,FAM129A,DAPK1,BNIP3,CDKN1A,ENSCAFG00000006238,DCP1B,CLSTN1,PTPN22,LRPAP1,OS9,ORMDL3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,MARF1,DKKL1,DAG1,PPP1R26,PARP9,APP,PSEN1,SYNJ2BP,MXI1,SPINK2,NR3C1,WWC2,DUSP22,EDN1,OXR1,DUSP26,CBX7,LRRC4,DDIT4,KLF11,FEZ2,INPP5K,CNOT4,WFS1,AZIN2,CTIF,ENSCAFG00000029553,ID3,PARK7,GPATCH2,STC2,ZFYVE1,IL18R1,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0012501	0.312	0.738	57	561	programmed cell death	BP	1	RHOT1,SMAD6,PLCG2,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,TM7SF3,TLR3,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,USP53,ITPR1,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,CDKN1A,JMY,NRP1,DMPK,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,APP,PSEN1,SPINK2,CLN8,PERP,SIAH1,OXR1,NOD2,DDIT4,SERINC3,TNFRSF11B,KLF11,HERPUD1,MAP3K7,WFS1,NAIF1,PARK7,ZMAT3	up_ACOR_VSMC
GO:0009719	0.312	0.764	22	395	response to endogenous stimulus	BP	1	SMAD9,LRP1,PRNP,VASN,FBN1,ADCY6,KANK2,COL6A1,ENSCAFG00000014978,CHRDL1,TIMP2,AKT2,NR3C1,ASPN,PARK7,ZFP36L1,FUT8,RAB31,SHC1,FBH1,GREM1,RGMA	down_VCAV_EC

GO:0009968	0.312	0.765	22	392	negative regulation of signal transduction	BP	1	SLC35F6,DCN,PRNP,VASN,FBN1,BGN,KANK2,AKT1S1,CHRDL1,CLSTN1,TMEM161A,ASPN,THY1,GLI3,PARK7,CDH2,SPRED1,RAB7B,GLIS2,GREM1,NPHP4,FOXO3	down_VCAV_EC
GO:0034765	0.312	0.803	9	91	regulation of ion transmembrane transport	BP	1	RELN,PDE4D,MEF2C,CHD7,APLNR,KCNJ3,KCNJ2,PLCG2,RIPK1	up_VCAV_EC
GO:0010522	0.312	0.873	3	24	regulation of calcium ion transport into cytosol	BP	1	CAV1,GSTO1,CORO1A	down_ACOR_VSMC
GO:0018958	0.312	0.874	3	20	phenol-containing compound metabolic	BP	1	MAOA,MOXD1,PARK7	up_ACOR_VSMC
GO:0031328	0.312	0.872	3	512	positive regulation of cellular biosynthetic	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0001906	0.312	0.874	3	20	cell killing	BP	1	EMP2,F2RL1,PPP3CB	up_VSAP_EC
GO:0010771	0.312	0.874	3	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	SLIT2,LRP4,FBLN1	up_VSAP_EC
GO:0006622	0.312	0.906	2	11	protein targeting to lysosome	BP	1	SCARB2,LAMP2	up_ACOR_VSMC
GO:0072376	0.312	0.906	2	11	protein activation cascade	BP	1	C1S,C7	up_ACOR_VSMC
GO:0023051	0.312	0.911	2	954	regulation of signaling	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:1901862	0.312	0.903	2	14	negative regulation of muscle tissue	BP	1	EPHB1,BMP2	up_VCAV_EC
GO:0006928	0.312	0.903	2	557	movement of cell or subcellular component	BP	1	TBX5,SLIT2	up_VPUL_VSMC
GO:0021591	0.312	0.905	2	12	ventricular system development	BP	1	KIF27,KDM2B	up_VSAP_EC
GO:0006189	0.312	0.958	1	4	'de novo' IMP biosynthetic process	BP	1	PFAS	down_ACOR_VSMC
GO:0030730	0.312	0.958	1	4	sequestering of triglyceride	BP	1	ABHD5	down_ACOR_VSMC
GO:0032534	0.312	0.958	1	4	regulation of microvillus assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0051124	0.312	0.958	1	4	synaptic growth at neuromuscular junction	BP	1	SIX4	down_ACOR_VSMC
GO:0060263	0.312	0.955	1	5	regulation of respiratory burst	BP	1	RAC1	down_ACOR_VSMC
GO:0034641	0.312	1	1	2171	cellular nitrogen compound metabolic	BP	1	GATA5	down_AFEM_VSMC
GO:0010712	0.312	0.952	1	7	regulation of collagen metabolic process	BP	1	LARP6	down_VCAV_EC
GO:0070584	0.312	0.952	1	7	mitochondrion morphogenesis	BP	1	POLDIP2	down_VCAV_EC
GO:0030852	0.312	0.954	1	6	regulation of granulocyte differentiation	BP	1	EVI2B	down_VSAP_EC
GO:0043950	0.312	0.954	1	6	positive regulation of cAMP-mediated signaling	BP	1	CALM1	down_VSAP_EC
GO:0032692	0.312	0.953	1	6	negative regulation of interleukin-1 production	BP	1	NR1H4	down_VSAP_EC
GO:1900120	0.312	0.952	1	7	regulation of receptor binding	BP	1	PLCL1	down_VSAP_EC
GO:1904923	0.312	0.954	1	6	regulation of autophagy of mitochondrion in response to mitochondrial	BP	1	CDC37	down_VSAP_EC
GO:0002949	0.312	0.958	1	4	tRNA threonylcarbamoyladenosine modification	BP	1	OSGEPL1	up_ACOR_VSMC
GO:0018065	0.312	0.958	1	4	protein-cofactor linkage	BP	1	LIPT2	up_ACOR_VSMC
GO:0033147	0.312	0.958	1	4	negative regulation of intracellular estrogen receptor signaling	BP	1	LBH	up_ACOR_VSMC
GO:0032446	0.312	0.95	1	255	protein modification by small protein conjugation	BP	1	EYA1	up_AFEM_VSMC
GO:0046903	0.312	0.95	1	255	secretion	BP	1	TLR2	up_AFEM_VSMC
GO:0007264	0.312	0.948	1	164	small GTPase mediated signal transduction	BP	1	CTNNAL1	up_AORT_EC
GO:0032989	0.312	0.952	1	292	cellular component morphogenesis	BP	1	WNT7A	up_AORT_VSMC
GO:0043010	0.312	0.948	1	96	camera-type eye development	BP	1	NTRK2	up_APUL_EC
GO:0021514	0.312	0.958	1	4	ventral spinal cord interneuron	BP	1	DLL4	up_VCAV_EC
GO:0045793	0.312	0.958	1	4	positive regulation of cell size	BP	1	EDN1	up_VCAV_EC
GO:0032446	0.312	0.95	1	255	protein modification by small protein conjugation	BP	1	LIMK1	up_VCAV_VSMC

GO:0034101	0.312	0.947	1	45	erythrocyte homeostasis	BP	1	ACVR2A	up_VPOR_EC
GO:0045664	0.312	0.948	1	144	regulation of neuron differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0098660	0.312	0.948	1	141	inorganic ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0000904	0.312	0.949	1	181	cell morphogenesis involved in differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0006636	0.31201511	0.949	1	14	unsaturated fatty acid biosynthetic process	BP	1	PTGDS	up_ACOR_EC
GO:0006457	0.312037535	0.86781	3	77	protein folding	BP	1	PDRG1,CLU,FKBP11	up_ACOR_EC
GO:0002711	0.312082781	0.94898	1	14	positive regulation of T cell mediated immunity	BP	1	FZD5	up_ACOR_EC
GO:2001239	0.312313406	0.9489	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	IFI6	up_ACOR_EC
GO:0035767	0.312425967	0.94886	1	14	endothelial cell chemotaxis	BP	1	NRP1	up_ACOR_EC
GO:0006898	0.313	0.849	4	57	receptor-mediated endocytosis	BP	1	LRPAP1,CLTB,RAB31,GREM1	down_VCAV_EC
GO:0030072	0.313	0.849	4	48	peptide hormone secretion	BP	1	NR1H4,PTPN11,HIF1A,REST	down_VSAP_EC
GO:0016202	0.313	0.869	3	39	regulation of striated muscle tissue	BP	1	BMPR1A,TSC22D3,GREM1	down_VCAV_EC
GO:0071706	0.313	0.869	3	40	tumor necrosis factor superfamily cytokine	BP	1	BPI,CYBA,MAVS	down_VCAV_EC
GO:0061180	0.313	0.874	3	20	mammary gland epithelium development	BP	1	LBH,FGFR2,RREB1	up_ACOR_VSMC
GO:0052547	0.313	0.867	3	82	regulation of peptidase activity	BP	1	CRYAB,F3,RECK	up_AFEM_EC
GO:0072523	0.313	0.903	2	14	purine-containing compound catabolic	BP	1	NUDT1,NUDT3	down_ACOR_VSMC
GO:0033866	0.313	0.899	2	22	nucleoside bisphosphate biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0034030	0.313	0.899	2	22	ribonucleoside bisphosphate biosynthetic	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0034033	0.313	0.899	2	22	purine nucleoside bisphosphate biosynthetic	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0051128	0.313	0.907	2	790	regulation of cellular component organization	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:1903532	0.313	0.947	1	78	positive regulation of secretion by cell	BP	1	STX4	down_ACOR_EC
GO:0032438	0.313	0.957	1	4	melanosome organization	BP	1	TRAPPC6A	down_ACOR_VSMC
GO:0045117	0.313	0.955	1	5	azole transport	BP	1	SLC25A19	down_ACOR_VSMC
GO:0048753	0.313	0.957	1	4	pigment granule organization	BP	1	TRAPPC6A	down_ACOR_VSMC
GO:0090161	0.313	0.955	1	5	Golgi ribbon formation	BP	1	PRMT5	down_ACOR_VSMC
GO:0006829	0.313	0.952	1	7	zinc ion transport	BP	1	SLC39A6	down_VCAV_EC
GO:0051180	0.313	0.952	1	7	vitamin transport	BP	1	FOLR2	down_VCAV_EC
GO:0071577	0.313	0.952	1	7	zinc ion transmembrane transport	BP	1	SLC39A6	down_VCAV_EC
GO:0072172	0.313	0.952	1	7	mesonephric tubule formation	BP	1	GREM1	down_VCAV_EC
GO:1900016	0.313	0.952	1	7	negative regulation of cytokine production involved in inflammatory	BP	1	CHID1	down_VCAV_EC
GO:0007595	0.313	0.953	1	6	lactation	BP	1	HIF1A	down_VSAP_EC
GO:0009109	0.313	0.953	1	6	coenzyme catabolic process	BP	1	ALDH1L2	down_VSAP_EC
GO:0060831	0.313	0.953	1	6	smoothened signaling pathway involved in dorsal/ventral neural tube	BP	1	PRKACB	down_VSAP_EC
GO:0002084	0.313	0.957	1	4	protein depalmitoylation	BP	1	LYPLAL1	up_ACOR_VSMC
GO:0098734	0.313	0.957	1	4	macromolecule depalmitoylation	BP	1	LYPLAL1	up_ACOR_VSMC
GO:0032377	0.313	0.958	1	4	regulation of intracellular lipid transport	BP	1	SCP2	up_ACOR_VSMC
GO:0032380	0.313	0.958	1	4	regulation of intracellular sterol transport	BP	1	SCP2	up_ACOR_VSMC
GO:0032383	0.313	0.958	1	4	regulation of intracellular cholesterol transport	BP	1	SCP2	up_ACOR_VSMC

GO:0034447	0.313	0.957	1	4	very-low-density lipoprotein particle	BP	1	LRPAP1	up_ACOR_VSMC
GO:0003097	0.313	0.957	1	4	renal water transport	BP	1	INPP5K	up_ACOR_VSMC
GO:0023061	0.313	0.947	1	95	signal release	BP	1	NR1H4	up_APUL_EC
GO:0070838	0.313	0.947	1	96	divalent metal ion transport	BP	1	HOXA3	up_APUL_EC
GO:0042908	0.313	0.962	1	3	xenobiotic transport	BP	1	LRRC8D	up_VCAV_EC
GO:0046520	0.313	0.955	1	5	sphingoid biosynthetic process	BP	1	SPTLC2	up_VCAV_EC
GO:0046903	0.313	0.95	1	255	secretion	BP	1	CA2	up_VCAV_VSMC
GO:0071222	0.313	0.947	1	46	cellular response to lipopolysaccharide	BP	1	MTDH	up_VPOR_EC
GO:0043410	0.313	0.948	1	144	positive regulation of MAPK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0048667	0.313	0.948	1	140	cell morphogenesis involved in neuron	BP	1	CHL1	up_VPOR_VSMC
GO:0048858	0.313	0.948	1	159	cell projection morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0050804	0.313	0.947	1	87	modulation of chemical synaptic transmission	BP	1	NETO1	up_VSAP_VSMC
GO:0051047	0.313	0.947	1	84	positive regulation of secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0099177	0.313	0.947	1	87	regulation of trans-synaptic signaling	BP	1	NETO1	up_VSAP_VSMC
GO:2000243	0.313087667	0.94863	1	14	positive regulation of reproductive process	BP	1	SOX9	up_ACOR_EC
GO:0072087	0.313996526	0.9483	1	14	renal vesicle development	BP	1	SOX9	up_ACOR_EC
GO:0048812	0.314	0.8	9	151	neuron projection morphogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,UST,BRSK1	down_VCAV_EC
GO:0071222	0.314	0.849	4	46	cellular response to lipopolysaccharide	BP	1	NR1H4,SERPINE1,MTDH,LYN	down_VSAP_EC
GO:0010770	0.314	0.852	4	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	NRP1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0050686	0.314	0.903	2	13	negative regulation of mRNA processing	BP	1	RNPS1,U2AF2	down_ACOR_VSMC
GO:0022029	0.314	0.899	2	23	telencephalon cell migration	BP	1	PEX5,GLI3	down_VCAV_EC
GO:2000008	0.314	0.904	2	12	regulation of protein localization to cell surface	BP	1	ACTN2,RAB11B	up_ACOR_VSMC
GO:0006518	0.314	0.898	2	290	peptide metabolic process	BP	1	PCSK1N,ENSCAFG00000028814	up_APUL_EC
GO:0001961	0.314	0.903	2	13	positive regulation of cytokine-mediated	BP	1	NLRC5,LSM14A	up_VCAV_EC
GO:0001101	0.314	0.947	1	65	response to acid chemical	BP	1	LYN	down_ACOR_EC
GO:0002764	0.314	0.946	1	80	immune response-regulating signaling	BP	1	LYN	down_ACOR_EC
GO:0061138	0.314	0.947	1	73	morphogenesis of a branching epithelium	BP	1	SULF1	down_ACOR_EC
GO:0030035	0.314	0.957	1	4	microspike assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0033034	0.314	0.957	1	4	positive regulation of myeloid cell apoptotic	BP	1	PIK3CD	down_ACOR_VSMC
GO:0034205	0.314	0.952	1	7	amyloid-beta formation	BP	1	PRNP	down_VCAV_EC
GO:0003181	0.314	0.952	1	7	atrioventricular valve morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0002902	0.314	0.953	1	6	regulation of B cell apoptotic process	BP	1	LYN	down_VSAP_EC
GO:2000679	0.314	0.953	1	6	positive regulation of transcription regulatory region DNA binding	BP	1	CTNNB1	down_VSAP_EC
GO:0003174	0.314	0.957	1	4	mitral valve development	BP	1	SMAD6	up_ACOR_VSMC
GO:0015693	0.314	0.957	1	4	magnesium ion transport	BP	1	NIPAL3	up_ACOR_VSMC
GO:0072189	0.314	0.957	1	4	ureter development	BP	1	BMP4	up_ACOR_VSMC
GO:0001944	0.314	0.95	1	263	vasculature development	BP	1	EYA1	up_AFEM_VSMC
GO:0048534	0.314	0.95	1	262	hematopoietic or lymphoid organ	BP	1	HOXA9	up_AFEM_VSMC
GO:0044806	0.314	0.962	1	3	G-quadruplex DNA unwinding	BP	1	BLM	up_VCAV_EC

GO:0010675	0.314	0.947	1	46	regulation of cellular carbohydrate metabolic	BP	1	FBP1	up_VPOR_EC
GO:0031333	0.314	0.946	1	46	negative regulation of protein complex assembly	BP	1	TWF1	up_VPOR_EC
GO:0051403	0.314	0.947	1	89	stress-activated MAPK cascade	BP	1	CDC42EP5	up_VFEM_EC
GO:0046700	0.314	0.948	1	147	heterocycle catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0006091	0.314	0.948	1	139	generation of precursor metabolites and energy	BP	1	FBP1	up_VFEM_VSMC
GO:0098655	0.314	0.948	1	142	cation transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0022038	0.314	0.957	1	4	corpus callosum development	BP	1	RTN4RL1	up_VSAP_EC
GO:0051547	0.314	0.957	1	4	regulation of keratinocyte migration	BP	1	FGF7	up_VSAP_EC
GO:0051549	0.314	0.957	1	4	positive regulation of keratinocyte migration	BP	1	FGF7	up_VSAP_EC
GO:0016311	0.314315222	0.84666	4	106	dephosphorylation	BP	1	THNSL2,DUSP26,PRKCD,PPP1R26	up_ACOR_EC
GO:0031076	0.314826241	0.94801	1	14	embryonic camera-type eye development	BP	1	FZD5	up_ACOR_EC
GO:1903556	0.314931226	0.94797	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4	up_ACOR_EC
GO:0009790	0.315	0.76	23	335	embryo development	BP	1	PRICKLE1,SULF1,PRKACB,ITGA2,SEC24D,ENSCAFG00000032470,TMED2,HOXB7,HIF1A,ZPR1,CTNNB1,PLOD3,MYO1E,SDC4,RBBP8,PRMT1,SH2B3,EXT1,INHBA,SIX4,NRP1,COL12A1,RTCB	down_VSAP_EC
GO:0009152	0.315	0.808	8	80	purine ribonucleotide biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,HIF1A	up_VCAV_EC
GO:0050896	0.315	0.836	7	2346	response to stimulus	BP	1	DKK2,LNPEP,ERC1,TAOK1,BPI,CTNNAL1,GPR155	up_AORT_EC
GO:0050866	0.315	0.825	6	48	negative regulation of cell activation	BP	1	BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0022607	0.315	0.84	5	969	cellular component assembly	BP	1	NR1H4,TUBB4A,ARHGEF26,SLITRK5,NTRK2	up_APUL_EC
GO:0034614	0.315	0.836	5	39	cellular response to reactive oxygen species	BP	1	PPARGC1B,ABL1,MAP3K5,PDK2,ZNF580	up_VSAP_EC
GO:0017015	0.315	0.868	3	40	regulation of transforming growth factor beta receptor signaling	BP	1	VASN,FBN1,ASPN	down_VCAV_EC
GO:1903844	0.315	0.868	3	40	regulation of cellular response to transforming growth factor beta	BP	1	VASN,FBN1,ASPN	down_VCAV_EC
GO:0050867	0.315	0.866	3	83	positive regulation of cell activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0051171	0.315	0.89	3	1697	regulation of nitrogen compound metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0010941	0.315	0.901	2	524	regulation of cell death	BP	1	IVNS1ABP,SRSF6	down_AFEM_EC
GO:0033146	0.315	0.904	2	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	LBH,SKP2	up_ACOR_VSMC
GO:0007600	0.315	0.946	1	73	sensory perception	BP	1	HOXA1	down_ACOR_EC
GO:0021554	0.315	0.957	1	4	optic nerve development	BP	1	NAV2	down_ACOR_VSMC
GO:0051640	0.315	0.948	1	174	organelle localization	BP	1	GPSM2	down_AFEM_EC
GO:0006656	0.315	0.951	1	7	phosphatidylcholine biosynthetic process	BP	1	LCAT	down_VCAV_EC
GO:0010043	0.315	0.951	1	7	response to zinc ion	BP	1	MT2A	down_VCAV_EC
GO:0051043	0.315	0.951	1	7	regulation of membrane protein ectodomain	BP	1	APOE	down_VSAP_EC
GO:0060306	0.315	0.951	1	7	regulation of membrane repolarization	BP	1	WDR1	down_VSAP_EC
GO:0060440	0.315	0.953	1	6	trachea formation	BP	1	CTNNB1	down_VSAP_EC
GO:0086009	0.315	0.951	1	7	membrane repolarization	BP	1	WDR1	down_VSAP_EC
GO:0033483	0.315	0.957	1	4	gas homeostasis	BP	1	EGLN1	up_ACOR_VSMC
GO:0090336	0.315	0.957	1	4	positive regulation of brown fat cell	BP	1	FNDC5	up_ACOR_VSMC
GO:0043069	0.315	0.949	1	262	negative regulation of programmed cell death	BP	1	EYA1	up_AFEM_VSMC

GO:1901701	0.315	0.949	1	271	cellular response to oxygen-containing	BP	1	TLR2	up_AFEM_VSMC
GO:0072511	0.315	0.946	1	97	divalent inorganic cation transport	BP	1	HOXA3	up_APUL_EC
GO:0006670	0.315	0.954	1	5	sphingosine metabolic process	BP	1	SPTLC2	up_VCAV_EC
GO:0006282	0.315	0.946	1	48	regulation of DNA repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0021543	0.315	0.946	1	49	pallium development	BP	1	SEMA3A	up_VPOR_EC
GO:0021953	0.315	0.946	1	49	central nervous system neuron differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0044270	0.315	0.947	1	147	cellular nitrogen compound catabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0050767	0.315	0.948	1	184	regulation of neurogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0048841	0.315	0.957	1	4	regulation of axon extension involved in	BP	1	PLXNA4	up_VSAP_EC
GO:0006914	0.315039499	0.83183	5	141	autophagy	BP	1	ATG16L2,CHMP4B,TP53INP2,VPS16,ENSCAFG00000010493	up_ACOR_EC
GO:0061919	0.315039499	0.83183	5	141	process utilizing autophagic mechanism	BP	1	ATG16L2,CHMP4B,TP53INP2,VPS16,ENSCAFG00000010493	up_ACOR_EC
GO:0032413	0.315292579	0.94761	1	15	negative regulation of ion transmembrane transporter activity	BP	1	ACTN2	up_ACOR_EC
GO:0060359	0.315757431	0.94768	1	14	response to ammonium ion	BP	1	AGRN	up_ACOR_EC
GO:0034142	0.315982351	0.9476	1	14	toll-like receptor 4 signaling pathway	BP	1	NR1H4	up_ACOR_EC
GO:0010941	0.316	0.739	45	524	regulation of cell death	BP	1	EPHB1,PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,MAP3K11,STK10,CD34,MEF2C,ATF3,TLR4,GATA3,TNFAIP8,FIGNL1,PELI1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,MADD,PAK2,SH3GLB1,NCK1,CASP10,PTGS2,RAPGEF2,PLCG2,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0048646	0.316	0.745	37	349	anatomical structure formation involved in morphogenesis	BP	1	VEGFD,ACTN2,LEP,GATA5,ANGPT1,SHROOM3,BMP4,FGFR2,TLR3,SEC24B,LATS2,CITED2,SPINT1,SASH1,LMO4,FGF18,NEBL,EGLN1,NRP1,SMARCD3,SPINT2,TBX20,TBX5,FZD3,FRS2,DAG1,LAMA3,PSEN1,SYNJ2BP,JUP,PERP,EDN1,JAM3,ERAP1,MYOZ2,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:0005975	0.316	0.765	20	183	carbohydrate metabolic process	BP	1	DHDH,ACACB,GOT1,INPP5E,PGM2L1,C1QTNF2,PHKA2,PPIP5K1,PDK2,GALK2,GALK1,PASK,KHK,GLB1L,TKFC,PC,NCOA2,CHST7,GNPDA1,DDIT4	up_VSAP_EC
GO:0043269	0.316	0.776	15	135	regulation of ion transport	BP	1	AMIGO1,SLC8B1,GABRE,ABL1,KCNE3,CHRM1,OSR1,CLIC5,KLHL24,RAB11B,CRACR2B,KCNB1,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0009100	0.316	0.794	10	139	glycoprotein metabolic process	BP	1	SULF1,ENSCAFG00000032470,CHSY1,HIF1A,GALNT1,CTNNB1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0072593	0.316	0.807	8	68	reactive oxygen species metabolic process	BP	1	PRDX4,F2RL1,BNIP3,CDKN1A,SESN1,DDIT4,CAT,PARK7	up_ACOR_VSMC
GO:0007548	0.316	0.808	8	68	sex differentiation	BP	1	HOXA11,HOXA9,HNF4A,IRX5,SLIT2,OSR1,PATZ1,CITED2	up_VSAP_EC
GO:0042445	0.316	0.834	5	46	hormone metabolic process	BP	1	TIPARP,GATA3,BMP2,HIF1A,ALDH1A3	up_VCAV_EC
GO:0048522	0.316	0.846	5	1484	positive regulation of cellular process	BP	1	EYA1,HOXA9,NETO1,HOXA11,SHOX2	up_VFEM_VSMC
GO:0032640	0.316	0.835	5	39	tumor necrosis factor production	BP	1	C5AR2,PIK3R1,MYD88,CYBA,MAVS	up_VSAP_EC
GO:0060419	0.316	0.871	3	22	heart growth	BP	1	MEF2C,EDN1,PROX1	up_VCAV_EC
GO:0002709	0.316	0.899	2	19	regulation of T cell mediated immunity	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0051646	0.316	0.903	2	12	mitochondrion localization	BP	1	MFN2,CLUH	up_VSAP_EC
GO:1901701	0.316	0.896	2	271	cellular response to oxygen-containing	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0070199	0.316	0.951	1	7	establishment of protein localization to	BP	1	NABP2	down_VCAV_EC
GO:1901028	0.316	0.951	1	7	regulation of mitochondrial outer membrane permeabilization involved	BP	1	SLC35F6	down_VCAV_EC
GO:0005975	0.316	0.948	1	183	carbohydrate metabolic process	BP	1	GBGT1	down_VPOR_EC

GO:0071363	0.316	0.948	1	188	cellular response to growth factor stimulus	BP	1	CITED2	down_VPOR_EC
GO:0044342	0.316	0.951	1	7	type B pancreatic cell proliferation	BP	1	NR4A1	down_VSAP_EC
GO:0097062	0.316	0.952	1	6	dendritic spine maintenance	BP	1	APOE	down_VSAP_EC
GO:2001224	0.316	0.954	1	5	positive regulation of neuron migration	BP	1	ARHGEF2	down_VSAP_EC
GO:0032400	0.316	0.952	1	6	melanosome localization	BP	1	SHROOM2	down_VSAP_EC
GO:0032401	0.316	0.952	1	6	establishment of melanosome localization	BP	1	SHROOM2	down_VSAP_EC
GO:0032906	0.316	0.952	1	6	transforming growth factor beta2 production	BP	1	HIF1A	down_VSAP_EC
GO:0032909	0.316	0.952	1	6	regulation of transforming growth factor beta2	BP	1	HIF1A	down_VSAP_EC
GO:0051875	0.316	0.952	1	6	pigment granule localization	BP	1	SHROOM2	down_VSAP_EC
GO:0051905	0.316	0.952	1	6	establishment of pigment granule localization	BP	1	SHROOM2	down_VSAP_EC
GO:0043062	0.316	0.946	1	99	extracellular structure organization	BP	1	NPNT	up_APUL_EC
GO:0070085	0.316	0.946	1	95	glycosylation	BP	1	GALNT17	up_APUL_EC
GO:0006103	0.316	0.954	1	5	2-oxoglutarate metabolic process	BP	1	AADAT	up_VCAV_EC
GO:0051084	0.316	0.954	1	5	'de novo' posttranslational protein	BP	1	SH3GLB1	up_VCAV_EC
GO:0007599	0.316	0.946	1	48	hemostasis	BP	1	SLC7A11	up_VPOR_EC
GO:0043123	0.316	0.946	1	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	MTDH	up_VPOR_EC
GO:0051225	0.316	0.946	1	49	spindle assembly	BP	1	MZT1	up_VPOR_EC
GO:0007610	0.316	0.947	1	146	behavior	BP	1	CHL1	up_VPOR_VSMC
GO:1904951	0.316	0.946	1	108	positive regulation of establishment of protein localization	BP	1	NR1H4	up_VPUL_EC
GO:2000392	0.316	0.957	1	4	regulation of lamellipodium	BP	1	ENPP2	up_VSAP_EC
GO:0044085	0.316068523	0.75201	31	1076	cellular component biogenesis	BP	1	MYOZ2,NR1H4,TMOD1,TRPS1,KCTD12,CALY,SOX9,ARHGAP6,ATG16L2,SYNPO2,KCNB1,FZD5,SMAD6,PLS1,ACTN2,ARHGAP28,PAK3,PTGER4,PREB,LRP4,CLSTN1,CLU,CHMP4B,TP53INP2,VPS16,NRP1,ARHGEF26,PRKCD,ENSCAFG00000010493,MFAP4,TUBB4A	up_ACOR_EC
GO:0007178	0.316086509	0.84541	4	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	RGMA,SMAD6,ADAMTSL2,LRP4	up_ACOR_EC
GO:0060997	0.31623494	0.94751	1	14	dendritic spine morphogenesis	BP	1	PAK3	up_ACOR_EC
GO:0032613	0.316968128	0.94725	1	14	interleukin-10 production	BP	1	PRKCD	up_ACOR_EC
GO:0009967	0.317	0.739	45	435	positive regulation of signal transduction	BP	1	CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,LIMS2,IL6R,CRADD,ABL1,EMP2,DLL1,EPN2,MAP3K5,PDGFD,C1QTNF2,HPSE,CCBE1,F2RL1,TRAF7,PIK3R1,RBCK1,FAM53B,SULF2,SHOX2,SASH1,CREBRF,MYD88,S100A4,TSPAN5,ENSCAFG00000011993,RAF1,CYBA,ZNF205,ACVRL1,UBQLN2,HTRA2,FLOT1,NCK1,MAVS,CITED2,BAG4,TRADD,DEDD2	up_VSAP_EC
GO:0007154	0.317	0.783	15	1622	cell communication	BP	1	C3AR1,BARX1,HTR7,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,SV2C,PDE1C,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0042326	0.317	0.793	10	163	negative regulation of phosphorylation	BP	1	KIRREL1,DCN,PRNP,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1,GREM1	down_VCAV_EC
GO:0001935	0.317	0.823	6	50	endothelial cell proliferation	BP	1	VEGFD,LEP,HTR2B,BMP4,TGFBR1,SYNJ2BP	up_ACOR_VSMC
GO:0070374	0.317	0.846	4	57	positive regulation of ERK1 and ERK2 cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,SHC1	down_VCAV_EC
GO:0044238	0.317	0.904	4	3383	primary metabolic process	BP	1	AK5,GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0060562	0.317	0.845	4	120	epithelial tube morphogenesis	BP	1	IRX3,DLL1,GREM1,LUZP1	up_AFEM_EC
GO:1903725	0.317	0.85	4	30	regulation of phospholipid metabolic process	BP	1	AMBRA1,PIK3R1,PIK3IP1,IDH1	up_VSAP_EC

GO:0080134	0.317	0.867	3	386	regulation of response to stress	BP	1	LYN,IGF1R,PDPN	down_ACOR_EC
GO:0048010	0.317	0.871	3	20	vascular endothelial growth factor receptor	BP	1	VEGFD,FGF18,NRP1	up_ACOR_VSMC
GO:0009615	0.317	0.865	3	83	response to virus	BP	1	GPAM,CHRM2,CCL5	up_AFEM_EC
GO:0032835	0.317	0.871	3	21	glomerulus development	BP	1	OSR1,KLF15,SULF2	up_VSAP_EC
GO:0006366	0.317	0.901	2	583	transcription by RNA polymerase II	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0031648	0.317	0.898	2	19	protein destabilization	BP	1	HTT,RAD23A	down_VSAP_EC
GO:0050891	0.317	0.902	2	12	multicellular organismal water homeostasis	BP	1	INPP5K,WFS1	up_ACOR_VSMC
GO:0030072	0.317	0.894	2	48	peptide hormone secretion	BP	1	LEP,CCL5	up_AFEM_EC
GO:0050866	0.317	0.895	2	48	negative regulation of cell activation	BP	1	BPI,CYLD	up_AFEM_EC
GO:0022607	0.317	0.908	2	969	cellular component assembly	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0048635	0.317	0.901	2	14	negative regulation of muscle organ	BP	1	EPHB1,BMP2	up_VCAV_EC
GO:2001239	0.317	0.901	2	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	CTNNA1,RIPK1	up_VCAV_EC
GO:0033059	0.317	0.902	2	12	cellular pigmentation	BP	1	RAB11B,HPS4	up_VSAP_EC
GO:0106049	0.317	0.956	1	4	regulation of cellular response to osmotic	BP	1	ARHGEF2	down_ACOR_VSMC
GO:1902218	0.317	0.956	1	4	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	ARHGEF2	down_ACOR_VSMC
GO:1902219	0.317	0.956	1	4	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0014070	0.317	0.947	1	172	response to organic cyclic compound	BP	1	GABPA	down_AFEM_EC
GO:0018208	0.317	0.951	1	7	peptidyl-proline modification	BP	1	CRTAP	down_VCAV_EC
GO:0034695	0.317	0.95	1	8	response to prostaglandin E	BP	1	ADCY6	down_VCAV_EC
GO:1902624	0.317	0.951	1	7	positive regulation of neutrophil migration	BP	1	RAC2	down_VCAV_EC
GO:0055082	0.317	0.947	1	189	cellular chemical homeostasis	BP	1	RAB11B	down_VPOR_EC
GO:0051246	0.317	0.961	1	832	regulation of protein metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0060020	0.317	0.952	1	6	Bergmann glial cell differentiation	BP	1	PTPN11	down_VSAP_EC
GO:1902743	0.317	0.947	1	16	regulation of lamellipodium	BP	1	KANK1	up_AFEM_EC
GO:0032880	0.317	0.949	1	266	regulation of protein localization	BP	1	TLR2	up_AFEM_VSMC
GO:0016053	0.317	0.946	1	97	organic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0046394	0.317	0.946	1	97	carboxylic acid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0051271	0.317	0.946	1	98	negative regulation of cellular component	BP	1	TBX5	up_APUL_EC
GO:0048227	0.317	0.954	1	5	plasma membrane to endosome transport	BP	1	USP6NL	up_VCAV_EC
GO:0097066	0.317	0.956	1	4	response to thyroid hormone	BP	1	KIT	up_VCAV_EC
GO:0097067	0.317	0.956	1	4	cellular response to thyroid hormone stimulus	BP	1	KIT	up_VCAV_EC
GO:0023058	0.317	0.954	1	5	adaptation of signaling pathway	BP	1	APLNR	up_VCAV_EC
GO:0034162	0.317	0.954	1	5	toll-like receptor 9 signaling pathway	BP	1	HMGB1	up_VCAV_EC
GO:0045898	0.317	0.954	1	5	regulation of RNA polymerase II transcriptional	BP	1	HMGB1	up_VCAV_EC
GO:0061156	0.317	0.956	1	4	pulmonary artery morphogenesis	BP	1	JAG1	up_VCAV_EC
GO:0048534	0.317	0.949	1	262	hematopoietic or lymphoid organ	BP	1	LRRC17	up_VCAV_VSMC
GO:0001503	0.317	0.946	1	109	ossification	BP	1	HOXA3	up_VPUL_EC
GO:0033993	0.317	0.947	1	186	response to lipid	BP	1	SLIT2	up_VPUL_VSMC

GO:0043065	0.317	0.947	1	188	positive regulation of apoptotic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0021825	0.317	0.956	1	4	substrate-dependent cerebral cortex tangential	BP	1	SLIT2	up_VSAP_EC
GO:0042176	0.317049342	0.83037	5	140	regulation of protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114,AZIN2	up_ACOR_EC
GO:0009266	0.317461266	0.89464	2	43	response to temperature stimulus	BP	1	PCSK1N,PRKACA	up_ACOR_EC
GO:0046888	0.317665817	0.947	1	14	negative regulation of hormone secretion	BP	1	KCNB1	up_ACOR_EC
GO:1905114	0.318	0.77	17	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	LGR6,ZRANB1,RECK,MLLT3,FERMT1,BMP4,FGFR2,LATS2,ZNRF3,TMEM108,CLSTN1,DMPK,FZD3,APP,PSEN1,INSYN1,DISC1	up_ACOR_VSMC
GO:0051090	0.318	0.775	15	134	regulation of DNA-binding transcription factor activity	BP	1	TLR3,PPARGC1A,AR,EGLN1,JMY,CLSTN1,APP,JUP,DDR2,EDN1,NOD2,ARID5B,WFS1,PARK7,IL18R1	up_ACOR_VSMC
GO:0016055	0.318	0.792	10	134	Wnt signaling pathway	BP	1	PRICKLE1,SULF1,ILK,SMARCA4,NXN,CTNNB1,APOE,DDIT3,TAX1BP3,DISC1	down_VSAP_EC
GO:0198738	0.318	0.792	10	134	cell-cell signaling by wnt	BP	1	PRICKLE1,SULF1,ILK,SMARCA4,NXN,CTNNB1,APOE,DDIT3,TAX1BP3,DISC1	down_VSAP_EC
GO:1902904	0.318	0.835	5	38	negative regulation of supramolecular fiber	BP	1	FGF13,ARHGAP28,MID1,TUBB4A,INPP5K	up_ACOR_VSMC
GO:0042325	0.318	0.831	5	463	regulation of phosphorylation	BP	1	ARHGEF2,ASPN,ACVR2A,FBP1,ENSCAFG00000032731	up_VPOR_EC
GO:0030316	0.318	0.867	3	31	osteoclast differentiation	BP	1	CTNNB1,TFRC,GLO1	down_VSAP_EC
GO:0055086	0.318	0.864	3	237	nucleobase-containing small molecule metabolic	BP	1	AK5,FBP1,GNPNAT1	up_VPOR_EC
GO:0030888	0.318	0.901	2	13	regulation of B cell proliferation	BP	1	MNDA,TFRC	down_ACOR_VSMC
GO:0021782	0.318	0.897	2	23	glial cell development	BP	1	LRP1,AKT2	down_VCAV_EC
GO:0032944	0.318	0.894	2	48	regulation of mononuclear cell	BP	1	LEP,GPAM	up_AFEM_EC
GO:0050670	0.318	0.894	2	48	regulation of lymphocyte proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0010647	0.318	0.899	2	460	positive regulation of cell communication	BP	1	BAMBI,ANKRD6	up_VPOR_VSMC
GO:0007399	0.318	0.9	2	564	nervous system development	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:0009395	0.318	0.901	2	12	phospholipid catabolic process	BP	1	ENPP2,IDH1	up_VSAP_EC
GO:0030201	0.318	0.902	2	12	heparan sulfate proteoglycan metabolic	BP	1	HPSE,SULF2	up_VSAP_EC
GO:0003333	0.318	0.902	2	12	amino acid transmembrane transport	BP	1	OSR1,SLC25A12	up_VSAP_EC
GO:0006122	0.318	0.95	1	7	mitochondrial electron transport, ubiquinol to	BP	1	UQCR10	down_VCAV_EC
GO:0032964	0.318	0.95	1	7	collagen biosynthetic process	BP	1	LARP6	down_VCAV_EC
GO:0043171	0.318	0.95	1	8	peptide catabolic process	BP	1	RNPEP	down_VCAV_EC
GO:0003413	0.318	0.952	1	6	chondrocyte differentiation involved in endochondral bone	BP	1	SERPINH1	down_VSAP_EC
GO:0006689	0.318	0.956	1	4	ganglioside catabolic process	BP	1	NEU3	up_ACOR_VSMC
GO:0010039	0.318	0.956	1	4	response to iron ion	BP	1	B2M	up_ACOR_VSMC
GO:0010996	0.318	0.96	1	3	response to auditory stimulus	BP	1	USP53	up_ACOR_VSMC
GO:0038166	0.318	0.956	1	4	angiotensin-activated signaling pathway	BP	1	ACTN2	up_ACOR_VSMC
GO:1901228	0.318	0.956	1	4	positive regulation of transcription from RNA polymerase II promoter involved in heart	BP	1	GATA5	up_ACOR_VSMC
GO:0006623	0.318	0.946	1	16	protein targeting to vacuole	BP	1	RAB7A	up_AFEM_EC
GO:0021602	0.318	0.946	1	16	cranial nerve morphogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0030003	0.318	0.946	1	157	cellular cation homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0007096	0.318	0.952	1	6	regulation of exit from mitosis	BP	1	ZW10	up_VCAV_EC
GO:2001138	0.318	0.953	1	5	regulation of phospholipid transport	BP	1	ATP8A1	up_VCAV_EC
GO:2001140	0.318	0.953	1	5	positive regulation of phospholipid transport	BP	1	ATP8A1	up_VCAV_EC

GO:0006733	0.318	0.945	1	45	oxidoreduction coenzyme metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0006020	0.318	0.956	1	4	inositol metabolic process	BP	1	PPIP5K1	up_VSAP_EC
GO:0033184	0.318	0.956	1	4	positive regulation of histone ubiquitination	BP	1	CDK9	up_VSAP_EC
GO:0043691	0.318	0.956	1	4	reverse cholesterol transport	BP	1	LCAT	up_VSAP_EC
GO:2001166	0.318	0.956	1	4	regulation of histone H2B ubiquitination	BP	1	CDK9	up_VSAP_EC
GO:2001168	0.318	0.956	1	4	positive regulation of histone H2B	BP	1	CDK9	up_VSAP_EC
GO:0032836	0.318	0.956	1	4	glomerular basement membrane development	BP	1	SULF2	up_VSAP_EC
GO:0051124	0.318	0.956	1	4	synaptic growth at neuromuscular junction	BP	1	LRP4	up_VSAP_EC
GO:0097090	0.318	0.956	1	4	presynaptic membrane organization	BP	1	LRP4	up_VSAP_EC
GO:0002237	0.318	0.945	1	85	response to molecule of bacterial origin	BP	1	TLR2	up_VSAP_VSMC
GO:0032722	0.318354738	0.94675	1	14	positive regulation of chemokine production	BP	1	MAVS	up_ACOR_EC
GO:0034109	0.318363571	0.94675	1	14	homotypic cell-cell adhesion	BP	1	PRKCD	up_ACOR_EC
GO:0009894	0.318537455	0.79633	9	277	regulation of catabolic process	BP	1	EDEM2,PIAS1,CLU,CHMP4B,TP53INP2,RARRES2,RNF114,AZIN2,PRKCD	up_ACOR_EC
GO:0097696	0.318626084	0.89399	2	43	STAT cascade	BP	1	LRRC15,LRRC4	up_ACOR_EC
GO:0060042	0.318666541	0.94664	1	14	retina morphogenesis in camera-type eye	BP	1	SOX9	up_ACOR_EC
GO:0098661	0.318743866	0.94661	1	14	inorganic anion transmembrane transport	BP	1	CLIC3	up_ACOR_EC
GO:0040007	0.318999012	0.79596	9	276	growth	BP	1	SOX9,PLS1,ESM1,FOXC2,TBX5,LRP4,C23H3orf58,NRP1,PYGO2	up_ACOR_EC
GO:0051338	0.319	0.752	27	288	regulation of transferase activity	BP	1	IRAK1,HMGCR,HNRNPD,UBE2S,SLC29A1,RFC2,CAV1,RFC5,RFC3,NF2,AURKB,CDKN2C,EZH2,GREM1,MAP3K20,RFC4,NEK2,CKS2,RAP2C,NUP62,EMP2,CLSPN,CDC20,CCNB3,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC
GO:0044419	0.319	0.787	11	117	interspecies interaction between organisms	BP	1	LYZ,CXCL8,TNIP1,IRF8,GUCY1A1,NECTIN2,PROX1,THOC1,SMARCA4,CNOT7,USP6NL	up_VCAV_EC
GO:1903522	0.319	0.812	7	58	regulation of blood circulation	BP	1	THRB,IRX5,KCNE3,CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0046677	0.319	0.821	6	54	response to antibiotic	BP	1	TNFAIP3,PDGFB,MEF2C,MAPK13,TIMELESS,RIPK1	up_VCAV_EC
GO:0071229	0.319	0.822	6	51	cellular response to acid chemical	BP	1	PDGFB,YES1,MTOR,ABCA1,PDGFD,ZEB1	up_VCAV_EC
GO:0045454	0.319	0.847	4	35	cell redox homeostasis	BP	1	QSOX2,PRDX1,ENSCAFG00000006478,TXNDC12	down_ACOR_VSMC
GO:0006479	0.319	0.846	4	45	protein methylation	BP	1	NR1H4,IWS1,PRMT1,KDM3A	down_VSAP_EC
GO:0008213	0.319	0.846	4	45	protein alkylation	BP	1	NR1H4,IWS1,PRMT1,KDM3A	down_VSAP_EC
GO:0001658	0.319	0.868	3	24	branching involved in ureteric bud	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0032786	0.319	0.9	2	13	positive regulation of DNA-templated transcription, elongation	BP	1	DDX39B,SUPT16H	down_ACOR_VSMC
GO:0061387	0.319	0.898	2	18	regulation of extent of cell growth	BP	1	IFRD1,NRP1	down_VSAP_EC
GO:0071108	0.319	0.902	2	11	protein K48-linked deubiquitination	BP	1	USP20,PARK7	up_ACOR_VSMC
GO:0060548	0.319	0.895	2	294	negative regulation of cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0030260	0.319	0.899	2	15	entry into host cell	BP	1	CXCL8,NECTIN2	up_VCAV_EC
GO:0044409	0.319	0.899	2	15	entry into host	BP	1	CXCL8,NECTIN2	up_VCAV_EC
GO:0051806	0.319	0.899	2	15	entry into cell of other organism involved in	BP	1	CXCL8,NECTIN2	up_VCAV_EC
GO:0051828	0.319	0.899	2	15	entry into other organism involved in symbiotic	BP	1	CXCL8,NECTIN2	up_VCAV_EC
GO:0090317	0.319	0.898	2	16	negative regulation of intracellular protein	BP	1	FERMT1,APOD	up_VCAV_EC
GO:0023056	0.319	0.898	2	462	positive regulation of signaling	BP	1	BAMBI,ANKRD6	up_VPOR_VSMC
GO:0048262	0.319	0.953	1	5	determination of dorsal/ventral asymmetry	BP	1	GREM1	down_ACOR_VSMC
GO:0032228	0.319	0.949	1	8	regulation of synaptic transmission, GABAergic	BP	1	PLCL1	down_VCAV_EC

GO:0061298	0.319	0.949	1	8	retina vasculature development in camera-	BP	1	PDGFRB	down_VCAV_EC
GO:1901798	0.319	0.95	1	7	positive regulation of signal transduction by p53 class mediator	BP	1	SPRED1	down_VCAV_EC
GO:0007507	0.319	0.947	1	194	heart development	BP	1	CITED2	down_VPOR_EC
GO:0007020	0.319	0.951	1	6	microtubule nucleation	BP	1	MZT1	down_VSAP_EC
GO:0010835	0.319	0.951	1	6	regulation of protein ADP-ribosylation	BP	1	PUM3	down_VSAP_EC
GO:0034205	0.319	0.95	1	7	amyloid-beta formation	BP	1	APOE	down_VSAP_EC
GO:0048308	0.319	0.951	1	6	organelle inheritance	BP	1	PLK3	down_VSAP_EC
GO:0060347	0.319	0.951	1	6	heart trabecula formation	BP	1	FHL2	down_VSAP_EC
GO:1904263	0.319	0.951	1	6	positive regulation of TORC1 signaling	BP	1	SEC13	down_VSAP_EC
GO:0006482	0.319	0.953	1	5	protein demethylation	BP	1	KDM3A	down_VSAP_EC
GO:0008214	0.319	0.953	1	5	protein dealkylation	BP	1	KDM3A	down_VSAP_EC
GO:0016577	0.319	0.953	1	5	histone demethylation	BP	1	KDM3A	down_VSAP_EC
GO:0030836	0.319	0.951	1	6	positive regulation of actin filament	BP	1	WDR1	down_VSAP_EC
GO:0045730	0.319	0.949	1	8	respiratory burst	BP	1	PGAM1	down_VSAP_EC
GO:0050996	0.319	0.951	1	6	positive regulation of lipid catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0070076	0.319	0.953	1	5	histone lysine demethylation	BP	1	KDM3A	down_VSAP_EC
GO:0006573	0.319	0.956	1	4	valine metabolic process	BP	1	ENSCAFG00000002977	up_ACOR_VSMC
GO:0033234	0.319	0.956	1	4	negative regulation of protein sumoylation	BP	1	PARK7	up_ACOR_VSMC
GO:0045823	0.319	0.956	1	4	positive regulation of heart contraction	BP	1	EDN1	up_ACOR_VSMC
GO:0007035	0.319	0.946	1	16	vacuolar acidification	BP	1	ATP6V0B	up_AFEM_EC
GO:0010830	0.319	0.946	1	16	regulation of myotube differentiation	BP	1	DMPK	up_AFEM_EC
GO:0035019	0.319	0.946	1	16	somatic stem cell population maintenance	BP	1	LBH	up_AFEM_EC
GO:0043502	0.319	0.946	1	16	regulation of muscle adaptation	BP	1	LMCD1	up_AFEM_EC
GO:0048641	0.319	0.946	1	16	regulation of skeletal muscle tissue	BP	1	DLL1	up_AFEM_EC
GO:0050879	0.319	0.946	1	16	multicellular organismal movement	BP	1	DMPK	up_AFEM_EC
GO:0050881	0.319	0.946	1	16	musculoskeletal movement	BP	1	DMPK	up_AFEM_EC
GO:1900024	0.319	0.946	1	16	regulation of substrate adhesion-dependent cell	BP	1	KANK1	up_AFEM_EC
GO:0072358	0.319	0.948	1	268	cardiovascular system development	BP	1	EYA1	up_AFEM_VSMC
GO:0006811	0.319	0.949	1	330	ion transport	BP	1	SLC20A2	up_AORT_VSMC
GO:0042592	0.319	0.953	1	522	homeostatic process	BP	1	HOXA3	up_APUL_VSMC
GO:0051339	0.319	0.956	1	4	regulation of lyase activity	BP	1	NOS2	up_VCAV_EC
GO:0010875	0.319	0.956	1	4	positive regulation of cholesterol efflux	BP	1	ABCA1	up_VCAV_EC
GO:0031943	0.319	0.956	1	4	regulation of glucocorticoid metabolic	BP	1	BMP2	up_VCAV_EC
GO:1900102	0.319	0.953	1	5	negative regulation of endoplasmic reticulum unfolded protein	BP	1	NCK1	up_VCAV_EC
GO:1903077	0.319	0.953	1	5	negative regulation of protein localization to	BP	1	PPP2R5A	up_VCAV_EC
GO:1904376	0.319	0.953	1	5	negative regulation of protein localization to cell	BP	1	PPP2R5A	up_VCAV_EC
GO:1901698	0.319	0.948	1	266	response to nitrogen compound	BP	1	CA2	up_VCAV_VSMC
GO:0048704	0.319	0.944	1	46	embryonic skeletal system morphogenesis	BP	1	HOXA3	up_VPOR_EC
GO:0009416	0.319	0.945	1	88	response to light stimulus	BP	1	MME	up_VFEM_EC

GO:0031100	0.319	0.956	1	4	animal organ regeneration	BP	1	SULF2	up_VSAP_EC
GO:0033578	0.319	0.956	1	4	protein glycosylation in Golgi	BP	1	LMF1	up_VSAP_EC
GO:0036315	0.319	0.956	1	4	cellular response to sterol	BP	1	OSBPL7	up_VSAP_EC
GO:1904396	0.319	0.956	1	4	regulation of neuromuscular junction	BP	1	LRP4	up_VSAP_EC
GO:0033673	0.319	0.945	1	84	negative regulation of kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0048771	0.319129045	0.89371	2	43	tissue remodeling	BP	1	PTH1R,FOXC2	up_ACOR_EC
GO:0009653	0.31987656	0.75726	23	773	anatomical structure morphogenesis	BP	1	MYOZ2,TMOD1,GATA4,BRSK1,SOX9,RHOU,AQP1,ENSCAFG00000004331,FZD5,LHX9,SMAD6,ACTN2,ESM1,PAK3,DLX3,MAPK8IP2,FOXC2,TBX5,LRP4,CLSTN1,NRP1,ARHGEF26,EFEMP1	up_ACOR_EC
GO:0051147	0.32	0.832	5	44	regulation of muscle cell differentiation	BP	1	MMP14,EZH2,GREM1,RBM14,CTH	down_ACOR_VSMC
GO:0072089	0.32	0.832	5	43	stem cell proliferation	BP	1	NF2,PDCD2,HMGB2,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0002460	0.32	0.83	5	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	SOCS5,FAM49B,PVR,TFRC,BTK	down_VSAP_EC
GO:0031333	0.32	0.832	5	46	negative regulation of protein complex assembly	BP	1	TMOD1,RIOK3,STMN1,HMGB1,TMOD3	up_VCAV_EC
GO:0008630	0.32	0.833	5	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	ACKR3,PIK3R1,HIC1,HTRA2,DDIT4	up_VSAP_EC
GO:0009966	0.32	0.835	5	868	regulation of signal transduction	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0110110	0.32	0.847	4	34	positive regulation of animal organ	BP	1	GREM1,HOXB7,B4GALT1,SIX4	down_ACOR_VSMC
GO:0043112	0.32	0.844	4	57	receptor metabolic process	BP	1	LRPAP1,FUT8,RAB31,GREM1	down_VCAV_EC
GO:0016575	0.32	0.868	3	23	histone deacetylation	BP	1	SREBF1,RBM14,TADA2A	down_ACOR_VSMC
GO:0097150	0.32	0.9	2	13	neuronal stem cell population maintenance	BP	1	SRRT,ASPM	down_ACOR_VSMC
GO:0006893	0.32	0.896	2	20	Golgi to plasma membrane transport	BP	1	EXOC5,BLZF1	down_VSAP_EC
GO:0032768	0.32	0.9	2	12	regulation of monooxygenase activity	BP	1	LEP,HTR2B	up_ACOR_VSMC
GO:0001569	0.32	0.899	2	14	branching involved in blood vessel	BP	1	DLL4,EDN1	up_VCAV_EC
GO:2000242	0.32	0.898	2	15	negative regulation of reproductive process	BP	1	ARHGDIB,FBXO5	up_VCAV_EC
GO:0009100	0.32	0.893	2	139	glycoprotein metabolic process	BP	1	OSTC,OGA	up_VPOR_EC
GO:0006123	0.32	0.953	1	5	mitochondrial electron transport, cytochrome c	BP	1	CYCS	down_ACOR_VSMC
GO:0002825	0.32	0.951	1	6	regulation of T-helper 1 type immune response	BP	1	SOCS5	down_VSAP_EC
GO:0010566	0.32	0.951	1	6	regulation of ketone biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0043371	0.32	0.951	1	6	negative regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0021697	0.32	0.951	1	6	cerebellar cortex formation	BP	1	PTPN11	down_VSAP_EC
GO:0031069	0.32	0.951	1	6	hair follicle morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0032928	0.32	0.955	1	4	regulation of superoxide anion generation	BP	1	F2RL1	up_ACOR_VSMC
GO:0032655	0.32	0.946	1	16	regulation of interleukin-12 production	BP	1	CMKLR1	up_AFEM_EC
GO:0046427	0.32	0.946	1	16	positive regulation of JAK-STAT cascade	BP	1	LEP	up_AFEM_EC
GO:0051705	0.32	0.946	1	16	multi-organism behavior	BP	1	GCNT4	up_AFEM_EC
GO:0070884	0.32	0.946	1	16	regulation of calcineurin-NFAT signaling cascade	BP	1	LMCD1	up_AFEM_EC
GO:0106056	0.32	0.946	1	16	regulation of calcineurin-mediated signaling	BP	1	LMCD1	up_AFEM_EC
GO:2000107	0.32	0.946	1	16	negative regulation of leukocyte apoptotic	BP	1	GPAM	up_AFEM_EC
GO:0032790	0.32	0.953	1	5	ribosome disassembly	BP	1	MRRF	up_VCAV_EC

GO:0036499	0.32	0.951	1	6	PERK-mediated unfolded protein response	BP	1	NCK1	up_VCAV_EC
GO:0048670	0.32	0.955	1	4	regulation of collateral sprouting	BP	1	IFRD1	up_VCAV_EC
GO:0016579	0.32	0.944	1	49	protein deubiquitination	BP	1	USP33	up_VPOR_EC
GO:0032504	0.32	0.946	1	152	multicellular organism reproduction	BP	1	CYP26B1	up_VPOR_VSMC
GO:0048609	0.32	0.946	1	152	multicellular organismal reproductive process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0007264	0.32	0.945	1	164	small GTPase mediated signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0032787	0.32	0.945	1	144	monocarboxylic acid metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0009725	0.32	0.946	1	188	response to hormone	BP	1	SLIT2	up_VPUL_VSMC
GO:0043068	0.32	0.946	1	190	positive regulation of programmed cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:0051493	0.32	0.946	1	188	regulation of cytoskeleton organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0006309	0.32	0.955	1	4	apoptotic DNA fragmentation	BP	1	DFFB	up_VSAP_EC
GO:0035331	0.32	0.955	1	4	negative regulation of hippo signaling	BP	1	LIMD1	up_VSAP_EC
GO:0050778	0.320064048	0.82814	5	141	positive regulation of immune response	BP	1	C7,NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC
GO:1901862	0.320203086	0.94609	1	14	negative regulation of muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0048635	0.320439621	0.946	1	14	negative regulation of muscle organ	BP	1	TBX5	up_ACOR_EC
GO:0070830	0.320454681	0.946	1	14	bicellular tight junction assembly	BP	1	FZD5	up_ACOR_EC
GO:0120192	0.320454681	0.946	1	14	tight junction assembly	BP	1	FZD5	up_ACOR_EC
GO:0034654	0.321	0.719	107	1236	nucleobase-containing compound biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0045935	0.321	0.733	50	491	positive regulation of nucleobase-containing compound metabolic process	BP	1	HOXA11,FZD1,THRB,HOXA9,CDON,WNT11,OSR2,INSIG2,PPARGC1B,HOXD3,CDH1,FGF7,DLL1,OSR1,MAP3K5,KLF15,ZBTB16,RARG,STAT6,F2RL1,ICE1,ZFP36L1,PIK3R1,MYC,SSBP2,ZEB1,SHOX2,CIZ1,FBXO4,IKZF2,TFE3,NUP98,NPAS2,CDK9,PRMT2,ZFP36L2,RAF1,TAF8,NFIB,ABHD14B,NCOA2,SMARCA2,ACVRL1,TNRC6C,PPP3CB,NCK1,MAVS,CITED2,CXXC1,LBH	up_VSAP_EC
GO:0051247	0.321	0.736	44	502	positive regulation of protein metabolic process	BP	1	PLK2,TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,TIPARP,TLR4,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,CASP8,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,TLR3,NCK1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,HMGB1,PMAIP1,RIPK1,PDGFD,UBE2D1,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0120031	0.321	0.785	11	154	plasma membrane bounded cell projection	BP	1	EXOC5,FSCN1,DPYSL3,RPGR,DYNLL1,TNIK,ANLN,KLF5,HTT,DISC1,NRP1	down_VSAP_EC
GO:0048518	0.321	0.802	10	1676	positive regulation of biological process	BP	1	ACVRL1,LYN,HOXA3,IGF1R,PDPN,SULF1,HOXA1,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0072006	0.321	0.811	7	59	nephron development	BP	1	HOXA11,WNT11,DLL1,OSR1,KLF15,IRX3,SULF2	up_VSAP_EC
GO:0032648	0.321	0.867	3	23	regulation of interferon-beta production	BP	1	CACTIN,HMGB2,POLR3F	down_ACOR_VSMC

GO:0050818	0.321	0.867	3	24	regulation of coagulation	BP	1	TFPI,CAV1,ANXA5	down_ACOR_VSMC
GO:0031110	0.321	0.867	3	24	regulation of microtubule polymerization or depolymerization	BP	1	STMN1,RAC1,ARHGEF2	down_ACOR_VSMC
GO:0010565	0.321	0.864	3	40	regulation of cellular ketone metabolic process	BP	1	AKT2,PARK7,LONP2	down_VCAV_EC
GO:0045807	0.321	0.865	3	35	positive regulation of endocytosis	BP	1	VEGFA,SERPINE1,APOE	down_VSAP_EC
GO:0043266	0.321	0.899	2	14	regulation of potassium ion transport	BP	1	NEDD4,CAV1	down_ACOR_VSMC
GO:0032607	0.321	0.901	2	11	interferon-alpha production	BP	1	TLR3,PTPN22	up_ACOR_VSMC
GO:0051560	0.321	0.9	2	12	mitochondrial calcium ion homeostasis	BP	1	MICU2,DISC1	up_ACOR_VSMC
GO:0051704	0.321	0.897	2	476	multi-organism process	BP	1	HOXA9,BPI	up_AORT_EC
GO:0007015	0.321	0.892	2	144	actin filament organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0043393	0.321	0.944	1	77	regulation of protein binding	BP	1	HOXA3	down_ACOR_EC
GO:0097191	0.321	0.944	1	79	extrinsic apoptotic signaling pathway	BP	1	STX4	down_ACOR_EC
GO:0086005	0.321	0.953	1	5	ventricular cardiac muscle cell action potential	BP	1	CAV1	down_ACOR_VSMC
GO:0035556	0.321	0.96	1	845	intracellular signal transduction	BP	1	PLCL1	down_VFEM_EC
GO:0090051	0.321	0.951	1	6	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	STARD13	down_VSAP_EC
GO:1901658	0.321	0.949	1	7	glycosyl compound catabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0009967	0.321	0.95	1	435	positive regulation of signal transduction	BP	1	GATA5	down_VSAP_VSMC
GO:0009584	0.321	0.955	1	4	detection of visible light	BP	1	GNAQ	up_ACOR_VSMC
GO:0048755	0.321	0.955	1	4	branching morphogenesis of a nerve	BP	1	FGFR2	up_ACOR_VSMC
GO:0030916	0.321	0.955	1	4	otic vesicle formation	BP	1	FGFR2	up_ACOR_VSMC
GO:0006024	0.321	0.946	1	16	glycosaminoglycan biosynthetic process	BP	1	XYLT1	up_AFEM_EC
GO:0019233	0.321	0.945	1	16	sensory perception of pain	BP	1	TMEM100	up_AFEM_EC
GO:0034308	0.321	0.945	1	16	primary alcohol metabolic process	BP	1	NAPEPLD	up_AFEM_EC
GO:0035725	0.321	0.945	1	16	sodium ion transmembrane transport	BP	1	FXYD1	up_AFEM_EC
GO:0003197	0.321	0.945	1	16	endocardial cushion development	BP	1	TMEM100	up_AFEM_EC
GO:1990868	0.321	0.945	1	16	response to chemokine	BP	1	CCL5	up_AFEM_EC
GO:1990869	0.321	0.945	1	16	cellular response to chemokine	BP	1	CCL5	up_AFEM_EC
GO:0006071	0.321	0.952	1	5	glycerol metabolic process	BP	1	GK5	up_VCAV_EC
GO:0060431	0.321	0.953	1	5	primary lung bud formation	BP	1	HHEX	up_VCAV_EC
GO:0002521	0.321	0.945	1	149	leukocyte differentiation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0019439	0.321	0.945	1	150	aromatic compound catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0045475	0.321	0.955	1	4	locomotor rhythm	BP	1	NCOA2	up_VSAP_EC
GO:1902668	0.321	0.955	1	4	negative regulation of axon guidance	BP	1	SLIT2	up_VSAP_EC
GO:0090287	0.321	0.944	1	91	regulation of cellular response to growth factor	BP	1	CAV1	up_VSAP_VSMC
GO:0071364	0.321722104	0.94554	1	14	cellular response to epidermal growth factor	BP	1	SOX9	up_ACOR_EC

GO:0006810	0.322	0.727	66	1244	transport	BP	1	GPAM,SLC35F6,SNX18,LRP1,PRNP,SDC4,FOLR2,TMEM230,FXYD1,TRPV2,CLIP3,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,MICALL2,LCAT,SNUPN,SSR2,SCP2,SLC39A6,CACNB3,ANXA11,ATP5MC1,SCAMP4,LRPAP1,THY1,CLTB,SSR3,PEX5,MFSD3,ATP6V0C,MYO1B,SCAMP2,OSBPL10,GLI3,PARK7,YIF1A,SLC17A9,SCARA5,ZFP36L1,SLC2A10,TPC3,CYBA,IFT57,MAVS,CDH2,TOM1,MGARP,RAB7B,SPNS1,SEC61B,RAB31,HM13,ARHGAP1,PCSK6,GREM1,EVI5L,LONP2,RAC2,CLIC4,SOAT1,PACSIN3,ANKRD54,SEC61A1,BRSK1	down_VCAV_EC
GO:0008283	0.322	0.732	49	545	cell proliferation	BP	1	HMGB1,MCM7,HMGA1,MNDA,HOXA3,SLC25A5,SRRT,GINS4,CDCA7L,BIRC5,PRMT1,CAV1,CDK1,FAM129B,NF2,MMP14,CDKN2C,EZH2,GREM1,CDK4,RNASEH2B,ARG2,MCM10,CKS2,PDCD2,MVD,E2F8,B4GALT1,TFRC,NRAS,PPARD,NUP62,EMP2,HMGB2,CDK2,SMARCB1,ENSCAFG00000005299,CORO1A,ASPM,MELK,ELF4,ARHGEF2,GLI1,TINF2,HMGN1,SIX4,MTBP,CTPS1,ANXA7	down_ACOR_VSMC
GO:0006955	0.322	0.756	22	327	immune response	BP	1	ARHGEF2,NR1H4,SOCS5,ENPP1,FAM49B,FLNB,MYO1C,KIF5B,CX3CL1,PTPN2,EIF2B1,PVR,SKAP2,CNOT7,TFRC,LYN,CDC37,GBP5,A2M,BTK,TNFAIP1,DEFB124	down_VSAP_EC
GO:0007409	0.322	0.781	12	109	axonogenesis	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,NFIB,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0022412	0.322	0.802	8	76	cellular process involved in reproduction in multicellular organism	BP	1	TRIP13,FBXO5,NCAPH,FOSL1,HMGB2,TTK,ASPM,TTLL1	down_ACOR_VSMC
GO:0008544	0.322	0.817	6	75	epidermis development	BP	1	ERRFI1,CASP3,FLNB,CTNNB1,PLOD3,INHBA	down_VSAP_EC
GO:0019827	0.322	0.843	4	59	stem cell population maintenance	BP	1	BMPR1A,TRIM8,CDH2,FOXO3	down_VCAV_EC
GO:0009119	0.322	0.846	4	32	ribonucleoside metabolic process	BP	1	ENPP4,PTGDR,ENSCAFG00000018611,NT5C2	up_ACOR_VSMC
GO:0051246	0.322	0.849	4	832	regulation of protein metabolic process	BP	1	CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0000245	0.322	0.866	3	24	spliceosomal complex assembly	BP	1	DDX39B,SF3A2,SF3A1	down_ACOR_VSMC
GO:0006939	0.322	0.864	3	32	smooth muscle contraction	BP	1	SULF1,HTR7,ACTA2	down_VSAP_EC
GO:0009891	0.322	0.865	3	521	positive regulation of biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0042136	0.322	0.868	3	21	neurotransmitter biosynthetic process	BP	1	DAGLB,ALDH9A1,ASS1	up_VSAP_EC
GO:0048640	0.322	0.868	3	21	negative regulation of developmental growth	BP	1	SLC6A4,SAV1,FXN	up_VSAP_EC
GO:0050994	0.322	0.898	2	14	regulation of lipid catabolic process	BP	1	ABHD5,CDK4	down_ACOR_VSMC
GO:0016579	0.322	0.892	2	49	protein deubiquitination	BP	1	USP54,CYLD	up_AFEM_EC
GO:0043388	0.322	0.897	2	16	positive regulation of DNA binding	BP	1	GATA3,HMGB1	up_VCAV_EC
GO:0006650	0.322	0.944	1	78	glycerophospholipid metabolic process	BP	1	ACSL3	down_ACOR_EC
GO:1901017	0.322	0.952	1	5	negative regulation of potassium ion transmembrane	BP	1	CAV1	down_ACOR_VSMC
GO:1901380	0.322	0.952	1	5	negative regulation of potassium ion	BP	1	CAV1	down_ACOR_VSMC
GO:0045671	0.322	0.948	1	8	negative regulation of osteoclast differentiation	BP	1	FBN1	down_VCAV_EC
GO:0070848	0.322	0.945	1	193	response to growth factor	BP	1	CITED2	down_VPOR_EC
GO:0006448	0.322	0.949	1	7	regulation of translational elongation	BP	1	AARS	down_VSAP_EC
GO:0044546	0.322	0.95	1	6	NLRP3 inflammasome complex assembly	BP	1	GBP5	down_VSAP_EC
GO:1900225	0.322	0.95	1	6	regulation of NLRP3 inflammasome complex	BP	1	GBP5	down_VSAP_EC
GO:0060601	0.322	0.95	1	6	lateral sprouting from an epithelium	BP	1	SULF1	down_VSAP_EC
GO:0006998	0.322	0.945	1	16	nuclear envelope organization	BP	1	DMPK	up_AFEM_EC
GO:0007338	0.322	0.945	1	16	single fertilization	BP	1	HOXA9	up_AFEM_EC
GO:0050854	0.322	0.945	1	16	regulation of antigen receptor-mediated	BP	1	CYLD	up_AFEM_EC

GO:0006873	0.322	0.945	1	160	cellular ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0090161	0.322	0.952	1	5	Golgi ribbon formation	BP	1	GCC2	up_VCAV_EC
GO:0006044	0.322	0.952	1	5	N-acetylglucosamine metabolic process	BP	1	CHST7	up_VCAV_EC
GO:0061042	0.322	0.952	1	5	vascular wound healing	BP	1	ADIPOR2	up_VCAV_EC
GO:1901977	0.322	0.955	1	4	negative regulation of cell cycle checkpoint	BP	1	THOC1	up_VCAV_EC
GO:2000002	0.322	0.955	1	4	negative regulation of DNA damage checkpoint	BP	1	THOC1	up_VCAV_EC
GO:0030509	0.322	0.943	1	47	BMP signaling pathway	BP	1	ACVR2A	up_VPOR_EC
GO:0019953	0.322	0.945	1	152	sexual reproduction	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003012	0.322	0.944	1	90	muscle system process	BP	1	MAP2K6	up_VFEM_EC
GO:0050808	0.322	0.944	1	93	synapse organization	BP	1	SIX1	up_VFEM_EC
GO:2001233	0.322	0.945	1	149	regulation of apoptotic signaling pathway	BP	1	EYA1	up_VFEM_VSMC
GO:0010720	0.322	0.944	1	110	positive regulation of cell development	BP	1	ARHGEF2	up_VPUL_EC
GO:0002407	0.322	0.955	1	4	dendritic cell chemotaxis	BP	1	ARHGEF5	up_VSAP_EC
GO:0061156	0.322	0.955	1	4	pulmonary artery morphogenesis	BP	1	CITED2	up_VSAP_EC
GO:0075044	0.322	0.955	1	4	autophagy of host cells involved in interaction	BP	1	ULK1	up_VSAP_EC
GO:0075071	0.322	0.955	1	4	autophagy involved in symbiotic interaction	BP	1	ULK1	up_VSAP_EC
GO:0031290	0.322	0.955	1	4	retinal ganglion cell axon guidance	BP	1	SLIT2	up_VSAP_EC
GO:0035546	0.322	0.955	1	4	interferon-beta secretion	BP	1	MAVS	up_VSAP_EC
GO:0035547	0.322	0.955	1	4	regulation of interferon-beta secretion	BP	1	MAVS	up_VSAP_EC
GO:0035549	0.322	0.955	1	4	positive regulation of interferon-beta secretion	BP	1	MAVS	up_VSAP_EC
GO:0019068	0.322096699	0.94515	1	15	virion assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0060043	0.322488861	0.94526	1	14	regulation of cardiac muscle cell proliferation	BP	1	TBX5	up_ACOR_EC
GO:0060612	0.322574614	0.94522	1	14	adipose tissue development	BP	1	NR1H4	up_ACOR_EC
GO:0060512	0.322638002	0.9452	1	14	prostate gland morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0098900	0.322939077	0.94484	1	15	regulation of action potential	BP	1	KCNB1	up_ACOR_EC
GO:0072359	0.323	0.738	38	368	circulatory system development	BP	1	FZD1,HOXA7,WNT11,ACKR3,AXIN2,ENPP2,ACACB,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,WARS2,SAV1,HPSE,CCBE1,RECK,PLPP3,DLX3,ZFP36L1,TBXA2R,SHOX2,SASH1,LOX,SMG9,HPGD,ZFAND5,ANPEP,ACVRL1,PPP3CB,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0030111	0.323	0.781	12	108	regulation of Wnt signaling pathway	BP	1	FZD1,WNT11,AXIN2,ABL1,RECK,PLPP3,FAM53B,SULF2,HIC1,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0022407	0.323	0.785	11	96	regulation of cell-cell adhesion	BP	1	LEP,CD83,MBP,BMP4,PDE5A,CITED2,CD274,PTPN22,SPINT2,DUSP22,PAG1	up_ACOR_VSMC
GO:0021700	0.323	0.802	8	65	developmental maturation	BP	1	RECK,FERMT1,GJA1,RND1,DAG1,APP,DMC1,DISC1	up_ACOR_VSMC
GO:0007292	0.323	0.864	3	32	female gamete generation	BP	1	ETV6,CTNNB1,INHBA	down_VSAP_EC
GO:1905897	0.323	0.863	3	34	regulation of response to endoplasmic reticulum	BP	1	HYOU1,PTPN2,USP14	down_VSAP_EC
GO:0032648	0.323	0.866	3	23	regulation of interferon-beta production	BP	1	TLR4,RIOK3,TLR3	up_VCAV_EC
GO:0007565	0.323	0.894	2	23	female pregnancy	BP	1	RECK,SYDE1	down_VCAV_EC
GO:0001776	0.323	0.894	2	23	leukocyte homeostasis	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0030048	0.323	0.894	2	23	actin filament-based movement	BP	1	WIPF1,MYO1B	down_VCAV_EC
GO:0060350	0.323	0.894	2	23	endochondral bone morphogenesis	BP	1	NAB2,THBS3	down_VCAV_EC
GO:0042981	0.323	0.896	2	471	regulation of apoptotic process	BP	1	CHL1,NKX2-5	up_VPOR_VSMC

GO:1902373	0.323	0.899	2	12	negative regulation of mRNA catabolic process	BP	1	AXIN2,TENT5C	up_VSAP_EC
GO:0030514	0.323	0.899	2	12	negative regulation of BMP signaling pathway	BP	1	FZD1,ABL1	up_VSAP_EC
GO:2000008	0.323	0.899	2	12	regulation of protein localization to cell surface	BP	1	RAB11B,STX4	up_VSAP_EC
GO:0050765	0.323	0.952	1	5	negative regulation of phagocytosis	BP	1	HMGB1	down_ACOR_VSMC
GO:0071514	0.323	0.948	1	8	genetic imprinting	BP	1	NDN	down_VCAV_EC
GO:0046827	0.323	0.95	1	6	positive regulation of protein export from	BP	1	GSK3B	down_VSAP_EC
GO:0043372	0.323	0.95	1	6	positive regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0045776	0.323	0.95	1	6	negative regulation of blood pressure	BP	1	PRCP	down_VSAP_EC
GO:0060633	0.323	0.954	1	4	negative regulation of transcription initiation from RNA polymerase II	BP	1	CLSTN1	up_ACOR_VSMC
GO:2000143	0.323	0.954	1	4	negative regulation of DNA-templated	BP	1	CLSTN1	up_ACOR_VSMC
GO:0007029	0.323	0.945	1	16	endoplasmic reticulum organization	BP	1	REEP2	up_AFEM_EC
GO:1902533	0.323	0.947	1	271	positive regulation of intracellular signal	BP	1	TLR2	up_AFEM_VSMC
GO:0007517	0.323	0.944	1	100	muscle organ development	BP	1	TBX5	up_APUL_EC
GO:0040013	0.323	0.944	1	100	negative regulation of locomotion	BP	1	TBX5	up_APUL_EC
GO:2001205	0.323	0.959	1	3	negative regulation of osteoclast development	BP	1	TJP2	up_VCAV_EC
GO:0030948	0.323	0.952	1	5	negative regulation of vascular endothelial growth factor receptor	BP	1	HHEX	up_VCAV_EC
GO:0046838	0.323	0.952	1	5	phosphorylated carbohydrate	BP	1	IMPA1	up_VCAV_EC
GO:0046855	0.323	0.952	1	5	inositol phosphate dephosphorylation	BP	1	IMPA1	up_VCAV_EC
GO:0070243	0.323	0.952	1	5	regulation of thymocyte apoptotic process	BP	1	HIF1A	up_VCAV_EC
GO:2000641	0.323	0.954	1	4	regulation of early endosome to late	BP	1	DNAJC13	up_VCAV_EC
GO:0006302	0.323	0.943	1	97	double-strand break repair	BP	1	EYA1	up_VFEM_EC
GO:0002313	0.323	0.954	1	4	mature B cell differentiation involved in	BP	1	DLL1	up_VSAP_EC
GO:0002335	0.323	0.954	1	4	mature B cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0044794	0.323	0.955	1	4	positive regulation by host of viral process	BP	1	PC	up_VSAP_EC
GO:2000047	0.323	0.954	1	4	regulation of cell-cell adhesion mediated by	BP	1	FLOT1	up_VSAP_EC
GO:2000049	0.323	0.954	1	4	positive regulation of cell-cell adhesion mediated by	BP	1	FLOT1	up_VSAP_EC
GO:0043268	0.323	0.954	1	4	positive regulation of potassium ion transport	BP	1	AMIGO1	up_VSAP_EC
GO:0035773	0.323209266	0.94474	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	NR1H4	up_ACOR_EC
GO:0071559	0.323404588	0.86052	3	75	response to transforming growth factor beta	BP	1	FNDC4,SMAD6,ADAMTSL2	up_ACOR_EC
GO:0046834	0.323782425	0.94478	1	14	lipid phosphorylation	BP	1	ENSCAFG00000004331	up_ACOR_EC
GO:0006884	0.323938078	0.94473	1	14	cell volume homeostasis	BP	1	AQP1	up_ACOR_EC
GO:0051146	0.324	0.794	9	76	striated muscle cell differentiation	BP	1	ACTN2,BMP4,NEBL,DMPK,TBX5,FRS2,EDN1,BVES,MYOZ2	up_ACOR_VSMC
GO:0051098	0.324	0.798	8	129	regulation of binding	BP	1	LRP1,LARP6,CLSTN1,PLCL1,LRPAP1,PARK7,MAPRE3,FBH1	down_VCAV_EC
GO:0050768	0.324	0.801	8	66	negative regulation of neurogenesis	BP	1	ITM2C,ZNF365,NRP1,ULK2,APP,PSEN1,ASAP1,B2M	up_ACOR_VSMC
GO:0002224	0.324	0.844	4	34	toll-like receptor signaling pathway	BP	1	HMGB1,IRAK1,CAV1,CACTIN	down_ACOR_VSMC
GO:0071383	0.324	0.842	4	58	cellular response to steroid hormone stimulus	BP	1	KANK2,NR3C1,PARK7,ZFP36L1	down_VCAV_EC
GO:0042133	0.324	0.845	4	30	neurotransmitter metabolic process	BP	1	ABAT,DAGLB,ALDH9A1,ASS1	up_VSAP_EC
GO:0051438	0.324	0.865	3	24	regulation of ubiquitin-protein transferase	BP	1	UBE2S,CDC20,DCUN1D5	down_ACOR_VSMC

GO:0051606	0.324	0.863	3	33	detection of stimulus	BP	1	GNAQ,RDH11,CALM1	down_VSAP_EC
GO:0060326	0.324	0.86	3	84	cell chemotaxis	BP	1	CMKLR1,CCL5,ADAM17	up_AFEM_EC
GO:0042127	0.324	0.863	3	452	regulation of cell proliferation	BP	1	MAB21L1,CAV1,SHOX2	up_VSAP_VSMC
GO:0000165	0.324	0.891	2	236	MAPK cascade	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0002684	0.324	0.892	2	239	positive regulation of immune system process	BP	1	LYN,STX4	down_ACOR_EC
GO:0070228	0.324	0.894	2	20	regulation of lymphocyte apoptotic process	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0046839	0.324	0.899	2	12	phospholipid dephosphorylation	BP	1	PLPP2,INPP5K	up_ACOR_VSMC
GO:0010922	0.324	0.897	2	14	positive regulation of phosphatase activity	BP	1	MEF2C,BMP2	up_VCAV_EC
GO:0060669	0.324	0.899	2	12	embryonic placenta morphogenesis	BP	1	GJB5,ZFP36L1	up_VSAP_EC
GO:0042391	0.324	0.943	1	81	regulation of membrane potential	BP	1	NEDD4	down_ACOR_EC
GO:0045088	0.324	0.943	1	81	regulation of innate immune response	BP	1	LYN	down_ACOR_EC
GO:2000042	0.324	0.947	1	8	negative regulation of double-strand break repair via homologous	BP	1	FBH1	down_VCAV_EC
GO:0071379	0.324	0.948	1	8	cellular response to prostaglandin stimulus	BP	1	ADCY6	down_VCAV_EC
GO:0034091	0.324	0.95	1	6	regulation of maintenance of sister chromatid	BP	1	NAA10	down_VSAP_EC
GO:0034182	0.324	0.95	1	6	regulation of maintenance of mitotic sister chromatid	BP	1	NAA10	down_VSAP_EC
GO:0019934	0.324	0.95	1	6	cGMP-mediated signaling	BP	1	APOE	down_VSAP_EC
GO:1901623	0.324	0.95	1	6	regulation of lymphocyte chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:2000765	0.324	0.95	1	6	regulation of cytoplasmic translation	BP	1	AARS	down_VSAP_EC
GO:1904153	0.324	0.954	1	4	negative regulation of retrograde protein	BP	1	OS9	up_ACOR_VSMC
GO:0014819	0.324	0.954	1	4	regulation of skeletal muscle contraction	BP	1	DMPK	up_ACOR_VSMC
GO:0002741	0.324	0.954	1	4	positive regulation of cytokine secretion involved in immune	BP	1	F2RL1	up_ACOR_VSMC
GO:0060136	0.324	0.954	1	4	embryonic process involved in female	BP	1	CITED2	up_ACOR_VSMC
GO:0003253	0.324	0.954	1	4	cardiac neural crest cell migration involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:0061209	0.324	0.954	1	4	cell proliferation involved in mesonephros	BP	1	BMP4	up_ACOR_VSMC
GO:0090073	0.324	0.954	1	4	positive regulation of protein homodimerization	BP	1	PARK7	up_ACOR_VSMC
GO:0051093	0.324	0.946	1	273	negative regulation of developmental process	BP	1	HOXA9	up_AFEM_VSMC
GO:0006790	0.324	0.943	1	99	sulfur compound metabolic process	BP	1	ENSCAFG00000028814	up_APUL_EC
GO:0062012	0.324	0.943	1	100	regulation of small molecule metabolic	BP	1	NR1H4	up_APUL_EC
GO:0048290	0.324	0.954	1	4	isotype switching to IgA isotypes	BP	1	THOC1	up_VCAV_EC
GO:0048296	0.324	0.954	1	4	regulation of isotype switching to IgA isotypes	BP	1	THOC1	up_VCAV_EC
GO:0032673	0.324	0.951	1	5	regulation of interleukin-4 production	BP	1	GATA3	up_VCAV_EC
GO:0035878	0.324	0.954	1	4	nail development	BP	1	ITGA6	up_VCAV_EC
GO:1902931	0.324	0.951	1	5	negative regulation of alcohol biosynthetic	BP	1	BMP2	up_VCAV_EC
GO:1901701	0.324	0.946	1	271	cellular response to oxygen-containing	BP	1	CA2	up_VCAV_VSMC
GO:0007030	0.324	0.943	1	49	Golgi organization	BP	1	GCC2	up_VPOR_EC
GO:0007423	0.324	0.944	1	155	sensory organ development	BP	1	EYA1	up_VFEM_VSMC
GO:0014706	0.324	0.943	1	112	striated muscle tissue development	BP	1	TBX5	up_VPUL_EC
GO:0045793	0.324	0.954	1	4	positive regulation of cell size	BP	1	PRR16	up_VSAP_EC

GO:0071680	0.324	0.954	1	4	response to indole-3-methanol	BP	1	CDH1	up_VSAP_EC
GO:0071681	0.324	0.954	1	4	cellular response to indole-3-methanol	BP	1	CDH1	up_VSAP_EC
GO:0010876	0.324	0.943	1	92	lipid localization	BP	1	CAV1	up_VSAP_VSMC
GO:0051235	0.324	0.943	1	90	maintenance of location	BP	1	CAV1	up_VSAP_VSMC
GO:0050731	0.324052899	0.89087	2	44	positive regulation of peptidyl-tyrosine	BP	1	LRP4,NRP1	up_ACOR_EC
GO:0046467	0.324241095	0.8907	2	45	membrane lipid biosynthetic process	BP	1	PIGS,PRKCD	up_ACOR_EC
GO:0006935	0.324651595	0.82472	5	143	chemotaxis	BP	1	MMP28,ELMO2,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0042330	0.324651595	0.82472	5	143	taxis	BP	1	MMP28,ELMO2,RARRES2,NRP1,PRKCD	up_ACOR_EC
GO:0045944	0.325	0.743	31	287	positive regulation of transcription by RNA polymerase II	BP	1	SMAD6,GATA5,PCGF5,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,CCNT1,CCPG1,CHD6,APP,CHD7,EDN1,NOD2,RPRD1B,ZKSCAN1,PARK7,TEAD1,SSBP2	up_ACOR_VSMC
GO:0006812	0.325	0.768	15	222	cation transport	BP	1	SLC39A7,ERO1A,ATP2B1,REM1,KIF5B,NDUFA4L2,CTNNB1,TFRC,LYN,DDIT3,NKAIN1,HTT,CALM1,YWHAH,HOMER1	down_VSAP_EC
GO:0110053	0.325	0.787	10	98	regulation of actin filament organization	BP	1	CAPG,LIMA1,NF2,STMN1,RAC1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0048762	0.325	0.794	9	77	mesenchymal cell differentiation	BP	1	GATA5,HTR2B,BMP4,FGFR2,CITED2,NRP1,DAG1,TGFBR1,EDN1	up_ACOR_VSMC
GO:1904018	0.325	0.8	8	69	positive regulation of vasculature development	BP	1	VEGFD,TLR3,SASH1,FGF18,NRP1,JUP,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0016032	0.325	0.805	7	94	viral process	BP	1	P4HB,SMARCA4,CNOT7,TFRC,APOE,REST,RAD23A	down_VSAP_EC
GO:0051188	0.325	0.814	6	81	cofactor biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:2000116	0.325	0.826	5	67	regulation of cysteine-type endopeptidase	BP	1	PTGS2,CRYAB,FAM162A,REST,PAK2	down_VSAP_EC
GO:0043624	0.325	0.829	5	39	cellular protein complex disassembly	BP	1	FGF13,DNAJC6,ACTN2,MID1,F2RL1	up_ACOR_VSMC
GO:0050789	0.325	0.878	5	3295	regulation of biological process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0042129	0.325	0.843	4	35	regulation of T cell proliferation	BP	1	HMGB1,ARG2,TFRC,CORO1A	down_ACOR_VSMC
GO:0072006	0.325	0.84	4	59	nephron development	BP	1	CLSTN1,GLI3,GREM1,SEC61A1	down_VCAV_EC
GO:0043401	0.325	0.841	4	46	steroid hormone mediated signaling	BP	1	SMARCA4,UBA5,YWHAH,KDM3A	down_VSAP_EC
GO:0006970	0.325	0.865	3	23	response to osmotic stress	BP	1	PLK3,ARHGEF2,ANXA7	down_ACOR_VSMC
GO:0014020	0.325	0.861	3	41	primary neural tube formation	BP	1	SDC4,LMO4,IFT57	down_VCAV_EC
GO:0048634	0.325	0.861	3	40	regulation of muscle organ development	BP	1	BMPR1A,TSC22D3,GREM1	down_VCAV_EC
GO:0031122	0.325	0.866	3	21	cytoplasmic microtubule organization	BP	1	RAB11A,HOOK3,SLK	up_VCAV_EC
GO:0097306	0.325	0.865	3	22	cellular response to alcohol	BP	1	PTGFR,CDH1,OSBPL7	up_VSAP_EC
GO:0003208	0.325	0.892	2	24	cardiac ventricle morphogenesis	BP	1	BMPR1A,SEMA3C	down_VCAV_EC
GO:0072091	0.325	0.892	2	24	regulation of stem cell proliferation	BP	1	GLI3,ZFP36L1	down_VCAV_EC
GO:0030149	0.325	0.898	2	12	sphingolipid catabolic process	BP	1	SMPD1,NEU3	up_ACOR_VSMC
GO:0046466	0.325	0.898	2	12	membrane lipid catabolic process	BP	1	SMPD1,NEU3	up_ACOR_VSMC
GO:0060602	0.325	0.898	2	12	branch elongation of an epithelium	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0010677	0.325	0.896	2	14	negative regulation of cellular carbohydrate	BP	1	FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0003008	0.325	0.892	2	336	system process	BP	1	MYBPC2,HTR7	up_VPUL_EC
GO:0045684	0.325	0.898	2	12	positive regulation of epidermis development	BP	1	HPSE,TRADD	up_VSAP_EC
GO:2001273	0.325	0.898	2	12	regulation of glucose import in response to	BP	1	KLF15,PIK3R1	up_VSAP_EC
GO:0006810	0.325	0.968	1	1244	transport	BP	1	SCAMP4	down_AORT_EC
GO:0014912	0.325	0.947	1	8	negative regulation of smooth muscle cell	BP	1	BMPR1A	down_VCAV_EC

GO:0032366	0.325	0.947	1	8	intracellular sterol transport	BP	1	SCP2	down_VCAV_EC
GO:0032367	0.325	0.947	1	8	intracellular cholesterol transport	BP	1	SCP2	down_VCAV_EC
GO:1900087	0.325	0.947	1	8	positive regulation of G1/S transition of mitotic	BP	1	LSM10	down_VCAV_EC
GO:0051239	0.325	0.958	1	859	regulation of multicellular organismal process	BP	1	PLCL1	down_VFEM_EC
GO:0006978	0.325	0.948	1	7	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	BP	1	CDKN1A	down_VSAP_EC
GO:0042772	0.325	0.948	1	7	DNA damage response, signal transduction resulting in transcription	BP	1	CDKN1A	down_VSAP_EC
GO:0060029	0.325	0.954	1	4	convergent extension involved in organogenesis	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:1905050	0.325	0.954	1	4	positive regulation of metallopeptidase activity	BP	1	MBP	up_ACOR_VSMC
GO:1902176	0.325	0.954	1	4	negative regulation of oxidative stress-induced intrinsic apoptotic	BP	1	PARK7	up_ACOR_VSMC
GO:0019216	0.325	0.943	1	101	regulation of lipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0031667	0.325	0.943	1	102	response to nutrient levels	BP	1	PCSK1N	up_APUL_EC
GO:0019430	0.325	0.951	1	5	removal of superoxide radicals	BP	1	GCH1	up_VCAV_EC
GO:0001916	0.325	0.949	1	6	positive regulation of T cell mediated cytotoxicity	BP	1	NECTIN2	up_VCAV_EC
GO:0071450	0.325	0.951	1	5	cellular response to oxygen radical	BP	1	GCH1	up_VCAV_EC
GO:0071451	0.325	0.951	1	5	cellular response to superoxide	BP	1	GCH1	up_VCAV_EC
GO:0010642	0.325	0.951	1	5	negative regulation of platelet-derived growth factor receptor signaling	BP	1	APOD	up_VCAV_EC
GO:0014003	0.325	0.951	1	5	oligodendrocyte development	BP	1	EIF2B2	up_VCAV_EC
GO:0031650	0.325	0.954	1	4	regulation of heat generation	BP	1	PTGS2	up_VCAV_EC
GO:0034141	0.325	0.951	1	5	positive regulation of toll-like receptor 3 signaling	BP	1	PELI1	up_VCAV_EC
GO:0061724	0.325	0.954	1	4	lipophagy	BP	1	SPTLC2	up_VCAV_EC
GO:0072178	0.325	0.951	1	5	nephric duct morphogenesis	BP	1	GATA3	up_VCAV_EC
GO:0009127	0.325	0.942	1	47	purine nucleoside monophosphate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0009168	0.325	0.942	1	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0050900	0.325	0.943	1	89	leukocyte migration	BP	1	HOXA7	up_VFEM_EC
GO:2000146	0.325	0.942	1	92	negative regulation of cell motility	BP	1	HOXA7	up_VFEM_EC
GO:0032438	0.325	0.954	1	4	melanosome organization	BP	1	HPS4	up_VSAP_EC
GO:0048753	0.325	0.954	1	4	pigment granule organization	BP	1	HPS4	up_VSAP_EC
GO:0009416	0.325	0.943	1	88	response to light stimulus	BP	1	NETO1	up_VSAP_VSMC
GO:0097164	0.325120667	0.89027	2	44	ammonium ion metabolic process	BP	1	AZIN2,PRKCD	up_ACOR_EC
GO:0007399	0.326	0.725	57	564	nervous system development	BP	1	FZD1,THRB,EMX2,PEX7,PCDH19,SEZ6L,CDON,WNT11,WASF3,AMIGO1,LRRN3,IRX5,SLIT2,HOXD3,SLC6A4,ABL1,DLL1,FUZ,KLF15,PLXNA4,ZBTB16,RARG,PLPP3,AMBRA1,ZFP36L1,IRX3,ZEB1,CTNS,SULF2,SHOX2,RTN4RL1,HOXC10,LRP4,DPYSL2,GDPD5,DAGLB,SMG9,MCPH1,KIF27,FBXO7,NTN4,NR2F6,KDM2B,NFIB,CYB5D2,CDNF,PQBP1,TTL,QARS,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,TGFBR2,CITED2,OGN	up_VSAP_EC
GO:0051347	0.326	0.773	13	182	positive regulation of transferase activity	BP	1	VEGFA,PTPN11,TRIB3,TNIK,ADAM17,MAGED1,CTNNB1,LYN,MMD,VLDLR,SH3GLB1,PAK2,MADD	down_VSAP_EC

GO:0043087	0.326	0.788	10	83	regulation of GTPase activity	BP	1	USP6NL,EVI5L,PKP4,CHN2,F2RL1,SGSM2,CCL5,SBF2,SH3BP4,BVES	up_ACOR_VSMC
GO:0023061	0.326	0.805	7	95	signal release	BP	1	NR1H4,PTPN11,HIF1A,GSK3B,REST,RAB11FIP1,INHBA	down_VSAP_EC
GO:0106106	0.326	0.817	6	48	cold-induced thermogenesis	BP	1	LEP,PLCL1,GJA1,PPARGC1A,PLAC8B,IL18R1	up_ACOR_VSMC
GO:0120161	0.326	0.817	6	48	regulation of cold-induced thermogenesis	BP	1	LEP,PLCL1,GJA1,PPARGC1A,PLAC8B,IL18R1	up_ACOR_VSMC
GO:0009142	0.326	0.827	5	46	nucleoside triphosphate biosynthetic process	BP	1	CYC1,ATP5F1A,ENSCAFG00000013366,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0002703	0.326	0.841	4	47	regulation of leukocyte mediated immunity	BP	1	FAM49B,PVR,TFRC,LYN	down_VSAP_EC
GO:0022604	0.326	0.838	4	122	regulation of cell morphogenesis	BP	1	PLXNA4,BVES,CDC42EP5,KANK1	up_AFEM_EC
GO:0051651	0.326	0.844	4	31	maintenance of location in cell	BP	1	MORC3,CIZ1,FTL,TAF8	up_VSAP_EC
GO:0042221	0.326	0.87	3	1012	response to chemical	BP	1	CITED2,RAB11B,HSD3B7	down_VPOR_EC
GO:0090304	0.326	0.884	3	1694	nucleic acid metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0008585	0.326	0.864	3	24	female gonad development	BP	1	KIT,TIPARP,EIF2B2	up_VCAV_EC
GO:0046545	0.326	0.864	3	24	development of primary female sexual	BP	1	KIT,TIPARP,EIF2B2	up_VCAV_EC
GO:0045746	0.326	0.896	2	14	negative regulation of Notch signaling pathway	BP	1	MMP14,BEND6	down_ACOR_VSMC
GO:0030101	0.326	0.897	2	12	natural killer cell activation	BP	1	LEP,IL18R1	up_ACOR_VSMC
GO:0007519	0.326	0.89	2	49	skeletal muscle tissue development	BP	1	DLL1,BVES	up_AFEM_EC
GO:0043433	0.326	0.889	2	49	negative regulation of DNA-binding transcription factor activity	BP	1	CMKLR1,CYLD	up_AFEM_EC
GO:0051241	0.326	0.892	2	336	negative regulation of multicellular organismal	BP	1	TBX5,NR1H4	up_VPUL_EC
GO:0006308	0.326	0.947	1	8	DNA catabolic process	BP	1	FBH1	down_VCAV_EC
GO:0001816	0.326	0.944	1	194	cytokine production	BP	1	HDAC7	down_VPOR_EC
GO:0006810	0.326	0.968	1	1244	transport	BP	1	JUP	down_VFEM_VSMC
GO:0010592	0.326	0.948	1	7	positive regulation of lamellipodium assembly	BP	1	FSCN1	down_VSAP_EC
GO:0046784	0.326	0.949	1	6	viral mRNA export from host cell nucleus	BP	1	DDX39B	down_VSAP_EC
GO:0033006	0.326	0.948	1	7	regulation of mast cell activation involved in	BP	1	LYN	down_VSAP_EC
GO:0043304	0.326	0.948	1	7	regulation of mast cell degranulation	BP	1	LYN	down_VSAP_EC
GO:0044788	0.326	0.949	1	6	modulation by host of viral process	BP	1	APOE	down_VSAP_EC
GO:0002029	0.326	0.954	1	4	desensitization of G protein-coupled receptor signaling pathway	BP	1	HTR2B	up_ACOR_VSMC
GO:2001034	0.326	0.954	1	4	positive regulation of double-strand break repair via nonhomologous	BP	1	PARP9	up_ACOR_VSMC
GO:0022401	0.326	0.954	1	4	negative adaptation of signaling pathway	BP	1	HTR2B	up_ACOR_VSMC
GO:0044770	0.326	0.943	1	161	cell cycle phase transition	BP	1	TAOK1	up_AORT_EC
GO:0010975	0.326	0.942	1	103	regulation of neuron projection development	BP	1	NTRK2	up_APUL_EC
GO:0033169	0.326	0.958	1	3	histone H3-K9 demethylation	BP	1	KDM3A	up_VCAV_EC
GO:0044282	0.326	0.942	1	89	small molecule catabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0033280	0.326	0.953	1	4	response to vitamin D	BP	1	BGLAP	up_VSAP_EC
GO:2000242	0.32608396	0.94368	1	15	negative regulation of reproductive process	BP	1	ARHGDIB	up_ACOR_EC
GO:0060421	0.326181494	0.9439	1	14	positive regulation of heart growth	BP	1	TBX5	up_ACOR_EC
GO:0031960	0.32619279	0.94364	1	15	response to corticosteroid	BP	1	AQP1	up_ACOR_EC
GO:0051384	0.32619279	0.94364	1	15	response to glucocorticoid	BP	1	AQP1	up_ACOR_EC
GO:0090288	0.326204179	0.88965	2	44	negative regulation of cellular response to growth factor stimulus	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC

GO:0008152	0.327	0.704	316	3714	metabolic process	BP	1	FADS2,ELK3,SCD,ACSL3,PRPSAP1,SQLE,FADS1,HMGB1,MCM6,RNPS1,LSS,SREBF1,ACLY,ARSI,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,PTBP1,ILF3,DDX39A,CBX5,ENSCAFG00000016095,PPRC1,USP4,SF3B2,BCAT1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPUL1,EDC3,NNT,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,SRSF2,RRM1,THOP1,MED17,U2AF2,INTS7,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,HOXA3,PPM1G,RRBP1,SNRPB2,TOP3A,TRIP13,PPP1R15B,SF1,PARPBP,POLA2,MPDU1,SRRT,GINS4,NOP56,CTDNEP1,RAD54L,POLE,DDX23,HSPA9,NAB2,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,XYLT1,FANCD2,U2AF1,TIMELESS,THRAP3,TRUB2,ENSCAFG00000018572,FAM129B,TCEA1,NF2,PFAS,EDC4,AURKB,NONO,MMP14,HNRNPL,TK1,CDKN2C,TOPBP1,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,SFSWAP,PCNA,DHX33,HOXA7,SMG9,TONSL,ARG2,MCM10,SF3B4,PHF5A,UHRF1,CKS2,PDCD2,HOXC10,RNF152,DIS3,TKT,GMNN,DHCR24,BRCA1,NOC4L,MV	down_ACOR_VSMC
GO:0051234	0.327	0.712	108	1283	establishment of localization	BP	1	HCLS1,GBP5,KIT,SELE,CXCL8,CP,OSBPL9,CALCRL,TNFAIP3,ATP8A1,LRRC8D,MX2,PDGFB,TMEM173,ATP2B1,EXOC3L2,RELN,PDE4D,IWS1,MEF2C,FERMT1,CHD7,SLC35A3,TLR4,QKI,STC1,GATA3,EDN1,RAB11A,KIF3C,APLNR,RAB27A,SLC39A8,EXOC6,CTTNBP2NL,SNCAIP,SLC49A3,IRF8,SLCO2A1,PIK3C2A,PPP3CA,YES1,SLC38A1,ARG2,NECTIN2,HOOK3,SNAP23,LRRC8C,HHEX,RAB6A,SPNS3,CAV2,BMP2K,RALBP1,SCAMP1,RSC1A1,PDZD8,ANKRD50,ABCA1,KCNJ3,OSBPL6,ELMO1,SNX2,SLCO3A1,MCC,THOC1,SH3GLB1,AKAP12,APOD,CENPC,SLC2A3,KCNJ2,EXOC5,CD200,SLC25A25,FES,HIST1H1A,EHD4,PLCG2,CTDSPL2,CREB1,PAN3,GCC2,STX11,SMG7,VPS54,HMGB1,TBC1D1,NOS2,PMAIP1,NUP133,SPTBN4,RIPK1,CHIC2,MCU,DNAJC13,ZW10,HIF1A,IPO11,ALS2,LMTK2,DOP1B,ENSCAFG00000002015,SHROOM2,ATP2A1,RABGAP1,PEAR1,USP6NL	up_VCAV_EC
GO:0010959	0.327	0.797	8	79	regulation of metal ion transport	BP	1	NEDD4,HOXA3,CAV1,SLC30A1,NKAIN1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0000956	0.327	0.815	6	55	nuclear-transcribed mRNA catabolic process	BP	1	TENT2,CNOT6,PAN3,CNOT7,SMG7,DCP2	up_VCAV_EC
GO:0016202	0.327	0.828	5	39	regulation of striated muscle tissue	BP	1	CDON,DLL1,SAV1,SHOX2,FLOT1	up_VSAP_EC
GO:0035282	0.327	0.843	4	30	segmentation	BP	1	AXIN2,DLL1,OSR1,IRX3	up_VSAP_EC
GO:0042592	0.327	0.862	3	522	homeostatic process	BP	1	NR1H4,HOXA3,PLCL1	up_APUL_EC
GO:0035306	0.327	0.863	3	24	positive regulation of dephosphorylation	BP	1	PPP2R5A,MEF2C,BMP2	up_VCAV_EC
GO:0042310	0.327	0.865	3	21	vasoconstriction	BP	1	CHRM1,TBXA2R,AGTR1	up_VSAP_EC
GO:0097756	0.327	0.865	3	21	negative regulation of blood vessel diameter	BP	1	CHRM1,TBXA2R,AGTR1	up_VSAP_EC
GO:1903391	0.327	0.864	3	21	regulation of adherens junction organization	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0019083	0.327	0.893	2	19	viral transcription	BP	1	SMARCA4,REST	down_VSAP_EC
GO:2000785	0.327	0.894	2	16	regulation of autophagosome assembly	BP	1	RALB,SH3GLB1	up_VCAV_EC
GO:0048812	0.327	0.889	2	151	neuron projection morphogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0042127	0.327	0.893	2	452	regulation of cell proliferation	BP	1	EYA1,SHOX2	up_VFEM_VSMC
GO:0042493	0.327	0.944	1	178	response to drug	BP	1	GABPA	down_AFEM_EC
GO:2000171	0.327	0.946	1	8	negative regulation of dendrite development	BP	1	TLX2	down_VCAV_EC
GO:0046716	0.327	0.949	1	6	muscle cell cellular homeostasis	BP	1	HIF1A	down_VSAP_EC

GO:0036490	0.327	0.949	1	6	regulation of translation in response to endoplasmic reticulum	BP	1	SESN2	down_VSAP_EC
GO:0046365	0.327	0.947	1	7	monosaccharide catabolic process	BP	1	GALE	down_VSAP_EC
GO:0006521	0.327	0.953	1	4	regulation of cellular amino acid metabolic	BP	1	PARK7	up_ACOR_VSMC
GO:0007220	0.327	0.953	1	4	Notch receptor processing	BP	1	PSEN1	up_ACOR_VSMC
GO:0030388	0.327	0.953	1	4	fructose 1,6-bisphosphate metabolic process	BP	1	PFKL	up_ACOR_VSMC
GO:0032287	0.327	0.953	1	4	peripheral nervous system myelin	BP	1	SH3TC2	up_ACOR_VSMC
GO:0086069	0.327	0.953	1	4	bundle of His cell to Purkinje myocyte	BP	1	JUP	up_ACOR_VSMC
GO:0072001	0.327	0.942	1	104	renal system development	BP	1	NPNT	up_APUL_EC
GO:0045019	0.327	0.95	1	5	negative regulation of nitric oxide biosynthetic	BP	1	CD34	up_VCAV_EC
GO:1904406	0.327	0.95	1	5	negative regulation of nitric oxide metabolic	BP	1	CD34	up_VCAV_EC
GO:0046949	0.327	0.949	1	6	fatty-acyl-CoA biosynthetic process	BP	1	ELOVL7	up_VCAV_EC
GO:0044092	0.327	0.945	1	270	negative regulation of molecular function	BP	1	LIMK1	up_VCAV_VSMC
GO:0008016	0.327	0.941	1	48	regulation of heart contraction	BP	1	SEMA3A	up_VPOR_EC
GO:0072522	0.327	0.942	1	91	purine-containing compound biosynthetic	BP	1	ADCY3	up_VFEM_EC
GO:1901361	0.327	0.943	1	154	organic cyclic compound catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:1901342	0.327	0.942	1	114	regulation of vasculature development	BP	1	CCL24	up_VPUL_EC
GO:0043576	0.327	0.953	1	4	regulation of respiratory gaseous exchange	BP	1	PASK	up_VSAP_EC
GO:0043650	0.327	0.953	1	4	dicarboxylic acid biosynthetic process	BP	1	GOT1	up_VSAP_EC
GO:0034638	0.327	0.953	1	4	phosphatidylcholine catabolic process	BP	1	ENPP2	up_VSAP_EC
GO:0031396	0.327	0.942	1	90	regulation of protein ubiquitination	BP	1	CAV1	up_VSAP_VSMC
GO:0048646	0.327601076	0.77923	11	349	anatomical structure formation involved in morphogenesis	BP	1	MYOZ2,TMOD1,SOX9,AQP1,ENSCAFG00000004331,FZD5,ACTN2,ESM1,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0032270	0.328	0.731	42	479	positive regulation of cellular protein metabolic process	BP	1	TEK,HCLS1,KIT,PPP2R5A,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,RELN,TLR4,GATA3,EDN1,RALB,APLNR,NEDD9,PELI1,YES1,CASP8,MTOR,MAP3K3,BMP2,SLK,PROX1,MADD,PAK2,PRKD2,TLR3,NCK1,PTGS2,MMD,RAPGEF2,BCL10,TAOK1,HMGB1,PMAIP1,RIPK1,PDGFD,UBE2D1,JCAD,ARHGEF2,CDON	up_VCAV_EC
GO:0031401	0.328	0.754	20	358	positive regulation of protein modification process	BP	1	NOTCH2,PDGFRB,PRNP,GLIPR2,BMPR1A,CLIP3,AKT2,CSPG4,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0071375	0.328	0.798	8	68	cellular response to peptide hormone stimulus	BP	1	GOT1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0034329	0.328	0.805	7	60	cell junction assembly	BP	1	WNT11,FAM107A,ABL1,HDAC7,CLDN1,ACVRL1,FLOT1	up_VSAP_EC
GO:0010001	0.328	0.814	6	54	glial cell differentiation	BP	1	RELN,TLR4,EIF2B2,MTOR,BMP2,MMP24	up_VCAV_EC
GO:0007411	0.328	0.839	4	45	axon guidance	BP	1	KIF5B,NEO1,EXT1,NRP1	down_VSAP_EC
GO:0097485	0.328	0.839	4	45	neuron projection guidance	BP	1	KIF5B,NEO1,EXT1,NRP1	down_VSAP_EC
GO:0080090	0.328	0.882	3	1734	regulation of primary metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0010628	0.328	0.861	3	527	positive regulation of gene expression	BP	1	NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0006081	0.328	0.862	3	27	cellular aldehyde metabolic process	BP	1	BMP2,KDM3A,ALDH1A3	up_VCAV_EC
GO:0051336	0.328	0.858	3	251	regulation of hydrolase activity	BP	1	ENSCAFG00000002015,ABHD5,ENSCAFG00000032731	up_VPOR_EC
GO:0035924	0.328	0.863	3	21	cellular response to vascular endothelial growth factor stimulus	BP	1	DLL1,CCBE1,GAS1	up_VSAP_EC
GO:0000469	0.328	0.897	2	12	cleavage involved in rRNA processing	BP	1	EXOSC7,RCL1	up_VSAP_EC

GO:0061178	0.328	0.896	2	12	regulation of insulin secretion involved in cellular response to	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0009152	0.328	0.941	1	80	purine ribonucleotide biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0021756	0.328	0.948	1	6	striatum development	BP	1	INHBA	down_VSAP_EC
GO:0036119	0.328	0.948	1	6	response to platelet-derived growth factor	BP	1	YES1	down_VSAP_EC
GO:0036120	0.328	0.948	1	6	cellular response to platelet-derived growth	BP	1	YES1	down_VSAP_EC
GO:2000406	0.328	0.948	1	6	positive regulation of T cell migration	BP	1	ADAM17	down_VSAP_EC
GO:0001967	0.328	0.953	1	4	suckling behavior	BP	1	APP	up_ACOR_VSMC
GO:0009445	0.328	0.953	1	4	putrescine metabolic process	BP	1	AZIN2	up_ACOR_VSMC
GO:0010715	0.328	0.953	1	4	regulation of extracellular matrix disassembly	BP	1	DDR2	up_ACOR_VSMC
GO:0042053	0.328	0.953	1	4	regulation of dopamine metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0042069	0.328	0.953	1	4	regulation of catecholamine metabolic	BP	1	PARK7	up_ACOR_VSMC
GO:0042118	0.328	0.953	1	4	endothelial cell activation	BP	1	TGFBR1	up_ACOR_VSMC
GO:1901723	0.328	0.953	1	4	negative regulation of cell proliferation involved in kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:0045892	0.328	0.946	1	328	negative regulation of transcription, DNA-	BP	1	ESR1	up_AORT_VSMC
GO:1902679	0.328	0.946	1	329	negative regulation of RNA biosynthetic process	BP	1	ESR1	up_AORT_VSMC
GO:1903507	0.328	0.946	1	329	negative regulation of nucleic acid-templated	BP	1	ESR1	up_AORT_VSMC
GO:0035743	0.328	0.95	1	5	CD4-positive, alpha-beta T cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:0051093	0.328	0.945	1	273	negative regulation of developmental process	BP	1	LRRC17	up_VCAV_VSMC
GO:0006520	0.328	0.942	1	114	cellular amino acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0000052	0.328	0.953	1	4	citrulline metabolic process	BP	1	ASS1	up_VSAP_EC
GO:0045324	0.328	0.953	1	4	late endosome to vacuole transport	BP	1	VPS36	up_VSAP_EC
GO:0007214	0.328	0.953	1	4	gamma-aminobutyric acid signaling pathway	BP	1	GABBR2	up_VSAP_EC
GO:0050790	0.328024419	0.7629	16	532	regulation of catalytic activity	BP	1	CDH3,PKIB,PCSK1N,ENSCAFG00000004331,FZD5,IFI6,DUSP26,DYNC1I1,PAK3,CST3,LRRC15,LRRC4,PRKCD,PPP1R26,DBNDD2,CCNYL1	up_ACOR_EC
GO:0043393	0.328059802	0.8574	3	77	regulation of protein binding	BP	1	PLCL1,IFIT2,CLSTN1	up_ACOR_EC
GO:0051641	0.328274475	0.74722	25	858	cellular localization	BP	1	SH3TC2,CDH3,NR1H4,BRSK1,CALY,KCNB1,EDEM2,AGRN,DYNC1I1,PLS1,ACTN2,TRIM8,PREB,DCLK2,MAVS,LRRC15,LRP4,LRRC4,CHMP4B,TP53INP2,VPS16,ABCB9,NRP1,HM13,PRKCD	up_ACOR_EC
GO:0006801	0.328275313	0.94286	1	15	superoxide metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0048729	0.32852918	0.80167	7	209	tissue morphogenesis	BP	1	BRSK1,SOX9,FZD5,FOXC2,TBX5,CLSTN1,NRP1	up_ACOR_EC
GO:0048667	0.328619796	0.82181	5	140	cell morphogenesis involved in neuron	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1	up_ACOR_EC
GO:0010608	0.329	0.765	15	154	posttranscriptional regulation of gene expression	BP	1	ILF3,EIF4A3,HNRNPD,PPP1R15B,SRRT,RAN,CAV1,THRAP3,TRUB2,FASTKD3,EIF5A,NCL,RBM14,NOLC1,PUM3	down_ACOR_VSMC
GO:0007015	0.329	0.768	14	144	actin filament organization	BP	1	FSCN1,CAPG,LIMA1,NF2,STMN1,RAC1,EMP2,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,ARPC1B,ARHGEF2	down_ACOR_VSMC
GO:0042692	0.329	0.776	12	105	muscle cell differentiation	BP	1	ACTN2,BMP4,FGFR2,NEBL,DMPK,NPNT,SMARCD3,TBX5,FRS2,EDN1,BVES,MYOZ2	up_ACOR_VSMC
GO:0001837	0.329	0.839	4	48	epithelial to mesenchymal transition	BP	1	TGFBR1,HIF1A,STRAP,GSK3B	down_VSAP_EC
GO:0030282	0.329	0.84	4	37	bone mineralization	BP	1	MEF2C,BMP2,BMP2K,HIF1A	up_VCAV_EC
GO:0000422	0.329	0.86	3	34	autophagy of mitochondrion	BP	1	HIF1A,CDC37,HTT	down_VSAP_EC
GO:0042129	0.329	0.859	3	35	regulation of T cell proliferation	BP	1	CTNNB1,TFRC,SDC4	down_VSAP_EC

GO:0061726	0.329	0.86	3	34	mitochondrion disassembly	BP	1	HIF1A,CDC37,HTT	down_VSAP_EC
GO:0051145	0.329	0.863	3	21	smooth muscle cell differentiation	BP	1	BMP4,FGFR2,NPNT	up_ACOR_VSMC
GO:0010596	0.329	0.863	3	21	negative regulation of endothelial cell migration	BP	1	SLIT2,TBXA2R,ACVRL1	up_VSAP_EC
GO:0015698	0.329	0.89	2	24	inorganic anion transport	BP	1	PRNP,CLIC4	down_VCAV_EC
GO:0008333	0.329	0.892	2	19	endosome to lysosome transport	BP	1	HOOK3,TRAK1	down_VSAP_EC
GO:0002067	0.329	0.896	2	12	glandular epithelial cell differentiation	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0009628	0.329	0.89	2	302	response to abiotic stimulus	BP	1	PCSK1N,HOXA1	up_APUL_EC
GO:2000145	0.329	0.889	2	279	regulation of cell motility	BP	1	HOXA7,TIAM1	up_VFEM_EC
GO:0010647	0.329	0.892	2	460	positive regulation of cell communication	BP	1	NETO1,SHOX2	up_VFEM_VSMC
GO:0008544	0.329	0.941	1	75	epidermis development	BP	1	HOXA7	down_ACOR_EC
GO:0010769	0.329	0.941	1	69	regulation of cell morphogenesis involved	BP	1	PDPN	down_ACOR_EC
GO:0060326	0.329	0.941	1	84	cell chemotaxis	BP	1	LYN	down_ACOR_EC
GO:0002507	0.329	0.947	1	7	tolerance induction	BP	1	LYN	down_VSAP_EC
GO:0045815	0.329	0.948	1	6	positive regulation of gene expression,	BP	1	CTNNB1	down_VSAP_EC
GO:0090208	0.329	0.948	1	6	positive regulation of triglyceride metabolic	BP	1	ABHD5	down_VSAP_EC
GO:0010559	0.329	0.948	1	6	regulation of glycoprotein biosynthetic process	BP	1	CTNNB1	down_VSAP_EC
GO:0055083	0.329	0.948	1	6	monovalent inorganic anion homeostasis	BP	1	ENPP1	down_VSAP_EC
GO:1903018	0.329	0.948	1	6	regulation of glycoprotein metabolic process	BP	1	CTNNB1	down_VSAP_EC
GO:0001773	0.329	0.953	1	4	myeloid dendritic cell activation	BP	1	PSEN1	up_ACOR_VSMC
GO:0042026	0.329	0.952	1	4	protein refolding	BP	1	B2M	up_ACOR_VSMC
GO:0043011	0.329	0.953	1	4	myeloid dendritic cell differentiation	BP	1	PSEN1	up_ACOR_VSMC
GO:0097202	0.329	0.952	1	4	activation of cysteine-type endopeptidase activity	BP	1	PERP	up_ACOR_VSMC
GO:0050708	0.329	0.941	1	101	regulation of protein secretion	BP	1	NR1H4	up_APUL_EC
GO:0072507	0.329	0.941	1	103	divalent inorganic cation homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0040007	0.329	0.944	1	276	growth	BP	1	LIMK1	up_VCAV_VSMC
GO:0050817	0.329	0.941	1	50	coagulation	BP	1	SLC7A11	up_VPOR_EC
GO:0007423	0.329	0.942	1	155	sensory organ development	BP	1	CYP26B1	up_VPOR_VSMC
GO:0032990	0.329	0.942	1	167	cell part morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0060322	0.329	0.943	1	193	head development	BP	1	SLIT2	up_VPUL_VSMC
GO:0035878	0.329	0.953	1	4	nail development	BP	1	PRKAB1	up_VSAP_EC
GO:1904683	0.329	0.953	1	4	regulation of metalloendopeptidase	BP	1	RECK	up_VSAP_EC
GO:2000647	0.329	0.953	1	4	negative regulation of stem cell proliferation	BP	1	FBLN1	up_VSAP_EC
GO:2001225	0.329	0.953	1	4	regulation of chloride transport	BP	1	GABRE	up_VSAP_EC
GO:0030260	0.329160811	0.94253	1	15	entry into host cell	BP	1	TRIM8	up_ACOR_EC
GO:0044409	0.329160811	0.94253	1	15	entry into host	BP	1	TRIM8	up_ACOR_EC
GO:0051806	0.329160811	0.94253	1	15	entry into cell of other organism involved in	BP	1	TRIM8	up_ACOR_EC
GO:0051828	0.329160811	0.94253	1	15	entry into other organism involved in symbiotic	BP	1	TRIM8	up_ACOR_EC
GO:0052548	0.329923774	0.85607	3	80	regulation of endopeptidase activity	BP	1	PCSK1N,IFI6,CST3	up_ACOR_EC
GO:0048871	0.33	0.775	12	120	multicellular organismal homeostasis	BP	1	ADGRF5,PRCP,CD34,TLR4,STMN1,EXOC5,LDB2,PTGS2,VPS54,ADIPOR2,NR1D2,KDM3A	up_VCAV_EC
GO:0030031	0.33	0.777	11	155	cell projection assembly	BP	1	EXOC5,FSCN1,DPYSL3,RPGR,DYNLL1,TNIK,ANLN,KLF5,HTT,DISC1,NRP1	down_VSAP_EC

GO:0007519	0.33	0.813	6	49	skeletal muscle tissue development	BP	1	CDON,DLL1,GTF3C5,SHOX2,FLOT1,CITED2	up_VSAP_EC
GO:1903034	0.33	0.825	5	40	regulation of response to wounding	BP	1	KLKB1,HPSE,F2RL1,RTN4RL1,MAP2K2	up_VSAP_EC
GO:0022406	0.33	0.859	3	35	membrane docking	BP	1	EXOC5,MSN,ESYT3	down_VSAP_EC
GO:0010464	0.33	0.862	3	21	regulation of mesenchymal cell	BP	1	BMP4,FGFR2,CLSTN1	up_ACOR_VSMC
GO:0002237	0.33	0.856	3	85	response to molecule of bacterial origin	BP	1	CD40,TBXA2R,ADAM17	up_AFEM_EC
GO:0046777	0.33	0.856	3	86	protein autophosphorylation	BP	1	HCK,GREM1,CAMK2A	up_AFEM_EC
GO:0032608	0.33	0.89	2	24	interferon-beta production	BP	1	RNF216,MAVS	down_VCAV_EC
GO:0044087	0.33	0.89	2	339	regulation of cellular component biogenesis	BP	1	CCL24,FLRT3	up_VPUL_EC
GO:0001910	0.33	0.895	2	12	regulation of leukocyte mediated cytotoxicity	BP	1	F2RL1,PPP3CB	up_VSAP_EC
GO:0032024	0.33	0.895	2	12	positive regulation of insulin secretion	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0090277	0.33	0.895	2	12	positive regulation of peptide hormone	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:1902533	0.33	0.889	2	271	positive regulation of intracellular signal	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0002237	0.33	0.941	1	85	response to molecule of bacterial origin	BP	1	LYN	down_ACOR_EC
GO:0060272	0.33	0.946	1	7	embryonic skeletal joint morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:1900017	0.33	0.948	1	6	positive regulation of cytokine production involved in inflammatory	BP	1	GBP5	down_VSAP_EC
GO:0001774	0.33	0.952	1	4	microglial cell activation	BP	1	APP	up_ACOR_VSMC
GO:0010819	0.33	0.952	1	4	regulation of T cell chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0010820	0.33	0.952	1	4	positive regulation of T cell chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0030238	0.33	0.952	1	4	male sex determination	BP	1	PTGDR	up_ACOR_VSMC
GO:0002269	0.33	0.952	1	4	leukocyte activation involved in inflammatory	BP	1	APP	up_ACOR_VSMC
GO:0002520	0.33	0.944	1	279	immune system development	BP	1	HOXA9	up_AFEM_VSMC
GO:0051222	0.33	0.941	1	103	positive regulation of protein transport	BP	1	NR1H4	up_APUL_EC
GO:0032460	0.33	0.949	1	5	negative regulation of protein oligomerization	BP	1	RIOK3	up_VCAV_EC
GO:0032463	0.33	0.949	1	5	negative regulation of protein	BP	1	RIOK3	up_VCAV_EC
GO:0055026	0.33	0.949	1	5	negative regulation of cardiac muscle tissue	BP	1	BMP2	up_VCAV_EC
GO:0006560	0.33	0.952	1	4	proline metabolic process	BP	1	ENSCAFG00000016140	up_VSAP_EC
GO:0009310	0.33	0.952	1	4	amine catabolic process	BP	1	IDO2	up_VSAP_EC
GO:0048793	0.33	0.952	1	4	pronephros development	BP	1	OSR1	up_VSAP_EC
GO:0060462	0.33	0.952	1	4	lung lobe development	BP	1	TGFBR2	up_VSAP_EC
GO:0060463	0.33	0.952	1	4	lung lobe morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0035860	0.33	0.952	1	4	glial cell-derived neurotrophic factor	BP	1	SULF2	up_VSAP_EC
GO:0050769	0.33	0.941	1	95	positive regulation of neurogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0032729	0.330835622	0.9419	1	15	positive regulation of interferon-gamma	BP	1	FZD5	up_ACOR_EC

GO:0031326	0.331	0.709	104	1176	regulation of cellular biosynthetic process	BP	1	ELK3,ACSL3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,SMC1A,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,PPP1R15B,SRRT,CTDNEP1,NAB2,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,NOLC1,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,HMGN1,CCT4,SIX4,NECAB3,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:0051172	0.331	0.72	58	663	negative regulation of nitrogen compound metabolic process	BP	1	EDNRB,HCLS1,CDA,TNFAIP3,TNIP1,PDGFB,CD34,PDE4D,MEF2C,ATF3,DLL4,RAPGEF1,WWP1,TLR4,GATA3,EDN1,HOXB8,SOX18,PPP3CA,TENT2,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,SH3BP5,ENC1,PROX1,UHRF2,MDFI,HMBOX1,PAK2,THOC1,SWAP70,SMARCA4,APOD,NCK1,TIMELESS,PTGS2,TCERG1,CREB1,BASP1,CNOT7,ENSCAFG00000002897,HMGB1,BLM,RAD17,MTA2,KDM5A,KDM3A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,IVNS1ABP,ELK3	up_VCAV_EC
GO:0051649	0.331	0.734	34	630	establishment of localization in cell	BP	1	SNX18,PRNP,TMEM230,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,MICALL2,SNUPN,SSR2,SCP2,THY1,CLTB,SSR3,PEX5,GLI3,PARK7,YIF1A,CYBA,IFT57,MAVS,CDH2,TOM1,MGARP,RAB7B,SEC61B,HM13,ARHGAP1,EVI5L,LONP2,RAC2,ANKRD54,SEC61A1,BRSK1	down_VCAV_EC
GO:0019637	0.331	0.737	31	342	organophosphate metabolic process	BP	1	ACSL3,PRPSAP1,ACLY,HMGCR,NNT,RRM1,RAN,CDK1,PFAS,RNASEH2B,TKT,MVD,ELOVL1,CYCS,PDXP,VAC14,ELOVL6,FDFT1,CYC1,ATP5F1A,DCK,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,PGD,NUS1,GK5,CTPS1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:2000112	0.331	0.818	6	1119	regulation of cellular macromolecule biosynthetic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0045619	0.331	0.824	5	44	regulation of lymphocyte differentiation	BP	1	HMGB1,PRELID1,MMP14,HMGB3,TOX	down_ACOR_VSMC
GO:0051701	0.331	0.823	5	45	interaction with host	BP	1	NEDD4,CAV1,TRIM35,SMC3,DDX39B	down_ACOR_VSMC
GO:0042157	0.331	0.823	5	51	lipoprotein metabolic process	BP	1	ZDHHC22,HHAT,ABCA1,APOD,ZDHHC6	up_VCAV_EC
GO:0006638	0.331	0.84	4	30	neutral lipid metabolic process	BP	1	LIPC,INSIG2,LMF1,ABHD16A	up_VSAP_EC
GO:0006639	0.331	0.84	4	30	acylglycerol metabolic process	BP	1	LIPC,INSIG2,LMF1,ABHD16A	up_VSAP_EC
GO:0050851	0.331	0.858	3	34	antigen receptor-mediated signaling	BP	1	PTPN2,EIF2B1,LYN	down_VSAP_EC
GO:0006366	0.331	0.861	3	583	transcription by RNA polymerase II	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0060284	0.331	0.887	2	212	regulation of cell development	BP	1	LYN,PDPN	down_ACOR_EC
GO:0006636	0.331	0.893	2	14	unsaturated fatty acid biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0061515	0.331	0.889	2	24	myeloid cell development	BP	1	NOTCH2,FBN1	down_VCAV_EC
GO:1900407	0.331	0.889	2	24	regulation of cellular response to oxidative	BP	1	PARK7,FUT8	down_VCAV_EC
GO:0032350	0.331	0.895	2	12	regulation of hormone metabolic process	BP	1	DKKL1,STC2	up_ACOR_VSMC
GO:0034103	0.331	0.895	2	12	regulation of tissue remodeling	BP	1	LEP,GJA1	up_ACOR_VSMC
GO:0071825	0.331	0.895	2	12	protein-lipid complex subunit organization	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0071827	0.331	0.895	2	12	plasma lipoprotein particle organization	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0120033	0.331	0.895	2	12	negative regulation of plasma membrane bounded cell projection	BP	1	EVI5L,EVL	up_ACOR_VSMC
GO:0008361	0.331	0.886	2	50	regulation of cell size	BP	1	PRR16,PLXNA4	up_AFEM_EC

GO:0090659	0.331	0.895	2	12	walking behavior	BP	1	CHD7,SPTBN4	up_VCAV_EC
GO:0023056	0.331	0.891	2	462	positive regulation of signaling	BP	1	NETO1,SHOX2	up_VFEM_VSMC
GO:0072079	0.331	0.895	2	12	nephron tubule formation	BP	1	OSR1,IRX3	up_VSAP_EC
GO:0007167	0.331	0.888	2	274	enzyme linked receptor protein signaling pathway	BP	1	CAV1,FGF5	up_VSAP_VSMC
GO:0031346	0.331	0.94	1	73	positive regulation of cell projection organization	BP	1	LYN	down_ACOR_EC
GO:0045732	0.331	0.94	1	78	positive regulation of protein catabolic process	BP	1	NEDD4	down_ACOR_EC
GO:0051346	0.331	0.94	1	78	negative regulation of hydrolase activity	BP	1	MYO1D	down_ACOR_EC
GO:0003071	0.331	0.949	1	5	renal system process involved in regulation of systemic arterial blood	BP	1	EMP2	down_ACOR_VSMC
GO:0030855	0.331	0.942	1	183	epithelial cell differentiation	BP	1	SRSF6	down_AFEM_EC
GO:0021544	0.331	0.945	1	8	subpallium development	BP	1	GLI3	down_VCAV_EC
GO:0030318	0.331	0.945	1	8	melanocyte differentiation	BP	1	GLI3	down_VCAV_EC
GO:0071709	0.331	0.945	1	8	membrane assembly	BP	1	CDH2	down_VCAV_EC
GO:0051173	0.331	0.957	1	874	positive regulation of nitrogen compound	BP	1	MOSPD1	down_VFEM_EC
GO:1900221	0.331	0.947	1	6	regulation of amyloid-beta clearance	BP	1	APOE	down_VSAP_EC
GO:0042127	0.331	0.947	1	452	regulation of cell proliferation	BP	1	TGFBR1	down_VSAP_VSMC
GO:0044058	0.331	0.952	1	4	regulation of digestive system process	BP	1	LEP	up_ACOR_VSMC
GO:0051923	0.331	0.952	1	4	sulfation	BP	1	TPST2	up_ACOR_VSMC
GO:0097484	0.331	0.952	1	4	dendrite extension	BP	1	TMEM108	up_ACOR_VSMC
GO:0046486	0.331	0.94	1	102	glycerolipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0034656	0.331	0.947	1	6	nucleobase-containing small molecule catabolic	BP	1	CDA	up_VCAV_EC
GO:0040034	0.331	0.949	1	5	regulation of development,	BP	1	GDPD5	up_VCAV_EC
GO:0051258	0.331	0.94	1	94	protein polymerization	BP	1	CDC42EP5	up_VFEM_EC
GO:0120035	0.331	0.941	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	SHOX2	up_VFEM_VSMC
GO:0001991	0.331	0.952	1	4	regulation of systemic arterial blood pressure by circulatory renin-	BP	1	F2RL1	up_VSAP_EC
GO:0003081	0.331	0.952	1	4	regulation of systemic arterial blood pressure by renin-angiotensin	BP	1	F2RL1	up_VSAP_EC
GO:0006525	0.331	0.952	1	4	arginine metabolic process	BP	1	ASS1	up_VSAP_EC
GO:0015810	0.331	0.952	1	4	aspartate transmembrane transport	BP	1	SLC25A12	up_VSAP_EC
GO:0042074	0.331	0.952	1	4	cell migration involved in gastrulation	BP	1	WNT11	up_VSAP_EC
GO:0045780	0.331	0.952	1	4	positive regulation of bone resorption	BP	1	PPARGC1B	up_VSAP_EC
GO:0045988	0.331	0.952	1	4	negative regulation of striated muscle	BP	1	KCNE3	up_VSAP_EC
GO:0046852	0.331	0.952	1	4	positive regulation of bone remodeling	BP	1	PPARGC1B	up_VSAP_EC
GO:0060484	0.331	0.952	1	4	lung-associated mesenchyme	BP	1	WNT11	up_VSAP_EC
GO:2000369	0.331	0.952	1	4	regulation of clathrin-dependent endocytosis	BP	1	UBQLN2	up_VSAP_EC
GO:2001212	0.331	0.952	1	4	regulation of vasculogenesis	BP	1	EMP2	up_VSAP_EC
GO:0003007	0.331	0.94	1	94	heart morphogenesis	BP	1	SHOX2	up_VSAP_VSMC

GO:1901566	0.332	0.73	37	598	organonitrogen compound biosynthetic process	BP	1	ASNS,CARS,PLOD2,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,PGAM1,PUM3,UGCG,SESN2,CHSY1,HIF1A,MRPL1,NMNAT2,GALNT1,ALDH18A1,YARS,TARS,NARS,EIF4EBP1,CNOT7,ALDOC,CTNNB1,PAPSS1,APOE,PLOD3,STT3A,EIF5,EIF2S1,EXT1,INHBA,RSL24D1,BCAT1,RPN1,CMPK1	down_VSAP_EC
GO:0018210	0.332	0.812	6	48	peptidyl-threonine modification	BP	1	GALNT3,CAMK2D,APP,PSKH1,LMTK2,INPP5K	up_ACOR_VSMC
GO:0070663	0.332	0.812	6	50	regulation of leukocyte proliferation	BP	1	LEP,BMP4,PDE5A,CD274,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0043903	0.332	0.811	6	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	CXCL8,IRF8,NECTIN2,PROX1,SMARCA4,CNOT7	up_VCAV_EC
GO:0006950	0.332	0.829	5	1102	response to stress	BP	1	NR1H4,MRC1,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0098727	0.332	0.835	4	60	maintenance of cell number	BP	1	BMPR1A,TRIM8,CDH2,FOXO3	down_VCAV_EC
GO:0000041	0.332	0.839	4	31	transition metal ion transport	BP	1	ATP7A,RAB11B,LMTK2,B2M	up_ACOR_VSMC
GO:1904659	0.332	0.838	4	36	glucose transmembrane transport	BP	1	EDN1,YES1,RSC1A1,SLC2A3	up_VCAV_EC
GO:0061077	0.332	0.859	3	25	chaperone-mediated protein folding	BP	1	FKBP11,CCT4,PPIB	down_ACOR_VSMC
GO:0045727	0.332	0.857	3	40	positive regulation of translation	BP	1	LARP6,EEF2,PYM1	down_VCAV_EC
GO:1901222	0.332	0.858	3	32	regulation of NIK/NF-kappaB signaling	BP	1	ILK,UACA,ENSCAFG00000002015	down_VSAP_EC
GO:0007189	0.332	0.861	3	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	CALCRL,ABCA1,RAPGEF2	up_VCAV_EC
GO:1901983	0.332	0.86	3	24	regulation of protein acetylation	BP	1	IWS1,GATA3,TAOK1	up_VCAV_EC
GO:0001947	0.332	0.861	3	21	heart looping	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:0061371	0.332	0.861	3	21	determination of heart left/right asymmetry	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:0032526	0.332	0.89	2	19	response to retinoic acid	BP	1	YES1,LYN	down_VSAP_EC
GO:0046426	0.332	0.889	2	20	negative regulation of JAK-STAT cascade	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:1904893	0.332	0.889	2	20	negative regulation of STAT cascade	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:0045992	0.332	0.894	2	12	negative regulation of embryonic development	BP	1	BMP4,FZD3	up_ACOR_VSMC
GO:0042446	0.332	0.893	2	14	hormone biosynthetic process	BP	1	BMP2,HIF1A	up_VCAV_EC
GO:0043067	0.332	0.891	2	479	regulation of programmed cell death	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0006778	0.332	0.894	2	12	porphyrin-containing compound metabolic	BP	1	CPOX,HMOX1	up_VSAP_EC
GO:0042168	0.332	0.894	2	12	heme metabolic process	BP	1	CPOX,HMOX1	up_VSAP_EC
GO:0048536	0.332	0.894	2	12	spleen development	BP	1	ABL1,CITED2	up_VSAP_EC
GO:0051093	0.332	0.887	2	273	negative regulation of developmental process	BP	1	HOXA9,CAV1	up_VSAP_VSMC
GO:0007033	0.332	0.94	1	82	vacuole organization	BP	1	SPG11	down_ACOR_EC
GO:0015672	0.332	0.94	1	89	monovalent inorganic cation transport	BP	1	NEDD4	down_ACOR_EC
GO:0002837	0.332	0.949	1	5	regulation of immune response to tumor cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0002418	0.332	0.949	1	5	immune response to tumor cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0002834	0.332	0.949	1	5	regulation of response to tumor cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0032042	0.332	0.947	1	6	mitochondrial DNA metabolic process	BP	1	SESN2	down_VSAP_EC
GO:0070741	0.332	0.947	1	6	response to interleukin-6	BP	1	PTPN2	down_VSAP_EC
GO:0071354	0.332	0.947	1	6	cellular response to interleukin-6	BP	1	PTPN2	down_VSAP_EC
GO:1905809	0.332	0.945	1	7	negative regulation of synapse organization	BP	1	APOE	down_VSAP_EC
GO:1905564	0.332	0.947	1	6	positive regulation of vascular endothelial cell	BP	1	ADAM17	down_VSAP_EC
GO:0001839	0.332	0.952	1	4	neural plate morphogenesis	BP	1	ENSCAFG00000006238	up_ACOR_VSMC

GO:0042033	0.332	0.952	1	4	chemokine biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0043252	0.332	0.952	1	4	sodium-independent organic anion transport	BP	1	SLCO1A2	up_ACOR_VSMC
GO:0045073	0.332	0.952	1	4	regulation of chemokine biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0045080	0.332	0.952	1	4	positive regulation of chemokine biosynthetic	BP	1	TLR3	up_ACOR_VSMC
GO:0045351	0.332	0.952	1	4	type I interferon biosynthetic process	BP	1	TLR3	up_ACOR_VSMC
GO:0050755	0.332	0.952	1	4	chemokine metabolic process	BP	1	TLR3	up_ACOR_VSMC
GO:0060681	0.332	0.952	1	4	branch elongation involved in ureteric bud	BP	1	BMP4	up_ACOR_VSMC
GO:0060900	0.332	0.952	1	4	embryonic camera-type eye formation	BP	1	FRS2	up_ACOR_VSMC
GO:0007528	0.332	0.941	1	17	neuromuscular junction development	BP	1	TNC	up_AFEM_EC
GO:0060078	0.332	0.941	1	17	regulation of postsynaptic membrane potential	BP	1	DMPK	up_AFEM_EC
GO:0099565	0.332	0.941	1	17	chemical synaptic transmission, postsynaptic	BP	1	DMPK	up_AFEM_EC
GO:0019221	0.332	0.94	1	102	cytokine-mediated signaling pathway	BP	1	NR1H4	up_APUL_EC
GO:0051604	0.332	0.94	1	102	protein maturation	BP	1	PCSK1N	up_APUL_EC
GO:0006928	0.332	0.949	1	557	movement of cell or subcellular component	BP	1	TBX5	up_APUL_VSMC
GO:0090670	0.332	0.949	1	5	RNA localization to Cajal body	BP	1	DCP2	up_VCAV_EC
GO:0090671	0.332	0.949	1	5	telomerase RNA localization to Cajal body	BP	1	DCP2	up_VCAV_EC
GO:0090672	0.332	0.949	1	5	telomerase RNA localization	BP	1	DCP2	up_VCAV_EC
GO:0090685	0.332	0.949	1	5	RNA localization to nucleus	BP	1	DCP2	up_VCAV_EC
GO:1904872	0.332	0.949	1	5	regulation of telomerase RNA localization to Cajal	BP	1	DCP2	up_VCAV_EC
GO:0070997	0.332	0.94	1	93	neuron death	BP	1	SIX1	up_VFEM_EC
GO:0071214	0.332	0.94	1	93	cellular response to abiotic stimulus	BP	1	MME	up_VFEM_EC
GO:0104004	0.332	0.94	1	93	cellular response to environmental stimulus	BP	1	MME	up_VFEM_EC
GO:0031344	0.332	0.941	1	161	regulation of cell projection organization	BP	1	SHOX2	up_VFEM_VSMC
GO:0002091	0.332	0.952	1	4	negative regulation of receptor internalization	BP	1	UBQLN2	up_VSAP_EC
GO:0090196	0.332	0.952	1	4	regulation of chemokine secretion	BP	1	F2RL1	up_VSAP_EC
GO:0046488	0.332703551	0.88592	2	44	phosphatidylinositol metabolic process	BP	1	ENSCAFG00000004331,PIGS	up_ACOR_EC
GO:0032270	0.333	0.723	49	479	positive regulation of cellular protein metabolic process	BP	1	ADRA1B,LEP,MAP3K8,MID1,HTR2B,RASSF2,MBP,SKP2,PRKAA2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,F2RL1,FAM129A,DAPK1,NRP1,PTPN22,NPNT,SMPD1,PRKCE,CCNT1,FRS2,RNF19A,PARP9,APP,PSEN1,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,MAP3K7,WFS1,ENSCAFG00000029553,PARK7,NGRN,CRKL	up_ACOR_VSMC
GO:0048646	0.333	0.73	36	349	anatomical structure formation involved in morphogenesis	BP	1	HOXA11,FZD1,HOXA7,CDON,WNT11,ACKR3,AXIN2,ENPP2,PPARGC1B,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,OSR1,FUZ,HPSE,RARG,CCBE1,MFN2,IRX3,TBXA2R,SASH1,KDM2B,NFIB,ANPEP,ACVRL1,FLOT1,PPP3CB,HMOX1,MAP2K2,TGFBR2,CITED2,LATS2	up_VSAP_EC
GO:0043436	0.333	0.738	28	303	oxoacid metabolic process	BP	1	SCD,SREBF1,ACLY,ENSCAFG00000016095,BCAT1,VARS,INSIG1,CAV1,XYLT1,PFAS,ARG2,BRCA1,ELOVL1,FARSA,SUCLG1,PPARD,AADAT,GSTO1,ELOVL6,SGPL1,RARS,CTH,PDHA1,GGH,LIPC,PGD,CTPS1,ACADL	down_ACOR_VSMC
GO:1901701	0.333	0.751	19	271	cellular response to oxygen-containing compound	BP	1	ARHGEF2,NR1H4,SERPINE1,ENPP1,PTPN11,TRIB3,SMARCA4,SESN2,MYO1C,MSN,HIF1A,PTPN2,YES1,MTDH,AGRN,GNAQ,CTNNB1,LYN,NR4A1	down_VSAP_EC
GO:0048584	0.333	0.759	16	592	positive regulation of response to stimulus	BP	1	CMKLR1,LEP,DLL1,F3,MLLT11,LMCD1,PLAGL2,GREM1,FAM53B,CLEC16A,CYLD,LGR6,NAPEPLD,CCL5,ADAM17,KANK1	up_AFEM_EC

GO:0051271	0.333	0.776	11	98	negative regulation of cellular component	BP	1	HOXA7,WNT11,C5AR2,SLIT2,CDH1,KCNE3,FUZ,RECK,TBXA2R,FBLN1,ACVRL1	up_VSAP_EC
GO:0034645	0.333	0.803	8	1546	cellular macromolecule biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,CHST7	up_VFEM_EC
GO:0051716	0.333	0.828	6	2001	cellular response to stimulus	BP	1	DKK2,LNPEP,ERC1,TAOK1,CTNNAL1,GPR155	up_AORT_EC
GO:0010038	0.333	0.81	6	62	response to metal ion	BP	1	MEF2C,PPP3CA,TJP1,ITPKB,CREB1,HIF1A	up_VCAV_EC
GO:0046883	0.333	0.811	6	49	regulation of hormone secretion	BP	1	HNF4A,SLC8B1,PASK,KCNB1,STX4,PPP3CB	up_VSAP_EC
GO:0032412	0.333	0.822	5	46	regulation of ion transmembrane	BP	1	RELN,PDE4D,MEF2C,PLCG2,RIPK1	up_VCAV_EC
GO:0010565	0.333	0.823	5	40	regulation of cellular ketone metabolic process	BP	1	INSIG2,ACACB,C1QTNF2,PDK2,LONP2	up_VSAP_EC
GO:0030490	0.333	0.837	4	35	maturation of SSU-rRNA	BP	1	NOC4L,NOP14,EMG1,NOB1	down_ACOR_VSMC
GO:2000278	0.333	0.837	4	37	regulation of DNA biosynthetic process	BP	1	PDGFB,HMBOX1,PRKD2,DCP2	up_VCAV_EC
GO:0061041	0.333	0.857	3	34	regulation of wound healing	BP	1	SERPINE1,APOE,LYN	down_VSAP_EC
GO:0021545	0.333	0.861	3	21	cranial nerve development	BP	1	EPHB1,CHD7,NAV2	up_VCAV_EC
GO:0006220	0.333	0.892	2	14	pyrimidine nucleotide metabolic process	BP	1	DCK,CTPS1	down_ACOR_VSMC
GO:0045844	0.333	0.888	2	24	positive regulation of striated muscle tissue	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0048636	0.333	0.888	2	24	positive regulation of muscle organ	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0010332	0.333	0.889	2	20	response to gamma radiation	BP	1	CRYAB,CDKN1A	down_VSAP_EC
GO:0045600	0.333	0.889	2	21	positive regulation of fat cell differentiation	BP	1	PTGS2,KLF5	down_VSAP_EC
GO:1902692	0.333	0.895	2	11	regulation of neuroblast proliferation	BP	1	CTNNA1,HIF1A	up_VCAV_EC
GO:0051049	0.333	0.89	2	479	regulation of transport	BP	1	HOXA3,NKX2-5	up_VPOR_VSMC
GO:0051130	0.333	0.888	2	342	positive regulation of cellular component	BP	1	CCL24,FLRT3	up_VPUL_EC
GO:0060429	0.333	0.888	2	341	epithelium development	BP	1	TBX5,FLRT3	up_VPUL_EC
GO:0006767	0.333	0.893	2	12	water-soluble vitamin metabolic process	BP	1	CLYBL,PNPO	up_VSAP_EC
GO:0043588	0.333	0.939	1	74	skin development	BP	1	HOXA7	down_ACOR_EC
GO:0002643	0.333	0.949	1	5	regulation of tolerance induction	BP	1	HMGB1	down_ACOR_VSMC
GO:0061900	0.333	0.944	1	8	glial cell activation	BP	1	LRP1	down_VCAV_EC
GO:0150076	0.333	0.944	1	8	neuroinflammatory response	BP	1	LRP1	down_VCAV_EC
GO:0033158	0.333	0.944	1	8	regulation of protein import into nucleus,	BP	1	MAVS	down_VCAV_EC
GO:0000423	0.333	0.946	1	6	mitophagy	BP	1	CDC37	down_VSAP_EC
GO:0090042	0.333	0.951	1	4	tubulin deacetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0090043	0.333	0.951	1	4	regulation of tubulin deacetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0042659	0.333	0.951	1	4	regulation of cell fate specification	BP	1	LMO4	up_ACOR_VSMC
GO:0051890	0.333	0.951	1	4	regulation of cardioblast differentiation	BP	1	TBX5	up_ACOR_VSMC
GO:1905941	0.333	0.951	1	4	positive regulation of gonad development	BP	1	CITED2	up_ACOR_VSMC
GO:2000018	0.333	0.951	1	4	regulation of male gonad development	BP	1	CITED2	up_ACOR_VSMC
GO:2000020	0.333	0.951	1	4	positive regulation of male gonad development	BP	1	CITED2	up_ACOR_VSMC
GO:0007420	0.333	0.94	1	169	brain development	BP	1	EMX2	up_VFEM_VSMC
GO:0050678	0.333	0.94	1	117	regulation of epithelial cell proliferation	BP	1	CCL24	up_VPUL_EC
GO:0034331	0.333	0.951	1	4	cell junction maintenance	BP	1	F2RL1	up_VSAP_EC
GO:0045351	0.333	0.951	1	4	type I interferon biosynthetic process	BP	1	MYD88	up_VSAP_EC
GO:0090336	0.333	0.951	1	4	positive regulation of brown fat cell	BP	1	NAPEPLD	up_VSAP_EC

GO:1900025	0.333	0.951	1	4	negative regulation of substrate adhesion-dependent cell spreading	BP	1	FBLN1	up_VSAP_EC
GO:0060340	0.333	0.951	1	4	positive regulation of type I interferon-mediated signaling pathway	BP	1	MAVS	up_VSAP_EC
GO:1905941	0.333	0.951	1	4	positive regulation of gonad development	BP	1	CITED2	up_VSAP_EC
GO:2000018	0.333	0.951	1	4	regulation of male gonad development	BP	1	CITED2	up_VSAP_EC
GO:2000020	0.333	0.951	1	4	positive regulation of male gonad development	BP	1	CITED2	up_VSAP_EC
GO:0045216	0.333310231	0.88557	2	44	cell-cell junction organization	BP	1	NR1H4,FZD5	up_ACOR_EC
GO:0006996	0.333327647	0.73203	37	1301	organelle organization	BP	1	MYOZ2,NR1H4,TMOD1,BRSK1,PKIB,SOX9,RHOU,ARHGAP6,PHF20,ATG16L2,AQP1,SYNPO2,IFI6,DIXDC1,PDLIM3,PLS1,ACTN2,ZMYND8,ARHGAP28,PAK3,PTGER4,ARHGDIB,ELMO2,PREB,DCLK2,MAVS,FIGNL1,LRRC4,CHMP4B,TP53INP2,VPS16,RIOX2,NRP1,PRKCD,PYGO2,ENSCAFG00000010493,TUBB4A	up_ACOR_EC
GO:0032787	0.333375598	0.8182	5	144	monocarboxylic acid metabolic process	BP	1	NR1H4,THNSL2,NIT2,PTGDS,ALDOC	up_ACOR_EC
GO:0032495	0.333524825	0.94088	1	15	response to muramyl dipeptide	BP	1	NOD2	up_ACOR_EC
GO:0003401	0.333730437	0.9408	1	15	axis elongation	BP	1	SOX9	up_ACOR_EC
GO:0090090	0.333778	0.8853	2	44	negative regulation of canonical Wnt signaling	BP	1	SOX9,LRP4	up_ACOR_EC
GO:0006733	0.333833018	0.8852	2	45	oxidoreduction coenzyme metabolic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0008361	0.334	0.81	6	50	regulation of cell size	BP	1	PRR16,ABL1,PLXNA4,DPYSL2,E2F4,TTL	up_VSAP_EC
GO:0002274	0.334	0.822	5	40	myeloid leukocyte activation	BP	1	TLR1,F2RL1,PRKCE,APP,PSEN1	up_ACOR_VSMC
GO:0051668	0.334	0.822	5	39	localization within membrane	BP	1	SEC24B,GLRB,AGRN,DAG1,AP2B1	up_ACOR_VSMC
GO:0009612	0.334	0.821	5	47	response to mechanical stimulus	BP	1	KIT,TMEM150C,CASP8,TLR3,BCL10	up_VCAV_EC
GO:0051101	0.334	0.837	4	35	regulation of DNA binding	BP	1	HMGB1,FAM129B,NEK2,HMGB2	down_ACOR_VSMC
GO:0065002	0.334	0.838	4	30	intracellular protein transmembrane transport	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0071806	0.334	0.838	4	30	protein transmembrane transport	BP	1	PEX7,PEX2,LONP2,PEX6	up_VSAP_EC
GO:0060968	0.334	0.859	3	23	regulation of gene silencing	BP	1	ATAD2,UHRF1,CDK2	down_ACOR_VSMC
GO:0016241	0.334	0.855	3	41	regulation of macroautophagy	BP	1	DCN,POLDIP2,CLEC16A	down_VCAV_EC
GO:0061326	0.334	0.855	3	41	renal tubule development	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0072080	0.334	0.855	3	41	nephron tubule development	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0009953	0.334	0.856	3	34	dorsal/ventral pattern formation	BP	1	PRKACB,CTNNB1,DDIT3	down_VSAP_EC
GO:0042221	0.334	0.865	3	1012	response to chemical	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:1903556	0.334	0.891	2	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	ARG2,CACTIN	down_ACOR_VSMC
GO:0021885	0.334	0.887	2	24	forebrain cell migration	BP	1	PEX5,GLI3	down_VCAV_EC
GO:0099003	0.334	0.885	2	50	vesicle-mediated transport in synapse	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0051234	0.334	0.966	1	1283	establishment of localization	BP	1	SCAMP4	down_AORT_EC
GO:0014044	0.334	0.944	1	8	Schwann cell development	BP	1	AKT2	down_VCAV_EC
GO:0022011	0.334	0.944	1	8	myelination in peripheral nervous system	BP	1	AKT2	down_VCAV_EC
GO:0032292	0.334	0.944	1	8	peripheral nervous system axon	BP	1	AKT2	down_VCAV_EC
GO:0035728	0.334	0.946	1	6	response to hepatocyte growth factor	BP	1	NRP1	down_VSAP_EC
GO:0035729	0.334	0.946	1	6	cellular response to hepatocyte growth factor	BP	1	NRP1	down_VSAP_EC
GO:0015701	0.334	0.951	1	4	bicarbonate transport	BP	1	SLC26A7	up_ACOR_VSMC
GO:0061046	0.334	0.951	1	4	regulation of branching involved in lung	BP	1	BMP4	up_ACOR_VSMC

GO:0061047	0.334	0.951	1	4	positive regulation of branching involved in lung	BP	1	BMP4	up_ACOR_VSMC
GO:0002526	0.334	0.94	1	17	acute inflammatory response	BP	1	F3	up_AFEM_EC
GO:0055013	0.334	0.94	1	17	cardiac muscle cell development	BP	1	BVES	up_AFEM_EC
GO:0060760	0.334	0.94	1	17	positive regulation of response to cytokine	BP	1	ADAM17	up_AFEM_EC
GO:0097300	0.334	0.94	1	17	programmed necrotic cell death	BP	1	CYLD	up_AFEM_EC
GO:1903146	0.334	0.94	1	17	regulation of autophagy of mitochondrion	BP	1	CLEC16A	up_AFEM_EC
GO:0007267	0.334	0.944	1	332	cell-cell signaling	BP	1	WNT7A	up_AORT_VSMC
GO:1901652	0.334	0.939	1	105	response to peptide	BP	1	NR1H4	up_APUL_EC
GO:0002437	0.334	0.946	1	6	inflammatory response to antigenic stimulus	BP	1	HMGB1	up_VCAV_EC
GO:0006026	0.334	0.948	1	5	aminoglycan catabolic process	BP	1	LYVE1	up_VCAV_EC
GO:0046697	0.334	0.948	1	5	decidualization	BP	1	PTGS2	up_VCAV_EC
GO:0002520	0.334	0.942	1	279	immune system development	BP	1	LRRC17	up_VCAV_VSMC
GO:0051480	0.334	0.939	1	50	regulation of cytosolic calcium ion concentration	BP	1	C3AR1	up_VPOR_EC
GO:0071219	0.334	0.939	1	50	cellular response to molecule of bacterial	BP	1	MTDH	up_VPOR_EC
GO:1902850	0.334	0.939	1	52	microtubule cytoskeleton organization involved in	BP	1	MZT1	up_VPOR_EC
GO:0048812	0.334	0.94	1	151	neuron projection morphogenesis	BP	1	CHL1	up_VPOR_VSMC
GO:0051301	0.334	0.939	1	117	cell division	BP	1	ARHGEF2	up_VPUL_EC
GO:0048732	0.334	0.939	1	116	gland development	BP	1	HOXA3	up_VPUL_EC
GO:0010942	0.334	0.941	1	200	positive regulation of cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:0030011	0.334	0.951	1	4	maintenance of cell polarity	BP	1	WNT11	up_VSAP_EC
GO:0032816	0.334	0.951	1	4	positive regulation of natural killer cell	BP	1	TOX	up_VSAP_EC
GO:0035090	0.334	0.951	1	4	maintenance of apical/basal cell polarity	BP	1	WNT11	up_VSAP_EC
GO:0039530	0.334	0.951	1	4	MDA-5 signaling pathway	BP	1	TKFC	up_VSAP_EC
GO:0045199	0.334	0.951	1	4	maintenance of epithelial cell apical/basal polarity	BP	1	WNT11	up_VSAP_EC
GO:0045672	0.334	0.951	1	4	positive regulation of osteoclast differentiation	BP	1	PPARGC1B	up_VSAP_EC
GO:2000096	0.334	0.951	1	4	positive regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	ABL1	up_VSAP_EC
GO:2001241	0.334	0.951	1	4	positive regulation of extrinsic apoptotic signaling pathway in	BP	1	HTRA2	up_VSAP_EC
GO:0010715	0.334	0.951	1	4	regulation of extracellular matrix disassembly	BP	1	DDR2	up_VSAP_EC
GO:0046541	0.334	0.951	1	4	saliva secretion	BP	1	CHRM1	up_VSAP_EC
GO:0003407	0.334061049	0.94067	1	15	neural retina development	BP	1	SOX9	up_ACOR_EC
GO:0030516	0.334160822	0.94063	1	15	regulation of axon extension	BP	1	NRP1	up_ACOR_EC
GO:0051051	0.334370301	0.83236	4	112	negative regulation of transport	BP	1	NR1H4,KCNB1,ACTN2,PTGER4	up_ACOR_EC
GO:0031214	0.334540473	0.88479	2	45	biomineral tissue development	BP	1	SOX9,PTH1R	up_ACOR_EC
GO:0009142	0.334727513	0.88462	2	46	nucleoside triphosphate biosynthetic process	BP	1	AK7,ALDOC	up_ACOR_EC
GO:0034340	0.33483653	0.94037	1	15	response to type I interferon	BP	1	MAVS	up_ACOR_EC
GO:0043535	0.334916838	0.88457	2	45	regulation of blood vessel endothelial cell migration	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:1904951	0.335	0.771	12	108	positive regulation of establishment of protein localization	BP	1	CD274,ARHGEF5,CDH1,ABL1,IL17RC,F2RL1,ICE1,PIK3R1,KCNB1,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0016236	0.335	0.78	10	88	macroautophagy	BP	1	RETREG1,AMBRA1,MFN2,POLDIP2,PIP4K2B,UBQLN2,HTRA2,ULK1,HMOX1,NPRL3	up_VSAP_EC

GO:0006486	0.335	0.806	6	91	protein glycosylation	BP	1	KRTCAP2,DDOST,GFPT2,B4GALT1,FUT8,RPN2	down_VCAV_EC
GO:0043413	0.335	0.806	6	91	macromolecule glycosylation	BP	1	KRTCAP2,DDOST,GFPT2,B4GALT1,FUT8,RPN2	down_VCAV_EC
GO:0010821	0.335	0.809	6	49	regulation of mitochondrion	BP	1	DDHD1,MFN2,FBXO7,ZNF205,HTRA2,BAG4	up_VSAP_EC
GO:0031497	0.335	0.82	5	49	chromatin assembly	BP	1	NASP,HIST1H1A,ASF1A,ATRX,HP1BP3	up_VCAV_EC
GO:0046916	0.335	0.855	3	35	cellular transition metal ion homeostasis	BP	1	SLC39A7,HIF1A,TFRC	down_VSAP_EC
GO:0009135	0.335	0.859	3	22	purine nucleoside diphosphate metabolic	BP	1	ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0009179	0.335	0.859	3	22	purine ribonucleoside diphosphate metabolic	BP	1	ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0046031	0.335	0.859	3	22	ADP metabolic process	BP	1	ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0070192	0.335	0.86	3	20	chromosome organization involved in meiotic cell	BP	1	ATRX,DMC1,SUN1	up_ACOR_VSMC
GO:0019319	0.335	0.858	3	26	hexose biosynthetic process	BP	1	ATF3,FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0042981	0.335	0.856	3	471	regulation of apoptotic process	BP	1	EYA1,MAP2K6,SIX1	up_VFEM_EC
GO:0030193	0.335	0.859	3	21	regulation of blood coagulation	BP	1	KLKB1,HPSE,F2RL1	up_VSAP_EC
GO:1900046	0.335	0.859	3	21	regulation of hemostasis	BP	1	KLKB1,HPSE,F2RL1	up_VSAP_EC
GO:0010955	0.335	0.891	2	14	negative regulation of protein processing	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0045806	0.335	0.89	2	15	negative regulation of endocytosis	BP	1	HMGB1,CAV1	down_ACOR_VSMC
GO:1903318	0.335	0.891	2	14	negative regulation of protein maturation	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:2000677	0.335	0.892	2	12	regulation of transcription regulatory region DNA	BP	1	PSEN1,PARK7	up_ACOR_VSMC
GO:0002548	0.335	0.889	2	17	monocyte chemotaxis	BP	1	PDGFB,HMGB1	up_VCAV_EC
GO:0030501	0.335	0.89	2	16	positive regulation of bone mineralization	BP	1	MEF2C,BMP2	up_VCAV_EC
GO:0008535	0.335	0.893	2	12	respiratory chain complex IV assembly	BP	1	SMIM20,COA1	up_VSAP_EC
GO:0001763	0.335	0.939	1	78	morphogenesis of a branching structure	BP	1	SULF1	down_ACOR_EC
GO:0031647	0.335	0.938	1	87	regulation of protein stability	BP	1	USP28	down_ACOR_EC
GO:0070372	0.335	0.938	1	85	regulation of ERK1 and ERK2 cascade	BP	1	LYN	down_ACOR_EC
GO:0070475	0.335	0.948	1	5	rRNA base methylation	BP	1	EMG1	down_ACOR_VSMC
GO:0009151	0.335	0.948	1	5	purine deoxyribonucleotide	BP	1	NUDT1	down_ACOR_VSMC
GO:0009200	0.335	0.948	1	5	deoxyribonucleoside triphosphate metabolic	BP	1	NUDT1	down_ACOR_VSMC
GO:0009215	0.335	0.948	1	5	purine deoxyribonucleoside	BP	1	NUDT1	down_ACOR_VSMC
GO:0010837	0.335	0.943	1	8	regulation of keratinocyte proliferation	BP	1	ZFP36L1	down_VCAV_EC
GO:0032369	0.335	0.943	1	8	negative regulation of lipid transport	BP	1	AKT2	down_VCAV_EC
GO:0033003	0.335	0.943	1	8	regulation of mast cell activation	BP	1	RAC2	down_VCAV_EC
GO:0051234	0.335	0.966	1	1283	establishment of localization	BP	1	JUP	down_VFEM_VSMC
GO:0002707	0.335	0.951	1	4	negative regulation of lymphocyte mediated	BP	1	DUSP22	up_ACOR_VSMC
GO:0048711	0.335	0.951	1	4	positive regulation of astrocyte differentiation	BP	1	APP	up_ACOR_VSMC
GO:0055119	0.335	0.951	1	4	relaxation of cardiac muscle	BP	1	PDE5A	up_ACOR_VSMC
GO:0002066	0.335	0.94	1	17	columnar/cuboidal epithelial cell	BP	1	DLL1	up_AFEM_EC
GO:0055025	0.335	0.94	1	17	positive regulation of cardiac muscle tissue	BP	1	GREM1	up_AFEM_EC
GO:0055081	0.335	0.94	1	17	anion homeostasis	BP	1	GPAM	up_AFEM_EC
GO:1903825	0.335	0.94	1	17	organic acid transmembrane transport	BP	1	SLC6A6	up_AFEM_EC
GO:1905039	0.335	0.94	1	17	carboxylic acid transmembrane transport	BP	1	SLC6A6	up_AFEM_EC
GO:0002791	0.335	0.939	1	104	regulation of peptide secretion	BP	1	NR1H4	up_APUL_EC

GO:0007399	0.335	0.948	1	564	nervous system development	BP	1	HOXA3	up_APUL_VSMC
GO:0031054	0.335	0.956	1	3	pre-miRNA processing	BP	1	TUT7	up_VCAV_EC
GO:0033034	0.335	0.951	1	4	positive regulation of myeloid cell apoptotic	BP	1	MEF2C	up_VCAV_EC
GO:0032956	0.335	0.939	1	116	regulation of actin cytoskeleton organization	BP	1	CCL24	up_VPUL_EC
GO:0003002	0.335	0.939	1	118	regionalization	BP	1	HOXA3	up_VPUL_EC
GO:0050801	0.335	0.94	1	200	ion homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0034397	0.335	0.951	1	4	telomere localization	BP	1	NUP98	up_VSAP_EC
GO:0035754	0.335	0.951	1	4	B cell chemotaxis	BP	1	HSD3B7	up_VSAP_EC
GO:0046337	0.335	0.951	1	4	phosphatidylethanolamine metabolic process	BP	1	NAPEPLD	up_VSAP_EC
GO:0060665	0.335	0.951	1	4	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial	BP	1	FGF7	up_VSAP_EC
GO:0071468	0.335	0.951	1	4	cellular response to acidic pH	BP	1	RAB11B	up_VSAP_EC
GO:0072529	0.335	0.951	1	4	pyrimidine-containing compound catabolic	BP	1	ALDH6A1	up_VSAP_EC
GO:0098911	0.335	0.951	1	4	regulation of ventricular cardiac muscle cell action	BP	1	KCNE3	up_VSAP_EC
GO:1905208	0.335	0.951	1	4	negative regulation of cardiocyte differentiation	BP	1	DLL1	up_VSAP_EC
GO:2000484	0.335	0.951	1	4	positive regulation of interleukin-8 secretion	BP	1	F2RL1	up_VSAP_EC
GO:0007617	0.335	0.951	1	4	mating behavior	BP	1	THRB	up_VSAP_EC
GO:0009309	0.335	0.951	1	4	amine biosynthetic process	BP	1	AZIN2	up_VSAP_EC
GO:0010838	0.335	0.951	1	4	positive regulation of keratinocyte proliferation	BP	1	FGF7	up_VSAP_EC
GO:0032225	0.335	0.951	1	4	regulation of synaptic transmission,	BP	1	FLOT1	up_VSAP_EC
GO:0042401	0.335	0.951	1	4	cellular biogenic amine biosynthetic process	BP	1	AZIN2	up_VSAP_EC
GO:0060292	0.335	0.951	1	4	long-term synaptic depression	BP	1	KCNB1	up_VSAP_EC
GO:1990778	0.335	0.939	1	91	protein localization to cell periphery	BP	1	CAV1	up_VSAP_VSMC
GO:0045862	0.335113895	0.83183	4	112	positive regulation of proteolysis	BP	1	EDEM2,PIAS1,CLU,RNF114	up_ACOR_EC
GO:0001836	0.335288289	0.93958	1	18	release of cytochrome c from mitochondria	BP	1	IFI6	up_ACOR_EC
GO:0032412	0.335467075	0.88419	2	46	regulation of ion transmembrane	BP	1	ACTN2,MAPK8IP2	up_ACOR_EC
GO:0044260	0.336	0.785	13	2593	cellular macromolecule metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:2001020	0.336	0.784	9	88	regulation of response to DNA damage stimulus	BP	1	HMGB1,USP1,WDR76,PARPBP,RAD51,TIMELESS,RNASEH2B,PCNA,DDX39B	down_ACOR_VSMC
GO:0006898	0.336	0.808	6	57	receptor-mediated endocytosis	BP	1	NEDD4,CAV1,GREM1,TFRC,HIST1H1A,EZR	down_ACOR_VSMC
GO:0009152	0.336	0.806	6	80	purine ribonucleotide biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1	down_VSAP_EC
GO:0045087	0.336	0.816	5	161	innate immune response	BP	1	LEP,RAB20,HCK,CYLD,CCL5	up_AFEM_EC
GO:0042752	0.336	0.836	4	34	regulation of circadian rhythm	BP	1	HNRNPD,TIMELESS,THRAP3,EZH2	down_ACOR_VSMC
GO:0006633	0.336	0.835	4	38	fatty acid biosynthetic process	BP	1	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0048699	0.336	0.833	4	371	generation of neurons	BP	1	HOOK3,ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0046889	0.336	0.857	3	24	positive regulation of lipid biosynthetic process	BP	1	ACSL3,SREBF1,CTDNEP1	down_ACOR_VSMC
GO:0002687	0.336	0.854	3	36	positive regulation of leukocyte migration	BP	1	VEGFA,SERPINE1,ADAM17	down_VSAP_EC
GO:0006959	0.336	0.859	3	21	humoral immune response	BP	1	CD83,C1S,C7	up_ACOR_VSMC
GO:0090630	0.336	0.857	3	23	activation of GTPase activity	BP	1	TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0001568	0.336	0.853	3	252	blood vessel development	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC

GO:0045935	0.336	0.855	3	491	positive regulation of nucleobase-containing compound metabolic	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0048584	0.336	0.858	3	592	positive regulation of response to stimulus	BP	1	NR1H4,CCL24,NEO1	up_VPUL_EC
GO:0044743	0.336	0.886	2	23	protein transmembrane import into intracellular	BP	1	PEX5,LONP2	down_VCAV_EC
GO:0090398	0.336	0.886	2	24	cellular senescence	BP	1	BMPR1A,PRMT6	down_VCAV_EC
GO:1903409	0.336	0.886	2	24	reactive oxygen species biosynthetic process	BP	1	PARK7,CYBA	down_VCAV_EC
GO:0030279	0.336	0.888	2	19	negative regulation of ossification	BP	1	CHSY1,HIF1A	down_VSAP_EC
GO:1903573	0.336	0.887	2	20	negative regulation of response to endoplasmic	BP	1	HYOU1,USP14	down_VSAP_EC
GO:0042221	0.336	0.899	2	1012	response to chemical	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0031638	0.336	0.89	2	15	zymogen activation	BP	1	KLKB1,CASP8	up_VCAV_EC
GO:0048585	0.336	0.888	2	475	negative regulation of response to stimulus	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0002696	0.336	0.938	1	80	positive regulation of leukocyte activation	BP	1	STX4	down_ACOR_EC
GO:0034475	0.336	0.947	1	5	U4 snRNA 3'-end processing	BP	1	EXOSC5	down_ACOR_VSMC
GO:0035089	0.336	0.947	1	5	establishment of apical/basal cell polarity	BP	1	FSCN1	down_ACOR_VSMC
GO:0048512	0.336	0.943	1	8	circadian behavior	BP	1	NAGLU	down_VCAV_EC
GO:0060479	0.336	0.943	1	8	lung cell differentiation	BP	1	THRB	down_VCAV_EC
GO:1904467	0.336	0.943	1	8	regulation of tumor necrosis factor secretion	BP	1	MAVS	down_VCAV_EC
GO:1902532	0.336	0.94	1	204	negative regulation of intracellular signal	BP	1	HDAC7	down_VPOR_EC
GO:0010874	0.336	0.944	1	7	regulation of cholesterol efflux	BP	1	APOE	down_VSAP_EC
GO:0034105	0.336	0.946	1	6	positive regulation of tissue remodeling	BP	1	TFRC	down_VSAP_EC
GO:0044848	0.336	0.945	1	6	biological phase	BP	1	CTNNB1	down_VSAP_EC
GO:0044851	0.336	0.945	1	6	hair cycle phase	BP	1	CTNNB1	down_VSAP_EC
GO:0048819	0.336	0.945	1	6	regulation of hair follicle maturation	BP	1	CTNNB1	down_VSAP_EC
GO:0033683	0.336	0.95	1	4	nucleotide-excision repair, DNA incision	BP	1	FAN1	up_ACOR_VSMC
GO:0045109	0.336	0.95	1	4	intermediate filament organization	BP	1	DES	up_ACOR_VSMC
GO:0046321	0.336	0.95	1	4	positive regulation of fatty acid oxidation	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0060685	0.336	0.95	1	4	regulation of prostatic bud formation	BP	1	BMP4	up_ACOR_VSMC
GO:0060686	0.336	0.95	1	4	negative regulation of prostatic bud formation	BP	1	BMP4	up_ACOR_VSMC
GO:2000369	0.336	0.95	1	4	regulation of clathrin-dependent endocytosis	BP	1	DNAJC6	up_ACOR_VSMC
GO:0033173	0.336	0.939	1	17	calcineurin-NFAT signaling cascade	BP	1	LMCD1	up_AFEM_EC
GO:0046717	0.336	0.94	1	17	acid secretion	BP	1	LEP	up_AFEM_EC
GO:0050810	0.336	0.94	1	17	regulation of steroid biosynthetic process	BP	1	LEP	up_AFEM_EC
GO:0097720	0.336	0.939	1	17	calcineurin-mediated signaling	BP	1	LMCD1	up_AFEM_EC
GO:1900015	0.336	0.939	1	17	regulation of cytokine production involved in inflammatory response	BP	1	LEP	up_AFEM_EC
GO:1904894	0.336	0.939	1	17	positive regulation of STAT cascade	BP	1	LEP	up_AFEM_EC
GO:2000026	0.336	0.947	1	560	regulation of multicellular organismal development	BP	1	TBX5	up_APUL_VSMC
GO:1901339	0.336	0.95	1	4	regulation of store-operated calcium channel	BP	1	PLCG2	up_VCAV_EC
GO:0043491	0.336	0.938	1	50	protein kinase B signaling	BP	1	MTDH	up_VPOR_EC
GO:0043010	0.336	0.938	1	96	camera-type eye development	BP	1	MAB21L1	up_VFEM_EC
GO:0060537	0.336	0.939	1	117	muscle tissue development	BP	1	TBX5	up_VPUL_EC

GO:0009584	0.336	0.95	1	4	detection of visible light	BP	1	CHRM1	up_VSAP_EC
GO:0042033	0.336	0.95	1	4	chemokine biosynthetic process	BP	1	MYD88	up_VSAP_EC
GO:0043545	0.336	0.95	1	4	molybdopterin cofactor metabolic process	BP	1	MOCOS	up_VSAP_EC
GO:0045073	0.336	0.95	1	4	regulation of chemokine biosynthetic process	BP	1	MYD88	up_VSAP_EC
GO:0045080	0.336	0.95	1	4	positive regulation of chemokine biosynthetic	BP	1	MYD88	up_VSAP_EC
GO:0045109	0.336	0.95	1	4	intermediate filament organization	BP	1	KLHL24	up_VSAP_EC
GO:0050755	0.336	0.95	1	4	chemokine metabolic process	BP	1	MYD88	up_VSAP_EC
GO:0051189	0.336	0.95	1	4	prosthetic group metabolic process	BP	1	MOCOS	up_VSAP_EC
GO:0090179	0.336	0.951	1	4	planar cell polarity pathway involved in	BP	1	FZD1	up_VSAP_EC
GO:0090219	0.336	0.95	1	4	negative regulation of lipid kinase activity	BP	1	PIK3IP1	up_VSAP_EC
GO:0098810	0.336	0.95	1	4	neurotransmitter reuptake	BP	1	SLC6A4	up_VSAP_EC
GO:0009445	0.336	0.95	1	4	putrescine metabolic process	BP	1	AZIN2	up_VSAP_EC
GO:0010766	0.336	0.95	1	4	negative regulation of sodium ion transport	BP	1	OSR1	up_VSAP_EC
GO:0034349	0.336	0.95	1	4	glial cell apoptotic process	BP	1	DLL1	up_VSAP_EC
GO:0060696	0.336	0.95	1	4	regulation of phospholipid catabolic process	BP	1	IDH1	up_VSAP_EC
GO:0072224	0.336	0.95	1	4	metanephric glomerulus development	BP	1	OSR1	up_VSAP_EC
GO:0072239	0.336	0.95	1	4	metanephric glomerulus vasculature development	BP	1	OSR1	up_VSAP_EC
GO:2001135	0.336	0.95	1	4	regulation of endocytic recycling	BP	1	RAB11B	up_VSAP_EC
GO:0090114	0.33608348	0.93989	1	15	COPII-coated vesicle budding	BP	1	PREB	up_ACOR_EC
GO:1902895	0.336500229	0.93973	1	15	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6	up_ACOR_EC
GO:0019752	0.336810186	0.78141	9	283	carboxylic acid metabolic process	BP	1	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,PTGDS,ALDOC,AZIN2,PM20D1	up_ACOR_EC
GO:0048762	0.336816665	0.85157	3	77	mesenchymal cell differentiation	BP	1	SOX9,FOXC2,NRP1	up_ACOR_EC
GO:0009628	0.337	0.736	27	302	response to abiotic stimulus	BP	1	EPHB1,KIT,CXCR4,LRRC8D,CD34,GPR4,GATA3,EDN1,FIGNL1,TMEM150C,CASP8,MTOR,BMP2,MAPK13,ENSCAFG00000010596,MMP24,TLR3,PTGS2,BCL10,USP28,PMAIP1,BLM,HIF1A,HP1BP3,TOPBP1,P2RX2,ARHGEF2	up_VCAV_EC
GO:0048729	0.337	0.767	12	209	tissue morphogenesis	BP	1	SDC4,BMPR1A,LMO4,CLSTN1,SEMA3C,TLX2,B4GALT1,GLI3,IFT57,RDH10,GREM1,BRSK1	down_VCAV_EC
GO:0006606	0.337	0.79	8	67	protein import into nucleus	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,RPAIN	up_ACOR_VSMC
GO:0010634	0.337	0.79	8	68	positive regulation of epithelial cell migration	BP	1	BMP4,SASH1,FGF18,NRP1,PRKCE,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0009894	0.337	0.787	8	277	regulation of catabolic process	BP	1	LEP,TENT5C,CLEC16A,RAB7A,AXIN2,ACACB,FAP,SAMD4B	up_AFEM_EC
GO:0043933	0.337	0.798	7	698	protein-containing complex subunit	BP	1	MZT1,ARHGEF2,FBP1,RSL24D1,RPL10L,TWF1,SRP54	up_VPOR_EC
GO:0042303	0.337	0.836	4	30	molting cycle	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0042633	0.337	0.836	4	30	hair cycle	BP	1	FERMT1,FGFR2,FZD3,ZDHHC21	up_ACOR_VSMC
GO:0060840	0.337	0.853	3	42	artery development	BP	1	BMPR1A,LOX,GLI3	down_VCAV_EC
GO:0071482	0.337	0.854	3	34	cellular response to light stimulus	BP	1	EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0050790	0.337	0.856	3	532	regulation of catalytic activity	BP	1	PCSK1N,NPNT,NTRK2	up_APUL_EC
GO:0048538	0.337	0.887	2	20	thymus development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0009395	0.337	0.891	2	12	phospholipid catabolic process	BP	1	PLCG2,SMPD1	up_ACOR_VSMC
GO:0035794	0.337	0.891	2	13	positive regulation of mitochondrial membrane permeability	BP	1	RHOT1,BNIP3	up_ACOR_VSMC

GO:1905710	0.337	0.891	2	13	positive regulation of membrane permeability	BP	1	RHOT1,BNIP3	up_ACOR_VSMC
GO:0009260	0.337	0.938	1	83	ribonucleotide biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0046390	0.337	0.938	1	83	ribose phosphate biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0048872	0.337	0.938	1	85	homeostasis of number of cells	BP	1	LYN	down_ACOR_EC
GO:0070234	0.337	0.947	1	5	positive regulation of T cell apoptotic process	BP	1	PRELID1	down_ACOR_VSMC
GO:0003177	0.337	0.943	1	8	pulmonary valve development	BP	1	NOTCH2	down_VCAV_EC
GO:0061014	0.337	0.943	1	8	positive regulation of mRNA catabolic process	BP	1	ZFP36L1	down_VCAV_EC
GO:0048729	0.337	0.94	1	209	tissue morphogenesis	BP	1	CITED2	down_VPOR_EC
GO:0060677	0.337	0.945	1	6	ureteric bud elongation	BP	1	SIX4	down_VSAP_EC
GO:0034367	0.337	0.944	1	7	protein-containing complex remodeling	BP	1	APOE	down_VSAP_EC
GO:0034368	0.337	0.944	1	7	protein-lipid complex remodeling	BP	1	APOE	down_VSAP_EC
GO:0034369	0.337	0.944	1	7	plasma lipoprotein particle remodeling	BP	1	APOE	down_VSAP_EC
GO:0010647	0.337	0.945	1	460	positive regulation of cell communication	BP	1	GATA5	down_VSAP_VSMC
GO:0006023	0.337	0.939	1	17	aminoglycan biosynthetic process	BP	1	XYLT1	up_AFEM_EC
GO:0007631	0.337	0.939	1	17	feeding behavior	BP	1	LEP	up_AFEM_EC
GO:0030858	0.337	0.939	1	17	positive regulation of epithelial cell	BP	1	TMEM100	up_AFEM_EC
GO:0042246	0.337	0.939	1	17	tissue regeneration	BP	1	LGR6	up_AFEM_EC
GO:0002763	0.337	0.939	1	17	positive regulation of myeloid leukocyte	BP	1	EVI2B	up_AFEM_EC
GO:0046530	0.337	0.939	1	17	photoreceptor cell differentiation	BP	1	THRB	up_AFEM_EC
GO:0060428	0.337	0.939	1	17	lung epithelium development	BP	1	THRB	up_AFEM_EC
GO:0071466	0.337	0.939	1	17	cellular response to xenobiotic stimulus	BP	1	NR3C1	up_AFEM_EC
GO:0120163	0.337	0.939	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_AFEM_EC
GO:0030035	0.337	0.95	1	4	microspike assembly	BP	1	FSCN1	up_VCAV_EC
GO:0090239	0.337	0.947	1	5	regulation of histone H4 acetylation	BP	1	IWS1	up_VCAV_EC
GO:0030178	0.337	0.937	1	52	negative regulation of Wnt signaling pathway	BP	1	BARX1	up_VPOR_EC
GO:0110053	0.337	0.938	1	98	regulation of actin filament organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0006644	0.337	0.938	1	118	phospholipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0008285	0.337	0.94	1	201	negative regulation of cell proliferation	BP	1	TBX5	up_VPUL_VSMC
GO:0002829	0.337	0.95	1	4	negative regulation of type 2 immune response	BP	1	STAT6	up_VSAP_EC
GO:0003198	0.337	0.95	1	4	epithelial to mesenchymal transition involved in endocardial cushion	BP	1	TGFBR2	up_VSAP_EC
GO:0010039	0.337	0.95	1	4	response to iron ion	BP	1	HMOX1	up_VSAP_EC
GO:0033147	0.337	0.95	1	4	negative regulation of intracellular estrogen receptor signaling	BP	1	LBH	up_VSAP_EC
GO:0045429	0.337	0.95	1	4	positive regulation of nitric oxide biosynthetic	BP	1	ASS1	up_VSAP_EC
GO:0046321	0.337	0.95	1	4	positive regulation of fatty acid oxidation	BP	1	C1QTNF2	up_VSAP_EC
GO:0060142	0.337	0.95	1	4	regulation of syncytium formation by plasma	BP	1	FLOT1	up_VSAP_EC
GO:0060143	0.337	0.95	1	4	positive regulation of syncytium formation by plasma membrane fusion	BP	1	FLOT1	up_VSAP_EC
GO:0060149	0.337	0.95	1	4	negative regulation of posttranscriptional gene	BP	1	ZC3H10	up_VSAP_EC
GO:0060965	0.337	0.95	1	4	negative regulation of gene silencing by miRNA	BP	1	ZC3H10	up_VSAP_EC

GO:0060967	0.337	0.95	1	4	negative regulation of gene silencing by RNA	BP	1	ZC3H10	up_VSAP_EC
GO:0072203	0.337	0.95	1	4	cell proliferation involved in metanephros	BP	1	OSR1	up_VSAP_EC
GO:1901739	0.337	0.95	1	4	regulation of myoblast fusion	BP	1	FLOT1	up_VSAP_EC
GO:1901741	0.337	0.95	1	4	positive regulation of myoblast fusion	BP	1	FLOT1	up_VSAP_EC
GO:1903147	0.337	0.95	1	4	negative regulation of autophagy of	BP	1	HTRA2	up_VSAP_EC
GO:1903799	0.337	0.95	1	4	negative regulation of production of miRNAs involved in gene silencing	BP	1	ZC3H10	up_VSAP_EC
GO:1904407	0.337	0.95	1	4	positive regulation of nitric oxide metabolic	BP	1	ASS1	up_VSAP_EC
GO:0060839	0.337	0.95	1	4	endothelial cell fate commitment	BP	1	DLL1	up_VSAP_EC
GO:0072148	0.337	0.95	1	4	epithelial cell fate commitment	BP	1	DLL1	up_VSAP_EC
GO:0002053	0.337079791	0.93951	1	15	positive regulation of mesenchymal cell	BP	1	SOX9	up_ACOR_EC
GO:0051701	0.337412211	0.88312	2	45	interaction with host	BP	1	TRIM8,CHMP4B	up_ACOR_EC
GO:0000060	0.33761766	0.9393	1	15	protein import into nucleus, translocation	BP	1	MAVS	up_ACOR_EC
GO:0043410	0.337838892	0.81484	5	144	positive regulation of MAPK cascade	BP	1	FZD5,NOD2,TNFRSF19,SH3RF3,NRP1	up_ACOR_EC
GO:0048583	0.338	0.701	110	1095	regulation of response to stimulus	BP	1	SH3TC2,ADRA1B,VEGFD,TLR1,SMAD6,LGR6,PLCG2,LEP,LBH,MID1,GATA5,HTR2B,RASSF2,ZRANB1,C28H10orf71,RECK,SKP2,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,FGFR2,TP53BP1,ABCA1,ELF1,CASTOR1,TLR3,SH3RF2,LATS2,PDE5A,CITED2,TP53INP1,ZNRF3,CD274,ZNF365,AR,PTGIR,SASH1,TMEM108,FGF18,ARHGEF26,NDRG2,CHN2,CDKN2B,ITPR1,LIMS2,ANKRD1,F2RL1,ENPP4,DAPK1,BNIP3,C1S,CRLF3,CLSTN1,CREBRF,NRP1,UBR1,PTPN22,DMPK,NPNT,OS9,UNC5B,SMPD1,APLP1,TBX20,C7,SESN3,SH3RF1,CCDC3,PRKCE,FRS2,RGS2,DAG1,FUT8,PARP9,APP,PSEN1,SYNJ2BP,SIPA1L1,CCL5,WWC2,DUSP22,SIAH1,EDN1,SESN1,OXR1,DUSP26,NOD2,LRRC4,DDIT4,JAM3,B2M,DISC1,SH3RF3,SERINC3,USP20,HERPUD1,MAP3K7,INPP5K,BMT2,WFS1,SH3BP4,ENSCAFG00000029553,PARK7,IL18R1,RREB1,CRKL	up_ACOR_VSMC
GO:0043549	0.338	0.736	26	244	regulation of kinase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,LATS2,PDE5A,SASH1,LMO4,FGF18,CDKN2B,CDKN1A,SMPD1,CCNT1,FRS2,APP,PSEN1,DDR2,DUSP22,EDN1,DUSP26,LRRC4,PRKAG3,MAP3K7,INPP5K,PARK7	up_ACOR_VSMC
GO:0042127	0.338	0.737	25	452	regulation of cell proliferation	BP	1	GPAM,PDGFRB,SLC35F6,NDN,PRNP,SDC4,KANK2,BMPR1A,OSMR,AKT2,CLSTN1,ENSCAFG00000013404,B4GALT1,GLI3,ZFP36L1,MYDGF,IFT57,CDH2,GSDME,DDR2,SHC1,GREM1,RAC2,FOXO3,ZBTB16	down_VCAV_EC
GO:0006952	0.338	0.749	18	319	defense response	BP	1	GPAM,LRP1,CFD,CHID1,CLSTN1,TRIM8,ENSCAFG00000013404,RNF216,B4GALT1,PARK7,BPI,CYBA,MAVS,LOXL3,RAB7B,A2M,SHC1,NAPEPLD	down_VCAV_EC
GO:0051235	0.338	0.778	10	90	maintenance of location	BP	1	SLC8B1,ACACB,ABL1,MORC3,CIZ1,FTL,TAF8,CYBA,KEAP1,SOAT1	up_VSAP_EC
GO:0098662	0.338	0.781	9	131	inorganic cation transmembrane transport	BP	1	SLC39A7,ERO1A,REM1,NDUFA4L2,LYN,DDIT3,HTT,CALM1,YWHAH	down_VSAP_EC
GO:0097191	0.338	0.783	9	79	extrinsic apoptotic signaling pathway	BP	1	ITM2C,BMP4,TLR3,AR,DAPK1,NRP1,UNC5B,SH3RF1,PARK7	up_ACOR_VSMC
GO:0042063	0.338	0.79	8	67	gliogenesis	BP	1	SH3TC2,WASF3,ZNF365,DAG1,APP,PSEN1,SUN1,CRKL	up_ACOR_VSMC
GO:0008360	0.338	0.818	5	46	regulation of cell shape	BP	1	FMNL3,CDC42EP4,EZR,CORO1A,ANXA7	down_ACOR_VSMC
GO:0009127	0.338	0.818	5	47	purine nucleoside monophosphate biosynthetic process	BP	1	PFAS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0009168	0.338	0.818	5	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	PFAS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0034613	0.338	0.834	4	576	cellular protein localization	BP	1	IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0001890	0.338	0.832	4	51	placenta development	BP	1	TMED2,PTGS2,HIF1A,RTCB	down_VSAP_EC

GO:0060402	0.338	0.834	4	35	calcium ion transport into cytosol	BP	1	PDE4D,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:1901564	0.338	0.858	4	2053	organonitrogen compound metabolic	BP	1	CYP1A1,LIMK1,C6,ENSCAFG00000028814	up_VCAV_VSMC
GO:1901654	0.338	0.835	4	31	response to ketone	BP	1	PTGFR,SLIT2,NCOA2,DDIT4	up_VSAP_EC
GO:0016125	0.338	0.852	3	41	sterol metabolic process	BP	1	LCAT,CYB5R3,SOAT1	down_VCAV_EC
GO:0051028	0.338	0.854	3	33	mRNA transport	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0048584	0.338	0.889	2	592	positive regulation of response to stimulus	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0051280	0.338	0.947	1	5	negative regulation of release of sequestered calcium ion into cytosol	BP	1	GSTO1	down_ACOR_VSMC
GO:0051284	0.338	0.947	1	5	positive regulation of sequestering of calcium	BP	1	GSTO1	down_ACOR_VSMC
GO:0060315	0.338	0.947	1	5	negative regulation of ryanodine-sensitive calcium-release channel	BP	1	GSTO1	down_ACOR_VSMC
GO:0006730	0.338	0.942	1	8	one-carbon metabolic process	BP	1	AHCYL1	down_VCAV_EC
GO:0032331	0.338	0.942	1	8	negative regulation of chondrocyte	BP	1	GREM1	down_VCAV_EC
GO:0045923	0.338	0.942	1	8	positive regulation of fatty acid metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0061037	0.338	0.942	1	8	negative regulation of cartilage development	BP	1	GREM1	down_VCAV_EC
GO:0086010	0.338	0.942	1	8	membrane depolarization during action potential	BP	1	TPC3	down_VCAV_EC
GO:0010719	0.338	0.944	1	7	negative regulation of epithelial to mesenchymal	BP	1	STRAP	down_VSAP_EC
GO:0010880	0.338	0.944	1	7	regulation of release of sequestered calcium ion into cytosol by	BP	1	CALM1	down_VSAP_EC
GO:0014808	0.338	0.944	1	7	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	CALM1	down_VSAP_EC
GO:0045652	0.338	0.943	1	7	regulation of megakaryocyte	BP	1	PRMT1	down_VSAP_EC
GO:1903514	0.338	0.944	1	7	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	1	CALM1	down_VSAP_EC
GO:0023056	0.338	0.945	1	462	positive regulation of signaling	BP	1	GATA5	down_VSAP_VSMC
GO:0042533	0.338	0.95	1	4	tumor necrosis factor biosynthetic process	BP	1	TLR1	up_ACOR_VSMC
GO:0042534	0.338	0.95	1	4	regulation of tumor necrosis factor	BP	1	TLR1	up_ACOR_VSMC
GO:0071073	0.338	0.95	1	4	positive regulation of phospholipid biosynthetic	BP	1	HTR2B	up_ACOR_VSMC
GO:0010823	0.338	0.939	1	17	negative regulation of mitochondrion	BP	1	CLEC16A	up_AFEM_EC
GO:0007409	0.338	0.938	1	109	axonogenesis	BP	1	SLITRK5	up_APUL_EC
GO:0001886	0.338	0.947	1	5	endothelial cell morphogenesis	BP	1	STC1	up_VCAV_EC
GO:1901798	0.338	0.944	1	7	positive regulation of signal transduction by p53 class mediator	BP	1	PMAIP1	up_VCAV_EC
GO:0010563	0.338	0.939	1	203	negative regulation of phosphorus metabolic	BP	1	SLIT2	up_VPUL_VSMC
GO:0045936	0.338	0.939	1	203	negative regulation of phosphate metabolic	BP	1	SLIT2	up_VPUL_VSMC
GO:0000185	0.338	0.95	1	4	activation of MAPKKK activity	BP	1	TRAF7	up_VSAP_EC
GO:0001562	0.338	0.95	1	4	response to protozoan	BP	1	BATF2	up_VSAP_EC
GO:0002029	0.338	0.95	1	4	desensitization of G protein-coupled receptor signaling pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0002707	0.338	0.95	1	4	negative regulation of lymphocyte mediated	BP	1	PPP3CB	up_VSAP_EC
GO:0015804	0.338	0.95	1	4	neutral amino acid transport	BP	1	CTNS	up_VSAP_EC
GO:0022401	0.338	0.95	1	4	negative adaptation of signaling pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0035584	0.338	0.95	1	4	calcium-mediated signaling using	BP	1	PTGFR	up_VSAP_EC

GO:0039536	0.338	0.95	1	4	negative regulation of RIG-I signaling pathway	BP	1	NLRX1	up_VSAP_EC
GO:0042118	0.338	0.95	1	4	endothelial cell activation	BP	1	HOXA9	up_VSAP_EC
GO:0042832	0.338	0.95	1	4	defense response to protozoan	BP	1	BATF2	up_VSAP_EC
GO:0042994	0.338	0.95	1	4	cytoplasmic sequestering of transcription factor	BP	1	KEAP1	up_VSAP_EC
GO:0044090	0.338	0.95	1	4	positive regulation of vacuole organization	BP	1	PIP4K2B	up_VSAP_EC
GO:0060837	0.338	0.95	1	4	blood vessel endothelial cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0090343	0.338	0.95	1	4	positive regulation of cell aging	BP	1	YPEL3	up_VSAP_EC
GO:1902307	0.338	0.95	1	4	positive regulation of sodium ion	BP	1	FXYD1	up_VSAP_EC
GO:2000774	0.338	0.95	1	4	positive regulation of cellular senescence	BP	1	YPEL3	up_VSAP_EC
GO:2000786	0.338	0.95	1	4	positive regulation of autophagosome assembly	BP	1	PIP4K2B	up_VSAP_EC
GO:0060136	0.338	0.95	1	4	embryonic process involved in female	BP	1	CITED2	up_VSAP_EC
GO:0051348	0.338	0.938	1	90	negative regulation of transferase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0035725	0.338383255	0.93877	1	16	sodium ion transmembrane transport	BP	1	SLC9A9	up_ACOR_EC
GO:0055010	0.338487853	0.93896	1	15	ventricular cardiac muscle tissue morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0120193	0.338652933	0.9389	1	15	tight junction organization	BP	1	FZD5	up_ACOR_EC
GO:0022612	0.338826255	0.88236	2	44	gland morphogenesis	BP	1	SOX9,NRP1	up_ACOR_EC
GO:0060236	0.33890258	0.9388	1	15	regulation of mitotic spindle organization	BP	1	CHMP4B	up_ACOR_EC
GO:2001233	0.339	0.754	16	149	regulation of apoptotic signaling pathway	BP	1	NACC2,ITM2C,BMP4,TP53INP1,AR,DAPK1,BNIP3,NRP1,UNC5B,SH3RF1,PSEN1,SIAH1,SERINC3,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:1901617	0.339	0.797	7	60	organic hydroxy compound biosynthetic	BP	1	PLCG2,PCBD1,PPIP5K1,MOXD1,DKKL1,PTS,PARK7	up_ACOR_VSMC
GO:0034097	0.339	0.794	7	238	response to cytokine	BP	1	LEP,RAB20,GREM2,CYLD,LRRC15,CCL5,ADAM17	up_AFEM_EC
GO:0048754	0.339	0.806	6	57	branching morphogenesis of an epithelial tube	BP	1	HOXB7,DLL4,EDN1,BMP2,HHEX,TIMELESS	up_VCAV_EC
GO:0035967	0.339	0.818	5	42	cellular response to topologically incorrect	BP	1	TM7SF3,HERPUD1,WFS1,DZIP3,STC2	up_ACOR_VSMC
GO:0046649	0.339	0.814	5	162	lymphocyte activation	BP	1	LEP,CD40,DLL1,GPAM,CYLD	up_AFEM_EC
GO:0072089	0.339	0.818	5	43	stem cell proliferation	BP	1	FERMT1,SOX18,CTNNA1,HIF1A,ARHGEF2	up_VCAV_EC
GO:0006754	0.339	0.833	4	36	ATP biosynthetic process	BP	1	CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0006497	0.339	0.833	4	38	protein lipidation	BP	1	ZDHHC22,HHAT,ABCA1,ZDHHC6	up_VCAV_EC
GO:2000736	0.339	0.857	3	21	regulation of stem cell differentiation	BP	1	LBH,BMP4,TBX5	up_ACOR_VSMC
GO:0030098	0.339	0.85	3	87	lymphocyte differentiation	BP	1	LEP,DLL1,CYLD	up_AFEM_EC
GO:0010557	0.339	0.853	3	492	positive regulation of macromolecule biosynthetic process	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0038202	0.339	0.885	2	24	TORC1 signaling	BP	1	AKT1S1,CLEC16A	down_VCAV_EC
GO:0046128	0.339	0.885	2	23	purine ribonucleoside metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:0014013	0.339	0.886	2	19	regulation of gliogenesis	BP	1	SLC45A3,CTNNB1	down_VSAP_EC
GO:0009892	0.339	0.893	2	835	negative regulation of metabolic process	BP	1	LIMK1,GATA5	up_VCAV_VSMC
GO:0051246	0.339	0.893	2	832	regulation of protein metabolic process	BP	1	LIMK1,C6	up_VCAV_VSMC
GO:0009113	0.339	0.946	1	5	purine nucleobase biosynthetic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0090201	0.339	0.947	1	5	negative regulation of release of cytochrome c	BP	1	PRELID1	down_ACOR_VSMC
GO:0048227	0.339	0.946	1	5	plasma membrane to endosome transport	BP	1	RAB35	down_ACOR_VSMC
GO:0050896	0.339	1	1	2346	response to stimulus	BP	1	GATA5	down_AFEM_VSMC
GO:0009988	0.339	0.942	1	8	cell-cell recognition	BP	1	B4GALT1	down_VCAV_EC

GO:0032703	0.339	0.942	1	8	negative regulation of interleukin-2 production	BP	1	PRNP	down_VCAV_EC
GO:0097094	0.339	0.942	1	8	craniofacial suture morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:2001024	0.339	0.942	1	8	negative regulation of response to drug	BP	1	PARK7	down_VCAV_EC
GO:0021604	0.339	0.944	1	6	cranial nerve structural organization	BP	1	NRP1	down_VSAP_EC
GO:0021612	0.339	0.944	1	6	facial nerve structural organization	BP	1	NRP1	down_VSAP_EC
GO:0001991	0.339	0.949	1	4	regulation of systemic arterial blood pressure by circulatory renin-	BP	1	F2RL1	up_ACOR_VSMC
GO:0003081	0.339	0.949	1	4	regulation of systemic arterial blood pressure by renin-angiotensin	BP	1	F2RL1	up_ACOR_VSMC
GO:0034309	0.339	0.949	1	4	primary alcohol biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0035372	0.339	0.949	1	4	protein localization to microtubule	BP	1	MID1	up_ACOR_VSMC
GO:0098719	0.339	0.949	1	4	sodium ion import across plasma membrane	BP	1	SLC8A1	up_ACOR_VSMC
GO:0006919	0.339	0.938	1	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	F3	up_AFEM_EC
GO:0002548	0.339	0.938	1	17	monocyte chemotaxis	BP	1	CCL5	up_AFEM_EC
GO:0044703	0.339	0.938	1	172	multi-organism reproductive process	BP	1	HOXA9	up_AORT_EC
GO:0043603	0.339	0.942	1	372	cellular amide metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0016311	0.339	0.937	1	106	dephosphorylation	BP	1	NPNT	up_APUL_EC
GO:0045785	0.339	0.937	1	107	positive regulation of cell adhesion	BP	1	NPNT	up_APUL_EC
GO:0006582	0.339	0.949	1	4	melanin metabolic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0035791	0.339	0.946	1	5	platelet-derived growth factor receptor-beta	BP	1	PDGFB	up_VCAV_EC
GO:0036302	0.339	0.95	1	4	atrioventricular canal development	BP	1	CHD7	up_VCAV_EC
GO:0042438	0.339	0.949	1	4	melanin biosynthetic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0046033	0.339	0.947	1	5	AMP metabolic process	BP	1	ADSS	up_VCAV_EC
GO:0045944	0.339	0.94	1	287	positive regulation of transcription by RNA polymerase II	BP	1	GATA5	up_VCAV_VSMC
GO:0048878	0.339	0.941	1	283	chemical homeostasis	BP	1	CA2	up_VCAV_VSMC
GO:0030335	0.339	0.938	1	165	positive regulation of cell migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0002741	0.339	0.949	1	4	positive regulation of cytokine secretion involved in immune	BP	1	F2RL1	up_VSAP_EC
GO:0006991	0.339	0.949	1	4	response to sterol depletion	BP	1	INSIG2	up_VSAP_EC
GO:0008298	0.339	0.949	1	4	intracellular mRNA localization	BP	1	ZFP36L1	up_VSAP_EC
GO:0016322	0.339	0.949	1	4	neuron remodeling	BP	1	NTN4	up_VSAP_EC
GO:0032933	0.339	0.949	1	4	SREBP signaling pathway	BP	1	INSIG2	up_VSAP_EC
GO:0048755	0.339	0.949	1	4	branching morphogenesis of a nerve	BP	1	SHOX2	up_VSAP_EC
GO:0051292	0.339	0.949	1	4	nuclear pore complex assembly	BP	1	NUP98	up_VSAP_EC
GO:0060307	0.339	0.949	1	4	regulation of ventricular cardiac muscle cell membrane repolarization	BP	1	KCNE3	up_VSAP_EC
GO:0071501	0.339	0.949	1	4	cellular response to sterol depletion	BP	1	INSIG2	up_VSAP_EC
GO:0090520	0.339	0.949	1	4	sphingolipid mediated signaling pathway	BP	1	PLPP3	up_VSAP_EC
GO:0099622	0.339	0.949	1	4	cardiac muscle cell membrane repolarization	BP	1	KCNE3	up_VSAP_EC
GO:0099623	0.339	0.949	1	4	regulation of cardiac muscle cell membrane	BP	1	KCNE3	up_VSAP_EC
GO:0099625	0.339	0.949	1	4	ventricular cardiac muscle cell membrane	BP	1	KCNE3	up_VSAP_EC

GO:0032928	0.339	0.949	1	4	regulation of superoxide anion generation	BP	1	F2RL1	up_VSAP_EC
GO:0060836	0.339	0.95	1	4	lymphatic endothelial cell differentiation	BP	1	ACVRL1	up_VSAP_EC
GO:0070849	0.339137429	0.93871	1	15	response to epidermal growth factor	BP	1	SOX9	up_ACOR_EC
GO:0014909	0.339551131	0.93855	1	15	smooth muscle cell migration	BP	1	SEMA6D	up_ACOR_EC
GO:0048588	0.339667271	0.88186	2	44	developmental cell growth	BP	1	SOX9,NRP1	up_ACOR_EC
GO:0047496	0.339827825	0.93844	1	15	vesicle transport along microtubule	BP	1	DYNC1I1	up_ACOR_EC
GO:2000785	0.339967542	0.93814	1	16	regulation of autophagosome assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0009987	0.34	0.702	307	5086	cellular process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SIPA1L1,SULF1,ARHGAP31,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,SLC39A7,SHROOM2,TAGLN2,NR1H4,FMNL3,PLK3,C1QTNF6,ENSCAFG00000013214,HSPA5,SERPINE1,ACTN1,SOCS5,ETV6,HM13,SPARC,VASP,ENSCAFG00000009211,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,PTPN14,ENPP1,ERRFI1,ITGA2,P4HA1,SEC24D,JCAD,TPM4,SNX25,CBX5,CASP3,FAM49B,SARS,ENSCAFG00000003477,HYOU1,PGK1,AKAP2,WSB1,BCAR3,NUAK1,PTPN11,EXOC5,ATP2B1,CORO1C,FSCN1,AARS,FLNB,SEC23A,MZT1,TPI1,ENSCAFG00000032470,DPYSL3,ENSCAFG00000028814,LRRC8A,HOOK3,TRIB3,PGAM1,IFRD1,FARP1,ENSCAFG00000007260,PUM3,FKBP11,UGCG,PM20D2,FBLIM1,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,SRP54,TGFBR1,PTGS2,REM1,WDR1,MYO1C,CANX,PPIB,CEMIP2,PIK3C2A,CHSY1,MSN,UACA,HOXB7,SEL1L,RPGR,KIF5B,ENSCAFG00000008716,LMAN1,HIF1A,HTR7,NDUFA4L2,FKBP10,CX3CL1,ENSCAFG00000000562,DYNLL1,TRAK1,FOXP4,SLC45A3,TUBB,USP12,TUBB2A,MRPL1,IWS1,NMNAT2,DNAJC10,YIPF5,TNIK,GALNT1,NAA10,NXN,UBA6,RGS2,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,M	down_VSAP_EC
GO:0050863	0.34	0.788	8	69	regulation of T cell activation	BP	1	LEP,CD83,BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0002244	0.34	0.833	4	35	hematopoietic progenitor cell differentiation	BP	1	KIT,GATA3,ENSCAFG00000003530,TENT2	up_VCAV_EC
GO:0006418	0.34	0.834	4	31	tRNA aminoacylation for protein translation	BP	1	WARS2,FARS2,QARS,LARS2	up_VSAP_EC
GO:1901983	0.34	0.855	3	24	regulation of protein acetylation	BP	1	BRCA1,NOC2L,TADA2A	down_ACOR_VSMC
GO:0006793	0.34	0.86	3	948	phosphorus metabolic process	BP	1	EXTL2,SUCLG2,NDUFA10	down_AFEM_EC
GO:1901861	0.34	0.851	3	41	regulation of muscle tissue development	BP	1	BMPR1A,TSC22D3,GREM1	down_VCAV_EC
GO:0043500	0.34	0.856	3	21	muscle adaptation	BP	1	GATA5,PDE5A,EDN1	up_ACOR_VSMC
GO:0003341	0.34	0.888	2	14	cilium movement	BP	1	CFAP298,TTLL1	down_ACOR_VSMC
GO:0044380	0.34	0.888	2	14	protein localization to cytoskeleton	BP	1	NUP62,TTK	down_ACOR_VSMC
GO:0048260	0.34	0.887	2	15	positive regulation of receptor-mediated	BP	1	GREM1,HIST1H1A	down_ACOR_VSMC
GO:0032989	0.34	0.883	2	292	cellular component morphogenesis	BP	1	RADIL,CDC42EP5	up_VFEM_EC
GO:0042148	0.34	0.946	1	5	strand invasion	BP	1	RAD51	down_ACOR_VSMC
GO:0009261	0.34	0.941	1	8	ribonucleotide catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0032516	0.34	0.942	1	8	positive regulation of phosphoprotein phosphatase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0032727	0.34	0.941	1	9	positive regulation of interferon-alpha	BP	1	MAVS	down_VCAV_EC
GO:0033278	0.34	0.949	1	4	cell proliferation in midbrain	BP	1	FZD3	up_ACOR_VSMC
GO:0010421	0.34	0.949	1	4	hydrogen peroxide-mediated programmed	BP	1	PARK7	up_ACOR_VSMC
GO:0034331	0.34	0.949	1	4	cell junction maintenance	BP	1	F2RL1	up_ACOR_VSMC
GO:0097468	0.34	0.949	1	4	programmed cell death in response to reactive oxygen species	BP	1	PARK7	up_ACOR_VSMC

GO:1905208	0.34	0.949	1	4	negative regulation of cardiocyte differentiation	BP	1	FRS2	up_ACOR_VSMC
GO:0032418	0.34	0.938	1	17	lysosome localization	BP	1	KXD1	up_AFEM_EC
GO:0043619	0.34	0.949	1	4	regulation of transcription from RNA polymerase II promoter in response to	BP	1	HIF1A	up_VCAV_EC
GO:0060314	0.34	0.944	1	6	regulation of ryanodine-sensitive calcium-release	BP	1	PDE4D	up_VCAV_EC
GO:0071677	0.34	0.946	1	5	positive regulation of mononuclear cell	BP	1	HMGB1	up_VCAV_EC
GO:0090026	0.34	0.946	1	5	positive regulation of monocyte chemotaxis	BP	1	HMGB1	up_VCAV_EC
GO:0009755	0.34	0.936	1	52	hormone-mediated signaling pathway	BP	1	RNF6	up_VPOR_EC
GO:0071772	0.34	0.937	1	50	response to BMP	BP	1	ACVR2A	up_VPOR_EC
GO:0071773	0.34	0.937	1	50	cellular response to BMP stimulus	BP	1	ACVR2A	up_VPOR_EC
GO:0001833	0.34	0.949	1	4	inner cell mass cell proliferation	BP	1	TAF8	up_VSAP_EC
GO:0002836	0.34	0.949	1	4	positive regulation of response to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0002839	0.34	0.949	1	4	positive regulation of immune response to	BP	1	CD274	up_VSAP_EC
GO:0006880	0.34	0.949	1	4	intracellular sequestering of iron ion	BP	1	FTL	up_VSAP_EC
GO:0007602	0.34	0.949	1	4	phototransduction	BP	1	CHRM1	up_VSAP_EC
GO:0009068	0.34	0.949	1	4	aspartate family amino acid catabolic process	BP	1	GOT1	up_VSAP_EC
GO:0009072	0.34	0.949	1	4	aromatic amino acid family metabolic process	BP	1	IDO2	up_VSAP_EC
GO:0019320	0.34	0.949	1	4	hexose catabolic process	BP	1	GALK1	up_VSAP_EC
GO:0031055	0.34	0.949	1	4	chromatin remodeling at centromere	BP	1	CENPP	up_VSAP_EC
GO:0031119	0.34	0.949	1	4	tRNA pseudouridine synthesis	BP	1	RPUSD4	up_VSAP_EC
GO:0034080	0.34	0.949	1	4	CENP-A containing nucleosome assembly	BP	1	CENPP	up_VSAP_EC
GO:0034116	0.34	0.949	1	4	positive regulation of heterotypic cell-cell	BP	1	FLOT1	up_VSAP_EC
GO:0035094	0.34	0.949	1	4	response to nicotine	BP	1	HMOX1	up_VSAP_EC
GO:0035269	0.34	0.949	1	4	protein O-linked mannosylation	BP	1	FKRP	up_VSAP_EC
GO:0038092	0.34	0.949	1	4	nodal signaling pathway	BP	1	CITED2	up_VSAP_EC
GO:0042573	0.34	0.949	1	4	retinoic acid metabolic process	BP	1	DHRS9	up_VSAP_EC
GO:0042574	0.34	0.949	1	4	retinal metabolic process	BP	1	DHRS4	up_VSAP_EC
GO:0061029	0.34	0.949	1	4	eyelid development in camera-type eye	BP	1	OSR2	up_VSAP_EC
GO:0061641	0.34	0.949	1	4	CENP-A containing chromatin organization	BP	1	CENPP	up_VSAP_EC
GO:0070257	0.34	0.949	1	4	positive regulation of mucus secretion	BP	1	CYBA	up_VSAP_EC
GO:0072189	0.34	0.949	1	4	ureter development	BP	1	OSR1	up_VSAP_EC
GO:0097577	0.34	0.949	1	4	sequestering of iron ion	BP	1	FTL	up_VSAP_EC
GO:1901030	0.34	0.949	1	4	positive regulation of mitochondrial outer membrane permeabilization involved	BP	1	ZNF205	up_VSAP_EC
GO:0046533	0.34	0.949	1	4	negative regulation of photoreceptor cell	BP	1	THRB	up_VSAP_EC
GO:0048305	0.34	0.949	1	4	immunoglobulin secretion	BP	1	STX4	up_VSAP_EC
GO:0050832	0.34	0.949	1	4	defense response to fungus	BP	1	IL17RC	up_VSAP_EC
GO:0051023	0.34	0.949	1	4	regulation of immunoglobulin secretion	BP	1	STX4	up_VSAP_EC
GO:0060219	0.34	0.949	1	4	camera-type eye photoreceptor cell	BP	1	THRB	up_VSAP_EC
GO:0044818	0.340484603	0.93818	1	15	mitotic G2/M transition checkpoint	BP	1	BRSK1	up_ACOR_EC

GO:0006793	0.341	0.701	95	948	phosphorus metabolic process	BP	1	FZD1,NAPEPLD,CDON,WNT11,ACSM3,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,EEF2K,IL6R,SLIT2,NADK,FGF7,ABL1,EMP2,OSR1,MAP3K5,CDC42EP5,INPP5E,PDGFD,C1QTNF2,CNPPD1,COQ9,NDUFS1,ENSCAFG00000004260,PLPP3,CAMKK2,TNKS1BP1,AMBRA1,F2RL1,RBL2,PHKA2,PPIP5K1,MORC3,DDR2,PDK2,ZFP36L1,TRAF7,FXN,GALK1,PIK3R1,ENTPD3,PLA2G6,MYC,PIK3IP1,CTNS,TMEM225B,RTN4RL1,SASH1,MYD88,NDUFS2,LRP4,PASK,NT5C2,STK16,NCEH1,FBXO7,MOCOS,LCAT,LIMD1,ACSS2,TKFC,CDK9,FBLN1,MVK,PNPO,DCAKD,ZFP36L2,ENSCAFG00000013366,RAF1,PNP,ZFYVE21,QARS,ACVRL1,IDH1,FLOT1,PLPP5,PPP3CB,NCK1,NDUFV1,MAVS,ULK1,MAP2K2,TGFBR2,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0001775	0.341	0.738	23	219	cell activation	BP	1	HOXA9,CD274,TBC1D10C,ABL1,DLL1,ZBTB16,TOX,STAT6,PATZ1,F2RL1,ZFP36L1,PIK3R1,BATF2,ZEB1,MYD88,FBXO7,CD83,ZFP36L2,PNP,STX4,PPP3CB,NCK1,TGFBR2	up_VSAP_EC
GO:0008284	0.341	0.751	16	238	positive regulation of cell proliferation	BP	1	VEGFA,SULF1,JCAD,ILK,TGFBR1,HIF1A,ESM1,ADAM17,CNOT7,CTNNB1,TFRC,LYN,PRMT1,DISC1,CDKN1A,MARCKSL1	down_VSAP_EC
GO:0019538	0.341	0.799	8	1713	protein metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2	up_APUL_EC
GO:0031668	0.341	0.803	6	79	cellular response to extracellular stimulus	BP	1	ASNS,HSPA5,SESN2,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0044238	0.341	0.851	6	3383	primary metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0045665	0.341	0.804	6	55	negative regulation of neuron differentiation	BP	1	EDNRB,IFRD1,PPP3CA,HMG20A,JAG1,RAPGEF2	up_VCAV_EC
GO:0032268	0.341	0.819	5	778	regulation of cellular protein metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,ASPN	down_ACOR_EC
GO:0070727	0.341	0.832	4	579	cellular macromolecule localization	BP	1	IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:1902106	0.341	0.833	4	31	negative regulation of leukocyte differentiation	BP	1	HOXA7,PIK3R1,MYC,FBXO7	up_VSAP_EC
GO:1903578	0.341	0.855	3	22	regulation of ATP metabolic process	BP	1	PPARGC1A,DDIT4,PARK7	up_ACOR_VSMC
GO:0051091	0.341	0.849	3	87	positive regulation of DNA-binding transcription factor activity	BP	1	GREM1,CAMK2A,PPARGC1A	up_AFEM_EC
GO:0048518	0.341	0.909	2	1676	positive regulation of biological process	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0050849	0.341	0.887	2	15	negative regulation of calcium-mediated	BP	1	HOMER3,MTOR	up_VCAV_EC
GO:0032872	0.341	0.936	1	77	regulation of stress-activated MAPK cascade	BP	1	IGF1R	down_ACOR_EC
GO:0048535	0.341	0.946	1	5	lymph node development	BP	1	TOX	down_ACOR_VSMC
GO:0050896	0.341	1	1	2346	response to stimulus	BP	1	MXRA5	down_AORT_VSMC
GO:0044273	0.341	0.941	1	8	sulfur compound catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0055070	0.341	0.941	1	8	copper ion homeostasis	BP	1	ATOX1	down_VCAV_EC
GO:2000273	0.341	0.944	1	6	positive regulation of signaling receptor activity	BP	1	ADAM17	down_VSAP_EC
GO:0040037	0.341	0.944	1	6	negative regulation of fibroblast growth factor receptor signaling	BP	1	SULF1	down_VSAP_EC
GO:0042636	0.341	0.949	1	4	negative regulation of hair cycle	BP	1	FERMT1	up_ACOR_VSMC
GO:0051799	0.341	0.949	1	4	negative regulation of hair follicle development	BP	1	FERMT1	up_ACOR_VSMC
GO:0071468	0.341	0.949	1	4	cellular response to acidic pH	BP	1	RAB11B	up_ACOR_VSMC
GO:0006020	0.341	0.949	1	4	inositol metabolic process	BP	1	IMPA1	up_VCAV_EC
GO:0015810	0.341	0.949	1	4	aspartate transmembrane transport	BP	1	LRRC8D	up_VCAV_EC
GO:0018027	0.341	0.949	1	4	peptidyl-lysine dimethylation	BP	1	KDM3A	up_VCAV_EC
GO:0019062	0.341	0.946	1	5	virion attachment to host cell	BP	1	NECTIN2	up_VCAV_EC
GO:0044406	0.341	0.946	1	5	adhesion of symbiont to host	BP	1	NECTIN2	up_VCAV_EC

GO:0044650	0.341	0.946	1	5	adhesion of symbiont to host cell	BP	1	NECTIN2	up_VCAV_EC
GO:1903706	0.341	0.937	1	119	regulation of hemopoiesis	BP	1	EVI2B	up_VPUL_EC
GO:0006729	0.341	0.949	1	4	tetrahydrobiopterin biosynthetic process	BP	1	PCBD1	up_VSAP_EC
GO:0006787	0.341	0.949	1	4	porphyrin-containing compound catabolic	BP	1	HMOX1	up_VSAP_EC
GO:0031294	0.341	0.949	1	4	lymphocyte costimulation	BP	1	CD274	up_VSAP_EC
GO:0033015	0.341	0.949	1	4	tetrapyrrole catabolic process	BP	1	HMOX1	up_VSAP_EC
GO:0042167	0.341	0.949	1	4	heme catabolic process	BP	1	HMOX1	up_VSAP_EC
GO:0046149	0.341	0.949	1	4	pigment catabolic process	BP	1	HMOX1	up_VSAP_EC
GO:0060710	0.341	0.949	1	4	chorio-allantoic fusion	BP	1	ZFP36L1	up_VSAP_EC
GO:1990441	0.341	0.949	1	4	negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	BP	1	NCK1	up_VSAP_EC
GO:0046146	0.341	0.949	1	4	tetrahydrobiopterin metabolic process	BP	1	PCBD1	up_VSAP_EC
GO:0007409	0.341111085	0.82756	4	109	axonogenesis	BP	1	BRSK1,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0055021	0.341205692	0.9379	1	15	regulation of cardiac muscle tissue growth	BP	1	TBX5	up_ACOR_EC
GO:0060284	0.3412314	0.79155	7	212	regulation of cell development	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:1905898	0.341495186	0.93754	1	16	positive regulation of response to endoplasmic	BP	1	EDEM2	up_ACOR_EC
GO:0032270	0.342	0.714	49	479	positive regulation of cellular protein metabolic process	BP	1	FZD1,PRR16,CDON,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,IL6R,CRADD,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CCBE1,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,TRAF7,MYC,EEF2,SASH1,FBXO4,LARP6,MYD88,LRP4,PHF1,RNF166,RPUSD4,CDK9,OSBPL7,RAF1,EIF3D,ACVRL1,UBQLN2,HTRA2,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0006810	0.342	0.729	32	1244	transport	BP	1	TRAPPC3L,LEP,KCNC4,CRY2,VPS26C,RAB20,GAS1,DLL1,CRYAB,KCND1,GPAM,CHRM2,SLC17A5,MYO1D,ATP6V1B2,SLC6A6,GREM1,CAMK2A,FXYD1,ICAM5,REEP2,BVES,RAB7A,ATP6V0B,NIPAL1,SLC46A2,CCL5,DMPK,SLC43A1,CLIC4,KXD1,ANXA11	up_AFEM_EC
GO:0043207	0.342	0.737	23	216	response to external biotic stimulus	BP	1	MAP3K14,PTGFR,ABL1,IL17RC,F2RL1,BATF2,PLA2G6,TBXA2R,SASH1,MYD88,WIPF1,CFD,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,CA5B,PQBP1,NCK1,MAVS,JCHAIN,DDIT4	up_VSAP_EC
GO:0051707	0.342	0.737	23	216	response to other organism	BP	1	MAP3K14,PTGFR,ABL1,IL17RC,F2RL1,BATF2,PLA2G6,TBXA2R,SASH1,MYD88,WIPF1,CFD,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,CA5B,PQBP1,NCK1,MAVS,JCHAIN,DDIT4	up_VSAP_EC
GO:0000226	0.342	0.757	14	197	microtubule cytoskeleton organization	BP	1	ARHGEF2,PLK3,MZT1,HOOK3,PPP1R12A,TUBB,ZPR1,CTNNB1,KPNB1,GSK3B,CCSER2,HTT,DISC1,MID1	down_VSAP_EC
GO:0050863	0.342	0.786	8	69	regulation of T cell activation	BP	1	CD274,ABL1,ZBTB16,ZEB1,CD83,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0002684	0.342	0.791	7	239	positive regulation of immune system process	BP	1	CMKLR1,LEP,GPAM,CYLD,EVI2B,CCL5,ADAM17	up_AFEM_EC
GO:0072073	0.342	0.795	7	60	kidney epithelium development	BP	1	HOXA11,WNT11,SLIT2,DLL1,OSR1,KLF15,IRX3	up_VSAP_EC
GO:0008104	0.342	0.818	5	763	protein localization	BP	1	LYN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0019725	0.342	0.881	2	245	cellular homeostasis	BP	1	LYN,STX4	down_ACOR_EC
GO:0003156	0.342	0.884	2	20	regulation of animal organ formation	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0061099	0.342	0.888	2	13	negative regulation of protein tyrosine kinase	BP	1	PSEN1,DUSP22	up_ACOR_VSMC
GO:0032722	0.342	0.887	2	14	positive regulation of chemokine production	BP	1	TLR4,TLR3	up_VCAV_EC
GO:0002052	0.342	0.94	1	9	positive regulation of neuroblast proliferation	BP	1	GLI3	down_VCAV_EC
GO:0032373	0.342	0.941	1	8	positive regulation of sterol transport	BP	1	SCP2	down_VCAV_EC

GO:0032376	0.342	0.941	1	8	positive regulation of cholesterol transport	BP	1	SCP2	down_VCAV_EC
GO:0032620	0.342	0.941	1	8	interleukin-17 production	BP	1	PRNP	down_VCAV_EC
GO:0044804	0.342	0.941	1	8	autophagy of nucleus	BP	1	WDR45	down_VCAV_EC
GO:0045737	0.342	0.941	1	8	positive regulation of cyclin-dependent protein serine/threonine kinase	BP	1	MAPRE3	down_VCAV_EC
GO:0050884	0.342	0.941	1	8	neuromuscular process controlling posture	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0036445	0.342	0.943	1	6	neuronal stem cell division	BP	1	ARHGEF2	down_VSAP_EC
GO:0031365	0.342	0.941	1	8	N-terminal protein amino acid modification	BP	1	NAA10	down_VSAP_EC
GO:0055057	0.342	0.943	1	6	neuroblast division	BP	1	ARHGEF2	down_VSAP_EC
GO:0003263	0.342	0.948	1	4	cardioblast proliferation	BP	1	TBX5	up_ACOR_VSMC
GO:1902683	0.342	0.948	1	4	regulation of receptor localization to synapse	BP	1	DAG1	up_ACOR_VSMC
GO:0071863	0.342	0.948	1	4	regulation of cell proliferation in bone	BP	1	FGFR2	up_ACOR_VSMC
GO:0071864	0.342	0.948	1	4	positive regulation of cell proliferation in bone	BP	1	FGFR2	up_ACOR_VSMC
GO:2000096	0.342	0.948	1	4	positive regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	MLLT3	up_ACOR_VSMC
GO:0006590	0.342	0.948	1	4	thyroid hormone generation	BP	1	GATA3	up_VCAV_EC
GO:0007274	0.342	0.945	1	5	neuromuscular synaptic transmission	BP	1	P2RX2	up_VCAV_EC
GO:0002689	0.342	0.945	1	5	negative regulation of leukocyte chemotaxis	BP	1	MMP28	up_VCAV_EC
GO:1903749	0.342	0.945	1	5	positive regulation of establishment of protein localization to	BP	1	SH3GLB1	up_VCAV_EC
GO:0055085	0.342	0.939	1	284	transmembrane transport	BP	1	CA2	up_VCAV_VSMC
GO:0006109	0.342	0.935	1	51	regulation of carbohydrate metabolic	BP	1	FBP1	up_VPOR_EC
GO:0048285	0.342	0.937	1	166	organelle fission	BP	1	CYP26B1	up_VPOR_VSMC
GO:0043254	0.342	0.937	1	164	regulation of protein complex assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0046649	0.342	0.937	1	162	lymphocyte activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0001819	0.342	0.936	1	120	positive regulation of cytokine production	BP	1	ARHGEF2	up_VPUL_EC
GO:0008015	0.342	0.936	1	120	blood circulation	BP	1	HTR7	up_VPUL_EC
GO:0031400	0.342	0.938	1	205	negative regulation of protein modification	BP	1	SLIT2	up_VPUL_VSMC
GO:1902532	0.342	0.938	1	204	negative regulation of intracellular signal	BP	1	SLIT2	up_VPUL_VSMC
GO:0035966	0.342044977	0.88026	2	47	response to topologically incorrect protein	BP	1	EDEM2,CLU	up_ACOR_EC
GO:1900024	0.342145919	0.93729	1	16	regulation of substrate adhesion-dependent cell	BP	1	NRP1	up_ACOR_EC
GO:0003338	0.34227395	0.93748	1	15	metanephros morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0006479	0.342409535	0.88018	2	45	protein methylation	BP	1	NR1H4,PYGO2	up_ACOR_EC
GO:0008213	0.342409535	0.88018	2	45	protein alkylation	BP	1	NR1H4,PYGO2	up_ACOR_EC
GO:0007589	0.342694496	0.93707	1	16	body fluid secretion	BP	1	AQP1	up_ACOR_EC

GO:0009892	0.343	0.703	74	835	negative regulation of metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,HNRNPD,SREBF2,SMC1A,NEDD4,U2AF2,SLC29A1,MTDH,PPP1R15B,PARPBP,SRRT,NAB2,SLC35C2,RAN,BIRC5,INSIG1,CAV1,TIMELESS,THRAP3,FAM129B,NF2,EDC4,AURKB,CDKN2C,EZH2,GREM1,SMARCC1,RNASEH2B,PLK3,HOXA7,SMG9,UHRF1,HOXC10,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,PPARD,YWHAB,NCL,NUP62,IQGAP1,SUV39H1,CACTIN,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,KNL1,ENSCAFG00000015189,HAT1,HIST2H2AC,TINF2,H2AFX,EXOSC5,SIX4,ANXA7	down_ACOR_VSMC
GO:0009150	0.343	0.753	15	161	purine ribonucleotide metabolic process	BP	1	ACLY,HMGCR,RAN,CDK1,PFAS,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:1901699	0.343	0.762	12	164	cellular response to nitrogen compound	BP	1	ARHGEF2,NR1H4,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,PTPN2,AGRN,GNAQ,CTNNB1,NR4A1	down_VSAP_EC
GO:0009101	0.343	0.784	8	113	glycoprotein biosynthetic process	BP	1	ENSCAFG00000032470,CHSY1,GALNT1,CTNNB1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0002520	0.343	0.783	8	279	immune system development	BP	1	HOXA9,LEP,HOXA7,DLL1,NFE2L1,CYLD,EVI2B,BVES	up_AFEM_EC
GO:0000723	0.343	0.802	6	54	telomere maintenance	BP	1	HMBOX1,SMG7,BLM,SMC5,ATRX,DCP2	up_VCAV_EC
GO:0032200	0.343	0.802	6	54	telomere organization	BP	1	HMBOX1,SMG7,BLM,SMC5,ATRX,DCP2	up_VCAV_EC
GO:0007405	0.343	0.854	3	21	neuroblast proliferation	BP	1	CTNNA1,HIF1A,ARHGEF2	up_VCAV_EC
GO:0030071	0.343	0.852	3	26	regulation of mitotic metaphase/anaphase	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0140029	0.343	0.851	3	28	exocytic process	BP	1	EXOC6,SNAP23,STX11	up_VCAV_EC
GO:1902099	0.343	0.852	3	26	regulation of metaphase/anaphase transition of cell cycle	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0061028	0.343	0.887	2	14	establishment of endothelial barrier	BP	1	RAP2C,EZR	down_ACOR_VSMC
GO:0043113	0.343	0.888	2	12	receptor clustering	BP	1	GLRB,AGRN	up_ACOR_VSMC
GO:0006109	0.343	0.879	2	51	regulation of carbohydrate metabolic	BP	1	LEP,ACACB	up_AFEM_EC
GO:0060538	0.343	0.879	2	51	skeletal muscle organ development	BP	1	DLL1,BVES	up_AFEM_EC
GO:0003283	0.343	0.941	1	8	atrial septum development	BP	1	NOTCH2	down_VCAV_EC
GO:0060413	0.343	0.941	1	8	atrial septum morphogenesis	BP	1	NOTCH2	down_VCAV_EC
GO:0030162	0.343	0.938	1	202	regulation of proteolysis	BP	1	CST3	down_VPOR_EC
GO:0006829	0.343	0.942	1	7	zinc ion transport	BP	1	SLC39A7	down_VSAP_EC
GO:0071577	0.343	0.942	1	7	zinc ion transmembrane transport	BP	1	SLC39A7	down_VSAP_EC
GO:0007016	0.343	0.953	1	3	cytoskeletal anchoring at plasma membrane	BP	1	DAG1	up_ACOR_VSMC
GO:0007617	0.343	0.948	1	4	mating behavior	BP	1	APP	up_ACOR_VSMC
GO:0045793	0.343	0.948	1	4	positive regulation of cell size	BP	1	EDN1	up_ACOR_VSMC
GO:1904951	0.343	0.936	1	108	positive regulation of establishment of protein localization	BP	1	NR1H4	up_APUL_EC
GO:0070886	0.343	0.945	1	5	positive regulation of calcineurin-NFAT signaling	BP	1	PPP3CA	up_VCAV_EC
GO:0106058	0.343	0.945	1	5	positive regulation of calcineurin-mediated	BP	1	PPP3CA	up_VCAV_EC
GO:0043496	0.343	0.943	1	6	regulation of protein homodimerization activity	BP	1	MEF2C	up_VCAV_EC
GO:0060576	0.343	0.945	1	5	intestinal epithelial cell development	BP	1	HIF1A	up_VCAV_EC
GO:0072643	0.343	0.945	1	5	interferon-gamma secretion	BP	1	GATA3	up_VCAV_EC
GO:0051338	0.343	0.939	1	288	regulation of transferase activity	BP	1	LIMK1	up_VCAV_VSMC
GO:0009156	0.343	0.935	1	50	ribonucleoside monophosphate	BP	1	FBP1	up_VPOR_EC
GO:0050877	0.343	0.937	1	164	nervous system process	BP	1	CHL1	up_VPOR_VSMC

GO:0051271	0.343	0.936	1	98	negative regulation of cellular component	BP	1	HOXA7	up_VFEM_EC
GO:0006338	0.343225731	0.87969	2	45	chromatin remodeling	BP	1	SOX9,RIOX2	up_ACOR_EC
GO:0031572	0.343232172	0.9371	1	15	G2 DNA damage checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0019233	0.343439197	0.93677	1	16	sensory perception of pain	BP	1	AQP1	up_ACOR_EC
GO:0043330	0.343511666	0.93674	1	16	response to exogenous dsRNA	BP	1	MAVS	up_ACOR_EC
GO:0072521	0.344	0.746	17	185	purine-containing compound metabolic process	BP	1	ACLY,HMGCR,RAN,CDK1,PFAS,MVD,ELOVL1,CYCS,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0030003	0.344	0.766	11	157	cellular cation homeostasis	BP	1	SLC39A7,ERO1A,ATP2B1,HIF1A,TFRC,APOE,LYN,DDIT3,HTT,CALM1,DISC1	down_VSAP_EC
GO:0050794	0.344	0.812	9	3075	regulation of cellular process	BP	1	CHL1,FGF5,HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0032608	0.344	0.852	3	24	interferon-beta production	BP	1	CACTIN,HMGB2,POLR3F	down_ACOR_VSMC
GO:0006941	0.344	0.849	3	36	striated muscle contraction	BP	1	CALM1,MYBPC2,HOMER1	down_VSAP_EC
GO:0051101	0.344	0.849	3	35	regulation of DNA binding	BP	1	CTNNB1,DDIT3,CALM1	down_VSAP_EC
GO:0051303	0.344	0.851	3	26	establishment of chromosome localization	BP	1	RAB11A,CENPC,ZW10	up_VCAV_EC
GO:0043067	0.344	0.85	3	479	regulation of programmed cell death	BP	1	EYA1,MAP2K6,SIX1	up_VFEM_EC
GO:0032371	0.344	0.885	2	15	regulation of sterol transport	BP	1	SREBF2,NUS1	down_ACOR_VSMC
GO:0032374	0.344	0.885	2	15	regulation of cholesterol transport	BP	1	SREBF2,NUS1	down_ACOR_VSMC
GO:0048259	0.344	0.881	2	24	regulation of receptor-mediated endocytosis	BP	1	LRPAP1,GREM1	down_VCAV_EC
GO:0045648	0.344	0.887	2	13	positive regulation of erythrocyte	BP	1	ISG15,FAM210B	up_ACOR_VSMC
GO:0030837	0.344	0.886	2	14	negative regulation of actin filament	BP	1	TMOD1,TMOD3	up_VCAV_EC
GO:0060997	0.344	0.886	2	14	dendritic spine morphogenesis	BP	1	EPHB1,RELN	up_VCAV_EC
GO:0006954	0.344	0.879	2	147	inflammatory response	BP	1	C3AR1,ENSCAFG00000032731	up_VPOR_EC
GO:0019953	0.344	0.879	2	152	sexual reproduction	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:1902969	0.344	0.945	1	5	mitotic DNA replication	BP	1	RAD51	down_ACOR_VSMC
GO:0001573	0.344	0.94	1	8	ganglioside metabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0018200	0.344	0.94	1	8	peptidyl-glutamic acid modification	BP	1	VKORC1	down_VCAV_EC
GO:2001044	0.344	0.94	1	8	regulation of integrin-mediated signaling	BP	1	LOXL3	down_VCAV_EC
GO:0031325	0.344	0.953	1	914	positive regulation of cellular metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0006089	0.344	0.941	1	7	lactate metabolic process	BP	1	HIF1A	down_VSAP_EC
GO:0001832	0.344	0.941	1	7	blastocyst growth	BP	1	ZPR1	down_VSAP_EC
GO:0009950	0.344	0.943	1	6	dorsal/ventral axis specification	BP	1	CTNNB1	down_VSAP_EC
GO:0010869	0.344	0.948	1	4	regulation of receptor biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0021514	0.344	0.948	1	4	ventral spinal cord interneuron	BP	1	LMO4	up_ACOR_VSMC
GO:0032800	0.344	0.948	1	4	receptor biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0048739	0.344	0.948	1	4	cardiac muscle fiber development	BP	1	BMP4	up_ACOR_VSMC
GO:0072217	0.344	0.948	1	4	negative regulation of metanephros	BP	1	BMP4	up_ACOR_VSMC
GO:1902946	0.344	0.948	1	4	protein localization to early endosome	BP	1	NRP1	up_ACOR_VSMC
GO:2000483	0.344	0.948	1	4	negative regulation of interleukin-8 secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:2000647	0.344	0.948	1	4	negative regulation of stem cell proliferation	BP	1	FERMT1	up_ACOR_VSMC
GO:0007178	0.344	0.935	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	NPNT	up_APUL_EC

GO:0010720	0.344	0.935	1	110	positive regulation of cell development	BP	1	NTRK2	up_APUL_EC
GO:0006349	0.344	0.948	1	4	regulation of gene expression by genetic	BP	1	ARID4B	up_VCAV_EC
GO:0032211	0.344	0.945	1	5	negative regulation of telomere maintenance via	BP	1	DCP2	up_VCAV_EC
GO:0042761	0.344	0.941	1	7	very long-chain fatty acid biosynthetic process	BP	1	ELOVL7	up_VCAV_EC
GO:0046006	0.344	0.943	1	6	regulation of activated T cell proliferation	BP	1	HMGB1	up_VCAV_EC
GO:0061436	0.344	0.945	1	5	establishment of skin barrier	BP	1	STMN1	up_VCAV_EC
GO:1900424	0.344	0.945	1	5	regulation of defense response to bacterium	BP	1	ARG2	up_VCAV_EC
GO:0022407	0.344	0.935	1	96	regulation of cell-cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0046578	0.344589387	0.84632	3	77	regulation of Ras protein signal transduction	BP	1	ARHGDIB,NRP1,ARHGEF26	up_ACOR_EC
GO:0016570	0.344699747	0.80965	5	143	histone modification	BP	1	NR1H4,PHF20,ZMYND8,PRKCD,PYGO2	up_ACOR_EC
GO:0052547	0.344721127	0.84607	3	82	regulation of peptidase activity	BP	1	PCSK1N,IFI6,CST3	up_ACOR_EC
GO:0046622	0.344853598	0.93646	1	15	positive regulation of organ growth	BP	1	TBX5	up_ACOR_EC
GO:0019725	0.345	0.736	22	245	cellular homeostasis	BP	1	CP,LRRC8D,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,LRRC8C,SLC12A7,PDZD8,SWAP70,SMARCA4,PDIA5,PLCG2,TAOK1,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0120035	0.345	0.746	17	160	regulation of plasma membrane bounded cell projection organization	BP	1	ENPP2,SLIT2,ABL1,CDC42EP5,FUZ,PLXNA4,CDC42EP2,F2RL1,SHOX2,RTN4RL1,LRP4,DPYSL2,FBXO7,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC
GO:0031326	0.345	0.771	11	1176	regulation of cellular biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:1901360	0.345	0.786	10	2016	organic cyclic compound metabolic process	BP	1	TBX15,EYA1,HOXA9,MME,HOXA10,HOXA7,SIX1,YBX3,CYP26B1,ADCY3	up_VFEM_EC
GO:0010959	0.345	0.777	9	79	regulation of metal ion transport	BP	1	AMIGO1,SLC8B1,ABL1,KCNE3,OSR1,KLHL24,CRACR2B,CYBA,FXYD1	up_VSAP_EC
GO:0045861	0.345	0.784	8	71	negative regulation of proteolysis	BP	1	RECK,PTPN3,CST3,OS9,SH3RF1,PSEN1,SPINK2,PARK7	up_ACOR_VSMC
GO:0009059	0.345	0.794	8	1563	macromolecule biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,CHST7	up_VFEM_EC
GO:0007159	0.345	0.799	6	79	leukocyte cell-cell adhesion	BP	1	SOCS5,FAM49B,MSN,PTPN2,TFRC,SDC4	down_VSAP_EC
GO:1902115	0.345	0.799	6	77	regulation of organelle assembly	BP	1	FSCN1,MSN,DYNLL1,SH3GLB1,SDC4,HTT	down_VSAP_EC
GO:0099003	0.345	0.801	6	50	vesicle-mediated transport in synapse	BP	1	DNAJC6,FBXL20,STX11,PSEN1,AP2B1,PREPL	up_ACOR_VSMC
GO:0007224	0.345	0.801	6	50	smoothened signaling pathway	BP	1	CDON,GLIS2,GAS1,SHOX2,TMEM17,TGFBR2	up_VSAP_EC
GO:0031929	0.345	0.812	5	62	TOR signaling	BP	1	SESN2,HIF1A,EIF4EBP1,DISC1,SEC13	down_VSAP_EC
GO:0051704	0.345	0.812	5	476	multi-organism process	BP	1	OAS3,ACVR2A,MTDH,RPL10L,NAALADL2	up_VPOR_EC
GO:0070266	0.345	0.885	2	14	necroptotic process	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:0008652	0.345	0.881	2	24	cellular amino acid biosynthetic process	BP	1	PARK7,GLS2	down_VCAV_EC
GO:1901607	0.345	0.881	2	24	alpha-amino acid biosynthetic process	BP	1	PARK7,GLS2	down_VCAV_EC
GO:0060445	0.345	0.886	2	13	branching involved in salivary gland	BP	1	NTN4,BTBD7	up_VCAV_EC
GO:0051704	0.345	0.883	2	476	multi-organism process	BP	1	HOXA9,HOXA11	up_VFEM_VSMC
GO:0006086	0.345	0.944	1	5	acetyl-CoA biosynthetic process from pyruvate	BP	1	PDHA1	down_ACOR_VSMC
GO:0051000	0.345	0.944	1	5	positive regulation of nitric-oxide synthase	BP	1	NUS1	down_ACOR_VSMC
GO:2000515	0.345	0.94	1	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	LOXL3	down_VCAV_EC
GO:0010604	0.345	0.953	1	919	positive regulation of macromolecule metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0021801	0.345	0.942	1	6	cerebral cortex radial glia guided migration	BP	1	CTNNB1	down_VSAP_EC
GO:0022030	0.345	0.942	1	6	telencephalon glial cell migration	BP	1	CTNNB1	down_VSAP_EC

GO:1901028	0.345	0.941	1	7	regulation of mitochondrial outer membrane permeabilization involved	BP	1	SH3GLB1	down_VSAP_EC
GO:0034397	0.345	0.948	1	4	telomere localization	BP	1	SUN1	up_ACOR_VSMC
GO:0060484	0.345	0.947	1	4	lung-associated mesenchyme	BP	1	FGFR2	up_ACOR_VSMC
GO:2000678	0.345	0.947	1	4	negative regulation of transcription regulatory region DNA binding	BP	1	PSEN1	up_ACOR_VSMC
GO:0045064	0.345	0.944	1	5	T-helper 2 cell differentiation	BP	1	GATA3	up_VCAV_EC
GO:0003013	0.345	0.935	1	121	circulatory system process	BP	1	HTR7	up_VPUL_EC
GO:0016032	0.345	0.935	1	94	viral process	BP	1	CAV1	up_VSAP_VSMC
GO:0009966	0.346	0.712	46	868	regulation of signal transduction	BP	1	NOTCH2,PDGFRB,SLC35F6,DCN,PRNP,VASN,FBN1,GLIPR2,BGN,KANK2,BMPR1A,EVC,RECK,IGFBP6,ARHGEF25,AKT1S1,CHRDL1,CLSTN1,CSPG4,PRMT6,TMEM161A,ASPN,THY1,ATP6V0C,GLI3,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,NCLN,SPRED1,RAB7B,GLIS2,SHC1,FBH1,GREM1,NPHP4,FOXO3,ANKRD54,CDK14	down_VCAV_EC
GO:0048584	0.346	0.722	32	592	positive regulation of response to stimulus	BP	1	NOTCH2,PDGFRB,DCN,CFD,PRNP,GLIPR2,BMPR1A,EVC,ENSCAFG00000014978,AKT2,CSPG4,TMEM161A,THY1,ATP6V0C,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,SPRED1,RAB7B,A2M,SHC1,FBH1,GREM1,RAC2,NAPEPLD	down_VCAV_EC
GO:0060341	0.346	0.728	27	255	regulation of cellular localization	BP	1	SH3TC2,ACTN2,LEP,TCAF1,FBXL20,PRKAA2,FERMT1,BMP4,SEC24B,AR,CDKN1A,PTPN22,OS9,SCP2,PRKCE,DAG1,PARP9,PSEN1,CHD7,JUP,RAB11B,KCNC4,INPP5K,PREPL,PARK7,BVES,PTPN14	up_ACOR_VSMC
GO:0065008	0.346	0.774	10	1056	regulation of biological quality	BP	1	C3AR1,HTR7,HOXA3,SLC7A11,SEMA3A,ENSCAFG00000005494,ACVR2A,ABHD5,TWF1,RNF6	up_VPOR_EC
GO:0002757	0.346	0.777	9	78	immune response-activating signal	BP	1	ABL1,F2RL1,RBCK1,MYD88,NLRX1,TKFC,CYBA,UNC93B1,FLOT1	up_VSAP_EC
GO:0009991	0.346	0.781	8	110	response to extracellular stimulus	BP	1	ASNS,HSPA5,SESN2,APOE,DDIT3,ATF3,EIF2S1,CDKN1A	down_VSAP_EC
GO:0048232	0.346	0.789	7	95	male gamete generation	BP	1	CELF1,PHC2,CCNYL1,CDYL,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0010556	0.346	0.806	6	1137	regulation of macromolecule	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0048634	0.346	0.814	5	40	regulation of muscle organ development	BP	1	CDON,DLL1,SAV1,SHOX2,FLOT1	up_VSAP_EC
GO:0010467	0.346	0.872	3	1787	gene expression	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0034243	0.346	0.885	2	14	regulation of transcription elongation from RNA polymerase II promoter	BP	1	EZH2,SUPT16H	down_ACOR_VSMC
GO:0035904	0.346	0.88	2	25	aorta development	BP	1	BMPR1A,LOX	down_VCAV_EC
GO:0046902	0.346	0.883	2	18	regulation of mitochondrial membrane	BP	1	SH3GLB1,PMAIP1	up_VCAV_EC
GO:0032504	0.346	0.878	2	152	multicellular organism reproduction	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0048609	0.346	0.878	2	152	multicellular organismal reproductive process	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0120039	0.346	0.877	2	158	plasma membrane bounded cell projection	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0043542	0.346	0.934	1	86	endothelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0006616	0.346	0.944	1	5	SRP-dependent cotranslational protein targeting to membrane,	BP	1	TRAM1	down_ACOR_VSMC
GO:0045019	0.346	0.944	1	5	negative regulation of nitric oxide biosynthetic	BP	1	CAV1	down_ACOR_VSMC
GO:0070365	0.346	0.944	1	5	hepatocyte differentiation	BP	1	E2F8	down_ACOR_VSMC
GO:0070862	0.346	0.944	1	5	negative regulation of protein exit from	BP	1	INSIG1	down_ACOR_VSMC
GO:1904406	0.346	0.944	1	5	negative regulation of nitric oxide metabolic	BP	1	CAV1	down_ACOR_VSMC
GO:0006779	0.346	0.94	1	8	porphyrin-containing compound biosynthetic	BP	1	UROS	down_VCAV_EC

GO:0006783	0.346	0.94	1	8	heme biosynthetic process	BP	1	UROS	down_VCAV_EC
GO:0033014	0.346	0.94	1	8	tetrapyrrole biosynthetic process	BP	1	UROS	down_VCAV_EC
GO:0050435	0.346	0.939	1	8	amyloid-beta metabolic process	BP	1	PRNP	down_VCAV_EC
GO:0051900	0.346	0.94	1	8	regulation of mitochondrial	BP	1	DCN	down_VCAV_EC
GO:0019400	0.346	0.94	1	7	alditol metabolic process	BP	1	TPI1	down_VSAP_EC
GO:0031954	0.346	0.939	1	8	positive regulation of protein	BP	1	VEGFA	down_VSAP_EC
GO:0017001	0.346	0.947	1	4	antibiotic catabolic process	BP	1	CAT	up_ACOR_VSMC
GO:0044241	0.346	0.947	1	4	lipid digestion	BP	1	LEP	up_ACOR_VSMC
GO:0097066	0.346	0.947	1	4	response to thyroid hormone	BP	1	CTSB	up_ACOR_VSMC
GO:0097067	0.346	0.947	1	4	cellular response to thyroid hormone stimulus	BP	1	CTSB	up_ACOR_VSMC
GO:0030001	0.346	0.936	1	172	metal ion transport	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0009991	0.346	0.935	1	110	response to extracellular stimulus	BP	1	PCSK1N	up_APUL_EC
GO:0034404	0.346	0.934	1	50	nucleobase-containing small molecule	BP	1	FBP1	up_VPOR_EC
GO:2000147	0.346	0.936	1	169	positive regulation of cell motility	BP	1	C3AR1	up_VPOR_VSMC
GO:0034762	0.346	0.935	1	122	regulation of transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0006631	0.346	0.934	1	93	fatty acid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0060079	0.346042166	0.93598	1	15	excitatory postsynaptic potential	BP	1	MAPK8IP2	up_ACOR_EC
GO:0009954	0.346394966	0.93559	1	16	proximal/distal pattern formation	BP	1	LRP4	up_ACOR_EC
GO:0014706	0.346418671	0.82363	4	112	striated muscle tissue development	BP	1	ACTN2,FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0003006	0.346534984	0.79653	6	180	developmental process involved in reproduction	BP	1	GATA4,SOX9,FZD5,LHX9,DLX3,PYGO2	up_ACOR_EC
GO:0018107	0.346849285	0.87754	2	45	peptidyl-threonine phosphorylation	BP	1	DCLK2,PRKCD	up_ACOR_EC
GO:0033993	0.347	0.755	13	186	response to lipid	BP	1	NR1H4,SERPINE1,SMARCA4,MSN,YES1,MTDH,ADAM17,CTNNB1,UBA5,LYN,REST,YWHAH,KDM3A	down_VSAP_EC
GO:0002250	0.347	0.783	8	68	adaptive immune response	BP	1	TP53BP1,CD274,C1S,DUSP22,JAM3,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0071695	0.347	0.812	5	45	anatomical structure maturation	BP	1	TRIP13,FBXO5,XYLT1,GREM1,ARCN1	down_ACOR_VSMC
GO:0010604	0.347	0.815	5	919	positive regulation of macromolecule metabolic	BP	1	EYA1,HOXA9,MAP2K6,SIX1,CYP26B1	up_VFEM_EC
GO:0071772	0.347	0.826	4	50	response to BMP	BP	1	SULF1,ILK,NEO1,ENSCAFG00000018360	down_VSAP_EC
GO:0071773	0.347	0.826	4	50	cellular response to BMP stimulus	BP	1	SULF1,ILK,NEO1,ENSCAFG00000018360	down_VSAP_EC
GO:0033554	0.347	0.829	4	708	cellular response to stress	BP	1	EYA1,MAP2K6,CDC42EP5,MTSS1	up_VFEM_EC
GO:0032642	0.347	0.851	3	22	regulation of chemokine production	BP	1	MBP,TLR3,F2RL1	up_ACOR_VSMC
GO:0044070	0.347	0.851	3	22	regulation of anion transport	BP	1	TCAF1,PSEN1,RAB11B	up_ACOR_VSMC
GO:2000026	0.347	0.883	2	560	regulation of multicellular organismal development	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0021766	0.347	0.881	2	20	hippocampus development	BP	1	UBA6,GSK3B	down_VSAP_EC
GO:2001259	0.347	0.885	2	13	positive regulation of cation channel activity	BP	1	RELN,PLCG2	up_VCAV_EC
GO:0006164	0.347	0.934	1	86	purine nucleotide biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0034141	0.347	0.943	1	5	positive regulation of toll-like receptor 3 signaling	BP	1	CAV1	down_ACOR_VSMC
GO:0034162	0.347	0.944	1	5	toll-like receptor 9 signaling pathway	BP	1	HMGB1	down_ACOR_VSMC
GO:2000010	0.347	0.944	1	5	positive regulation of protein localization to cell	BP	1	SLC29A1	down_ACOR_VSMC
GO:0006805	0.347	0.939	1	8	xenobiotic metabolic process	BP	1	CYP1B1	down_VCAV_EC
GO:0031954	0.347	0.939	1	8	positive regulation of protein	BP	1	GREM1	down_VCAV_EC

GO:0032689	0.347	0.939	1	8	negative regulation of interferon-gamma	BP	1	PRNP	down_VCAV_EC
GO:0090382	0.347	0.939	1	8	phagosome maturation	BP	1	RAB31	down_VCAV_EC
GO:1990748	0.347	0.939	1	8	cellular detoxification	BP	1	PARK7	down_VCAV_EC
GO:1903539	0.347	0.947	1	4	protein localization to postsynaptic membrane	BP	1	DAG1	up_ACOR_VSMC
GO:0021855	0.347	0.947	1	4	hypothalamus cell migration	BP	1	NRP1	up_ACOR_VSMC
GO:0048670	0.347	0.947	1	4	regulation of collateral sprouting	BP	1	ULK2	up_ACOR_VSMC
GO:0060742	0.347	0.947	1	4	epithelial cell differentiation involved in prostate gland	BP	1	FGFR2	up_ACOR_VSMC
GO:1903753	0.347	0.947	1	4	negative regulation of p38MAPK cascade	BP	1	PTPN22	up_ACOR_VSMC
GO:0035239	0.347	0.937	1	299	tube morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0007155	0.347	0.939	1	324	cell adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0120039	0.347	0.935	1	158	plasma membrane bounded cell projection	BP	1	CHL1	up_VPOR_VSMC
GO:1901570	0.347716377	0.93506	1	16	fatty acid derivative biosynthetic process	BP	1	PTGDS	up_ACOR_EC
GO:1901998	0.347863777	0.935	1	16	toxin transport	BP	1	NRP1	up_ACOR_EC
GO:0006998	0.34793891	0.93497	1	16	nuclear envelope organization	BP	1	CHMP4B	up_ACOR_EC
GO:0050794	0.348	0.709	76	3075	regulation of cellular process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,KCNC4,LBH,PRR16,CRY2,RAB20,GAS1,ANGPT4,HOXA7,CD40,DLL1,CRYAB,F3,PLXNA4,BPI,GPAM,FIBIN,MLLT11,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,TWIST2,MAB21L1,THRB,LGI4,MYO1D,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,HTR1D,NFE2L1,OVOL1,FAM53B,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,RASGEF1B,POSTN,LRRC15,FAM13A,MYBL1,RECK,NR3C1,PTHLH,TBXA2R,EVI2B,DCUN1D3,EAF1,BVES,LGR6,RAB7A,AXIN2,YEATS2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,FOSL2,KANK1,TNC	up_AFEM_EC
GO:1901565	0.348	0.711	45	442	organonitrogen compound catabolic process	BP	1	ENOSF1,ZRANB1,FBXL20,ENSCAFG00000002977,SKP2,SH3RF2,PDE5A,MAOA,ISG15,ZNRF3,CTSS,PTPN3,KLHL20,ENPP4,CTSB,BNIP3,EGLN1,UBR1,OS9,STT3B,SMPD1,UBE2H,MOXD1,RNF24,SARDH,RNF19A,LYPLAL1,PSEN1,LAMP2,CLN8,SIAH1,CTSF,PCYOX1,DISC1,RNF181,NEU3,USP20,HERPUD1,FAF2,CNOT4,WFS1,AZIN2,DZIP3,ERAP1,PARK7	up_ACOR_VSMC
GO:0006644	0.348	0.756	13	118	phospholipid metabolic process	BP	1	NAPEPLD,ENPP2,INPP5E,PLPP3,AMBRA1,PIK3R1,PLA2G6,PIK3IP1,LCAT,MVK,ZFYVE21,IDH1,PLPP5	up_VSAP_EC
GO:0051090	0.348	0.779	8	134	regulation of DNA-binding transcription factor	BP	1	PRNP,CLSTN1,PARK7,MAVS,RAB7B,GLIS2,DDR2,GREM1	down_VCAV_EC
GO:0008406	0.348	0.799	6	57	gonad development	BP	1	KIT,TIPARP,EIF2B2,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:0045137	0.348	0.799	6	57	development of primary sexual characteristics	BP	1	KIT,TIPARP,EIF2B2,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:0072175	0.348	0.824	4	60	epithelial tube formation	BP	1	SDC4,LMO4,IFT57,GREM1	down_VCAV_EC
GO:0002429	0.348	0.846	3	35	immune response-activating cell surface receptor signaling	BP	1	PTPN2,EIF2B1,LYN	down_VSAP_EC
GO:0045069	0.348	0.85	3	22	regulation of viral genome replication	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0023014	0.348	0.878	2	248	signal transduction by protein phosphorylation	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0070509	0.348	0.88	2	21	calcium ion import	BP	1	CTNNB1,HOMER1	down_VSAP_EC
GO:0006493	0.348	0.88	2	20	protein O-linked glycosylation	BP	1	GALNT1,PLOD3	down_VSAP_EC
GO:0061384	0.348	0.885	2	12	heart trabecula morphogenesis	BP	1	EGLN1,CHD7	up_ACOR_VSMC
GO:0032006	0.348	0.877	2	52	regulation of TOR signaling	BP	1	LEP,CLEC16A	up_AFEM_EC

GO:0006977	0.348	0.943	1	5	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BP	1	CASP2	down_ACOR_VSMC
GO:0035437	0.348	0.943	1	5	maintenance of protein localization in endoplasmic reticulum	BP	1	INSIG1	down_ACOR_VSMC
GO:0051131	0.348	0.943	1	5	chaperone-mediated protein complex assembly	BP	1	SLC29A1	down_ACOR_VSMC
GO:0072431	0.348	0.943	1	5	signal transduction involved in mitotic G1 DNA damage checkpoint	BP	1	CASP2	down_ACOR_VSMC
GO:1902400	0.348	0.943	1	5	intracellular signal transduction involved in G1 DNA damage	BP	1	CASP2	down_ACOR_VSMC
GO:0002082	0.348	0.939	1	8	regulation of oxidative phosphorylation	BP	1	PARK7	down_VCAV_EC
GO:0015937	0.348	0.939	1	8	coenzyme A biosynthetic process	BP	1	ACAT1	down_VCAV_EC
GO:0050829	0.348	0.939	1	8	defense response to Gram-negative bacterium	BP	1	BPI	down_VCAV_EC
GO:0007398	0.348	0.941	1	6	ectoderm development	BP	1	CTNNB1	down_VSAP_EC
GO:0021800	0.348	0.941	1	6	cerebral cortex tangential migration	BP	1	NRP1	down_VSAP_EC
GO:0043981	0.348	0.946	1	4	histone H4-K5 acetylation	BP	1	PHF20	up_ACOR_VSMC
GO:0043982	0.348	0.946	1	4	histone H4-K8 acetylation	BP	1	PHF20	up_ACOR_VSMC
GO:0046325	0.348	0.946	1	4	negative regulation of glucose import	BP	1	LEP	up_ACOR_VSMC
GO:1900409	0.348	0.946	1	4	positive regulation of cellular response to	BP	1	PARK7	up_ACOR_VSMC
GO:1902884	0.348	0.946	1	4	positive regulation of response to oxidative	BP	1	PARK7	up_ACOR_VSMC
GO:1903209	0.348	0.946	1	4	positive regulation of oxidative stress-induced	BP	1	PARK7	up_ACOR_VSMC
GO:0046580	0.348	0.935	1	18	negative regulation of Ras protein signal	BP	1	KANK1	up_AFEM_EC
GO:0022603	0.348	0.937	1	301	regulation of anatomical structure morphogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0060548	0.348	0.937	1	294	negative regulation of cell death	BP	1	EYA1	up_AFEM_VSMC
GO:0031098	0.348	0.934	1	109	stress-activated protein kinase signaling cascade	BP	1	MAPK10	up_APUL_EC
GO:0003373	0.348	0.946	1	4	dynamin family protein polymerization involved in membrane fission	BP	1	MX2	up_VCAV_EC
GO:0003374	0.348	0.946	1	4	dynamin family protein polymerization involved in mitochondrial fission	BP	1	MX2	up_VCAV_EC
GO:0000972	0.348	0.943	1	5	transcription-dependent tethering of RNA polymerase II gene DNA at	BP	1	NUP133	up_VCAV_EC
GO:0002190	0.348	0.943	1	5	cap-independent translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0044068	0.348	0.943	1	5	modulation by symbiont of host cellular process	BP	1	TNIP1	up_VCAV_EC
GO:1903358	0.348	0.943	1	5	regulation of Golgi organization	BP	1	USP6NL	up_VCAV_EC
GO:0031290	0.348	0.946	1	4	retinal ganglion cell axon guidance	BP	1	EPHB1	up_VCAV_EC
GO:0009124	0.348	0.933	1	51	nucleoside monophosphate	BP	1	FBP1	up_VPOR_EC
GO:0048858	0.348	0.935	1	159	cell projection morphogenesis	BP	1	CHL1	up_VPOR_VSMC
GO:0051272	0.348	0.935	1	170	positive regulation of cellular component	BP	1	C3AR1	up_VPOR_VSMC
GO:0006486	0.348	0.933	1	91	protein glycosylation	BP	1	GALNT17	up_VSAP_VSMC
GO:0043413	0.348	0.933	1	91	macromolecule glycosylation	BP	1	GALNT17	up_VSAP_VSMC

GO:0048518	0.348485796	0.71292	47	1676	positive regulation of biological process	BP	1	C7,CDH3,NR1H4,GATA4,PKIB,CALY,SOX9,PTH1R,AQP1,ENSCAFG00000004331,SYNPO2,KCNB1,EDEM2,FZD5,CCDC3,SEMA6D,DUSP26,DIXDC1,RASL11A,NOD2,IL33,SMAD6,PLS1,ACTN2,ESM1,PAK3,TRIM8,TNFRSF19,PTGER4,PIAS1,MAVS,FOXC2,LRRC15,IFIT2,TBX5,LRP4,CLSTN1,SH3RF3,CLU,CHMP4B,TP53INP2,RARRES2,RNF114,NRP1,AZIN2,AGPAT2,PRKCD	up_ACOR_EC
GO:0001667	0.348585234	0.80663	5	146	ameboidal-type cell migration	BP	1	SOX9,ENSCAFG00000004331,ARHGDIB,FOXC2,NRP1	up_ACOR_EC
GO:0043123	0.348586212	0.87643	2	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	NOD2,TNFRSF19	up_ACOR_EC
GO:0035136	0.348798868	0.93462	1	16	forelimb morphogenesis	BP	1	TBX5	up_ACOR_EC
GO:0001568	0.34881144	0.77781	8	252	blood vessel development	BP	1	AQP1,ENSCAFG00000004331,FZD5,SMAD6,ESM1,DLX3,FOXC2,NRP1	up_ACOR_EC
GO:0051704	0.349	0.72	31	476	multi-organism process	BP	1	P4HB,CELF1,NR1H4,SERPINE1,ETV6,COTL1,TMED2,SMARCA4,PTGS2,PHC2,MTDH,DDX39B,ADAM17,ACTA2,CNOT7,CTNNB1,TFRC,APOE,LYN,BNIP3,CCNYL1,GBP5,REST,CALM1,RAD23A,CDYL,INHBA,SPINK2,SNRPA1,DEFB124,KDM3A	down_VSAP_EC
GO:0048878	0.349	0.744	16	283	chemical homeostasis	BP	1	GPAM,DCN,PRNP,ENSCAFG00000014978,LCAT,ENSCAFG00000018277,SLC39A6,THY1,ATP6V0C,PARK7,SCARA5,CYBA,ORMDL3,ATOX1,FOXO3,SOAT1	down_VCAV_EC
GO:0001701	0.349	0.754	13	134	in utero embryonic development	BP	1	HINFP,GINS4,PRMT1,SLC30A1,NEK2,RNASEH2B,E2F8,FOSL1,PLK4,SMARCB1,RBBP8,EMG1,RTCB	down_ACOR_VSMC
GO:0051047	0.349	0.779	8	84	positive regulation of secretion	BP	1	FERMT1,GATA3,EDN1,RAB27A,CREB1,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0017038	0.349	0.786	7	96	protein import	BP	1	PRICKLE1,ZPR1,KPNB1,APOE,KPNA4,KPNA1,CDKN1A	down_VSAP_EC
GO:0035690	0.349	0.787	7	91	cellular response to drug	BP	1	ARHGEF2,PPP1R12A,AGRN,GNAQ,CTNNB1,TFRC,REST	down_VSAP_EC
GO:0031398	0.349	0.798	6	51	positive regulation of protein ubiquitination	BP	1	SKP2,PTPN22,NOD2,FAM107A,DCUN1D4,WFS1	up_ACOR_VSMC
GO:0032388	0.349	0.809	5	62	positive regulation of intracellular transport	BP	1	PLK3,MYO1C,MSN,ZPR1,GSK3B	down_VSAP_EC
GO:0043406	0.349	0.808	5	62	positive regulation of MAP kinase activity	BP	1	VEGFA,PTPN11,TNIK,MAGED1,MADD	down_VSAP_EC
GO:0048813	0.349	0.811	5	39	dendrite morphogenesis	BP	1	ZNF365,NRP1,SLITRK5,SIPA1L1,WASL	up_ACOR_VSMC
GO:0017015	0.349	0.811	5	40	regulation of transforming growth factor beta receptor signaling	BP	1	SMAD6,FERMT1,CITED2,CDKN2B,NPNT	up_ACOR_VSMC
GO:1903844	0.349	0.811	5	40	regulation of cellular response to transforming growth factor beta	BP	1	SMAD6,FERMT1,CITED2,CDKN2B,NPNT	up_ACOR_VSMC
GO:0046883	0.349	0.809	5	49	regulation of hormone secretion	BP	1	CHD7,EDN1,CREB1,MCU,HIF1A	up_VCAV_EC
GO:0045927	0.349	0.823	4	61	positive regulation of growth	BP	1	GPAM,BMPR1A,TRPV2,PEX5	down_VCAV_EC
GO:0045055	0.349	0.824	4	52	regulated exocytosis	BP	1	LYN,GSK3B,REST,RAB11FIP1	down_VSAP_EC
GO:0099003	0.349	0.824	4	50	vesicle-mediated transport in synapse	BP	1	CANX,CTNNB1,GSK3B,AP3S1	down_VSAP_EC
GO:0007229	0.349	0.827	4	32	integrin-mediated signaling pathway	BP	1	FERMT1,CTNNA1,ITGA6,ITGB3	up_VCAV_EC
GO:0048522	0.349	0.84	4	1484	positive regulation of cellular process	BP	1	HOXA3,TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:2000377	0.349	0.845	3	41	regulation of reactive oxygen species metabolic	BP	1	PARK7,CYBA,FOXO3	down_VCAV_EC
GO:1903305	0.349	0.846	3	36	regulation of regulated secretory pathway	BP	1	LYN,GSK3B,REST	down_VSAP_EC
GO:0060255	0.349	0.87	3	1782	regulation of macromolecule metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0070301	0.349	0.848	3	25	cellular response to hydrogen peroxide	BP	1	TNFAIP3,MAPK13,RIPK1	up_VCAV_EC
GO:0035773	0.349	0.882	2	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0071364	0.349	0.883	2	14	cellular response to epidermal growth factor	BP	1	NCL,IQGAP1	down_ACOR_VSMC
GO:2000401	0.349	0.884	2	13	regulation of lymphocyte migration	BP	1	STK10,APOD	up_VCAV_EC
GO:0001845	0.349	0.943	1	5	phagolysosome assembly	BP	1	CORO1A	down_ACOR_VSMC

GO:1900424	0.349	0.943	1	5	regulation of defense response to bacterium	BP	1	ARG2	down_ACOR_VSMC
GO:0048009	0.349	0.938	1	8	insulin-like growth factor receptor signaling	BP	1	IGFBP6	down_VCAV_EC
GO:0050766	0.349	0.938	1	8	positive regulation of phagocytosis	BP	1	CYBA	down_VCAV_EC
GO:0009620	0.349	0.938	1	8	response to fungus	BP	1	COTL1	down_VSAP_EC
GO:0045663	0.349	0.939	1	7	positive regulation of myoblast differentiation	BP	1	HIF1AN	down_VSAP_EC
GO:0010875	0.349	0.946	1	4	positive regulation of cholesterol efflux	BP	1	ABCA1	up_ACOR_VSMC
GO:0075044	0.349	0.946	1	4	autophagy of host cells involved in interaction	BP	1	ULK2	up_ACOR_VSMC
GO:0075071	0.349	0.946	1	4	autophagy involved in symbiotic interaction	BP	1	ULK2	up_ACOR_VSMC
GO:0010171	0.349	0.934	1	18	body morphogenesis	BP	1	GREM2	up_AFEM_EC
GO:0060113	0.349	0.934	1	18	inner ear receptor cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:0090303	0.349	0.934	1	18	positive regulation of wound healing	BP	1	KANK1	up_AFEM_EC
GO:0022610	0.349	0.938	1	326	biological adhesion	BP	1	ARG2	up_AORT_VSMC
GO:0048646	0.349	0.938	1	349	anatomical structure formation involved in	BP	1	WNT7A	up_AORT_VSMC
GO:0006820	0.349	0.933	1	109	anion transport	BP	1	NTRK2	up_APUL_EC
GO:0045723	0.349	0.943	1	5	positive regulation of fatty acid biosynthetic process	BP	1	PTGS2	up_VCAV_EC
GO:0097152	0.349	0.943	1	5	mesenchymal cell apoptotic process	BP	1	HIF1A	up_VCAV_EC
GO:0006518	0.349	0.937	1	290	peptide metabolic process	BP	1	ENSCAFG00000028814	up_VCAV_VSMC
GO:0040013	0.349	0.933	1	100	negative regulation of locomotion	BP	1	HOXA7	up_VFEM_EC
GO:0007265	0.349	0.934	1	121	Ras protein signal transduction	BP	1	ARHGEF2	up_VPUL_EC
GO:0034504	0.349355107	0.8215	4	111	protein localization to nucleus	BP	1	TRIM8,DCLK2,MAVS,PRKCD	up_ACOR_EC
GO:0035019	0.349854374	0.93419	1	16	somatic stem cell population maintenance	BP	1	SOX9	up_ACOR_EC
GO:0051253	0.35	0.727	24	359	negative regulation of RNA metabolic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,CBX5,FHL2,SMARCA4,PTPN2,MORF4L2,PEG3,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,HIF1AN,SIX4	down_VSAP_EC
GO:0044703	0.35	0.756	12	172	multi-organism reproductive process	BP	1	CELF1,ETV6,TMED2,PTGS2,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0001505	0.35	0.78	8	69	regulation of neurotransmitter levels	BP	1	SLC6A4,ABAT,DAGLB,STX4,KCNC4,ALDH9A1,ASS1,FLOT1	up_VSAP_EC
GO:0007165	0.35	0.798	7	1496	signal transduction	BP	1	NR1H4,MAPK10,PLCL1,ARHGEF26,NPNT,NTRK2,PDE1A	up_APUL_EC
GO:0043534	0.35	0.797	6	57	blood vessel endothelial cell migration	BP	1	HMGB1,GREM1,PRCP,EMP2,NUS1,AMOTL1	down_ACOR_VSMC
GO:0006333	0.35	0.797	6	59	chromatin assembly or disassembly	BP	1	NASP,SMARCA4,HIST1H1A,ASF1A,ATRX,HP1BP3	up_VCAV_EC
GO:0050877	0.35	0.806	5	164	nervous system process	BP	1	HOXC10,THRB,TMEM100,REEP2,DMPK	up_AFEM_EC
GO:0021675	0.35	0.827	4	29	nerve development	BP	1	CITED2,NRP1,DAG1,CHD7	up_ACOR_VSMC
GO:0002694	0.35	0.821	4	126	regulation of leukocyte activation	BP	1	LEP,BPI,GPAM,CYLD	up_AFEM_EC
GO:0008645	0.35	0.825	4	37	hexose transmembrane transport	BP	1	EDN1,YES1,RSC1A1,SLC2A3	up_VCAV_EC
GO:0015749	0.35	0.825	4	37	monosaccharide transmembrane transport	BP	1	EDN1,YES1,RSC1A1,SLC2A3	up_VCAV_EC
GO:0034219	0.35	0.825	4	37	carbohydrate transmembrane transport	BP	1	EDN1,YES1,RSC1A1,SLC2A3	up_VCAV_EC
GO:0009416	0.35	0.843	3	88	response to light stimulus	BP	1	CRY2,MFAP4,DCUN1D3	up_AFEM_EC
GO:0071230	0.35	0.848	3	23	cellular response to amino acid stimulus	BP	1	PDGFD,ZEB1,CASTOR1	up_VSAP_EC
GO:1901863	0.35	0.878	2	25	positive regulation of muscle tissue	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0030850	0.35	0.879	2	20	prostate gland development	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0032922	0.35	0.88	2	19	circadian regulation of gene expression	BP	1	BHLHE40,MAGED1	down_VSAP_EC

GO:0009755	0.35	0.875	2	52	hormone-mediated signaling pathway	BP	1	LBH,CRY2	up_AFEM_EC
GO:0009966	0.35	0.887	2	868	regulation of signal transduction	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0045912	0.35	0.881	2	15	negative regulation of carbohydrate metabolic	BP	1	FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0048858	0.35	0.875	2	159	cell projection morphogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0007340	0.35	0.943	1	5	acrosome reaction	BP	1	B4GALT1	down_ACOR_VSMC
GO:0040034	0.35	0.942	1	5	regulation of development,	BP	1	HMGN1	down_ACOR_VSMC
GO:0046596	0.35	0.938	1	8	regulation of viral entry into host cell	BP	1	TRIM8	down_VCAV_EC
GO:0060055	0.35	0.938	1	8	angiogenesis involved in wound healing	BP	1	B4GALT1	down_VCAV_EC
GO:0000466	0.35	0.938	1	8	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	PDCD11	down_VSAP_EC
GO:0034134	0.35	0.939	1	7	toll-like receptor 2 signaling pathway	BP	1	LYN	down_VSAP_EC
GO:0090335	0.35	0.939	1	7	regulation of brown fat cell differentiation	BP	1	PTGS2	down_VSAP_EC
GO:0106070	0.35	0.946	1	4	regulation of adenylate cyclase-activating G protein-coupled receptor	BP	1	APLP1	up_ACOR_VSMC
GO:0106072	0.35	0.946	1	4	negative regulation of adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	APLP1	up_ACOR_VSMC
GO:0007214	0.35	0.946	1	4	gamma-aminobutyric acid signaling pathway	BP	1	PLCL1	up_ACOR_VSMC
GO:0099563	0.35	0.946	1	4	modification of synaptic structure	BP	1	WASF3	up_ACOR_VSMC
GO:0000184	0.35	0.934	1	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	CTIF	up_AFEM_EC
GO:0003300	0.35	0.934	1	18	cardiac muscle hypertrophy	BP	1	LMCD1	up_AFEM_EC
GO:0014896	0.35	0.934	1	18	muscle hypertrophy	BP	1	LMCD1	up_AFEM_EC
GO:0014897	0.35	0.934	1	18	striated muscle hypertrophy	BP	1	LMCD1	up_AFEM_EC
GO:0002063	0.35	0.934	1	18	chondrocyte development	BP	1	AXIN2	up_AFEM_EC
GO:0042116	0.35	0.934	1	18	macrophage activation	BP	1	BPI	up_AFEM_EC
GO:0055006	0.35	0.934	1	18	cardiac cell development	BP	1	BVES	up_AFEM_EC
GO:0060420	0.35	0.934	1	18	regulation of heart growth	BP	1	ACACB	up_AFEM_EC
GO:0061387	0.35	0.934	1	18	regulation of extent of cell growth	BP	1	PLXNA4	up_AFEM_EC
GO:0055080	0.35	0.934	1	176	cation homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0044057	0.35	0.933	1	110	regulation of system process	BP	1	NPNT	up_APUL_EC
GO:0097475	0.35	0.946	1	4	motor neuron migration	BP	1	RELN	up_VCAV_EC
GO:0044089	0.35	0.934	1	170	positive regulation of cellular component	BP	1	NKX2-5	up_VPOR_VSMC
GO:0000904	0.35	0.934	1	181	cell morphogenesis involved in differentiation	BP	1	SHOX2	up_VFEM_VSMC
GO:0022604	0.35	0.933	1	122	regulation of cell morphogenesis	BP	1	CCL24	up_VPUL_EC
GO:0002221	0.350166054	0.87548	2	46	pattern recognition receptor signaling	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0002758	0.350166054	0.87548	2	46	innate immune response-activating signal	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0016569	0.350344506	0.80531	5	144	covalent chromatin modification	BP	1	NR1H4,PHF20,ZMYND8,PRKCD,PYGO2	up_ACOR_EC
GO:1902116	0.350548632	0.93391	1	16	negative regulation of organelle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0043392	0.350620979	0.93388	1	16	negative regulation of DNA binding	BP	1	CLSTN1	up_ACOR_EC

GO:0010604	0.351	0.702	59	919	positive regulation of macromolecule metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,MYH9,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,TMED2,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,MSN,HIF1A,ACTG2,TNIK,ZPR1,YES1,PEG3,DDX39B,ADAM17,ACTA2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,APOE,KLF5,LYN,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,GTF2H1,ARMCX3,REST,CALM1,DISC1,RAD23A,PAK2,INHBA,NR4A1,TMTC3,NRP1,SH3RF3,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0042493	0.351	0.736	19	178	response to drug	BP	1	FZD1,EMX2,SLIT2,CDH1,SLC6A4,ABL1,CHRM1,OSR1,MAP3K5,MYC,ABAT,CASTOR1,PNP,ZNF580,NCOA2,PPP3CB,HMOX1,TGFBR2,DDIT4	up_VSAP_EC
GO:0051235	0.351	0.772	9	90	maintenance of location	BP	1	SREBF2,INSIG1,CAV1,ABHD5,SLC30A1,YWHAB,GSTO1,CORO1A,ASPM	down_ACOR_VSMC
GO:0010646	0.351	0.774	9	945	regulation of cell communication	BP	1	BARX1,ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0031503	0.351	0.779	8	79	protein-containing complex localization	BP	1	EXOC3L2,RELN,IWS1,HHEX,MZT1,THOC1,SMG7,NUP133	up_VCAV_EC
GO:0048754	0.351	0.796	6	57	branching morphogenesis of an epithelial tube	BP	1	TIMELESS,MMP14,GREM1,HOXB7,B4GALT1,SIX4	down_ACOR_VSMC
GO:0018108	0.351	0.806	5	79	peptidyl-tyrosine phosphorylation	BP	1	PDGFRB,PRNP,CSPG4,ARL2BP,GREM1	down_VCAV_EC
GO:0048519	0.351	0.821	5	1554	negative regulation of biological process	BP	1	HOXC10,EYA1,HOXA9,FBP1,SHOX2	up_VFEM_VSMC
GO:0061326	0.351	0.809	5	41	renal tubule development	BP	1	HOXA11,WNT11,DLL1,OSR1,IRX3	up_VSAP_EC
GO:0072080	0.351	0.809	5	41	nephron tubule development	BP	1	HOXA11,WNT11,DLL1,OSR1,IRX3	up_VSAP_EC
GO:0034764	0.351	0.822	4	50	positive regulation of transmembrane transport	BP	1	NR1H4,PTPN11,HTT,CALM1	down_VSAP_EC
GO:0070665	0.351	0.826	4	31	positive regulation of leukocyte proliferation	BP	1	MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:1904888	0.351	0.826	4	31	cranial skeletal system development	BP	1	TBX15,INSIG2,IRX5,TGFBR2	up_VSAP_EC
GO:0060401	0.351	0.843	3	42	cytosolic calcium ion transport	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0072089	0.351	0.844	3	43	stem cell proliferation	BP	1	NUMBL,GLI3,ZFP36L1	down_VCAV_EC
GO:0016444	0.351	0.848	3	23	somatic cell DNA recombination	BP	1	THOC1,SWAP70,HMGB1	up_VCAV_EC
GO:0002200	0.351	0.848	3	23	somatic diversification of immune receptors	BP	1	THOC1,SWAP70,HMGB1	up_VCAV_EC
GO:0002562	0.351	0.848	3	23	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	THOC1,SWAP70,HMGB1	up_VCAV_EC
GO:0009892	0.351	0.85	3	835	negative regulation of metabolic process	BP	1	HOXC10,FBP1,SHOX2	up_VFEM_VSMC
GO:0021872	0.351	0.879	2	19	forebrain generation of neurons	BP	1	INHBA,NRP1	down_VSAP_EC
GO:0030521	0.351	0.879	2	19	androgen receptor signaling pathway	BP	1	SMARCA4,KDM3A	down_VSAP_EC
GO:2000514	0.351	0.883	2	13	regulation of CD4-positive, alpha-beta T cell	BP	1	CD83,CD274	up_ACOR_VSMC
GO:0050663	0.351	0.875	2	52	cytokine secretion	BP	1	LEP,GPAM	up_AFEM_EC
GO:0006111	0.351	0.881	2	15	regulation of gluconeogenesis	BP	1	FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0031016	0.351	0.881	2	15	pancreas development	BP	1	HHEX,PROX1	up_VCAV_EC
GO:0010608	0.351	0.875	2	154	posttranscriptional regulation of gene	BP	1	PUM3,EIF5	up_VPOR_EC
GO:0009126	0.351	0.932	1	100	purine nucleoside monophosphate metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0009167	0.351	0.932	1	100	purine ribonucleoside monophosphate metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0061436	0.351	0.942	1	5	establishment of skin barrier	BP	1	STMN1	down_ACOR_VSMC
GO:1903011	0.351	0.942	1	5	negative regulation of bone development	BP	1	GREM1	down_ACOR_VSMC
GO:0033617	0.351	0.937	1	8	mitochondrial respiratory chain complex IV	BP	1	COA1	down_VCAV_EC
GO:0048340	0.351	0.937	1	8	paraxial mesoderm morphogenesis	BP	1	BMPR1A	down_VCAV_EC

GO:0060117	0.351	0.945	1	4	auditory receptor cell development	BP	1	SEC24B	up_ACOR_VSMC
GO:0015732	0.351	0.945	1	4	prostaglandin transport	BP	1	LEP	up_ACOR_VSMC
GO:0072102	0.351	0.945	1	4	glomerulus morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0090399	0.351	0.945	1	4	replicative senescence	BP	1	CDKN1A	up_ACOR_VSMC
GO:0006821	0.351	0.933	1	18	chloride transport	BP	1	CLIC4	up_AFEM_EC
GO:0032272	0.351	0.933	1	18	negative regulation of protein polymerization	BP	1	KANK1	up_AFEM_EC
GO:0046626	0.351	0.933	1	18	regulation of insulin receptor signaling	BP	1	KANK1	up_AFEM_EC
GO:0051155	0.351	0.933	1	18	positive regulation of striated muscle cell	BP	1	GREM1	up_AFEM_EC
GO:0060563	0.351	0.933	1	18	neuroepithelial cell differentiation	BP	1	DLL1	up_AFEM_EC
GO:1903432	0.351	0.933	1	18	regulation of TORC1 signaling	BP	1	CLEC16A	up_AFEM_EC
GO:0061061	0.351	0.934	1	179	muscle structure development	BP	1	SGCD	up_AORT_EC
GO:0097366	0.351	0.942	1	5	response to bronchodilator	BP	1	GUCY1B1	up_VCAV_EC
GO:0044255	0.351	0.936	1	293	cellular lipid metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0046434	0.351	0.932	1	52	organophosphate catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0032101	0.351	0.933	1	173	regulation of response to external stimulus	BP	1	C3AR1	up_VPOR_VSMC
GO:0009150	0.351	0.933	1	161	purine ribonucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0071222	0.35112619	0.8749	2	46	cellular response to lipopolysaccharide	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0016925	0.351338967	0.93358	1	16	protein sumoylation	BP	1	PIAS1	up_ACOR_EC
GO:0032410	0.351689009	0.93321	1	17	negative regulation of transporter activity	BP	1	ACTN2	up_ACOR_EC
GO:0015909	0.351804359	0.93339	1	16	long-chain fatty acid transport	BP	1	CFI	up_ACOR_EC
GO:1904063	0.351925492	0.93312	1	17	negative regulation of cation transmembrane	BP	1	ACTN2	up_ACOR_EC
GO:0009056	0.351993433	0.73016	22	755	catabolic process	BP	1	PLCL1,THNSL2,ATG16L2,SARDH,EDEM2,KLHL25,PLCE1,CFI,PIAS1,CLU,ALDOC,CHMP4B,TP53INP2,RARRES2,VPS16,RNF114,UBE2H,AZIN2,HM13,PRKCD,PM20D1,ENSCAFG00000010493	up_ACOR_EC
GO:0060249	0.352	0.76	11	110	anatomical structure homeostasis	BP	1	RPA1,HNRNPD,SLC29A1,RAD51,AURKB,NEK2,TFRC,SMC6,CORO1A,TINF2,CCT4	down_ACOR_VSMC
GO:0007423	0.352	0.759	11	155	sensory organ development	BP	1	BCAR3,PTPN11,SMARCA4,HIF1A,CTNNB1,CRYAB,PDS5B,SDC4,INHBA,SIX4,NRP1	down_VSAP_EC
GO:0060348	0.352	0.778	8	78	bone development	BP	1	NAB2,INSIG1,XYLT1,MMP14,GREM1,POC1A,SERPINH1,AMER1	down_ACOR_VSMC
GO:0006606	0.352	0.785	7	67	protein import into nucleus	BP	1	POLA2,RAN,ENSCAFG00000011598,IPO4,NUP62,NUP188,DMAP1	down_ACOR_VSMC
GO:0007030	0.352	0.822	4	49	Golgi organization	BP	1	PLK3,LMAN1,HTT,BLZF1	down_VSAP_EC
GO:0060993	0.352	0.843	3	42	kidney morphogenesis	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC
GO:0014902	0.352	0.844	3	34	myotube differentiation	BP	1	ACTN1,SIX4,HOMER1	down_VSAP_EC
GO:0032675	0.352	0.844	3	34	regulation of interleukin-6 production	BP	1	ARHGEF2,NR1H4,SOCS5	down_VSAP_EC
GO:0032612	0.352	0.848	3	22	interleukin-1 production	BP	1	ABCA1,F2RL1,NOD2	up_ACOR_VSMC
GO:0035272	0.352	0.848	3	21	exocrine system development	BP	1	FGFR2,NRP1,DAG1	up_ACOR_VSMC
GO:0006357	0.352	0.846	3	547	regulation of transcription by RNA polymerase II	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0008219	0.352	0.847	3	611	cell death	BP	1	NR1H4,PTGER2,ARHGEF2	up_VPUL_EC
GO:1901566	0.352	0.881	2	598	organonitrogen compound biosynthetic	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0009649	0.352	0.882	2	13	entrainment of circadian clock	BP	1	RBM4B,GNAQ	up_ACOR_VSMC
GO:0030104	0.352	0.882	2	13	water homeostasis	BP	1	INPP5K,WFS1	up_ACOR_VSMC
GO:0000302	0.352	0.874	2	52	response to reactive oxygen species	BP	1	CRYAB,SOD1	up_AFEM_EC

GO:0010595	0.352	0.874	2	52	positive regulation of endothelial cell migration	BP	1	ANGPT4,ADAM17	up_AFEM_EC
GO:0045017	0.352	0.874	2	52	glycerolipid biosynthetic process	BP	1	GPAM,AGPAT2	up_AFEM_EC
GO:0003197	0.352	0.88	2	16	endocardial cushion development	BP	1	BMP2,JAG1	up_VCAV_EC
GO:0038084	0.352	0.882	2	13	vascular endothelial growth factor signaling	BP	1	DLL1,CCBE1	up_VSAP_EC
GO:0060445	0.352	0.882	2	13	branching involved in salivary gland	BP	1	FGF7,NTN4	up_VSAP_EC
GO:0031349	0.352	0.931	1	90	positive regulation of defense response	BP	1	LYN	down_ACOR_EC
GO:0035268	0.352	0.942	1	5	protein mannosylation	BP	1	NUS1	down_ACOR_VSMC
GO:0097502	0.352	0.942	1	5	mannosylation	BP	1	NUS1	down_ACOR_VSMC
GO:1903649	0.352	0.942	1	5	regulation of cytoplasmic transport	BP	1	EZR	down_ACOR_VSMC
GO:2001138	0.352	0.942	1	5	regulation of phospholipid transport	BP	1	PRELID1	down_ACOR_VSMC
GO:2001140	0.352	0.942	1	5	positive regulation of phospholipid transport	BP	1	PRELID1	down_ACOR_VSMC
GO:0006796	0.352	0.951	1	938	phosphate-containing compound metabolic	BP	1	PLCL1	down_VFEM_EC
GO:0007097	0.352	0.938	1	7	nuclear migration	BP	1	HOOK3	down_VSAP_EC
GO:0051647	0.352	0.938	1	7	nucleus localization	BP	1	HOOK3	down_VSAP_EC
GO:0048011	0.352	0.938	1	7	neurotrophin TRK receptor signaling	BP	1	PTPN11	down_VSAP_EC
GO:0002313	0.352	0.945	1	4	mature B cell differentiation involved in	BP	1	PLCG2	up_ACOR_VSMC
GO:0002335	0.352	0.945	1	4	mature B cell differentiation	BP	1	PLCG2	up_ACOR_VSMC
GO:0030224	0.352	0.933	1	18	monocyte differentiation	BP	1	HOXA7	up_AFEM_EC
GO:0002534	0.352	0.933	1	18	cytokine production involved in inflammatory	BP	1	LEP	up_AFEM_EC
GO:0045661	0.352	0.933	1	18	regulation of myoblast differentiation	BP	1	DLL1	up_AFEM_EC
GO:0045747	0.352	0.933	1	18	positive regulation of Notch signaling pathway	BP	1	DLL1	up_AFEM_EC
GO:0070231	0.352	0.933	1	18	T cell apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0070664	0.352	0.933	1	18	negative regulation of leukocyte proliferation	BP	1	GREM1	up_AFEM_EC
GO:1903131	0.352	0.933	1	18	mononuclear cell differentiation	BP	1	HOXA7	up_AFEM_EC
GO:0051253	0.352	0.937	1	359	negative regulation of RNA metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0014706	0.352	0.932	1	112	striated muscle tissue development	BP	1	TBX5	up_APUL_EC
GO:0002701	0.352	0.94	1	6	negative regulation of production of molecular mediator of immune	BP	1	THOC1	up_VCAV_EC
GO:0006699	0.352	0.942	1	5	bile acid biosynthetic process	BP	1	PROX1	up_VCAV_EC
GO:0070841	0.352	0.942	1	5	inclusion body assembly	BP	1	SNCAIP	up_VCAV_EC
GO:0016049	0.352	0.932	1	124	cell growth	BP	1	FLRT3	up_VPUL_EC
GO:0009948	0.352418145	0.93314	1	16	anterior/posterior axis specification	BP	1	FZD5	up_ACOR_EC
GO:0018108	0.352475419	0.84085	3	79	peptidyl-tyrosine phosphorylation	BP	1	LRP4,NRP1,PRKCD	up_ACOR_EC

GO:0018130	0.353	0.688	108	1261	heterocycle biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0051128	0.353	0.693	80	790	regulation of cellular component organization	BP	1	SYNPO2L,FGF13,DNAJC6,SMAD6,ARHGAP28,ACTN2,PLCG2,DCBLD2,MID1,CDC7,USP6NL,ZRANB1,FEZ1,PRKAA2,ITM2C,BMP4,LCAT,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,GJA1,ATRX,SEC24B,WASF3,PPARGC1A,ATXN2,RERG,ZNF365,AR,LMO4,ZMYM2,F2RL1,MARCH5,BNIP3,EGLN1,CDKN1A,JMY,CRLF3,CLSTN1,NRP1,LRPAP1,ULK2,DMPK,EVL,SLITRK5,TBX20,PRKCE,DAG1,APP,PSEN1,SGSM2,SYNJ2BP,SIPA1L1,DDR2,DUSP22,SSH3,EDN1,GTF2A1L,LRRC4,ASAP1,FAM107A,JAM3,B2M,DISC1,KIF9,SCAMP5,IGFBP7,FEZ2,INPP5K,RAB5C,WASL,NAIF1,DOCK5,SH3BP4,HMBOX1,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0044089	0.353	0.742	16	170	positive regulation of cellular component biogenesis	BP	1	FSCN1,ANLN,SDC1,CAV1,NF2,DHX33,RAC1,NUP62,FOSL1,PLK4,IQGAP2,CDC42EP4,CORO1A,ARPC1B,PSMC1,TPBG	down_ACOR_VSMC
GO:0034504	0.353	0.759	11	111	protein localization to nucleus	BP	1	POLA2,CTDNEP1,RAN,CDK1,NF2,ENSCAFG00000011598,IPO4,NUP62,NUP188,DMAP1,SIX4	down_ACOR_VSMC
GO:0021537	0.353	0.777	8	73	telencephalon development	BP	1	RELN,CHD7,BMP2,PROX1,ENSCAFG00000010224,HIF1A,ALDH1A3,CDON	up_VCAV_EC
GO:0031503	0.353	0.793	6	79	protein-containing complex localization	BP	1	MZT1,RPGR,DYNLL1,IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0006323	0.353	0.794	6	58	DNA packaging	BP	1	PSME4,NASP,HIST1H1A,ASF1A,ATRX,HP1BP3	up_VCAV_EC
GO:0007093	0.353	0.794	6	59	mitotic cell cycle checkpoint	BP	1	PLK2,TAOK1,BLM,RAD17,ZW10,TOPBP1	up_VCAV_EC
GO:0034330	0.353	0.804	5	80	cell junction organization	BP	1	NUMBL,RHOD,RASSF8,THY1,GREM1	down_VCAV_EC
GO:0030902	0.353	0.807	5	41	hindbrain development	BP	1	SEZ6L,ABL1,DLL1,KDM2B,NFIB	up_VSAP_EC
GO:2001022	0.353	0.842	3	42	positive regulation of response to DNA damage	BP	1	TMEM161A,SPRED1,FBH1	down_VCAV_EC
GO:0030199	0.353	0.848	3	21	collagen fibril organization	BP	1	FMOD,P4HA1,DDR2	up_ACOR_VSMC
GO:0051403	0.353	0.84	3	89	stress-activated MAPK cascade	BP	1	LEP,CYLD,CDC42EP5	up_AFEM_EC
GO:0048522	0.353	0.861	3	1484	positive regulation of cellular process	BP	1	TLR2,EYA1,HOXA9	up_AFEM_VSMC
GO:0035914	0.353	0.847	3	22	skeletal muscle cell differentiation	BP	1	CDON,GTF3C5,CITED2	up_VSAP_EC
GO:0033077	0.353	0.847	3	22	T cell differentiation in thymus	BP	1	ZFP36L1,ZEB1,ZFP36L2	up_VSAP_EC
GO:0042304	0.353	0.88	2	15	regulation of fatty acid biosynthetic process	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:0042982	0.353	0.88	2	15	amyloid precursor protein metabolic process	BP	1	DHCR24,NECAB3	down_ACOR_VSMC
GO:0045022	0.353	0.88	2	15	early endosome to late endosome transport	BP	1	EMP2,EZR	down_ACOR_VSMC
GO:0008344	0.353	0.876	2	25	adult locomotory behavior	BP	1	PARK7,ENSCAFG00000017708	down_VCAV_EC
GO:0033143	0.353	0.876	2	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	KANK2,PARK7	down_VCAV_EC
GO:0070232	0.353	0.882	2	13	regulation of T cell apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0051173	0.353	0.885	2	874	positive regulation of nitrogen compound	BP	1	EYA1,HOXA9	up_AFEM_VSMC

GO:0031440	0.353	0.882	2	13	regulation of mRNA 3'-end processing	BP	1	ZFP36L1,CDK9	up_VSAP_EC
GO:0070371	0.353	0.931	1	91	ERK1 and ERK2 cascade	BP	1	LYN	down_ACOR_EC
GO:0034982	0.353	0.942	1	5	mitochondrial protein processing	BP	1	PMPCA	down_ACOR_VSMC
GO:0006103	0.353	0.941	1	5	2-oxoglutarate metabolic process	BP	1	AADAT	down_ACOR_VSMC
GO:0046931	0.353	0.941	1	5	pore complex assembly	BP	1	NDC1	down_ACOR_VSMC
GO:1903580	0.353	0.941	1	5	positive regulation of ATP metabolic process	BP	1	CDK1	down_ACOR_VSMC
GO:0034694	0.353	0.936	1	9	response to prostaglandin	BP	1	ADCY6	down_VCAV_EC
GO:0043923	0.353	0.938	1	7	positive regulation by host of viral transcription	BP	1	SMARCA4	down_VSAP_EC
GO:1904293	0.353	0.938	1	7	negative regulation of ERAD pathway	BP	1	USP14	down_VSAP_EC
GO:0070242	0.353	0.938	1	7	thymocyte apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:0030035	0.353	0.945	1	4	microspike assembly	BP	1	ACTN2	up_ACOR_VSMC
GO:2000392	0.353	0.945	1	4	regulation of lamellipodium	BP	1	RREB1	up_ACOR_VSMC
GO:0042737	0.353	0.933	1	18	drug catabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0048146	0.353	0.933	1	18	positive regulation of fibroblast proliferation	BP	1	FOSL2	up_AFEM_EC
GO:1902807	0.353	0.932	1	18	negative regulation of cell cycle G1/S phase	BP	1	DCUN1D3	up_AFEM_EC
GO:2000134	0.353	0.932	1	18	negative regulation of G1/S transition of mitotic	BP	1	DCUN1D3	up_AFEM_EC
GO:0003006	0.353	0.932	1	180	developmental process involved in reproduction	BP	1	HOXA9	up_AORT_EC
GO:0002715	0.353	0.941	1	5	regulation of natural killer cell mediated immunity	BP	1	NECTIN2	up_VCAV_EC
GO:0042269	0.353	0.941	1	5	regulation of natural killer cell mediated cytotoxicity	BP	1	NECTIN2	up_VCAV_EC
GO:0072070	0.353	0.941	1	5	loop of Henle development	BP	1	JAG1	up_VCAV_EC
GO:0000724	0.353	0.931	1	57	double-strand break repair via homologous	BP	1	CXHXorf57	up_VPOR_EC
GO:0030705	0.353	0.931	1	56	cytoskeleton-dependent intracellular transport	BP	1	HOOK3	up_VPOR_EC
GO:0051222	0.353	0.931	1	103	positive regulation of protein transport	BP	1	TLR2	up_VSAP_VSMC
GO:0008610	0.354	0.734	19	177	lipid biosynthetic process	BP	1	PEX7,ACSM3,LIPC,INSIG2,ACACB,CERS4,HSD3B7,HSD17B8,ENSCAFG00000000071,PLA2G6,PTGES,HACD4,LCAT,DHRS9,MVK,FAXDC2,IDH1,CYB5R3,B3GALT4	up_VSAP_EC
GO:0009260	0.354	0.776	8	83	ribonucleotide biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,HIF1A	up_VCAV_EC
GO:0046390	0.354	0.776	8	83	ribose phosphate biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,HIF1A	up_VCAV_EC
GO:1990845	0.354	0.795	6	51	adaptive thermogenesis	BP	1	PPARGC1B,EBF2,STAT6,MFN2,HOXC10,PRKAB1	up_VSAP_EC
GO:0045055	0.354	0.805	5	52	regulated exocytosis	BP	1	KIT,RAB27A,SNAP23,FES,STX11	up_VCAV_EC
GO:0006351	0.354	0.852	3	1069	transcription, DNA-templated	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0060271	0.354	0.84	3	89	cilium assembly	BP	1	CYLD,DNAL1,SPATA6	up_AFEM_EC
GO:0043066	0.354	0.874	2	253	negative regulation of apoptotic process	BP	1	IGF1R,PDPN	down_ACOR_EC
GO:0048675	0.354	0.875	2	26	axon extension	BP	1	NDN,TRPV2	down_VCAV_EC
GO:0071674	0.354	0.876	2	23	mononuclear cell migration	BP	1	SERPINE1,LYN	down_VSAP_EC
GO:0006749	0.354	0.88	2	14	glutathione metabolic process	BP	1	ENSCAFG00000028814,PARK7	up_ACOR_VSMC
GO:0097529	0.354	0.873	2	52	myeloid leukocyte migration	BP	1	CMKLR1,CCL5	up_AFEM_EC
GO:0006940	0.354	0.88	2	14	regulation of smooth muscle contraction	BP	1	DOCK4,GUCY1A1	up_VCAV_EC
GO:0060998	0.354	0.88	2	14	regulation of dendritic spine development	BP	1	RELN,MEF2C	up_VCAV_EC
GO:0050804	0.354	0.931	1	87	modulation of chemical synaptic transmission	BP	1	STX4	down_ACOR_EC
GO:0099177	0.354	0.931	1	87	regulation of trans-synaptic signaling	BP	1	STX4	down_ACOR_EC

GO:0048570	0.354	0.941	1	5	notochord morphogenesis	BP	1	GLI1	down_ACOR_VSMC
GO:0060346	0.354	0.941	1	5	bone trabecula formation	BP	1	GREM1	down_ACOR_VSMC
GO:0072161	0.354	0.941	1	5	mesenchymal cell differentiation involved in	BP	1	AMER1	down_ACOR_VSMC
GO:2001012	0.354	0.941	1	5	mesenchymal cell differentiation involved in renal system	BP	1	AMER1	down_ACOR_VSMC
GO:0000226	0.354	0.933	1	197	microtubule cytoskeleton organization	BP	1	GPSM2	down_AFEM_EC
GO:0048532	0.354	0.935	1	9	anatomical structure arrangement	BP	1	BMPR1A	down_VCAV_EC
GO:0010646	0.354	0.95	1	945	regulation of cell communication	BP	1	PLCL1	down_VFEM_EC
GO:0002043	0.354	0.937	1	7	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	JCAD	down_VSAP_EC
GO:0015810	0.354	0.944	1	4	aspartate transmembrane transport	BP	1	SLC25A12	up_ACOR_VSMC
GO:0033085	0.354	0.944	1	4	negative regulation of T cell differentiation in	BP	1	BMP4	up_ACOR_VSMC
GO:1901264	0.354	0.932	1	18	carbohydrate derivative transport	BP	1	SLC17A5	up_AFEM_EC
GO:0036444	0.354	0.939	1	6	calcium import into the mitochondrion	BP	1	MCU	up_VCAV_EC
GO:0045835	0.354	0.941	1	5	negative regulation of meiotic nuclear division	BP	1	FBXO5	up_VCAV_EC
GO:2001279	0.354	0.944	1	4	regulation of unsaturated fatty acid biosynthetic	BP	1	PTGS2	up_VCAV_EC
GO:0051924	0.354	0.93	1	53	regulation of calcium ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0044703	0.354	0.932	1	172	multi-organism reproductive process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0042326	0.354	0.932	1	163	negative regulation of phosphorylation	BP	1	FBP1	up_VFEM_VSMC
GO:0034248	0.354	0.932	1	125	regulation of cellular amide metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0060284	0.354	0.933	1	212	regulation of cell development	BP	1	SLIT2	up_VPUL_VSMC
GO:0006690	0.354085045	0.93245	1	16	icosanoid metabolic process	BP	1	PTGDS	up_ACOR_EC
GO:0032728	0.354148066	0.93243	1	16	positive regulation of interferon-beta	BP	1	MAVS	up_ACOR_EC
GO:0001755	0.354282741	0.93237	1	16	neural crest cell migration	BP	1	NRP1	up_ACOR_EC
GO:0021602	0.354693515	0.9322	1	16	cranial nerve morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0044267	0.355	0.692	83	1583	cellular protein metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,PRNP,UBA52,GLIPR2,BGN,LARP6,COA1,BMPR1A,KRTCAP2,VKORC1,RECK,CLIP3,AKT1S1,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,HR,RPL23,RPL13,PLCL1,DDOST,CSPG4,PRMT6,GFPT2,ASPN,PIGS,HS3ST3B1,EIF3K,THY1,RNF216,WDR45,MRPL37,B4GALT1,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RPL27,COPS7A,ARL2BP,IFT57,MAVS,MRPS11,CDH2,LOXL3,GSDME,CAMK2D,RPS27,FUT8,SPRED1,A2M,SEC61B,MAPRE3,CDKL2,HM13,DDR2,SHC1,CRTAP,ENSCAFG00000015122,PYM1,FBH1,GREM1,RPN2,KLHL29,LONP2,FOXO3,PACSIN3,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0031344	0.355	0.737	17	161	regulation of cell projection organization	BP	1	ENPP2,SLIT2,ABL1,CDC42EP5,FUZ,PLXNA4,CDC42EP2,F2RL1,SHOX2,RTN4RL1,LRP4,DPYSL2,FBXO7,PQBP1,TTL,NCK1,MAP2K2	up_VSAP_EC
GO:0065007	0.355	0.805	10	3499	biological regulation	BP	1	CHL1,FGF5,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:1903037	0.355	0.803	5	65	regulation of leukocyte cell-cell adhesion	BP	1	SOCS5,FAM49B,PTPN2,TFRC,SDC4	down_VSAP_EC
GO:0014065	0.355	0.807	5	39	phosphatidylinositol 3-kinase signaling	BP	1	LEP,HTR2B,F2RL1,UNC5B,EDN1	up_ACOR_VSMC
GO:0048706	0.355	0.819	4	59	embryonic skeletal system development	BP	1	TBX15,GLI3,IRX5,RDH10	down_VCAV_EC
GO:0043491	0.355	0.819	4	50	protein kinase B signaling	BP	1	ILK,SESN2,MTDH,DDIT3	down_VSAP_EC
GO:0032268	0.355	0.824	4	778	regulation of cellular protein metabolic process	BP	1	PLCL1,PCSK1N,NPNT,NTRK2	up_APUL_EC
GO:0048534	0.355	0.84	3	262	hematopoietic or lymphoid organ	BP	1	BARX1,HOXA3,ACVR2A	up_VPOR_EC

GO:0002381	0.355	0.877	2	19	immunoglobulin production involved in immunoglobulin	BP	1	TFRC,BTK	down_VSAP_EC
GO:1904292	0.355	0.88	2	13	regulation of ERAD pathway	BP	1	OS9,HERPUD1	up_ACOR_VSMC
GO:0045055	0.355	0.873	2	52	regulated exocytosis	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0006952	0.355	0.875	2	319	defense response	BP	1	NR1H4,BPI	up_APUL_EC
GO:1905063	0.355	0.941	1	5	regulation of vascular smooth muscle cell	BP	1	CTH	down_ACOR_VSMC
GO:2000209	0.355	0.941	1	5	regulation of anoikis	BP	1	CAV1	down_ACOR_VSMC
GO:2000811	0.355	0.941	1	5	negative regulation of anoikis	BP	1	CAV1	down_ACOR_VSMC
GO:0051932	0.355	0.935	1	9	synaptic transmission, GABAergic	BP	1	PLCL1	down_VCAV_EC
GO:1900449	0.355	0.935	1	9	regulation of glutamate receptor signaling	BP	1	PRNP	down_VCAV_EC
GO:0000122	0.355	0.933	1	218	negative regulation of transcription by RNA polymerase II	BP	1	HDAC7	down_VPOR_EC
GO:0006793	0.355	0.95	1	948	phosphorus metabolic process	BP	1	PLCL1	down_VFEM_EC
GO:0046831	0.355	0.939	1	6	regulation of RNA export from nucleus	BP	1	IWS1	down_VSAP_EC
GO:0030277	0.355	0.937	1	7	maintenance of gastrointestinal	BP	1	STRAP	down_VSAP_EC
GO:0051240	0.355	0.938	1	489	positive regulation of multicellular organismal	BP	1	GATA5	down_VSAP_VSMC
GO:0033080	0.355	0.944	1	4	immature T cell proliferation in thymus	BP	1	BMP4	up_ACOR_VSMC
GO:0033084	0.355	0.944	1	4	regulation of immature T cell proliferation in	BP	1	BMP4	up_ACOR_VSMC
GO:1901339	0.355	0.944	1	4	regulation of store-operated calcium channel	BP	1	PLCG2	up_ACOR_VSMC
GO:0007200	0.355	0.932	1	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	CHRM2	up_AFEM_EC
GO:0001909	0.355	0.932	1	18	leukocyte mediated cytotoxicity	BP	1	LEP	up_AFEM_EC
GO:0046902	0.355	0.932	1	18	regulation of mitochondrial membrane	BP	1	CAMK2A	up_AFEM_EC
GO:0051781	0.355	0.932	1	18	positive regulation of cell division	BP	1	LBH	up_AFEM_EC
GO:0061309	0.355	0.941	1	5	cardiac neural crest cell development involved in outflow tract	BP	1	JAG1	up_VCAV_EC
GO:0021563	0.355	0.944	1	4	glossopharyngeal nerve development	BP	1	NAV2	up_VCAV_EC
GO:0021895	0.355	0.941	1	5	cerebral cortex neuron differentiation	BP	1	GDPD5	up_VCAV_EC
GO:0032071	0.355	0.941	1	5	regulation of endodeoxyribonuclease	BP	1	HMGB1	up_VCAV_EC
GO:0010975	0.355	0.93	1	103	regulation of neuron projection development	BP	1	SHOX2	up_VSAP_VSMC
GO:0051705	0.355100115	0.93203	1	16	multi-organism behavior	BP	1	MAPK8IP2	up_ACOR_EC
GO:0032212	0.355638455	0.93181	1	16	positive regulation of telomere maintenance via	BP	1	PKIB	up_ACOR_EC
GO:1904358	0.355638455	0.93181	1	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	PKIB	up_ACOR_EC
GO:0010830	0.355933518	0.93169	1	16	regulation of myotube differentiation	BP	1	RBM38	up_ACOR_EC
GO:0000904	0.356	0.734	18	181	cell morphogenesis involved in differentiation	BP	1	EPHB1,TEK,IFRD1,RELN,MEF2C,STC1,GATA3,RAB11A,NEDD9,PPP3CA,PREX2,PROX1,STMN1,FLNB,RAPGEF2,CREB1,SPTBN4,ENSCAFG00000002015	up_VCAV_EC
GO:0008015	0.356	0.749	13	120	blood circulation	BP	1	THRB,RNPEP,IRX5,SLIT2,EMP2,KCNE3,CHRM1,DLL1,F2RL1,TBXA2R,AGTR1,E2F4,ACVRL1	up_VSAP_EC
GO:0034248	0.356	0.752	12	125	regulation of cellular amide metabolic process	BP	1	ILF3,EIF4A3,HNRNPD,PPP1R15B,TRUB2,PLK3,FASTKD3,EIF5A,NCL,RBM14,NOLC1,PUM3	down_ACOR_VSMC
GO:0006887	0.356	0.781	7	99	exocytosis	BP	1	EXOC5,LYN,GSK3B,SDC4,REST,SCAMP1,RAB11FIP1	down_VSAP_EC
GO:0008406	0.356	0.792	6	57	gonad development	BP	1	SF1,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC

GO:0045137	0.356	0.792	6	57	development of primary sexual characteristics	BP	1	SF1,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC
GO:0003206	0.356	0.793	6	51	cardiac chamber morphogenesis	BP	1	FZD1,WNT11,SAV1,SHOX2,TGFBR2,CITED2	up_VSAP_EC
GO:0065003	0.356	0.821	4	616	protein-containing complex assembly	BP	1	IGF1R,RPSA,ACSL3,STX4	down_ACOR_EC
GO:0032943	0.356	0.818	4	60	mononuclear cell proliferation	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0046651	0.356	0.818	4	60	lymphocyte proliferation	BP	1	GPAM,PRNP,SDC4,RAC2	down_VCAV_EC
GO:0090316	0.356	0.819	4	48	positive regulation of intracellular protein	BP	1	PLK3,MYO1C,ZPR1,GSK3B	down_VSAP_EC
GO:0097659	0.356	0.851	3	1072	nucleic acid-templated transcription	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:2000242	0.356	0.878	2	15	negative regulation of reproductive process	BP	1	FBXO5,TTK	down_ACOR_VSMC
GO:0002376	0.356	0.879	2	622	immune system process	BP	1	CITED2,HSD3B7	down_VPOR_EC
GO:0015748	0.356	0.877	2	16	organophosphate ester transport	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0050772	0.356	0.88	2	13	positive regulation of axonogenesis	BP	1	SHOX2,MAP2K2	up_VSAP_EC
GO:1901890	0.356	0.88	2	13	positive regulation of cell junction assembly	BP	1	ABL1,FLOT1	up_VSAP_EC
GO:0006364	0.356	0.93	1	87	rRNA processing	BP	1	WDR12	down_ACOR_EC
GO:0009651	0.356	0.941	1	5	response to salt stress	BP	1	ANXA7	down_ACOR_VSMC
GO:0030539	0.356	0.94	1	5	male genitalia development	BP	1	DHCR24	down_ACOR_VSMC
GO:0033238	0.356	0.937	1	7	regulation of cellular amine metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0048569	0.356	0.937	1	7	post-embryonic animal organ development	BP	1	MYO1E	down_VSAP_EC
GO:0048846	0.356	0.938	1	6	axon extension involved in axon guidance	BP	1	NRP1	down_VSAP_EC
GO:1902284	0.356	0.938	1	6	neuron projection extension involved in neuron projection	BP	1	NRP1	down_VSAP_EC
GO:0019884	0.356	0.944	1	4	antigen processing and presentation of exogenous antigen	BP	1	B2M	up_ACOR_VSMC
GO:0033210	0.356	0.944	1	4	leptin-mediated signaling pathway	BP	1	LEP	up_ACOR_VSMC
GO:0044320	0.356	0.944	1	4	cellular response to leptin stimulus	BP	1	LEP	up_ACOR_VSMC
GO:0098771	0.356	0.931	1	180	inorganic ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0006396	0.356	0.935	1	368	RNA processing	BP	1	ESR1	up_AORT_VSMC
GO:0006790	0.356	0.93	1	99	sulfur compound metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0060070	0.356	0.93	1	105	canonical Wnt signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0050708	0.356	0.93	1	101	regulation of protein secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0001954	0.356458092	0.93123	1	17	positive regulation of cell-matrix adhesion	BP	1	NRP1	up_ACOR_EC
GO:0036503	0.356773029	0.8714	2	47	ERAD pathway	BP	1	EDEM2,HM13	up_ACOR_EC
GO:0043086	0.357	0.759	10	170	negative regulation of catalytic activity	BP	1	CST3,DCN,BGN,RECK,AKT1S1,TIMP2,ASPN,THY1,PARK7,SPRED1	down_VCAV_EC
GO:0050900	0.357	0.761	10	89	leukocyte migration	BP	1	HOXA7,ARHGEF5,C5AR2,SLC8B1,SLIT2,IL17RC,HSD3B7,F2RL1,MYD88,ZNF580	up_VSAP_EC
GO:0022607	0.357	0.796	6	969	cellular component assembly	BP	1	ACVRL1,IGF1R,SPG11,RPSA,ACSL3,STX4	down_ACOR_EC
GO:0051271	0.357	0.789	6	98	negative regulation of cellular component	BP	1	DCN,BMPR1A,RECK,THY1,SPRED1,FOXO3	down_VCAV_EC
GO:0060348	0.357	0.79	6	78	bone development	BP	1	SULF1,SERPINH1,SPARC,PTPN11,CHSY1,PLS3	down_VSAP_EC
GO:0007568	0.357	0.792	6	50	aging	BP	1	MARCH5,CDKN1A,APP,PSEN1,CLN8,PRELP	up_ACOR_VSMC
GO:0019219	0.357	0.798	6	1151	regulation of nucleobase-containing compound metabolic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0071222	0.357	0.804	5	46	cellular response to lipopolysaccharide	BP	1	IRAK1,MTDH,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0046824	0.357	0.822	4	30	positive regulation of nucleocytoplasmic	BP	1	LEP,PTPN22,PSEN1,JUP	up_ACOR_VSMC

GO:0048469	0.357	0.821	4	31	cell maturation	BP	1	GJA1,RND1,APP,DMC1	up_ACOR_VSMC
GO:0019218	0.357	0.843	3	25	regulation of steroid metabolic process	BP	1	SREBF1,SF1,INSIG1	down_ACOR_VSMC
GO:0032774	0.357	0.851	3	1073	RNA biosynthetic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0042752	0.357	0.84	3	34	regulation of circadian rhythm	BP	1	BHLHE40,MAGED1,GNAQ	down_VSAP_EC
GO:0010771	0.357	0.845	3	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	NRP1,ULK2,PSEN1	up_ACOR_VSMC
GO:0006066	0.357	0.838	3	89	alcohol metabolic process	BP	1	LEP,MOXD1,NAPEPLD	up_AFEM_EC
GO:0046364	0.357	0.842	3	27	monosaccharide biosynthetic process	BP	1	ATF3,FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:1901616	0.357	0.878	2	15	organic hydroxy compound catabolic	BP	1	PDXP,NUDT3	down_ACOR_VSMC
GO:2000648	0.357	0.878	2	14	positive regulation of stem cell proliferation	BP	1	PDCD2,ASPM	down_ACOR_VSMC
GO:0050729	0.357	0.874	2	25	positive regulation of inflammatory response	BP	1	PARK7,NAPEPLD	down_VCAV_EC
GO:0051150	0.357	0.879	2	13	regulation of smooth muscle cell differentiation	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0034109	0.357	0.878	2	14	homotypic cell-cell adhesion	BP	1	ITGB3,PEAR1	up_VCAV_EC
GO:0051270	0.357	0.873	2	296	regulation of cellular component movement	BP	1	HOXA7,TIAM1	up_VFEM_EC
GO:0060964	0.357	0.879	2	13	regulation of gene silencing by miRNA	BP	1	ZC3H10,LIMD1	up_VSAP_EC
GO:1900078	0.357	0.879	2	13	positive regulation of cellular response to	BP	1	KLF15,PIK3R1	up_VSAP_EC
GO:0021537	0.357	0.929	1	73	telencephalon development	BP	1	NRP2	down_ACOR_EC
GO:0044539	0.357	0.94	1	5	long-chain fatty acid import	BP	1	ACSL3	down_ACOR_VSMC
GO:0060363	0.357	0.94	1	5	cranial suture morphogenesis	BP	1	INSIG1	down_ACOR_VSMC
GO:0071320	0.357	0.934	1	9	cellular response to cAMP	BP	1	ZFP36L1	down_VCAV_EC
GO:0023051	0.357	0.949	1	954	regulation of signaling	BP	1	PLCL1	down_VFEM_EC
GO:2000404	0.357	0.936	1	7	regulation of T cell migration	BP	1	ADAM17	down_VSAP_EC
GO:0003373	0.357	0.943	1	4	dynamin family protein polymerization involved in membrane fission	BP	1	MX1	up_ACOR_VSMC
GO:0003374	0.357	0.943	1	4	dynamin family protein polymerization involved in mitochondrial fission	BP	1	MX1	up_ACOR_VSMC
GO:0042308	0.357	0.94	1	5	negative regulation of protein import into	BP	1	FERMT1	up_ACOR_VSMC
GO:1904590	0.357	0.94	1	5	negative regulation of protein import	BP	1	FERMT1	up_ACOR_VSMC
GO:0001836	0.357	0.931	1	18	release of cytochrome c from mitochondria	BP	1	MLLT11	up_AFEM_EC
GO:0009628	0.357	0.934	1	302	response to abiotic stimulus	BP	1	EYA1	up_AFEM_VSMC
GO:0006629	0.357	0.935	1	382	lipid metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0090306	0.357	0.943	1	4	spindle assembly involved in meiosis	BP	1	FBXO5	up_VCAV_EC
GO:1902624	0.357	0.936	1	7	positive regulation of neutrophil migration	BP	1	CXCL8	up_VCAV_EC
GO:0017000	0.357	0.943	1	4	antibiotic biosynthetic process	BP	1	KDM3A	up_VCAV_EC
GO:0035907	0.357	0.94	1	5	dorsal aorta development	BP	1	DLL4	up_VCAV_EC
GO:0035912	0.357	0.94	1	5	dorsal aorta morphogenesis	BP	1	DLL4	up_VCAV_EC
GO:0003207	0.357	0.94	1	5	cardiac chamber formation	BP	1	MEF2C	up_VCAV_EC
GO:1901652	0.357	0.93	1	105	response to peptide	BP	1	AVPR1A	up_VFEM_EC
GO:0051186	0.357	0.931	1	159	cofactor metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043207	0.357	0.932	1	216	response to external biotic stimulus	BP	1	IL22RA1	up_VPUL_VSMC
GO:0051707	0.357	0.932	1	216	response to other organism	BP	1	IL22RA1	up_VPUL_VSMC

GO:0098542	0.357	0.929	1	100	defense response to other organism	BP	1	TLR2	up_VSAP_VSMC
GO:0051092	0.357061495	0.87122	2	47	positive regulation of NF-kappaB transcription	BP	1	NOD2,CLU	up_ACOR_EC
GO:0090224	0.35741413	0.93107	1	16	regulation of spindle organization	BP	1	CHMP4B	up_ACOR_EC
GO:0048568	0.357795037	0.7995	5	148	embryonic organ development	BP	1	SOX9,FZD5,FOXC2,RARRES2,EFEMP1	up_ACOR_EC
GO:0006915	0.358	0.696	55	550	apoptotic process	BP	1	RHOT1,SMAD6,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,TLR3,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,USP53,ITPR1,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,CDKN1A,JMY,NRP1,DMPK,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,APP,PSEN1,SPINK2,CLN8,PERP,SIAH1,OXR1,NOD2,DDIT4,SERINC3,TNFRSF11B,KLF11,HERPUD1,MAP3K7,WFS1,NAIF1,PARK7,ZMAT3	up_ACOR_VSMC
GO:0051252	0.358	0.719	27	1051	regulation of RNA metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,PPARGC1A,SAMD4B	up_AFEM_EC
GO:0007399	0.358	0.74	15	564	nervous system development	BP	1	IRX3,IRX5,HOXC10,LEP,DLL1,VXN,PLXNA4,NEFH,THRB,LGI4,CAMK2A,LUZP1,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0046034	0.358	0.761	10	88	ATP metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0009306	0.358	0.765	9	127	protein secretion	BP	1	NR1H4,PTPN11,SEL1L,HIF1A,LYN,GBP5,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0045089	0.358	0.773	8	70	positive regulation of innate immune response	BP	1	TLR1,COCH,TLR3,F2RL1,PTPN22,PRKCE,PARP9,NOD2	up_ACOR_VSMC
GO:2001235	0.358	0.773	8	69	positive regulation of apoptotic signaling	BP	1	PLEKHF1,CRADD,TRAF7,RBCK1,ZNF205,HTRA2,NCK1,DEDD2	up_VSAP_EC
GO:0007369	0.358	0.801	5	63	gastrulation	BP	1	ITGA2,CTNNB1,EXT1,INHBA,COL12A1	down_VSAP_EC
GO:1903708	0.358	0.801	5	65	positive regulation of hemopoiesis	BP	1	SOCS5,HIF1A,EVI2B,PRMT1,INHBA	down_VSAP_EC
GO:1903707	0.358	0.802	5	48	negative regulation of hemopoiesis	BP	1	HOXB8,ITPKB,HMGB1,CUL4A,TJP2	up_VCAV_EC
GO:2001056	0.358	0.819	4	38	positive regulation of cysteine-type	BP	1	HMGB1,PDCD2,CYCS,AIFM1	down_ACOR_VSMC
GO:0042775	0.358	0.841	3	28	mitochondrial ATP synthesis coupled	BP	1	CDK1,CYCS,CYC1	down_ACOR_VSMC
GO:0009855	0.358	0.839	3	42	determination of bilateral symmetry	BP	1	IFT57,PCSK6,GREM1	down_VCAV_EC
GO:0000027	0.358	0.876	2	16	ribosomal large subunit assembly	BP	1	DDX28,ENSCAFG00000015189	down_ACOR_VSMC
GO:0032435	0.358	0.877	2	15	negative regulation of proteasomal ubiquitin-dependent protein	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC
GO:0051649	0.358	0.878	2	630	establishment of localization in cell	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:0042310	0.358	0.874	2	21	vasoconstriction	BP	1	HTR7,ACTA2	down_VSAP_EC
GO:0097756	0.358	0.874	2	21	negative regulation of blood vessel diameter	BP	1	HTR7,ACTA2	down_VSAP_EC
GO:0032873	0.358	0.879	2	13	negative regulation of stress-activated MAPK	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0070303	0.358	0.879	2	13	negative regulation of stress-activated protein kinase signaling cascade	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0072583	0.358	0.879	2	13	clathrin-dependent endocytosis	BP	1	DNM1,UBQLN2	up_VSAP_EC
GO:0048878	0.358	0.872	2	283	chemical homeostasis	BP	1	STIM1,CAV1	up_VSAP_VSMC
GO:0006869	0.358	0.929	1	81	lipid transport	BP	1	ACSL3	down_ACOR_EC
GO:0009070	0.358	0.94	1	5	serine family amino acid biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0046600	0.358	0.94	1	5	negative regulation of centriole replication	BP	1	RBM14	down_ACOR_VSMC
GO:0061042	0.358	0.939	1	5	vascular wound healing	BP	1	ADIPOR2	down_ACOR_VSMC
GO:0072075	0.358	0.94	1	5	metanephric mesenchyme	BP	1	SIX4	down_ACOR_VSMC
GO:1902337	0.358	0.939	1	5	regulation of apoptotic process involved in	BP	1	B4GALT1	down_ACOR_VSMC

GO:1904748	0.358	0.939	1	5	regulation of apoptotic process involved in	BP	1	B4GALT1	down_ACOR_VSMC
GO:0006953	0.358	0.936	1	7	acute-phase response	BP	1	PTGS2	down_VSAP_EC
GO:0018200	0.358	0.935	1	8	peptidyl-glutamic acid modification	BP	1	NAA10	down_VSAP_EC
GO:0034377	0.358	0.936	1	7	plasma lipoprotein particle assembly	BP	1	APOE	down_VSAP_EC
GO:0065005	0.358	0.936	1	7	protein-lipid complex assembly	BP	1	APOE	down_VSAP_EC
GO:0033631	0.358	0.943	1	4	cell-cell adhesion mediated by integrin	BP	1	NPNT	up_ACOR_VSMC
GO:0001655	0.358	0.929	1	116	urogenital system development	BP	1	NPNT	up_APUL_EC
GO:0043455	0.358	0.939	1	5	regulation of secondary metabolic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0071545	0.358	0.937	1	6	inositol phosphate catabolic process	BP	1	IMPA1	up_VCAV_EC
GO:1903726	0.358	0.937	1	6	negative regulation of phospholipid metabolic	BP	1	PDGFB	up_VCAV_EC
GO:0007623	0.358	0.929	1	55	circadian rhythm	BP	1	HTR7	up_VPOR_EC
GO:0009306	0.358	0.93	1	127	protein secretion	BP	1	NR1H4	up_VPUL_EC
GO:1901652	0.358	0.929	1	105	response to peptide	BP	1	CAV1	up_VSAP_VSMC
GO:0009967	0.35831281	0.74536	13	435	positive regulation of signal transduction	BP	1	CDH3,NR1H4,SOX9,FZD5,DIXDC1,NOD2,ESM1,TNFRSF19,MAVS,SH3RF3,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0051591	0.358621566	0.93056	1	16	response to cAMP	BP	1	AQP1	up_ACOR_EC
GO:0050801	0.359	0.731	18	200	ion homeostasis	BP	1	EDNRB,CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,ABCA1,SWAP70,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0050794	0.359	0.779	12	3075	regulation of cellular process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,RGS1,STK32B,WIF1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0007548	0.359	0.78	7	68	sex differentiation	BP	1	SF1,DHCR24,HMGB2,SGPL1,ASPM,HOXA9,SIX4	down_ACOR_VSMC
GO:0006606	0.359	0.78	7	67	protein import into nucleus	BP	1	HCLS1,TMEM173,FERMT1,PPP3CA,APOD,NUP133,IPO11	up_VCAV_EC
GO:0007548	0.359	0.78	7	68	sex differentiation	BP	1	KIT,CHD7,TIPARP,EIF2B2,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:0071219	0.359	0.791	6	50	cellular response to molecule of bacterial	BP	1	TLR1,ABCA1,SASH1,ANKRD1,PRKCE,NOD2	up_ACOR_VSMC
GO:0051240	0.359	0.801	5	489	positive regulation of multicellular organismal	BP	1	C3AR1,ARHGEF2,SEMA3A,ACVR2A,MTDH	up_VPOR_EC
GO:0071426	0.359	0.819	4	35	ribonucleoprotein complex export from	BP	1	DDX39A,RAN,NUP62,DDX39B	down_ACOR_VSMC
GO:0032535	0.359	0.814	4	128	regulation of cellular component size	BP	1	PRR16,PLXNA4,CDC42EP5,KANK1	up_AFEM_EC
GO:0030218	0.359	0.838	3	42	erythrocyte differentiation	BP	1	ZFP36L1,FOXO3,ANKRD54	down_VCAV_EC
GO:0060324	0.359	0.842	3	24	face development	BP	1	CHD7,TIPARP,ALDH1A3	up_VCAV_EC
GO:0040011	0.359	0.84	3	505	locomotion	BP	1	HOXA7,SIX1,TIAM1	up_VFEM_EC
GO:1905515	0.359	0.843	3	22	non-motile cilium assembly	BP	1	FUZ,TMEM17,TTC8	up_VSAP_EC
GO:0030097	0.359	0.871	2	244	hemopoiesis	BP	1	LYN,HOXA7	down_ACOR_EC
GO:0007264	0.359	0.87	2	164	small GTPase mediated signal transduction	BP	1	ARHGEF2,FBP1	up_VPOR_EC
GO:0060443	0.359	0.878	2	13	mammary gland morphogenesis	BP	1	STAT6,TGFBR2	up_VSAP_EC
GO:0060972	0.359	0.878	2	13	left/right pattern formation	BP	1	DLL1,CITED2	up_VSAP_EC
GO:0002253	0.359	0.929	1	92	activation of immune response	BP	1	LYN	down_ACOR_EC
GO:0009161	0.359	0.929	1	103	ribonucleoside monophosphate	BP	1	TNRC6B	down_ACOR_EC
GO:0016032	0.359	0.929	1	94	viral process	BP	1	NEDD4	down_ACOR_EC
GO:0072522	0.359	0.929	1	91	purine-containing compound biosynthetic	BP	1	TNRC6B	down_ACOR_EC
GO:0006071	0.359	0.939	1	5	glycerol metabolic process	BP	1	GK5	down_ACOR_VSMC
GO:0048313	0.359	0.939	1	5	Golgi inheritance	BP	1	PLK3	down_ACOR_VSMC
GO:0043368	0.359	0.933	1	9	positive T cell selection	BP	1	LOXL3	down_VCAV_EC

GO:0060977	0.359	0.937	1	6	coronary vasculature morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0006020	0.359	0.943	1	4	inositol metabolic process	BP	1	PPIP5K1	up_ACOR_VSMC
GO:0006349	0.359	0.943	1	4	regulation of gene expression by genetic	BP	1	PCGF5	up_ACOR_VSMC
GO:0097475	0.359	0.943	1	4	motor neuron migration	BP	1	NRP1	up_ACOR_VSMC
GO:0030540	0.359	0.939	1	5	female genitalia development	BP	1	CHD7	up_VCAV_EC
GO:0009081	0.359	0.937	1	6	branched-chain amino acid metabolic process	BP	1	BCAT1	up_VCAV_EC
GO:0071680	0.359	0.943	1	4	response to indole-3-methanol	BP	1	CTNNA1	up_VCAV_EC
GO:0071681	0.359	0.943	1	4	cellular response to indole-3-methanol	BP	1	CTNNA1	up_VCAV_EC
GO:0000725	0.359	0.928	1	58	recombinational repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0001649	0.359	0.928	1	54	osteoblast differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0032990	0.359	0.93	1	167	cell part morphogenesis	BP	1	CHL1	up_VPOR_VSMC
GO:0070085	0.359	0.929	1	95	glycosylation	BP	1	GALNT17	up_VSAP_VSMC
GO:0031349	0.36	0.759	10	90	positive regulation of defense response	BP	1	TLR1,COCH,TLR3,F2RL1,PTPN22,PRKCE,PARP9,APP,NOD2,PARK7	up_ACOR_VSMC
GO:0046034	0.36	0.787	6	88	ATP metabolic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0060326	0.36	0.787	6	84	cell chemotaxis	BP	1	VEGFA,SERPINE1,ADAM17,MMP28,LYN,NRP1	down_VSAP_EC
GO:0043434	0.36	0.799	5	80	response to peptide hormone	BP	1	ENSCAFG00000014978,AKT2,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0030038	0.36	0.819	4	31	contractile actin filament bundle assembly	BP	1	ARHGAP28,NRP1,EVL,INPP5K	up_ACOR_VSMC
GO:0030968	0.36	0.819	4	33	endoplasmic reticulum unfolded protein	BP	1	HERPUD1,WFS1,DZIP3,STC2	up_ACOR_VSMC
GO:0043149	0.36	0.819	4	31	stress fiber assembly	BP	1	ARHGAP28,NRP1,EVL,INPP5K	up_ACOR_VSMC
GO:0051173	0.36	0.822	4	874	positive regulation of nitrogen compound	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0001944	0.36	0.836	3	263	vasculature development	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0003143	0.36	0.842	3	22	embryonic heart tube morphogenesis	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:1904019	0.36	0.842	3	22	epithelial cell apoptotic process	BP	1	ABL1,ZFP36L1,TGFBR2	up_VSAP_EC
GO:0044070	0.36	0.842	3	22	regulation of anion transport	BP	1	GABRE,OSR1,RAB11B	up_VSAP_EC
GO:0000288	0.36	0.872	2	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	SAMD4B,ZFP36L1	down_VCAV_EC
GO:0014066	0.36	0.872	2	26	regulation of phosphatidylinositol 3-	BP	1	DCN,MYDGF	down_VCAV_EC
GO:0001707	0.36	0.872	2	25	mesoderm formation	BP	1	BMPR1A,TLX2	down_VCAV_EC
GO:0051173	0.36	0.881	2	874	positive regulation of nitrogen compound	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0043489	0.36	0.877	2	13	RNA stabilization	BP	1	AXIN2,TENT5C	up_VSAP_EC
GO:0019752	0.36	0.871	2	283	carboxylic acid metabolic process	BP	1	GATM,CAV1	up_VSAP_VSMC
GO:0006790	0.36	0.928	1	99	sulfur compound metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0006241	0.36	0.939	1	5	CTP biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0009147	0.36	0.939	1	5	pyrimidine nucleoside triphosphate metabolic	BP	1	CTPS1	down_ACOR_VSMC
GO:0009148	0.36	0.939	1	5	pyrimidine nucleoside triphosphate biosynthetic	BP	1	CTPS1	down_ACOR_VSMC
GO:0009208	0.36	0.939	1	5	pyrimidine ribonucleoside triphosphate metabolic	BP	1	CTPS1	down_ACOR_VSMC
GO:0009209	0.36	0.939	1	5	pyrimidine ribonucleoside triphosphate biosynthetic	BP	1	CTPS1	down_ACOR_VSMC
GO:0040031	0.36	0.939	1	5	snRNA modification	BP	1	ENSCAFG00000019620	down_ACOR_VSMC
GO:0046036	0.36	0.939	1	5	CTP metabolic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0071971	0.36	0.939	1	5	extracellular exosome assembly	BP	1	SDC1	down_ACOR_VSMC

GO:0090670	0.36	0.939	1	5	RNA localization to Cajal body	BP	1	CCT4	down_ACOR_VSMC
GO:0090671	0.36	0.939	1	5	telomerase RNA localization to Cajal body	BP	1	CCT4	down_ACOR_VSMC
GO:0090672	0.36	0.939	1	5	telomerase RNA localization	BP	1	CCT4	down_ACOR_VSMC
GO:0090685	0.36	0.939	1	5	RNA localization to nucleus	BP	1	CCT4	down_ACOR_VSMC
GO:1903551	0.36	0.939	1	5	regulation of extracellular exosome assembly	BP	1	SDC1	down_ACOR_VSMC
GO:1904872	0.36	0.939	1	5	regulation of telomerase RNA localization to Cajal	BP	1	CCT4	down_ACOR_VSMC
GO:0032365	0.36	0.933	1	9	intracellular lipid transport	BP	1	SCP2	down_VCAV_EC
GO:1902745	0.36	0.933	1	9	positive regulation of lamellipodium	BP	1	RAC2	down_VCAV_EC
GO:0009084	0.36	0.935	1	7	glutamine family amino acid biosynthetic process	BP	1	ALDH18A1	down_VSAP_EC
GO:0060026	0.36	0.935	1	7	convergent extension	BP	1	PTK7	down_VSAP_EC
GO:0060546	0.36	0.935	1	7	negative regulation of necroptotic process	BP	1	ARHGEF2	down_VSAP_EC
GO:0060547	0.36	0.935	1	7	negative regulation of necrotic cell death	BP	1	ARHGEF2	down_VSAP_EC
GO:0021562	0.36	0.942	1	4	vestibulocochlear nerve development	BP	1	NRP1	up_ACOR_VSMC
GO:0031290	0.36	0.942	1	4	retinal ganglion cell axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0035546	0.36	0.942	1	4	interferon-beta secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:0035547	0.36	0.942	1	4	regulation of interferon-beta secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:0035549	0.36	0.942	1	4	positive regulation of interferon-beta secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:1902668	0.36	0.942	1	4	negative regulation of axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0051493	0.36	0.93	1	188	regulation of cytoskeleton organization	BP	1	TAOK1	up_AORT_EC
GO:0009259	0.36	0.93	1	166	ribonucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:1901615	0.36	0.929	1	128	organic hydroxy compound metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0051960	0.36	0.931	1	216	regulation of nervous system development	BP	1	SLIT2	up_VPUL_VSMC
GO:0002763	0.3601241	0.92969	1	17	positive regulation of myeloid leukocyte	BP	1	CLSTN1	up_ACOR_EC
GO:0006812	0.36039904	0.77596	7	222	cation transport	BP	1	AQP1,KCNB1,ACTN2,MAPK8IP2,SLC9A9,PM20D1,ATP7B	up_ACOR_EC
GO:0000122	0.361	0.72	23	218	negative regulation of transcription by RNA polymerase II	BP	1	LEP,NACC2,BMP4,FGFR2,ATRX,TRPS1,ZNF174,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,WFS1,HMBOX1,RREB1	up_ACOR_VSMC
GO:0009889	0.361	0.757	11	1190	regulation of biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:1903320	0.361	0.757	10	102	regulation of protein modification by small protein conjugation or	BP	1	USP4,UBE2S,U2AF2,SLC29A1,CAV1,FANCI,CDC20,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0008202	0.361	0.764	9	80	steroid metabolic process	BP	1	LEP,LCAT,ABCA1,LIPE,SCP2,DKKL1,APP,CLN8,LMF1	up_ACOR_VSMC
GO:1901617	0.361	0.779	7	60	organic hydroxy compound biosynthetic	BP	1	INSIG2,GOT1,PPIP5K1,PCBD1,MVK,PNPO,CYB5R3	up_VSAP_EC
GO:0071772	0.361	0.801	5	50	response to BMP	BP	1	GATA3,SMAD1,BMP2,CTDSPL2,SKIL	up_VCAV_EC
GO:0071773	0.361	0.801	5	50	cellular response to BMP stimulus	BP	1	GATA3,SMAD1,BMP2,CTDSPL2,SKIL	up_VCAV_EC
GO:0000079	0.361	0.84	3	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CDKN2C,CKS2,CCNB3	down_ACOR_VSMC
GO:0080135	0.361	0.87	2	240	regulation of cellular response to stress	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0019076	0.361	0.875	2	15	viral release from host cell	BP	1	TRIM35,SMC3	down_ACOR_VSMC
GO:0035890	0.361	0.875	2	15	exit from host	BP	1	TRIM35,SMC3	down_ACOR_VSMC
GO:0035891	0.361	0.875	2	15	exit from host cell	BP	1	TRIM35,SMC3	down_ACOR_VSMC
GO:0052126	0.361	0.875	2	15	movement in host environment	BP	1	TRIM35,SMC3	down_ACOR_VSMC

GO:0052192	0.361	0.875	2	15	movement in environment of other organism involved in	BP	1	TRIM35,SMC3	down_ACOR_VSMC
GO:0071310	0.361	0.876	2	634	cellular response to organic substance	BP	1	CITED2,RAB11B	down_VPOR_EC
GO:0050710	0.361	0.877	2	13	negative regulation of cytokine secretion	BP	1	F2RL1,PTPN22	up_ACOR_VSMC
GO:0051179	0.361	0.9	2	1747	localization	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0060548	0.361	0.87	2	294	negative regulation of cell death	BP	1	EYA1,SIX1	up_VFEM_EC
GO:0001961	0.361	0.877	2	13	positive regulation of cytokine-mediated	BP	1	CREBRF,MAVS	up_VSAP_EC
GO:0009123	0.361	0.928	1	104	nucleoside monophosphate	BP	1	TNRC6B	down_ACOR_EC
GO:0023061	0.361	0.928	1	95	signal release	BP	1	STX4	down_ACOR_EC
GO:0032071	0.361	0.939	1	5	regulation of endodeoxyribonuclease	BP	1	HMGB1	down_ACOR_VSMC
GO:0034375	0.361	0.938	1	5	high-density lipoprotein particle remodeling	BP	1	LIPC	down_ACOR_VSMC
GO:0060339	0.361	0.939	1	5	negative regulation of type I interferon-mediated signaling	BP	1	CACTIN	down_ACOR_VSMC
GO:0048523	0.361	0.96	1	1399	negative regulation of cellular process	BP	1	CST3	down_AORT_EC
GO:0009187	0.361	0.932	1	10	cyclic nucleotide metabolic process	BP	1	ADCY6	down_VCAV_EC
GO:0046850	0.361	0.933	1	9	regulation of bone remodeling	BP	1	GREM1	down_VCAV_EC
GO:0061323	0.361	0.935	1	7	cell proliferation involved in heart morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:1902473	0.361	0.942	1	4	regulation of protein localization to synapse	BP	1	DAG1	up_ACOR_VSMC
GO:0032104	0.361	0.942	1	4	regulation of response to extracellular stimulus	BP	1	LEP	up_ACOR_VSMC
GO:0032107	0.361	0.942	1	4	regulation of response to nutrient levels	BP	1	LEP	up_ACOR_VSMC
GO:0051152	0.361	0.938	1	5	positive regulation of smooth muscle cell	BP	1	KIT	up_VCAV_EC
GO:0014009	0.361	0.938	1	5	glial cell proliferation	BP	1	PRKCH	up_VCAV_EC
GO:0007160	0.361	0.927	1	56	cell-matrix adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0010817	0.361	0.928	1	102	regulation of hormone levels	BP	1	CYP26B1	up_VFEM_EC
GO:1903320	0.361	0.928	1	102	regulation of protein modification by small protein conjugation or	BP	1	CAV1	up_VSAP_VSMC
GO:0019216	0.361	0.928	1	101	regulation of lipid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0000904	0.361209687	0.78486	6	181	cell morphogenesis involved in differentiation	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1,ARHGEF26	up_ACOR_EC
GO:0008016	0.361483158	0.86844	2	48	regulation of heart contraction	BP	1	GNAO1,RNLS	up_ACOR_EC
GO:0051173	0.362	0.692	56	874	positive regulation of nitrogen compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,MYH9,NR1H4,PLK3,HSPA5,SOCS5,JCAD,BCAR3,PTPN11,TRIB3,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,MSN,HIF1A,TNIK,ZPR1,YES1,PEG3,DDX39B,ADAM17,CNOT7,MAGED1,CTNNB1,TFRC,APOE,KLF5,LYN,DDIT3,FAM162A,MMD,ATF3,GSK3B,VLDLR,GTF2H1,ARMCX3,REST,CALM1,DISC1,RAD23A,PAK2,INHBA,NR4A1,TMTC3,NRP1,SH3RF3,ARF4,YWHAH,MADD,KDM3A,MID1	down_VSAP_EC
GO:0032270	0.362	0.714	26	479	positive regulation of cellular protein metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,PRNP,GLIPR2,LARP6,BMPR1A,CLIP3,AKT2,CSPG4,PARK7,EEF2,MYDGF,SASH1,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,PACSIN3	down_VCAV_EC
GO:0120039	0.362	0.761	9	158	plasma membrane bounded cell projection	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,UST,BRSK1	down_VCAV_EC
GO:0023051	0.362	0.765	9	954	regulation of signaling	BP	1	BARX1,ARHGEF2,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0009617	0.362	0.767	8	133	response to bacterium	BP	1	CFD,ENSCAFG00000013404,FKBP5,SASH1,BPI,CYBA,MAVS,SHC1	down_VCAV_EC
GO:0071496	0.362	0.776	7	97	cellular response to external stimulus	BP	1	ASNS,HSPA5,SESN2,BNIP3,ATF3,EIF2S1,CDKN1A	down_VSAP_EC

GO:0022898	0.362	0.8	5	48	regulation of transmembrane	BP	1	RELN,PDE4D,MEF2C,PLCG2,RIPK1	up_VCAV_EC
GO:0042147	0.362	0.816	4	38	retrograde transport, endosome to Golgi	BP	1	RAB6A,SNX2,GCC2,VPS54	up_VCAV_EC
GO:0043507	0.362	0.84	3	23	positive regulation of JUN kinase activity	BP	1	MAP3K11,EDN1,RIPK1	up_VCAV_EC
GO:0097581	0.362	0.87	2	26	lamellipodium organization	BP	1	RHOD,RAC2	down_VCAV_EC
GO:1901224	0.362	0.872	2	20	positive regulation of NIK/NF-kappaB signaling	BP	1	ILK,ENSCAFG00000002015	down_VSAP_EC
GO:0032370	0.362	0.877	2	13	positive regulation of lipid transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0030808	0.362	0.875	2	15	regulation of nucleotide biosynthetic process	BP	1	NOS2,HIF1A	up_VCAV_EC
GO:1900371	0.362	0.875	2	15	regulation of purine nucleotide biosynthetic	BP	1	NOS2,HIF1A	up_VCAV_EC
GO:0010557	0.362	0.873	2	492	positive regulation of macromolecule biosynthetic process	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0044381	0.362	0.876	2	13	glucose import in response to insulin	BP	1	KLF15,PIK3R1	up_VSAP_EC
GO:0044262	0.362	0.928	1	89	cellular carbohydrate metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0003012	0.362	0.927	1	90	muscle system process	BP	1	SULF1	down_ACOR_EC
GO:0034330	0.362	0.927	1	80	cell junction organization	BP	1	ACVRL1	down_ACOR_EC
GO:0090596	0.362	0.927	1	84	sensory organ morphogenesis	BP	1	HOXA1	down_ACOR_EC
GO:0007141	0.362	0.938	1	5	male meiosis I	BP	1	TRIP13	down_ACOR_VSMC
GO:0019062	0.362	0.938	1	5	virion attachment to host cell	BP	1	SLC29A1	down_ACOR_VSMC
GO:0044406	0.362	0.938	1	5	adhesion of symbiont to host	BP	1	SLC29A1	down_ACOR_VSMC
GO:0044650	0.362	0.938	1	5	adhesion of symbiont to host cell	BP	1	SLC29A1	down_ACOR_VSMC
GO:0009218	0.362	0.934	1	7	pyrimidine ribonucleotide metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0015682	0.362	0.934	1	7	ferric iron transport	BP	1	TFRC	down_VSAP_EC
GO:0072512	0.362	0.934	1	7	trivalent inorganic cation transport	BP	1	TFRC	down_VSAP_EC
GO:0019367	0.362	0.938	1	5	fatty acid elongation, saturated fatty acid	BP	1	ELOVL7	up_ACOR_VSMC
GO:0019368	0.362	0.938	1	5	fatty acid elongation, unsaturated fatty acid	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034625	0.362	0.938	1	5	fatty acid elongation, monounsaturated fatty	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034626	0.362	0.938	1	5	fatty acid elongation, polyunsaturated fatty acid	BP	1	ELOVL7	up_ACOR_VSMC
GO:0035338	0.362	0.938	1	5	long-chain fatty-acyl-CoA biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0036302	0.362	0.942	1	4	atrioventricular canal development	BP	1	CHD7	up_ACOR_VSMC
GO:0043619	0.362	0.942	1	4	regulation of transcription from RNA polymerase II promoter in response to	BP	1	CHD6	up_ACOR_VSMC
GO:0051124	0.362	0.942	1	4	synaptic growth at neuromuscular junction	BP	1	APP	up_ACOR_VSMC
GO:0071680	0.362	0.941	1	4	response to indole-3-methanol	BP	1	JUP	up_ACOR_VSMC
GO:0071681	0.362	0.941	1	4	cellular response to indole-3-methanol	BP	1	JUP	up_ACOR_VSMC
GO:0001817	0.362	0.929	1	182	regulation of cytokine production	BP	1	BPI	up_AORT_EC
GO:0009101	0.362	0.928	1	113	glycoprotein biosynthetic process	BP	1	GALNT17	up_APUL_EC
GO:0061564	0.362	0.928	1	119	axon development	BP	1	SLITRK5	up_APUL_EC
GO:0070391	0.362	0.938	1	5	response to lipoteichoic acid	BP	1	TLR4	up_VCAV_EC
GO:0071223	0.362	0.938	1	5	cellular response to lipoteichoic acid	BP	1	TLR4	up_VCAV_EC
GO:0043567	0.362	0.936	1	6	regulation of insulin-like growth factor receptor	BP	1	BMP2	up_VCAV_EC
GO:0030001	0.362	0.929	1	172	metal ion transport	BP	1	NETO1	up_VFEM_VSMC
GO:0010639	0.362	0.928	1	128	negative regulation of organelle organization	BP	1	ARHGEF2	up_VPUL_EC

GO:0051098	0.362	0.928	1	129	regulation of binding	BP	1	HOXA3	up_VPUL_EC
GO:0033182	0.362	0.938	1	5	regulation of histone ubiquitination	BP	1	CDK9	up_VSAP_EC
GO:0016053	0.362	0.928	1	97	organic acid biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0046394	0.362	0.928	1	97	carboxylic acid biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0046486	0.362	0.928	1	102	glycerolipid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0015031	0.362133353	0.73574	15	510	protein transport	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0046530	0.362426172	0.92871	1	17	photoreceptor cell differentiation	BP	1	SOX9	up_ACOR_EC
GO:0000122	0.362480279	0.77428	7	218	negative regulation of transcription by RNA polymerase II	BP	1	NR1H4,TRPS1,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1	up_ACOR_EC
GO:0030858	0.362870478	0.92852	1	17	positive regulation of epithelial cell	BP	1	SOX9	up_ACOR_EC
GO:0051960	0.362880192	0.77397	7	216	regulation of nervous system development	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,LRP4,NRP1	up_ACOR_EC
GO:0072659	0.362926727	0.83347	3	82	protein localization to plasma membrane	BP	1	PLS1,ACTN2,LRRC15	up_ACOR_EC
GO:0002684	0.363	0.715	25	239	positive regulation of immune system process	BP	1	CD274,PPARGC1B,ABL1,ANKRD54,ZBTB16,TOX,STAT6,F2RL1,ZFP36L1,RBCK1,MYD88,CFD,NLRX1,TKFC,CD83,PNP,ZNF580,CYBA,STX4,PQBP1,UNC93B1,FLOT1,NCK1,MAVS,TGFBR2	up_VSAP_EC
GO:0050863	0.363	0.777	7	69	regulation of T cell activation	BP	1	HMGB1,PRELID1,CAV1,ARG2,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0050770	0.363	0.8	5	39	regulation of axonogenesis	BP	1	NRP1,ULK2,PSEN1,SIPA1L1,SSH3	up_ACOR_VSMC
GO:2000377	0.363	0.8	5	41	regulation of reactive oxygen species metabolic	BP	1	F2RL1,CYBA,ZNF205,ASS1,TGFBR2	up_VSAP_EC
GO:1901615	0.363	0.811	4	128	organic hydroxy compound metabolic	BP	1	LEP,MOXD1,NAPEPLD,GCNT4	up_AFEM_EC
GO:0009185	0.363	0.839	3	23	ribonucleoside diphosphate metabolic	BP	1	ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0007165	0.363	0.855	3	1496	signal transduction	BP	1	LIMK1,GATA5,CA2	up_VCAV_VSMC
GO:0031328	0.363	0.837	3	512	positive regulation of cellular biosynthetic	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0034121	0.363	0.84	3	22	regulation of toll-like receptor signaling	BP	1	F2RL1,CYBA,FLOT1	up_VSAP_EC
GO:0070897	0.363	0.874	2	16	transcription preinitiation complex assembly	BP	1	HMGB1,PSMC1	down_ACOR_VSMC
GO:0003170	0.363	0.87	2	25	heart valve development	BP	1	NOTCH2,BMPR1A	down_VCAV_EC
GO:0034637	0.363	0.87	2	25	cellular carbohydrate biosynthetic process	BP	1	AKT2,B4GALT1	down_VCAV_EC
GO:0032414	0.363	0.871	2	21	positive regulation of ion transmembrane transporter activity	BP	1	HTT,CALM1	down_VSAP_EC
GO:0006801	0.363	0.874	2	15	superoxide metabolic process	BP	1	GCH1,NOS2	up_VCAV_EC
GO:0043044	0.363	0.875	2	14	ATP-dependent chromatin remodeling	BP	1	PSME4,SMARCA4	up_VCAV_EC
GO:0002762	0.363	0.874	2	15	negative regulation of myeloid leukocyte	BP	1	CUL4A,TJP2	up_VCAV_EC
GO:0045935	0.363	0.873	2	491	positive regulation of nucleobase-containing compound metabolic	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0051196	0.363	0.876	2	13	regulation of coenzyme metabolic process	BP	1	PDK2,DDIT4	up_VSAP_EC
GO:0071404	0.363	0.938	1	5	cellular response to low-density lipoprotein	BP	1	SREBF2	down_ACOR_VSMC
GO:0071677	0.363	0.938	1	5	positive regulation of mononuclear cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0090026	0.363	0.938	1	5	positive regulation of monocyte chemotaxis	BP	1	HMGB1	down_ACOR_VSMC
GO:0006355	0.363	0.947	1	974	regulation of transcription, DNA-	BP	1	MOSPD1	down_VFEM_EC
GO:0098780	0.363	0.934	1	7	response to mitochondrial depolarisation	BP	1	CDC37	down_VSAP_EC
GO:0010765	0.363	0.938	1	5	positive regulation of sodium ion transport	BP	1	FXYD1	up_ACOR_VSMC
GO:0035331	0.363	0.941	1	4	negative regulation of hippo signaling	BP	1	WWC2	up_ACOR_VSMC

GO:0070647	0.363	0.931	1	311	protein modification by small protein conjugation	BP	1	EYA1	up_AFEM_VSMC
GO:0006520	0.363	0.927	1	114	cellular amino acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:2000291	0.363	0.938	1	5	regulation of myoblast proliferation	BP	1	ZNF609	up_VCAV_EC
GO:0032269	0.363	0.931	1	306	negative regulation of cellular protein metabolic	BP	1	LIMK1	up_VCAV_VSMC
GO:0002262	0.363	0.927	1	54	myeloid cell homeostasis	BP	1	ACVR2A	up_VPOR_EC
GO:0048589	0.363	0.928	1	188	developmental growth	BP	1	HOXA11	up_VFEM_VSMC
GO:0032535	0.363	0.927	1	128	regulation of cellular component size	BP	1	CCL24	up_VPUL_EC
GO:0002791	0.363	0.927	1	104	regulation of peptide secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0007409	0.363	0.927	1	109	axonogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0062012	0.363	0.927	1	100	regulation of small molecule metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:2000142	0.363582566	0.92821	1	17	regulation of DNA-templated transcription,	BP	1	CLSTN1	up_ACOR_EC
GO:0002526	0.363791647	0.92813	1	17	acute inflammatory response	BP	1	CLSTN1	up_ACOR_EC
GO:0010033	0.364	0.698	41	772	response to organic substance	BP	1	PCOLCE,GPAM,PDGFRB,SMAD9,LRP1,DCN,NDN,PRNP,VASN,FBN1,ADCY6,BGN,SLC10A3,KANK2,COL6A1,NUMBL,ENSCAFG00000014978,AKT1S1,CHRDL1,TIMP2,AKT2,NR3C1,ENSCAFG00000013404,EPHX1,TMEM161A,GFPT2,ASPN,PARK7,ZFP36L1,SASH1,MAVS,GSDME,FUT8,RAB7B,SEC61B,RAB31,HM13,SHC1,GREM1,FOXO3,RGMA	down_VCAV_EC
GO:0031399	0.364	0.708	30	559	regulation of protein modification process	BP	1	NOTCH2,PDGFRB,KIRREL1,DCN,PRNP,GLIPR2,BGN,BMPR1A,CLIP3,AKT1S1,AKT2,EEF2K,PLCL1,CSPG4,PRMT6,ASPN,THY1,PARK7,MYDGF,SASH1,ARL2BP,MAVS,CDH2,GSDME,SPRED1,MAPRE3,DDR2,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0090304	0.364	0.767	10	1694	nucleic acid metabolic process	BP	1	ACVRL1,YEATS2,YBX3,HIVEP2,HOXA7,SULF1,ELK3,HOXA1,WDR12,NEDD4	down_ACOR_EC
GO:0006109	0.364	0.787	6	51	regulation of carbohydrate metabolic	BP	1	ACACB,C1QTNF2,PDK2,PASK,NCOA2,DDIT4	up_VSAP_EC
GO:0034332	0.364	0.816	4	32	adherens junction organization	BP	1	ACTN2,NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0097327	0.364	0.838	3	25	response to antineoplastic agent	BP	1	RAD51,TIMELESS,CDK4	down_ACOR_VSMC
GO:0006694	0.364	0.835	3	42	steroid biosynthetic process	BP	1	HSD3B7,SCP2,CYB5R3	down_VCAV_EC
GO:0022612	0.364	0.834	3	44	gland morphogenesis	BP	1	SEMA3C,B4GALT1,GLI3	down_VCAV_EC
GO:0035710	0.364	0.839	3	22	CD4-positive, alpha-beta T cell activation	BP	1	CD83,CD274,IL18R1	up_ACOR_VSMC
GO:0010629	0.364	0.837	3	502	negative regulation of gene expression	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0010596	0.364	0.871	2	21	negative regulation of endothelial cell migration	BP	1	STARD13,APOE	down_VSAP_EC
GO:1902017	0.364	0.87	2	21	regulation of cilium assembly	BP	1	DYNLL1,HTT	down_VSAP_EC
GO:0060571	0.364	0.875	2	13	morphogenesis of an epithelial fold	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0044085	0.364	0.883	2	1076	cellular component biogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0006024	0.364	0.873	2	16	glycosaminoglycan biosynthetic process	BP	1	PDGFB,CHST7	up_VCAV_EC
GO:0030593	0.364	0.871	2	19	neutrophil chemotaxis	BP	1	CXCL8,PDE4D	up_VCAV_EC
GO:0030003	0.364	0.866	2	157	cellular cation homeostasis	BP	1	C3AR1,ENSCAFG00000005494	up_VPOR_EC
GO:0072594	0.364	0.867	2	155	establishment of protein localization to organelle	BP	1	GCC2,SRP54	up_VPOR_EC
GO:0043603	0.364	0.87	2	372	cellular amide metabolic process	BP	1	NR1H4,ENSCAFG00000028814	up_VPUL_EC
GO:0001553	0.364	0.938	1	5	luteinization	BP	1	SGPL1	down_ACOR_VSMC
GO:0007028	0.364	0.937	1	5	cytoplasm organization	BP	1	FOSL1	down_ACOR_VSMC
GO:0030574	0.364	0.937	1	5	collagen catabolic process	BP	1	MMP14	down_ACOR_VSMC
GO:0032211	0.364	0.937	1	5	negative regulation of telomere maintenance via	BP	1	TINF2	down_ACOR_VSMC

GO:0002190	0.364	0.938	1	5	cap-independent translational initiation	BP	1	RBM14	down_ACOR_VSMC
GO:0018149	0.364	0.932	1	9	peptide cross-linking	BP	1	DCN	down_VCAV_EC
GO:0046189	0.364	0.931	1	9	phenol-containing compound biosynthetic	BP	1	PARK7	down_VCAV_EC
GO:0071867	0.364	0.931	1	9	response to monoamine	BP	1	ADCY6	down_VCAV_EC
GO:0071868	0.364	0.931	1	9	cellular response to monoamine stimulus	BP	1	ADCY6	down_VCAV_EC
GO:0071869	0.364	0.931	1	9	response to catecholamine	BP	1	ADCY6	down_VCAV_EC
GO:0071870	0.364	0.931	1	9	cellular response to catecholamine stimulus	BP	1	ADCY6	down_VCAV_EC
GO:1903506	0.364	0.947	1	977	regulation of nucleic acid-templated transcription	BP	1	MOSPD1	down_VFEM_EC
GO:1901881	0.364	0.933	1	7	positive regulation of protein depolymerization	BP	1	WDR1	down_VSAP_EC
GO:2000516	0.364	0.933	1	7	positive regulation of CD4-positive, alpha-beta T cell activation	BP	1	SOCS5	down_VSAP_EC
GO:0010629	0.364	0.935	1	502	negative regulation of gene expression	BP	1	GATA5	down_VSAP_VSMC
GO:0042148	0.364	0.937	1	5	strand invasion	BP	1	DMC1	up_ACOR_VSMC
GO:0009164	0.364	0.937	1	5	nucleoside catabolic process	BP	1	ENPP4	up_ACOR_VSMC
GO:0010603	0.364	0.941	1	4	regulation of cytoplasmic mRNA processing body	BP	1	ATXN2	up_ACOR_VSMC
GO:0042454	0.364	0.937	1	5	ribonucleoside catabolic process	BP	1	ENPP4	up_ACOR_VSMC
GO:0045596	0.364	0.928	1	186	negative regulation of cell differentiation	BP	1	HOXA9	up_AORT_EC
GO:0072359	0.364	0.932	1	368	circulatory system development	BP	1	WNT7A	up_AORT_VSMC
GO:0048710	0.364	0.937	1	5	regulation of astrocyte differentiation	BP	1	BMP2	up_VCAV_EC
GO:0046519	0.364	0.935	1	6	sphingoid metabolic process	BP	1	SPTLC2	up_VCAV_EC
GO:0061418	0.364	0.937	1	5	regulation of transcription from RNA polymerase II promoter in response to	BP	1	HIF1A	up_VCAV_EC
GO:0040017	0.364	0.928	1	180	positive regulation of locomotion	BP	1	C3AR1	up_VPOR_VSMC
GO:0009165	0.364	0.926	1	104	nucleotide biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0040008	0.364	0.928	1	179	regulation of growth	BP	1	FBP1	up_VFEM_VSMC
GO:0006812	0.364	0.929	1	222	cation transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0046148	0.36462845	0.92777	1	17	pigment biosynthetic process	BP	1	CDH3	up_ACOR_EC
GO:0001654	0.365	0.765	8	110	eye development	BP	1	BCAR3,SMARCA4,HIF1A,CTNNB1,CRYAB,PDS5B,INHBA,NRP1	down_VSAP_EC
GO:0048880	0.365	0.765	8	110	sensory system development	BP	1	BCAR3,SMARCA4,HIF1A,CTNNB1,CRYAB,PDS5B,INHBA,NRP1	down_VSAP_EC
GO:0150063	0.365	0.765	8	110	visual system development	BP	1	BCAR3,SMARCA4,HIF1A,CTNNB1,CRYAB,PDS5B,INHBA,NRP1	down_VSAP_EC
GO:0065007	0.365	0.836	6	3499	biological regulation	BP	1	HOXC10,TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0006909	0.365	0.799	5	42	phagocytosis	BP	1	LEP,CDC7,ABCA1,F2RL1,TXNDC5	up_ACOR_VSMC
GO:1903531	0.365	0.799	5	41	negative regulation of secretion by cell	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1	up_VSAP_EC
GO:0006099	0.365	0.873	2	15	tricarboxylic acid cycle	BP	1	SUCLG1,PDHA1	down_ACOR_VSMC
GO:0001960	0.365	0.873	2	15	negative regulation of cytokine-mediated	BP	1	CAV1,CACTIN	down_ACOR_VSMC
GO:0060761	0.365	0.873	2	15	negative regulation of response to cytokine	BP	1	CAV1,CACTIN	down_ACOR_VSMC
GO:2000179	0.365	0.874	2	14	positive regulation of neural precursor cell	BP	1	ASPM,GLI1	down_ACOR_VSMC
GO:0045740	0.365	0.876	2	12	positive regulation of DNA replication	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0006955	0.365	0.868	2	327	immune response	BP	1	NR1H4,BPI	up_APUL_EC
GO:0120035	0.365	0.866	2	160	regulation of plasma membrane bounded cell projection organization	BP	1	SEMA3A,RNF6	up_VPOR_EC

GO:0009649	0.365	0.874	2	13	entrainment of circadian clock	BP	1	CHRM1,NR2F6	up_VSAP_EC
GO:0048663	0.365	0.874	2	13	neuron fate commitment	BP	1	DLL1,HOXC10	up_VSAP_EC
GO:0046470	0.365	0.874	2	13	phosphatidylcholine metabolic process	BP	1	ENPP2,LCAT	up_VSAP_EC
GO:1901653	0.365	0.926	1	84	cellular response to peptide	BP	1	IGF1R	down_ACOR_EC
GO:0006817	0.365	0.937	1	5	phosphate ion transport	BP	1	SLC20A1	down_ACOR_VSMC
GO:0006901	0.365	0.937	1	5	vesicle coating	BP	1	PREB	down_ACOR_VSMC
GO:0030575	0.365	0.937	1	5	nuclear body organization	BP	1	SF1	down_ACOR_VSMC
GO:0043584	0.365	0.937	1	5	nose development	BP	1	SIX4	down_ACOR_VSMC
GO:0071624	0.365	0.935	1	6	positive regulation of granulocyte chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:0090023	0.365	0.935	1	6	positive regulation of neutrophil chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:0031400	0.365	0.928	1	205	negative regulation of protein modification	BP	1	IVNS1ABP	down_AFEM_EC
GO:0005979	0.365	0.931	1	9	regulation of glycogen biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0010518	0.365	0.931	1	9	positive regulation of phospholipase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0010962	0.365	0.931	1	9	regulation of glucan biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0070873	0.365	0.931	1	9	regulation of glycogen metabolic process	BP	1	AKT2	down_VCAV_EC
GO:2001141	0.365	0.947	1	979	regulation of RNA biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0048523	0.365	0.959	1	1399	negative regulation of cellular process	BP	1	JUP	down_VFEM_VSMC
GO:0034086	0.365	0.933	1	7	maintenance of sister chromatid cohesion	BP	1	NAA10	down_VSAP_EC
GO:0034088	0.365	0.933	1	7	maintenance of mitotic sister chromatid cohesion	BP	1	NAA10	down_VSAP_EC
GO:0043558	0.365	0.933	1	7	regulation of translational initiation in response to	BP	1	EIF2S1	down_VSAP_EC
GO:0002418	0.365	0.937	1	5	immune response to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0002834	0.365	0.937	1	5	regulation of response to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0002837	0.365	0.937	1	5	regulation of immune response to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0006833	0.365	0.937	1	5	water transport	BP	1	INPP5K	up_ACOR_VSMC
GO:0018230	0.365	0.937	1	5	peptidyl-L-cysteine S-palmitoylation	BP	1	ZDHHC21	up_ACOR_VSMC
GO:0018231	0.365	0.937	1	5	peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-	BP	1	ZDHHC21	up_ACOR_VSMC
GO:0042490	0.365	0.927	1	19	mechanoreceptor differentiation	BP	1	DLL1	up_AFEM_EC
GO:0048483	0.365	0.927	1	19	autonomic nervous system development	BP	1	PLXNA4	up_AFEM_EC
GO:1903036	0.365	0.927	1	19	positive regulation of response to wounding	BP	1	KANK1	up_AFEM_EC
GO:1901700	0.365	0.932	1	364	response to oxygen-containing compound	BP	1	ESR1	up_AORT_VSMC
GO:0048732	0.365	0.927	1	116	gland development	BP	1	HOXA3	up_APUL_EC
GO:0060537	0.365	0.926	1	117	muscle tissue development	BP	1	TBX5	up_APUL_EC
GO:0061061	0.365	0.927	1	179	muscle structure development	BP	1	SHOX2	up_VFEM_VSMC
GO:0051129	0.365	0.929	1	221	negative regulation of cellular component	BP	1	SLIT2	up_VPUL_VSMC
GO:0051260	0.365	0.926	1	100	protein homooligomerization	BP	1	CAV1	up_VSAP_VSMC
GO:0001756	0.365004021	0.9276	1	17	somitogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0071466	0.365441454	0.92741	1	17	cellular response to xenobiotic stimulus	BP	1	AQP1	up_ACOR_EC
GO:1901214	0.365718078	0.83153	3	81	regulation of neuron death	BP	1	CHMP4B,NRP1,PM20D1	up_ACOR_EC
GO:0034599	0.365825229	0.83145	3	81	cellular response to oxidative stress	BP	1	AQP1,GUCY1B1,PRKCD	up_ACOR_EC

GO:0008285	0.366	0.719	21	201	negative regulation of cell proliferation	BP	1	SMAD6,PRDX4,NACC2,FERMT1,BMP4,PDE5A,TP53INP1,RERG,CD274,PTGIR,NDRG2,CDKN2B,LIMS2,CDKN1A,CLSTN1,TBX5,APP,SYNJ2BP,KLF11,SH3BP4,PTPN14	up_ACOR_VSMC
GO:0043543	0.366	0.766	8	84	protein acylation	BP	1	IWS1,GATA3,ZDHHC22,HHAT,CDYL,ESCO1,TAOK1,ZDHHC6	up_VCAV_EC
GO:0019932	0.366	0.782	6	82	second-messenger-mediated signaling	BP	1	FHL2,GNAQ,APOE,GSK3B,HTT,CALM1	down_VSAP_EC
GO:1901861	0.366	0.798	5	41	regulation of muscle tissue development	BP	1	CDON,DLL1,SAV1,SHOX2,FLOT1	up_VSAP_EC
GO:0030838	0.366	0.814	4	37	positive regulation of actin filament	BP	1	IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0035296	0.366	0.815	4	32	regulation of tube diameter	BP	1	CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0097746	0.366	0.815	4	32	regulation of blood vessel diameter	BP	1	CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0032368	0.366	0.836	3	26	regulation of lipid transport	BP	1	SREBF2,PRELID1,NUS1	down_ACOR_VSMC
GO:0055088	0.366	0.834	3	37	lipid homeostasis	BP	1	NR1H4,SESN2,APOE	down_VSAP_EC
GO:0019359	0.366	0.837	3	23	nicotinamide nucleotide biosynthetic process	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0019363	0.366	0.837	3	23	pyridine nucleotide biosynthetic process	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0045744	0.366	0.872	2	15	negative regulation of G protein-coupled receptor signaling pathway	BP	1	STMN1,YWHAB	down_ACOR_VSMC
GO:0072523	0.366	0.873	2	14	purine-containing compound catabolic	BP	1	PDE5A,ENPP4	up_ACOR_VSMC
GO:0010001	0.366	0.865	2	54	glial cell differentiation	BP	1	DLL1,LGI4	up_AFEM_EC
GO:0071622	0.366	0.874	2	13	regulation of granulocyte chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0014009	0.366	0.937	1	5	glial cell proliferation	BP	1	NF2	down_ACOR_VSMC
GO:0031125	0.366	0.934	1	6	rRNA 3'-end processing	BP	1	EXOSC5	down_ACOR_VSMC
GO:0051152	0.366	0.937	1	5	positive regulation of smooth muscle cell	BP	1	CTH	down_ACOR_VSMC
GO:2000291	0.366	0.937	1	5	regulation of myoblast proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0010470	0.366	0.93	1	9	regulation of gastrulation	BP	1	BMPR1A	down_VCAV_EC
GO:0045577	0.366	0.931	1	9	regulation of B cell differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0006812	0.366	0.928	1	222	cation transport	BP	1	RAB11B	down_VPOR_EC
GO:0050435	0.366	0.931	1	8	amyloid-beta metabolic process	BP	1	APOE	down_VSAP_EC
GO:0008038	0.366	0.932	1	7	neuron recognition	BP	1	NRP1	down_VSAP_EC
GO:0060439	0.366	0.933	1	7	trachea morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0090148	0.366	0.933	1	7	membrane fission	BP	1	SLC25A46	down_VSAP_EC
GO:0002551	0.366	0.936	1	5	mast cell chemotaxis	BP	1	VEGFD	up_ACOR_VSMC
GO:0002888	0.366	0.937	1	5	positive regulation of myeloid leukocyte	BP	1	F2RL1	up_ACOR_VSMC
GO:0048841	0.366	0.94	1	4	regulation of axon extension involved in	BP	1	NRP1	up_ACOR_VSMC
GO:0097531	0.366	0.936	1	5	mast cell migration	BP	1	VEGFD	up_ACOR_VSMC
GO:0070265	0.366	0.927	1	19	necrotic cell death	BP	1	CYLD	up_AFEM_EC
GO:1905954	0.366	0.927	1	19	positive regulation of lipid localization	BP	1	ACACB	up_AFEM_EC
GO:0001817	0.366	0.927	1	182	regulation of cytokine production	BP	1	C3AR1	up_VPOR_VSMC
GO:0016311	0.366	0.926	1	106	dephosphorylation	BP	1	EYA1	up_VFEM_EC
GO:0007268	0.366	0.926	1	130	chemical synaptic transmission	BP	1	HTR7	up_VPUL_EC
GO:0022411	0.366	0.926	1	130	cellular component disassembly	BP	1	ARHGEF2	up_VPUL_EC
GO:0032970	0.366	0.926	1	130	regulation of actin filament-based process	BP	1	CCL24	up_VPUL_EC
GO:0098916	0.366	0.926	1	130	anterograde trans-synaptic signaling	BP	1	HTR7	up_VPUL_EC

GO:0046883	0.36620907	0.86543	2	49	regulation of hormone secretion	BP	1	NR1H4,KCNB1	up_ACOR_EC
GO:0051173	0.367	0.68	77	874	positive regulation of nitrogen compound metabolic process	BP	1	ACSL3,HMGB1,SREBF1,IRAK1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,NEDD4,U2AF2,SLC29A1,PRELID1,RFC2,INSIG1,CAV1,CDK1,RFC5,RFC3,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,AURKB,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,SF3B4,CKS2,PDCD2,BRCA1,FASTKD3,EIF5A,E2F8,TFRC,PPARD,RAP2C,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,EZR,CLSPN,RBM14,RAD23A,CDC20,PSMC1,AIFM1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0051129	0.367	0.731	15	221	negative regulation of cellular component organization	BP	1	ARHGEF2,DPYSL3,IFRD1,NAA10,CRYAB,APOE,BNIP3,TWF1,GSK3B,LRRTM2,CAPG,NRP1,YWHAH,KDM3A,MID1	down_VSAP_EC
GO:0006790	0.367	0.748	11	99	sulfur compound metabolic process	BP	1	ACSM3,ACACB,PDK2,FXN,CTNS,ACSS2,MVK,MPST,IDH1,CHST7,ENSCAFG00000006478	up_VSAP_EC
GO:0051170	0.367	0.766	8	69	import into nucleus	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,RPAIN	up_ACOR_VSMC
GO:0007281	0.367	0.774	7	60	germ cell development	BP	1	BMP4,PDE5A,MARF1,AFF4,SPINK2,DMC1,JAM3	up_ACOR_VSMC
GO:0060538	0.367	0.784	6	51	skeletal muscle organ development	BP	1	CDON,DLL1,GTF3C5,SHOX2,FLOT1,CITED2	up_VSAP_EC
GO:0035023	0.367	0.796	5	46	regulation of Rho protein signal transduction	BP	1	ENSCAFG00000030005,STMN1,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0006869	0.367	0.793	5	81	lipid transport	BP	1	AKT2,LCAT,SCP2,OSBPL10,SOAT1	down_VCAV_EC
GO:0048608	0.367	0.808	4	129	reproductive structure development	BP	1	HOXA9,IRX5,LEP,TNC	up_AFEM_EC
GO:0031109	0.367	0.834	3	36	microtubule polymerization or	BP	1	ARHGEF2,MZT1,MID1	down_VSAP_EC
GO:0048513	0.367	0.841	3	906	animal organ development	BP	1	HOXC10,HOXA9,SGCD	up_AORT_EC
GO:0006511	0.367	0.866	2	253	ubiquitin-dependent protein catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0033260	0.367	0.872	2	15	nuclear DNA replication	BP	1	RAD51,GMNN	down_ACOR_VSMC
GO:1901566	0.367	0.872	2	598	organonitrogen compound biosynthetic	BP	1	DARS,EIF3M	down_AFEM_EC
GO:0099024	0.367	0.873	2	13	plasma membrane invagination	BP	1	ABCA1,F2RL1	up_ACOR_VSMC
GO:0090311	0.367	0.872	2	15	regulation of protein deacetylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0044088	0.367	0.87	2	17	regulation of vacuole organization	BP	1	RALB,SH3GLB1	up_VCAV_EC
GO:0040012	0.367	0.866	2	303	regulation of locomotion	BP	1	HOXA7,TIAM1	up_VFEM_EC
GO:0007289	0.367	0.936	1	5	spermatid nucleus differentiation	BP	1	HMGB2	down_ACOR_VSMC
GO:0060218	0.367	0.936	1	5	hematopoietic stem cell differentiation	BP	1	HSPA9	down_ACOR_VSMC
GO:1902532	0.367	0.927	1	204	negative regulation of intracellular signal	BP	1	IVNS1ABP	down_AFEM_EC
GO:0007417	0.367	0.927	1	235	central nervous system development	BP	1	CITED2	down_VPOR_EC
GO:0043968	0.367	0.932	1	7	histone H2A acetylation	BP	1	MORF4L2	down_VSAP_EC
GO:0032689	0.367	0.931	1	8	negative regulation of interferon-gamma	BP	1	NR1H4	down_VSAP_EC
GO:0033003	0.367	0.931	1	8	regulation of mast cell activation	BP	1	LYN	down_VSAP_EC
GO:0072182	0.367	0.932	1	7	regulation of nephron tubule epithelial cell	BP	1	CTNNB1	down_VSAP_EC
GO:2000136	0.367	0.932	1	7	regulation of cell proliferation involved in	BP	1	CTNNB1	down_VSAP_EC
GO:0003071	0.367	0.936	1	5	renal system process involved in regulation of systemic arterial blood	BP	1	F2RL1	up_ACOR_VSMC
GO:0051045	0.367	0.936	1	5	negative regulation of membrane protein	BP	1	PTPN3	up_ACOR_VSMC
GO:0008333	0.367	0.926	1	19	endosome to lysosome transport	BP	1	RAB7A	up_AFEM_EC
GO:0010092	0.367	0.926	1	19	specification of animal organ identity	BP	1	AXIN2	up_AFEM_EC
GO:0072210	0.367	0.927	1	19	metanephric nephron development	BP	1	GREM1	up_AFEM_EC

GO:0097006	0.367	0.927	1	19	regulation of plasma lipoprotein particle levels	BP	1	PLAGL2	up_AFEM_EC
GO:0007265	0.367	0.926	1	121	Ras protein signal transduction	BP	1	ARHGEF26	up_APUL_EC
GO:0072176	0.367	0.934	1	6	nephric duct development	BP	1	GATA3	up_VCAV_EC
GO:0009887	0.367	0.929	1	314	animal organ morphogenesis	BP	1	GATA5	up_VCAV_VSMC
GO:0070647	0.367	0.929	1	311	protein modification by small protein conjugation	BP	1	LIMK1	up_VCAV_VSMC
GO:0019221	0.367	0.925	1	102	cytokine-mediated signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0018212	0.367142721	0.83052	3	81	peptidyl-tyrosine modification	BP	1	LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0032886	0.367250109	0.83045	3	81	regulation of microtubule-based process	BP	1	DIXDC1,CHMP4B,TUBB4A	up_ACOR_EC
GO:1900015	0.367367014	0.92658	1	17	regulation of cytokine production involved in inflammatory response	BP	1	NOD2	up_ACOR_EC
GO:1902229	0.367641219	0.92646	1	17	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	CLU	up_ACOR_EC
GO:0051568	0.367755023	0.92641	1	17	histone H3-K4 methylation	BP	1	PYGO2	up_ACOR_EC
GO:0051179	0.368	0.666	172	1747	localization	BP	1	EXPH5,SH3TC2,FGF13,RHOT1,VEGFD,TLR1,DNAJC6,ACTN2,LGR6,PLCG2,LEP,MID1,SLC26A7,KCNE3,CDC7,HTR2B,TCAF1,USP6NL,MBP,ZRANB1,FBXL20,RECK,NACC2,PRKAA2,FERMT1,BMP4,SYT16,LCAT,TPC3,EVI5L,TM7SF3,ABCA1,GJA1,SCARB2,ATRX,HRH1,SH3RF2,SEC24B,LATS2,TP53INP1,ATXN2,GLRB,CD274,NIPAL3,AR,SARAF,SASH1,SLC2A5,STX11,GPR155,LMO4,PTPN3,TMEM108,CLCN3,FGF18,MICU2,IFT43,ITPR1,KLHL20,ANKRD1,F2RL1,HRH2,MARCH5,DAPK1,APOL6,BNIP3,SLC17A5,CACNB3,AKAP6,CDKN1A,LRRC8C,ABCA4,NRP1,PTPN22,GPM6A,LRPAP1,DMPK,TCN2,NPNT,OS9,ATP7A,SCP2,EVL,SPINT2,KCNJ4,OSBPL1A,TBX20,TBX5,SLCO1A2,PRKCE,FZD3,AGRN,MYO1B,SCG5,POLR2M,DAG1,FUT8,POMK,PARP9,APP,LAMA3,PSEN1,SEMA6D,PCSK6,SGSM2,SYNJ2BP,CHD7,PIK3C3,MFSD9,LAMP2,JUP,CCL5,DDR2,CLN8,ENSCAFG00000001846,DUSP22,ATP6V0E1,RAB11B,EDN1,DYNC1I2,SLC25A20,GTF2A1L,AKTIP,KCNC4,NOD2,LRRC4,ARID5B,LMTK2,FAM107A,JAM3,B2M,DISC1,AP2B1,PLIN2,FXYD1,SCAMP5,SCRN2,SAR1B,HERPUD1,TXNDC5,CFI,GAA,SUN1,VPS26A,INPP5K,FAF2,RAB5C,PREPL,PFKL,WFS1,AZIN2,RPAIN,WASL,ATP2C1,SLC25A12,NDUFA4L2,NAIF1,DO	up_ACOR_VSMC
GO:1901137	0.368	0.716	21	232	carbohydrate derivative biosynthetic process	BP	1	ACLY,RRM1,MPDU1,SLC35C2,B3GNT2,XYLT1,PFAS,TKT,B4GALT1,ELOVL1,UGDH,ELOVL6,CYC1,ATP5F1A,ENSCAFG00000013366,PDHA1,NUS1,GK5,CTPS1,NECAB3,ATP5F1D	down_ACOR_VSMC
GO:0003013	0.368	0.739	13	121	circulatory system process	BP	1	THRB,RNPEP,IRX5,SLIT2,EMP2,KCNE3,CHRM1,DLL1,F2RL1,TBXA2R,AGTR1,E2F4,ACVRL1	up_VSAP_EC
GO:0051260	0.368	0.747	11	100	protein homooligomerization	BP	1	ACACB,C1QTNF2,CLDN1,SCARA5,CLYBL,KCNB1,PCBD1,KCNC4,HTRA2,FLOT1,HMOX1	up_VSAP_EC
GO:0035690	0.368	0.752	10	91	cellular response to drug	BP	1	SLIT2,CDH1,ABL1,CHRM1,MAP3K5,CASTOR1,ZNF580,PPP3CB,HMOX1,DDIT4	up_VSAP_EC
GO:0002696	0.368	0.758	9	80	positive regulation of leukocyte activation	BP	1	LEP,CD83,TP53BP1,CD274,F2RL1,CDKN1A,PTPN22,APP,NOD2	up_ACOR_VSMC
GO:0003007	0.368	0.771	7	94	heart morphogenesis	BP	1	TMED2,ILK,FHL2,TGFBR1,HIF1A,CTNNB1,NRP1	down_VSAP_EC
GO:0050679	0.368	0.773	7	62	positive regulation of epithelial cell proliferation	BP	1	VEGFD,HTR2B,BMP4,FGFR2,TGFBR1,WDR48,RREB1	up_ACOR_VSMC
GO:0060560	0.368	0.774	7	58	developmental growth involved in	BP	1	BMP4,FGFR2,TMEM108,ENSCAFG00000006238,NRP1,ULK2,APP	up_ACOR_VSMC
GO:0097237	0.368	0.796	5	42	cellular response to toxic substance	BP	1	ABL1,SESN1,MAP3K5,ZNF580,HMOX1	up_VSAP_EC
GO:0006939	0.368	0.813	4	32	smooth muscle contraction	BP	1	TPCN2,CHRM1,TBXA2R,SULF2	up_VSAP_EC
GO:0007283	0.368	0.83	3	91	spermatogenesis	BP	1	HOXA9,OVOL1,SPATA6	up_AFEM_EC
GO:0034446	0.368	0.836	3	23	substrate adhesion-dependent cell spreading	BP	1	RADIL,ABL1,FBLN1	up_VSAP_EC
GO:0090311	0.368	0.871	2	15	regulation of protein deacetylation	BP	1	SREBF1,TADA2A	down_ACOR_VSMC

GO:0007200	0.368	0.87	2	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	GPR4,EDN1	up_VCAV_EC
GO:0031344	0.368	0.864	2	161	regulation of cell projection organization	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0031341	0.368	0.873	2	13	regulation of cell killing	BP	1	F2RL1,PPP3CB	up_VSAP_EC
GO:0045843	0.368	0.873	2	13	negative regulation of striated muscle tissue	BP	1	DLL1,SAV1	up_VSAP_EC
GO:0014029	0.368	0.936	1	5	neural crest formation	BP	1	NOLC1	down_ACOR_VSMC
GO:0031665	0.368	0.936	1	5	negative regulation of lipopolysaccharide-mediated signaling	BP	1	CACTIN	down_ACOR_VSMC
GO:0036491	0.368	0.936	1	5	regulation of translation initiation in response to endoplasmic reticulum	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0036492	0.368	0.936	1	5	eiF2alpha phosphorylation in response to endoplasmic	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0050667	0.368	0.936	1	5	homocysteine metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0090128	0.368	0.936	1	5	regulation of synapse maturation	BP	1	CDC20	down_ACOR_VSMC
GO:0010002	0.368	0.93	1	9	cardioblast differentiation	BP	1	GREM1	down_VCAV_EC
GO:0050919	0.368	0.929	1	10	negative chemotaxis	BP	1	SEMA3C	down_VCAV_EC
GO:1900745	0.368	0.93	1	9	positive regulation of p38MAPK cascade	BP	1	SASH1	down_VCAV_EC
GO:0044417	0.368	0.932	1	7	translocation of molecules into host	BP	1	DDX39B	down_VSAP_EC
GO:0051836	0.368	0.932	1	7	translocation of molecules into other organism involved in symbiotic	BP	1	DDX39B	down_VSAP_EC
GO:0050829	0.368	0.931	1	8	defense response to Gram-negative bacterium	BP	1	SERPINE1	down_VSAP_EC
GO:0097201	0.368	0.931	1	8	negative regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	HIF1AN	down_VSAP_EC
GO:0002643	0.368	0.936	1	5	regulation of tolerance induction	BP	1	CD274	up_ACOR_VSMC
GO:0007260	0.368	0.926	1	19	tyrosine phosphorylation of STAT protein	BP	1	LEP	up_AFEM_EC
GO:0032456	0.368	0.926	1	19	endocytic recycling	BP	1	BVES	up_AFEM_EC
GO:0033619	0.368	0.926	1	19	membrane protein proteolysis	BP	1	ADAM17	up_AFEM_EC
GO:0048016	0.368	0.926	1	19	inositol phosphate-mediated signaling	BP	1	LMCD1	up_AFEM_EC
GO:0051973	0.368	0.926	1	19	positive regulation of telomerase activity	BP	1	GREM1	up_AFEM_EC
GO:2000059	0.368	0.926	1	19	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0031665	0.368	0.936	1	5	negative regulation of lipopolysaccharide-mediated signaling	BP	1	TNFAIP3	up_VCAV_EC
GO:0046640	0.368	0.934	1	6	regulation of alpha-beta T cell proliferation	BP	1	ARG2	up_VCAV_EC
GO:0048642	0.368	0.936	1	5	negative regulation of skeletal muscle tissue	BP	1	EPHB1	up_VCAV_EC
GO:0060676	0.368	0.933	1	6	ureteric bud formation	BP	1	GATA3	up_VCAV_EC
GO:1901071	0.368	0.934	1	6	glucosamine-containing compound metabolic	BP	1	CHST7	up_VCAV_EC
GO:0030036	0.368	0.927	1	223	actin cytoskeleton organization	BP	1	SLIT2	up_VPUL_VSMC
GO:1904951	0.368	0.925	1	108	positive regulation of establishment of protein localization	BP	1	TLR2	up_VSAP_VSMC
GO:0060428	0.368045524	0.92628	1	17	lung epithelium development	BP	1	ADAMTSL2	up_ACOR_EC
GO:0050886	0.368158347	0.92624	1	17	endocrine process	BP	1	AQP1	up_ACOR_EC
GO:0110111	0.36843795	0.92611	1	17	negative regulation of animal organ	BP	1	FOXC2	up_ACOR_EC
GO:0000281	0.368491824	0.92587	1	18	mitotic cytokinesis	BP	1	CHMP4B	up_ACOR_EC

GO:0046782	0.368531543	0.92607	1	17	regulation of viral transcription	BP	1	TRIM8	up_ACOR_EC
GO:0009987	0.369	0.784	21	5086	cellular process	BP	1	NR1H4,TBX5,MAPK10,BPI,HTR7,HOXA3,PLCL1,TUBB4A,PCSK1N,GALNT17,ARHGEF26,LZTS1,ZDHHC16,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,ENSCAFG00000028814,PDE1A,PDLIM3	up_APUL_EC
GO:0000226	0.369	0.72	19	197	microtubule cytoskeleton organization	BP	1	PLK2,RAB11A,HOOK3,SLK,CEP68,MZT1,ENSCAFG00000010224,STMN1,FES,SENP6,GCC2,TAOK1,ZW10,ATRX,HAUS3,GAS2L3,ARHGEF2,FBXO5,SASS6	up_VCAV_EC
GO:0048568	0.369	0.733	14	148	embryonic organ development	BP	1	EIF4A3,HOXA3,INSIG1,MMP14,HOXA7,HOXB7,E2F8,PLK4,HOXB5,HOXC4,PHACTR4,TBX15,GLI1,SIX4	down_ACOR_VSMC
GO:0050776	0.369	0.749	10	173	regulation of immune response	BP	1	CFD,PRNP,THY1,PARK7,CYBA,MAVS,LOXL3,RAB7B,A2M,RAC2	down_VCAV_EC
GO:0048858	0.369	0.754	9	159	cell projection morphogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,UST,BRSK1	down_VCAV_EC
GO:0060828	0.369	0.757	9	82	regulation of canonical Wnt signaling pathway	BP	1	FZD1,WNT11,AXIN2,RECK,FAM53B,SULF2,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0017148	0.369	0.811	4	36	negative regulation of translation	BP	1	ILF3,EIF4A3,NCL,RBM14	down_ACOR_VSMC
GO:0006112	0.369	0.813	4	30	energy reserve metabolic process	BP	1	LEP,PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0120162	0.369	0.813	4	31	positive regulation of cold-induced thermogenesis	BP	1	LEP,GJA1,PPARGC1A,PLAC8B	up_ACOR_VSMC
GO:0060759	0.369	0.811	4	37	regulation of response to cytokine stimulus	BP	1	NLRC5,OTUD4,CNOT7,LSM14A	up_VCAV_EC
GO:0001841	0.369	0.831	3	44	neural tube formation	BP	1	SDC4,LMO4,IFT57	down_VCAV_EC
GO:0006289	0.369	0.832	3	35	nucleotide-excision repair	BP	1	GTF2H1,RBBP8,RAD23A	down_VSAP_EC
GO:0006633	0.369	0.832	3	38	fatty acid biosynthetic process	BP	1	TRIB3,PTGS2,SLC45A3	down_VSAP_EC
GO:0031399	0.369	0.834	3	559	regulation of protein modification process	BP	1	PLCL1,NPNT,NTRK2	up_APUL_EC
GO:0031638	0.369	0.871	2	15	zymogen activation	BP	1	MMP14,DHCR24	down_ACOR_VSMC
GO:0019646	0.369	0.933	1	6	aerobic electron transport chain	BP	1	CYCS	down_ACOR_VSMC
GO:0045124	0.369	0.935	1	5	regulation of bone resorption	BP	1	TFRC	down_ACOR_VSMC
GO:0048642	0.369	0.936	1	5	negative regulation of skeletal muscle tissue	BP	1	SIX4	down_ACOR_VSMC
GO:1905331	0.369	0.929	1	9	negative regulation of morphogenesis of an	BP	1	GREM1	down_VCAV_EC
GO:0045622	0.369	0.931	1	7	regulation of T-helper cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0021825	0.369	0.939	1	4	substrate-dependent cerebral cortex tangential	BP	1	NRP1	up_ACOR_VSMC
GO:1902991	0.369	0.936	1	5	regulation of amyloid precursor protein	BP	1	APP	up_ACOR_VSMC
GO:0000226	0.369	0.926	1	197	microtubule cytoskeleton organization	BP	1	TAOK1	up_AORT_EC
GO:0045321	0.369	0.926	1	191	leukocyte activation	BP	1	BPI	up_AORT_EC
GO:0003334	0.369	0.939	1	4	keratinocyte development	BP	1	FLNB	up_VCAV_EC
GO:0006591	0.369	0.935	1	5	ornithine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0007608	0.369	0.936	1	5	sensory perception of smell	BP	1	NAV2	up_VCAV_EC
GO:0015849	0.369	0.924	1	56	organic acid transport	BP	1	SLC7A11	up_VPOR_EC
GO:0002685	0.369	0.924	1	55	regulation of leukocyte migration	BP	1	C3AR1	up_VPOR_EC
GO:0046942	0.369	0.924	1	56	carboxylic acid transport	BP	1	SLC7A11	up_VPOR_EC
GO:0007169	0.369	0.926	1	178	transmembrane receptor protein tyrosine kinase	BP	1	FGF5	up_VPOR_VSMC
GO:0040008	0.369	0.926	1	179	regulation of growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0099537	0.369	0.925	1	131	trans-synaptic signaling	BP	1	HTR7	up_VPUL_EC
GO:1900044	0.369	0.935	1	5	regulation of protein K63-linked ubiquitination	BP	1	SASH1	up_VSAP_EC
GO:0045088	0.369049306	0.82917	3	81	regulation of innate immune response	BP	1	NR1H4,NOD2,MAVS	up_ACOR_EC
GO:0051495	0.369240526	0.829	3	82	positive regulation of cytoskeleton organization	BP	1	SYNPO2,ACTN2,NRP1	up_ACOR_EC

GO:0046887	0.369830478	0.92528	1	18	positive regulation of hormone secretion	BP	1	NR1H4	up_ACOR_EC
GO:0051496	0.369925008	0.92546	1	17	positive regulation of stress fiber assembly	BP	1	NRP1	up_ACOR_EC
GO:0033993	0.37	0.723	17	186	response to lipid	BP	1	CXCL8,TIE1,TNFAIP3,PPARG,TNIP1,PDE4D,MEF2C,TFPI,IRF8,PELI1,YES1,ABCA1,SMARCA4,PLCG2,GCH1,UFSP2,KDM3A	up_VCAV_EC
GO:0090287	0.37	0.751	10	91	regulation of cellular response to growth factor	BP	1	FZD1,SLIT2,ABL1,DLL1,EPN2,CCBE1,ZEB1,SULF2,ACVRL1,CITED2	up_VSAP_EC
GO:0002694	0.37	0.754	9	126	regulation of leukocyte activation	BP	1	SOCS5,FAM49B,PTPN2,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0009152	0.37	0.791	5	80	purine ribonucleotide biosynthetic process	BP	1	ADCY6,ATP5MC1,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0043087	0.37	0.791	5	83	regulation of GTPase activity	BP	1	SNX18,AKT2,SYDE1,ARHGAP1,EVI5L	down_VCAV_EC
GO:0042158	0.37	0.81	4	40	lipoprotein biosynthetic process	BP	1	ZDHHC22,HHAT,ABCA1,ZDHHC6	up_VCAV_EC
GO:1903900	0.37	0.809	4	40	regulation of viral life cycle	BP	1	CXCL8,NECTIN2,PROX1,CNOT7	up_VCAV_EC
GO:0034332	0.37	0.812	4	32	adherens junction organization	BP	1	FAM107A,CDH1,ABL1,ACVRL1	up_VSAP_EC
GO:0043536	0.37	0.811	4	32	positive regulation of blood vessel endothelial	BP	1	ABL1,HDAC7,STAT5A,HMOX1	up_VSAP_EC
GO:0006140	0.37	0.833	3	28	regulation of nucleotide metabolic process	BP	1	CDA,NOS2,HIF1A	up_VCAV_EC
GO:0007091	0.37	0.834	3	27	metaphase/anaphase transition of mitotic cell	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0010965	0.37	0.834	3	27	regulation of mitotic sister chromatid separation	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0044784	0.37	0.834	3	27	metaphase/anaphase transition of cell cycle	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0048167	0.37	0.833	3	28	regulation of synaptic plasticity	BP	1	PLK2,RELN,MEF2C	up_VCAV_EC
GO:0050000	0.37	0.833	3	27	chromosome localization	BP	1	RAB11A,CENPC,ZW10	up_VCAV_EC
GO:0050905	0.37	0.833	3	26	neuromuscular process	BP	1	TMEM150C,GCH1,ALDH1A3	up_VCAV_EC
GO:0048525	0.37	0.866	2	25	negative regulation of viral process	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0006811	0.37	0.865	2	330	ion transport	BP	1	HOXA3,NTRK2	up_APUL_EC
GO:0045579	0.37	0.935	1	5	positive regulation of B cell differentiation	BP	1	MMP14	down_ACOR_VSMC
GO:0055062	0.37	0.935	1	5	phosphate ion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:0060788	0.37	0.935	1	5	ectodermal placode formation	BP	1	SIX4	down_ACOR_VSMC
GO:0071697	0.37	0.935	1	5	ectodermal placode morphogenesis	BP	1	SIX4	down_ACOR_VSMC
GO:0072505	0.37	0.935	1	5	divalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:0072506	0.37	0.935	1	5	trivalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:0034122	0.37	0.929	1	9	negative regulation of toll-like receptor signaling	BP	1	RAB7B	down_VCAV_EC
GO:0009893	0.37	0.945	1	995	positive regulation of metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0046639	0.37	0.931	1	7	negative regulation of alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:0006688	0.37	0.935	1	5	glycosphingolipid biosynthetic process	BP	1	UGCG	up_ACOR_VSMC
GO:0032836	0.37	0.939	1	4	glomerular basement membrane development	BP	1	NID1	up_ACOR_VSMC
GO:0060393	0.37	0.925	1	19	regulation of pathway-restricted SMAD protein	BP	1	GREM1	up_AFEM_EC
GO:0007507	0.37	0.925	1	194	heart development	BP	1	SGCD	up_AORT_EC
GO:0055082	0.37	0.925	1	189	cellular chemical homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0010571	0.37	0.939	1	4	positive regulation of nuclear cell cycle DNA	BP	1	ATRX	up_VCAV_EC
GO:0015695	0.37	0.933	1	6	organic cation transport	BP	1	RALBP1	up_VCAV_EC
GO:0008211	0.37	0.935	1	5	glucocorticoid metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0016358	0.37	0.923	1	58	dendrite development	BP	1	SEMA3A	up_VPOR_EC
GO:1901293	0.37	0.924	1	106	nucleoside phosphate biosynthetic process	BP	1	ADCY3	up_VFEM_EC

GO:0031175	0.37	0.926	1	224	neuron projection development	BP	1	SLIT2	up_VPUL_VSMC
GO:0045056	0.37	0.935	1	5	transcytosis	BP	1	RAB11B	up_VSAP_EC
GO:0009892	0.370118953	0.71085	24	835	negative regulation of metabolic process	BP	1	NR1H4,TRPS1,PLCL1,PKIB,SOX9,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,ZMYND8,CST3,PIAS1,FOXC2,LRRC15,CLSTN1,LRRC4,SFMBT2,CHMP4B,RIOX2,AZIN2,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0050810	0.370212562	0.92534	1	17	regulation of steroid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:0051234	0.371	0.668	126	1283	establishment of localization	BP	1	EXPH5,SH3TC2,FGF13,RHOT1,TLR1,DNAJC6,ACTN2,PLCG2,LEP,SLC26A7,KCNE3,CDC7,HTR2B,TCAF1,USP6NL,MBP,FBXL20,FERMT1,BMP4,SYT16,LCAT,TPC3,EVI5L,TM7SF3,ABCA1,GJA1,SCARB2,SEC24B,ATXN2,CD274,NIPAL3,SARAF,SLC2A5,STX11,GPR155,PTPN3,TMEM108,CLCN3,MICU2,IFT43,ITPR1,KLHL20,ANKRD1,F2RL1,HRH2,DAPK1,APOL6,BNIP3,SLC17A5,CACNB3,AKAP6,CDKN1A,LRRC8C,ABCA4,NRP1,PTPN22,LRPAP1,DMPK,TCN2,NPNT,OS9,ATP7A,SCP2,KCNJ4,OSBPL1A,SLCO1A2,PRKCE,MYO1B,SCG5,APP,PSEN1,PCSK6,SGSM2,SYNJ2BP,CHD7,PIK3C3,MFSD9,LAMP2,JUP,CCL5,CLN8,ENSCAFG00000001846,ATP6V0E1,RAB11B,EDN1,DYNC1I2,SLC25A20,GTF2A1L,AKTIP,KCNC4,NOD2,LMTK2,B2M,AP2B1,PLIN2,FXYD1,SCAMP5,SCRN2,SAR1B,HERPUD1,TXNDC5,CFI,SUN1,VPS26A,INPP5K,FAF2,RAB5C,PREPL,PFKL,WFS1,AZIN2,RPAIN,ATP2C1,SLC25A12,NDUFA4L2,NAIF1,DYNC1I1,PARK7,SLC8A1,SLC2A12,STC2,ENSCAFG00000013536,BVES,LMF1,PIK3C2A,PTPN14	up_ACOR_VSMC
GO:1901362	0.371	0.67	110	1293	organic cyclic compound biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,MTOR,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,CCAR1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,LBR,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0006914	0.371	0.729	15	141	autophagy	BP	1	PLEKHF1,TPCN2,RETREG1,AMBRA1,MFN2,POLDIP2,ATG2A,FBXO7,PIP4K2B,UBQLN2,HTRA2,ULK1,HMOX1,NPRL3,FUNDC2	up_VSAP_EC
GO:0061919	0.371	0.729	15	141	process utilizing autophagic mechanism	BP	1	PLEKHF1,TPCN2,RETREG1,AMBRA1,MFN2,POLDIP2,ATG2A,FBXO7,PIP4K2B,UBQLN2,HTRA2,ULK1,HMOX1,NPRL3,FUNDC2	up_VSAP_EC
GO:0071826	0.371	0.743	11	117	ribonucleoprotein complex subunit organization	BP	1	USP4,EDC3,SLC29A1,DDX28,DDX39B,SF3A2,PRMT5,ENSCAFG00000015189,GEMIN7,SF3A1,EIF3M	down_ACOR_VSMC
GO:0021537	0.371	0.763	8	73	telencephalon development	BP	1	EMX2,CDON,SLIT2,PLXNA4,RTN4RL1,MCPH1,KDM2B,NFIB	up_VSAP_EC
GO:0051783	0.371	0.77	7	72	regulation of nuclear division	BP	1	PDGFB,EDN1,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0009260	0.371	0.779	6	83	ribonucleotide biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1	down_VSAP_EC
GO:0046390	0.371	0.779	6	83	ribose phosphate biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1	down_VSAP_EC
GO:0051983	0.371	0.793	5	47	regulation of chromosome segregation	BP	1	SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:1903312	0.371	0.833	3	25	negative regulation of mRNA metabolic process	BP	1	RNPS1,U2AF2,THRAP3	down_ACOR_VSMC
GO:0072358	0.371	0.829	3	268	cardiovascular system development	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0043507	0.371	0.834	3	23	positive regulation of JUN kinase activity	BP	1	ARHGEF5,MAP3K5,SASH1	up_VSAP_EC

GO:0042475	0.371	0.865	2	26	odontogenesis of dentin-containing tooth	BP	1	BMPR1A,GLI3	down_VCAV_EC
GO:0001947	0.371	0.866	2	21	heart looping	BP	1	TMED2,HIF1A	down_VSAP_EC
GO:0061371	0.371	0.866	2	21	determination of heart left/right asymmetry	BP	1	TMED2,HIF1A	down_VSAP_EC
GO:0045143	0.371	0.871	2	13	homologous chromosome segregation	BP	1	DMC1,SUN1	up_ACOR_VSMC
GO:0050764	0.371	0.871	2	13	regulation of phagocytosis	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0000183	0.371	0.935	1	5	chromatin silencing at rDNA	BP	1	SUV39H1	down_ACOR_VSMC
GO:0021873	0.371	0.935	1	5	forebrain neuroblast division	BP	1	ASPM	down_ACOR_VSMC
GO:0031958	0.371	0.935	1	5	corticosteroid receptor signaling pathway	BP	1	NEDD4	down_ACOR_VSMC
GO:0042921	0.371	0.935	1	5	glucocorticoid receptor signaling pathway	BP	1	NEDD4	down_ACOR_VSMC
GO:0000002	0.371	0.928	1	9	mitochondrial genome maintenance	BP	1	MPV17	down_VCAV_EC
GO:0006541	0.371	0.928	1	9	glutamine metabolic process	BP	1	GLS2	down_VCAV_EC
GO:0051569	0.371	0.928	1	9	regulation of histone H3-K4 methylation	BP	1	PRMT6	down_VCAV_EC
GO:0070885	0.371	0.929	1	9	negative regulation of calcineurin-NFAT signaling	BP	1	PRNP	down_VCAV_EC
GO:0106057	0.371	0.929	1	9	negative regulation of calcineurin-mediated	BP	1	PRNP	down_VCAV_EC
GO:1990774	0.371	0.928	1	9	tumor necrosis factor secretion	BP	1	MAVS	down_VCAV_EC
GO:0001783	0.371	0.929	1	8	B cell apoptotic process	BP	1	LYN	down_VSAP_EC
GO:0071071	0.371	0.929	1	8	regulation of phospholipid biosynthetic process	BP	1	NR1H4	down_VSAP_EC
GO:0070234	0.371	0.935	1	5	positive regulation of T cell apoptotic process	BP	1	CD274	up_ACOR_VSMC
GO:0070254	0.371	0.935	1	5	mucus secretion	BP	1	PRKCE	up_ACOR_VSMC
GO:0070255	0.371	0.935	1	5	regulation of mucus secretion	BP	1	PRKCE	up_ACOR_VSMC
GO:0030593	0.371	0.925	1	19	neutrophil chemotaxis	BP	1	CCL5	up_AFEM_EC
GO:0006644	0.371	0.924	1	118	phospholipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0008015	0.371	0.924	1	120	blood circulation	BP	1	HTR7	up_APUL_EC
GO:0048871	0.371	0.924	1	120	multicellular organismal homeostasis	BP	1	PLCL1	up_APUL_EC
GO:0060562	0.371	0.924	1	120	epithelial tube morphogenesis	BP	1	NPNT	up_APUL_EC
GO:0002376	0.371	0.935	1	622	immune system process	BP	1	HOXA3	up_APUL_VSMC
GO:0006658	0.371	0.932	1	6	phosphatidylserine metabolic process	BP	1	SERINC5	up_VCAV_EC
GO:0010935	0.371	0.932	1	6	regulation of macrophage cytokine production	BP	1	TLR4	up_VCAV_EC
GO:0050909	0.371	0.932	1	6	sensory perception of taste	BP	1	P2RX2	up_VCAV_EC
GO:0048268	0.371	0.935	1	5	clathrin coat assembly	BP	1	SNAP91	up_VCAV_EC
GO:0019827	0.371	0.923	1	59	stem cell population maintenance	BP	1	HOOK3	up_VPOR_EC
GO:0019693	0.371	0.925	1	172	ribose phosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0051249	0.371	0.923	1	107	regulation of lymphocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:0043551	0.371062419	0.92496	1	17	regulation of phosphatidylinositol 3-	BP	1	ENSCAFG00000004331	up_ACOR_EC
GO:1905207	0.371075339	0.92496	1	17	regulation of cardiocyte differentiation	BP	1	TBX5	up_ACOR_EC
GO:0055013	0.371722492	0.92467	1	17	cardiac muscle cell development	BP	1	ACTN2	up_ACOR_EC
GO:1902533	0.372	0.719	18	271	positive regulation of intracellular signal transduction	BP	1	VEGFA,JCAD,PTPN11,ILK,TNIK,PTPN2,MTDH,MAGED1,CTNNB1,ENSCAFG00000002015,LYN,HTT,CALM1,NRP1,SH3RF3,MADD,SEC13,MID1	down_VSAP_EC
GO:0009117	0.372	0.737	12	208	nucleotide metabolic process	BP	1	GPAM,ADCY6,H6PD,NT5C2,PGLS,ATP5MC1,UQCR10,ADK,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0051260	0.372	0.767	7	100	protein homooligomerization	BP	1	VASP,DPYSL3,CRYAB,APOE,GBP5,PRMT1,TNFAIP1	down_VSAP_EC

GO:0070085	0.372	0.777	6	95	glycosylation	BP	1	KRTCAP2,DDOST,GFPT2,B4GALT1,FUT8,RPN2	down_VCAV_EC
GO:0008154	0.372	0.778	6	81	actin polymerization or depolymerization	BP	1	VASP,WDR1,ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0018212	0.372	0.789	5	81	peptidyl-tyrosine modification	BP	1	PDGFRB,PRNP,CSPG4,ARL2BP,GREM1	down_VCAV_EC
GO:0009799	0.372	0.829	3	43	specification of symmetry	BP	1	IFT57,PCSK6,GREM1	down_VCAV_EC
GO:0038061	0.372	0.83	3	34	NIK/NF-kappaB signaling	BP	1	ILK,UACA,ENSCAFG00000002015	down_VSAP_EC
GO:0010876	0.372	0.827	3	92	lipid localization	BP	1	LEP,CRY2,ACACB	up_AFEM_EC
GO:0051336	0.372	0.863	2	251	regulation of hydrolase activity	BP	1	LYN,MYO1D	down_ACOR_EC
GO:0002698	0.372	0.865	2	25	negative regulation of immune effector process	BP	1	LOXL3,A2M	down_VCAV_EC
GO:0016242	0.372	0.871	2	13	negative regulation of macroautophagy	BP	1	FEZ1,FEZ2	up_ACOR_VSMC
GO:0060443	0.372	0.871	2	13	mammary gland morphogenesis	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0022603	0.372	0.863	2	301	regulation of anatomical structure morphogenesis	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0051403	0.372	0.923	1	89	stress-activated MAPK cascade	BP	1	IGF1R	down_ACOR_EC
GO:0006983	0.372	0.934	1	5	ER overload response	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0007346	0.372	0.925	1	210	regulation of mitotic cell cycle	BP	1	GPSM2	down_AFEM_EC
GO:0001732	0.372	0.928	1	9	formation of cytoplasmic translation initiation	BP	1	EIF3K	down_VCAV_EC
GO:0007622	0.372	0.928	1	9	rhythmic behavior	BP	1	NAGLU	down_VCAV_EC
GO:0036474	0.372	0.928	1	9	cell death in response to hydrogen peroxide	BP	1	PARK7	down_VCAV_EC
GO:0044458	0.372	0.928	1	9	motile cilium assembly	BP	1	IFT57	down_VCAV_EC
GO:0060037	0.372	0.928	1	9	pharyngeal system development	BP	1	BMPR1A	down_VCAV_EC
GO:0090141	0.372	0.928	1	9	positive regulation of mitochondrial fission	BP	1	DCN	down_VCAV_EC
GO:0006098	0.372	0.929	1	8	pentose-phosphate shunt	BP	1	PGAM1	down_VSAP_EC
GO:0010829	0.372	0.93	1	7	negative regulation of glucose transmembrane	BP	1	ENPP1	down_VSAP_EC
GO:0051156	0.372	0.929	1	8	glucose 6-phosphate metabolic process	BP	1	PGAM1	down_VSAP_EC
GO:0031571	0.372	0.929	1	8	mitotic G1 DNA damage checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0044783	0.372	0.929	1	8	G1 DNA damage checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0044819	0.372	0.929	1	8	mitotic G1/S transition checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0046174	0.372	0.929	1	8	polyol catabolic process	BP	1	TPI1	down_VSAP_EC
GO:2000251	0.372	0.93	1	7	positive regulation of actin cytoskeleton	BP	1	NRP1	down_VSAP_EC
GO:0051881	0.372	0.924	1	19	regulation of mitochondrial membrane	BP	1	MLLT11	up_AFEM_EC
GO:0003002	0.372	0.923	1	118	regionalization	BP	1	HOXA3	up_APUL_EC
GO:0035456	0.372	0.932	1	6	response to interferon-beta	BP	1	TMEM173	up_VCAV_EC
GO:0060644	0.372	0.934	1	5	mammary gland epithelial cell differentiation	BP	1	HIF1A	up_VCAV_EC
GO:0051248	0.372	0.927	1	316	negative regulation of protein metabolic process	BP	1	LIMK1	up_VCAV_VSMC
GO:0007179	0.372	0.922	1	57	transforming growth factor beta receptor	BP	1	ASPN	up_VPOR_EC
GO:0060322	0.372	0.924	1	193	head development	BP	1	EMX2	up_VFEM_VSMC
GO:0002790	0.372	0.924	1	133	peptide secretion	BP	1	NR1H4	up_VPUL_EC
GO:0030099	0.372	0.924	1	133	myeloid cell differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0002295	0.372	0.934	1	5	T-helper cell lineage commitment	BP	1	STAT6	up_VSAP_EC
GO:0002363	0.372	0.934	1	5	alpha-beta T cell lineage commitment	BP	1	STAT6	up_VSAP_EC
GO:0043373	0.372	0.934	1	5	CD4-positive, alpha-beta T cell lineage commitment	BP	1	STAT6	up_VSAP_EC

GO:0045785	0.372	0.923	1	107	positive regulation of cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0055025	0.37209308	0.92451	1	17	positive regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0016043	0.373	0.663	168	1973	cellular component organization	BP	1	EPHB1,PLK2,TEK,HCLS1,IL7R,GBP5,SELP,KIT,SELE,PRKCH,ARHGEF15,IFRD1,ENSCAFG00000007112,TIE1,CDA,ADAMTS9,ATP8A1,LRRC8D,MX2,AMOT,PDGFB,MALL,PODXL,BAIAP2L1,RELN,VWF,LAMC2,IWS1,OCLN,MEF2C,FERMT1,CHD7,RAPGEF1,TLR4,STC1,GATA3,EDN1,RAB11A,RALB,ARAP3,RAB27A,SMAD1,SNCAIP,PSME4,NEDD9,IRF8,SNAP91,ARHGAP28,TMOD1,FIGNL1,PPP3CA,NASP,MTSS1,NECTIN2,MTOR,ACPP,HOOK3,SNAP23,LRRC8C,TJP1,HEX,LNX2,CAV2,PREX2,SLC12A7,SLK,CEP68,BMP2K,SCAF11,CNOT6,PDZD8,ABCA1,NCKAP1,GDPD5,MZT1,RIOK3,PROX1,UHRF2,IQGAP2,ENSCAFG00000010224,EPB41,ELMO1,ARID4B,STMN1,FLNB,SNX2,HMBOX1,BAZ1A,PAK2,PRKD2,SH3GLB1,SWAP70,SMARCA4,APOD,CENPC,NCK1,ESCO1,KCNJ2,EXOC5,FES,NSD1,MRRF,HIST1H1A,TOP1,EHD4,RAPGEF2,PLCG2,CREB1,BCL10,SENP6,PAN3,GCC2,TAOK1,PRPF39,CTNNA1,CNOT7,FMNL3,STX11,SMG7,GCH1,SERAC1,VPS54,ASF1A,HMGB1,TBC1D1,PMAIP1,ARPC5L,BLM,NUP133,SPTBN4,RIPK1,SMC5,LSM14A,ITGA6,RAD21,MCU,DNAJC13,OLFML2A,ARHGDIB,ZW10,KDM5A,HIF1A,KDM3A,ARHGAP26,ALS2,IQUB,ATRX,HAUS3,ALDH1A3,HIST2H2AC,HP1BP3,ENSCAFG000000	up_VCAV_EC
GO:0019637	0.373	0.716	19	342	organophosphate metabolic process	BP	1	GPAM,PDGFRB,ADCY6,ENSCAFG00000014978,LCAT,H6PD,NT5C2,ENTPD3,PGLS,ATP5MC1,GFPT2,UQCR10,PIGS,ADK,PARK7,AMPD2,ACSS2,NAPEPLD,ACAT1	down_VCAV_EC
GO:0001775	0.373	0.725	15	219	cell activation	BP	1	SOCS5,FAM49B,TGFBR1,MSN,CX3CL1,PTPN2,CTNNB1,TFRC,APOE,LYN,SLC7A11,ITGB3,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0010648	0.373	0.741	11	407	negative regulation of cell communication	BP	1	LEP,LBH,CRY2,GREM1,GREM2,CYLD,LRRC15,RAB7A,AXIN2,ADAM17,KANK1	up_AFEM_EC
GO:0045333	0.373	0.768	7	74	cellular respiration	BP	1	PRELID1,CDK1,FASTKD3,SUCLG1,CYCS,CYC1,PDHA1	down_ACOR_VSMC
GO:0030278	0.373	0.79	5	66	regulation of ossification	BP	1	ILK,CHSY1,HIF1A,CTNNB1,REST	down_VSAP_EC
GO:0002065	0.373	0.808	4	37	columnar/cuboidal epithelial cell	BP	1	BMP2,PROX1,JAG1,HIF1A	up_VCAV_EC
GO:0010811	0.373	0.808	4	36	positive regulation of cell-substrate adhesion	BP	1	TEK,FERMT1,NEDD9,ENSCAFG00000002015	up_VCAV_EC
GO:0031047	0.373	0.809	4	33	gene silencing by RNA	BP	1	MOV10,PPP3CA,TUT7,CNOT7	up_VCAV_EC
GO:0021545	0.373	0.834	3	21	cranial nerve development	BP	1	CITED2,NRP1,CHD7	up_ACOR_VSMC
GO:0070936	0.373	0.831	3	28	protein K48-linked ubiquitination	BP	1	TNFAIP3,PELI1,UBE2D1	up_VCAV_EC
GO:2000573	0.373	0.831	3	28	positive regulation of DNA biosynthetic process	BP	1	PDGFB,HMBOX1,PRKD2	up_VCAV_EC
GO:0043069	0.373	0.862	2	262	negative regulation of programmed cell death	BP	1	IGF1R,PDPN	down_ACOR_EC
GO:0010507	0.373	0.864	2	26	negative regulation of autophagy	BP	1	POLDIP2,CLEC16A	down_VCAV_EC
GO:0050905	0.373	0.864	2	26	neuromuscular process	BP	1	PEX5,ENSCAFG00000017708	down_VCAV_EC
GO:0017145	0.373	0.87	2	13	stem cell division	BP	1	LBH,FGFR2	up_ACOR_VSMC
GO:0021532	0.373	0.87	2	13	neural tube patterning	BP	1	BMP4,PSEN1	up_ACOR_VSMC
GO:0042246	0.373	0.866	2	17	tissue regeneration	BP	1	IFRD1,APOD	up_VCAV_EC
GO:0006873	0.373	0.861	2	160	cellular ion homeostasis	BP	1	C3AR1,ENSCAFG00000005494	up_VPOR_EC
GO:0010941	0.373	0.867	2	524	regulation of cell death	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0009628	0.373	0.863	2	302	response to abiotic stimulus	BP	1	EYA1,MME	up_VFEM_EC
GO:0006605	0.373	0.922	1	99	protein targeting	BP	1	NEDD4	down_ACOR_EC
GO:0008340	0.373	0.934	1	5	determination of adult lifespan	BP	1	RAD54L	down_ACOR_VSMC
GO:0072396	0.373	0.934	1	5	response to cell cycle checkpoint signaling	BP	1	SMC1A	down_ACOR_VSMC

GO:0072402	0.373	0.934	1	5	response to DNA integrity checkpoint signaling	BP	1	SMC1A	down_ACOR_VSMC
GO:0072423	0.373	0.934	1	5	response to DNA damage checkpoint signaling	BP	1	SMC1A	down_ACOR_VSMC
GO:0044260	0.373	1	1	2593	cellular macromolecule metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0006359	0.373	0.927	1	10	regulation of transcription by RNA polymerase III	BP	1	NAB2	down_VCAV_EC
GO:0001516	0.373	0.93	1	7	prostaglandin biosynthetic process	BP	1	PTGS2	down_VSAP_EC
GO:0043928	0.373	0.928	1	8	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	BP	1	CNOT7	down_VSAP_EC
GO:0046457	0.373	0.93	1	7	prostanoid biosynthetic process	BP	1	PTGS2	down_VSAP_EC
GO:0060628	0.373	0.929	1	8	regulation of ER to Golgi vesicle-mediated transport	BP	1	YIPF5	down_VSAP_EC
GO:0090036	0.373	0.93	1	7	regulation of protein kinase C signaling	BP	1	VEGFA	down_VSAP_EC
GO:0045603	0.373	0.934	1	5	positive regulation of endothelial cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0060501	0.373	0.934	1	5	positive regulation of epithelial cell proliferation involved in lung morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0006952	0.373	0.927	1	319	defense response	BP	1	TLR2	up_AFEM_VSMC
GO:0006700	0.373	0.934	1	5	C21-steroid hormone biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0034329	0.373	0.922	1	60	cell junction assembly	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0070374	0.373	0.922	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0099536	0.373	0.923	1	133	synaptic signaling	BP	1	HTR7	up_VPUL_EC
GO:0000209	0.373039561	0.82626	3	83	protein polyubiquitination	BP	1	NOD2,RNF114,UBE2H	up_ACOR_EC
GO:0051881	0.373249654	0.92357	1	19	regulation of mitochondrial membrane potential	BP	1	IFI6	up_ACOR_EC
GO:0046717	0.373307893	0.92397	1	17	acid secretion	BP	1	CFI	up_ACOR_EC
GO:0030224	0.373404855	0.9237	1	18	monocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:1903131	0.373404855	0.9237	1	18	mononuclear cell differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0106106	0.37340618	0.86096	2	48	cold-induced thermogenesis	BP	1	PLCL1,FOXC2	up_ACOR_EC
GO:0120161	0.37340618	0.86096	2	48	regulation of cold-induced thermogenesis	BP	1	PLCL1,FOXC2	up_ACOR_EC
GO:0055081	0.373898997	0.92371	1	17	anion homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0009892	0.374	0.675	72	835	negative regulation of metabolic process	BP	1	EDNRB,HCLS1,PPP2R5A,CDA,TNFAIP3,TNIP1,PDGFB,CD34,PDE4D,MOV10,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,GATA3,EDN1,HOXB8,SOX18,PPP3CA,FAM3C,MTOR,TENT2,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,TUT7,SH3BP5,CNOT6,ENC1,PROX1,UHRF2,MDFI,ENSCAFG00000010596,HMBOX1,PAK2,THOC1,SWAP70,SMARCA4,APOD,NCK1,TIMELESS,PTGS2,RAPGEF2,TCERG1,CREB1,BASP1,PAN3,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,BLM,RAD17,MTA2,KDM5A,HIF1A,KDM3A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,IVNS1ABP,FKBP15,ELK3	up_VCAV_EC
GO:0043604	0.374	0.704	25	288	amide biosynthetic process	BP	1	ACLY,ILF3,EIF4A3,HNRNPD,VARS,RRBP1,PPP1R15B,MRPS18B,TRUB2,DHX33,ARG2,FASTKD3,EIF5A,ELOVL1,FARSA,NCL,MRPL37,ELOVL6,RBM14,NOLC1,RARS,PUM3,PDHA1,MRPL18,EIF3M	down_ACOR_VSMC
GO:1902903	0.374	0.736	12	125	regulation of supramolecular fiber organization	BP	1	CAPG,COLGALT1,LIMA1,NF2,STMN1,RAC1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B,ARHGEF2	down_ACOR_VSMC
GO:0002764	0.374	0.753	9	80	immune response-regulating signaling	BP	1	ABL1,F2RL1,RBCK1,MYD88,NLRX1,TKFC,CYBA,UNC93B1,FLOT1	up_VSAP_EC
GO:0051099	0.374	0.768	7	70	positive regulation of binding	BP	1	HMGB1,HOXA3,CAV1,FAM129B,STMN1,GMNN,HMGB2	down_ACOR_VSMC
GO:0052548	0.374	0.767	7	80	regulation of endopeptidase activity	BP	1	CASP8,PAK2,PTGS2,BCL10,HMGB1,PMAIP1,PSMB9	up_VCAV_EC

GO:0031023	0.374	0.778	6	58	microtubule organizing center organization	BP	1	PLK2,CEP68,FES,GCC2,HAUS3,SASS6	up_VCAV_EC
GO:0003018	0.374	0.791	5	42	vascular process in circulatory system	BP	1	SLIT2,CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0072524	0.374	0.807	4	37	pyridine-containing compound metabolic	BP	1	NNT,PDXP,PDHA1,PGD	down_ACOR_VSMC
GO:0007369	0.374	0.804	4	63	gastrulation	BP	1	BMPR1A,COL6A1,LAMA3,TLX2	down_VCAV_EC
GO:0006979	0.374	0.803	4	130	response to oxidative stress	BP	1	CRYAB,NFE2L1,PPARGC1A,SOD1	up_AFEM_EC
GO:0048489	0.374	0.828	3	38	synaptic vesicle transport	BP	1	CTNNB1,GSK3B,AP3S1	down_VSAP_EC
GO:0097480	0.374	0.828	3	38	establishment of synaptic vesicle localization	BP	1	CTNNB1,GSK3B,AP3S1	down_VSAP_EC
GO:0019941	0.374	0.861	2	258	modification-dependent protein catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0000060	0.374	0.868	2	15	protein import into nucleus, translocation	BP	1	POLA2,IPO4	down_ACOR_VSMC
GO:0016180	0.374	0.867	2	15	snRNA processing	BP	1	INTS7,EXOSC5	down_ACOR_VSMC
GO:0030330	0.374	0.863	2	25	DNA damage response, signal transduction by p53 class mediator	BP	1	SPRED1,FOXO3	down_VCAV_EC
GO:0001961	0.374	0.869	2	13	positive regulation of cytokine-mediated	BP	1	CREBRF,PARP9	up_ACOR_VSMC
GO:0006874	0.374	0.922	1	91	cellular calcium ion homeostasis	BP	1	LYN	down_ACOR_EC
GO:0008627	0.374	0.933	1	5	intrinsic apoptotic signaling pathway in response to osmotic	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0033572	0.374	0.934	1	5	transferrin transport	BP	1	TFRC	down_ACOR_VSMC
GO:0002230	0.374	0.927	1	9	positive regulation of defense response to virus	BP	1	MAVS	down_VCAV_EC
GO:1903204	0.374	0.927	1	9	negative regulation of oxidative stress-induced	BP	1	PARK7	down_VCAV_EC
GO:0000289	0.374	0.929	1	7	nuclear-transcribed mRNA poly(A) tail shortening	BP	1	CNOT7	down_VSAP_EC
GO:0010758	0.374	0.928	1	8	regulation of macrophage chemotaxis	BP	1	MMP28	down_VSAP_EC
GO:0010107	0.374	0.933	1	5	potassium ion import	BP	1	KCNJ4	up_ACOR_VSMC
GO:0034114	0.374	0.933	1	5	regulation of heterotypic cell-cell adhesion	BP	1	MBP	up_ACOR_VSMC
GO:1904754	0.374	0.937	1	4	positive regulation of vascular associated smooth muscle cell	BP	1	DOCK5	up_ACOR_VSMC
GO:0003013	0.374	0.922	1	121	circulatory system process	BP	1	HTR7	up_APUL_EC
GO:0034143	0.374	0.931	1	6	regulation of toll-like receptor 4 signaling	BP	1	PELI1	up_VCAV_EC
GO:0031023	0.374	0.922	1	58	microtubule organizing center organization	BP	1	GCC2	up_VPOR_EC
GO:0044242	0.374	0.921	1	57	cellular lipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0071383	0.374	0.922	1	58	cellular response to steroid hormone stimulus	BP	1	RNF6	up_VPOR_EC
GO:0001654	0.374	0.922	1	110	eye development	BP	1	MAB21L1	up_VFEM_EC
GO:0042110	0.374	0.922	1	109	T cell activation	BP	1	CYP26B1	up_VFEM_EC
GO:0150063	0.374	0.922	1	110	visual system development	BP	1	MAB21L1	up_VFEM_EC
GO:0048880	0.374	0.922	1	110	sensory system development	BP	1	MAB21L1	up_VFEM_EC
GO:0050673	0.374	0.923	1	135	epithelial cell proliferation	BP	1	CCL24	up_VPUL_EC
GO:0043900	0.374	0.922	1	104	regulation of multi-organism process	BP	1	CAV1	up_VSAP_VSMC
GO:0043433	0.374357014	0.86029	2	49	negative regulation of DNA-binding transcription factor activity	BP	1	NR1H4,CLSTN1	up_ACOR_EC
GO:0010569	0.37479346	0.92331	1	17	regulation of double-strand break repair via homologous	BP	1	FIGNL1	up_ACOR_EC

GO:0051234	0.375	0.677	67	1283	establishment of localization	BP	1	GPAM,SLC35F6,SNX18,LRP1,PRNP,SDC4,FOLR2,TMEM230,NABP2,FXYD1,TRPV2,CLIP3,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,MICALL2,LCAT,SNUPN,SSR2,SCP2,SLC39A6,CACNB3,ANXA11,ATP5MC1,SCAMP4,LRPAP1,THY1,CLTB,SSR3,PEX5,MFSD3,ATP6V0C,MYO1B,SCAMP2,OSBPL10,GLI3,PARK7,YIF1A,SLC17A9,SCARA5,ZFP36L1,SLC2A10,TPC3,CYBA,IFT57,MAVS,CDH2,TOM1,MGARP,RAB7B,SPNS1,SEC61B,RAB31,HM13,ARHGAP1,PCSK6,GREM1,EVI5L,LONP2,RAC2,CLIC4,SOAT1,PACSIN3,ANKRD54,SEC61A1,BRSK1	down_VCAV_EC
GO:0030182	0.375	0.694	33	327	neuron differentiation	BP	1	THRB,EMX2,CDON,WNT11,AMIGO1,IRX5,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,HOXC10,LRP4,DPYSL2,GDPD5,FBXO7,NTN4,NR2F6,NFIB,CYB5D2,CDNF,PQBP1,TTL,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0035239	0.375	0.697	31	299	tube morphogenesis	BP	1	VEGFD,LEP,ANGPT1,SHROOM3,BMP4,FGFR2,GJA1,TLR3,SEC24B,CITED2,SPINT1,SASH1,LMO4,FGF18,EGLN1,CLSTN1,NRP1,NPNT,SPINT2,TBX20,FZD3,DAG1,PSEN1,SYNJ2BP,CHD7,JUP,EDN1,HPGD,JAM3,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0051960	0.375	0.735	12	216	regulation of nervous system development	BP	1	BMPR1A,TRPV2,NUMBL,THY1,TLX2,GLI3,CDH2,UST,PRKCSH,THRB,RGMA,BRSK1	down_VCAV_EC
GO:0051962	0.375	0.736	12	112	positive regulation of nervous system development	BP	1	CDON,WASF3,AMIGO1,LRRN3,HOXD3,IRX3,ZEB1,SHOX2,GDPD5,CYB5D2,NCK1,MAP2K2	up_VSAP_EC
GO:0002009	0.375	0.744	10	177	morphogenesis of an epithelium	BP	1	SDC4,LMO4,CLSTN1,SEMA3C,B4GALT1,GLI3,IFT57,RDH10,GREM1,BRSK1	down_VCAV_EC
GO:0034765	0.375	0.746	10	91	regulation of ion transmembrane transport	BP	1	AMIGO1,ABL1,KCNE3,OSR1,CLIC5,KLHL24,KCNB1,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0045088	0.375	0.752	9	81	regulation of innate immune response	BP	1	TLR1,LEP,COCH,TLR3,F2RL1,PTPN22,PRKCE,PARP9,NOD2	up_ACOR_VSMC
GO:0006955	0.375	0.749	9	327	immune response	BP	1	LEP,RAB20,CD40,DLL1,CTSS,BPI,HCK,CYLD,CCL5	up_AFEM_EC
GO:0090287	0.375	0.752	9	91	regulation of cellular response to growth factor	BP	1	FERMT1,GATA3,HHEX,PRKD2,CTDSPL2,SKIL,HIF1A,JCAD,ZEB1	up_VCAV_EC
GO:0071826	0.375	0.757	8	117	ribonucleoprotein complex subunit	BP	1	CELF1,KIF5B,PRPF3,DDX39B,CNOT7,STRAP,EIF2S1,RSL24D1	down_VSAP_EC
GO:0071560	0.375	0.766	7	72	cellular response to transforming growth	BP	1	MEF2C,FERMT1,SMAD1,YES1,SKIL,ENSCAFG00000002015,ZEB1	up_VCAV_EC
GO:1903322	0.375	0.776	6	59	positive regulation of protein modification by small protein conjugation	BP	1	UBE2S,CAV1,FANCI,CDC20,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0007596	0.375	0.79	5	47	blood coagulation	BP	1	TFPI,TFPI2,CAV1,ITGB3,PIK3CD	down_ACOR_VSMC
GO:0031123	0.375	0.789	5	48	RNA 3'-end processing	BP	1	INTS7,FBL,ENSCAFG00000019620,WDR33,EXOSC5	down_ACOR_VSMC
GO:0032944	0.375	0.79	5	48	regulation of mononuclear cell	BP	1	HMGB1,MNDA,ARG2,TFRC,CORO1A	down_ACOR_VSMC
GO:0050670	0.375	0.79	5	48	regulation of lymphocyte proliferation	BP	1	HMGB1,MNDA,ARG2,TFRC,CORO1A	down_ACOR_VSMC
GO:0045834	0.375	0.791	5	41	positive regulation of lipid metabolic process	BP	1	HTR2B,PPARGC1A,CCDC3,PRKCE,ENSCAFG00000029553	up_ACOR_VSMC
GO:0006909	0.375	0.791	5	42	phagocytosis	BP	1	ABL1,F2RL1,CYBA,XKR8,ARHGAP12	up_VSAP_EC
GO:2001242	0.375	0.804	4	62	regulation of intrinsic apoptotic signaling	BP	1	TMEM161A,PARK7,GSDME,FBH1	down_VCAV_EC
GO:2000779	0.375	0.83	3	25	regulation of double-strand break repair	BP	1	PARPBP,RAD51,TIMELESS	down_ACOR_VSMC
GO:0032602	0.375	0.832	3	23	chemokine production	BP	1	MBP,TLR3,F2RL1	up_ACOR_VSMC
GO:0040007	0.375	0.826	3	276	growth	BP	1	SEMA3A,FBP1,RNF6	up_VPOR_EC
GO:0009891	0.375	0.829	3	521	positive regulation of biosynthetic process	BP	1	EYA1,HOXA9,SIX1	up_VFEM_EC
GO:0002832	0.375	0.867	2	15	negative regulation of response to biotic	BP	1	ARG2,CACTIN	down_ACOR_VSMC
GO:0048332	0.375	0.862	2	26	mesoderm morphogenesis	BP	1	BMPR1A,TLX2	down_VCAV_EC
GO:0099175	0.375	0.864	2	21	regulation of postsynapse organization	BP	1	APOE,ARF4	down_VSAP_EC
GO:0006468	0.375	0.866	2	544	protein phosphorylation	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0009888	0.375	0.865	2	545	tissue development	BP	1	SGCD,DUSP2	up_AORT_EC
GO:0001755	0.375	0.866	2	16	neural crest cell migration	BP	1	EDNRB,HIF1A	up_VCAV_EC

GO:0061337	0.375	0.866	2	16	cardiac conduction	BP	1	KCNJ2,SPTBN4	up_VCAV_EC
GO:0032990	0.375	0.86	2	167	cell part morphogenesis	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0035330	0.375	0.933	1	5	regulation of hippo signaling	BP	1	NF2	down_ACOR_VSMC
GO:0002092	0.375	0.927	1	9	positive regulation of receptor internalization	BP	1	GREM1	down_VCAV_EC
GO:0031103	0.375	0.927	1	9	axon regeneration	BP	1	RGMA	down_VCAV_EC
GO:0045616	0.375	0.927	1	9	regulation of keratinocyte differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0071360	0.375	0.927	1	9	cellular response to exogenous dsRNA	BP	1	MAVS	down_VCAV_EC
GO:1902236	0.375	0.927	1	9	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	PARK7	down_VCAV_EC
GO:0035640	0.375	0.929	1	7	exploration behavior	BP	1	APOE	down_VSAP_EC
GO:0036342	0.375	0.933	1	5	post-anal tail morphogenesis	BP	1	FZD3	up_ACOR_VSMC
GO:0071850	0.375	0.933	1	5	mitotic cell cycle arrest	BP	1	CDKN1A	up_ACOR_VSMC
GO:1902285	0.375	0.937	1	4	semaphorin-plexin signaling pathway involved in neuron	BP	1	NRP1	up_ACOR_VSMC
GO:0006974	0.375	0.926	1	333	cellular response to DNA damage stimulus	BP	1	EYA1	up_AFEM_VSMC
GO:0014733	0.375	0.933	1	5	regulation of skeletal muscle adaptation	BP	1	PPP3CA	up_VCAV_EC
GO:0035020	0.375	0.933	1	5	regulation of Rac protein signal transduction	BP	1	ARAP3	up_VCAV_EC
GO:0043501	0.375	0.933	1	5	skeletal muscle adaptation	BP	1	PPP3CA	up_VCAV_EC
GO:0002830	0.375	0.933	1	5	positive regulation of type 2 immune response	BP	1	GATA3	up_VCAV_EC
GO:0010043	0.375	0.929	1	7	response to zinc ion	BP	1	CREB1	up_VCAV_EC
GO:0030517	0.375	0.933	1	5	negative regulation of axon extension	BP	1	IFRD1	up_VCAV_EC
GO:0006952	0.375	0.926	1	319	defense response	BP	1	C6	up_VCAV_VSMC
GO:0045596	0.375	0.923	1	186	negative regulation of cell differentiation	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006163	0.375	0.923	1	174	purine nucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0030855	0.375	0.923	1	183	epithelial cell differentiation	BP	1	SPINK5	up_VFEM_VSMC
GO:0090407	0.375	0.923	1	177	organophosphate biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043269	0.375	0.922	1	135	regulation of ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0002753	0.375058068	0.92319	1	17	cytoplasmic pattern recognition receptor	BP	1	NOD2	up_ACOR_EC
GO:0060760	0.375286167	0.92309	1	17	positive regulation of response to cytokine	BP	1	MAVS	up_ACOR_EC
GO:0032504	0.375894666	0.78523	5	152	multicellular organism reproduction	BP	1	SOX9,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0048609	0.375894666	0.78523	5	152	multicellular organismal reproductive process	BP	1	SOX9,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0031175	0.376	0.704	24	224	neuron projection development	BP	1	EPYC,FEZ1,ITM2C,FGFR2,SEC24B,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,DAG1,APP,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,WASL	up_ACOR_VSMC
GO:0010648	0.376	0.707	22	407	negative regulation of cell communication	BP	1	SLC35F6,DCN,PRNP,VASN,FBN1,BGN,KANK2,AKT1S1,CHRDL1,CLSTN1,TMEM161A,ASPN,THY1,GLI3,PARK7,CDH2,SPRED1,RAB7B,GLIS2,GREM1,NPHP4,FOXO3	down_VCAV_EC
GO:0051345	0.376	0.721	16	151	positive regulation of hydrolase activity	BP	1	TNNT2,HTR2B,USP6NL,MBP,EVI5L,FGFR2,PKP4,F2RL1,DAPK1,NPNT,SGSM2,CCL5,PERP,DYNC1I2,DYNC1I1,LMF1	up_ACOR_VSMC
GO:0051251	0.376	0.766	7	69	positive regulation of lymphocyte activation	BP	1	HMGB1,CAV1,MMP14,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0002831	0.376	0.79	5	42	regulation of response to biotic stimulus	BP	1	CD274,SASH1,F2RL1,PTPN22,PARP9	up_ACOR_VSMC
GO:0046488	0.376	0.826	3	44	phosphatidylinositol metabolic process	BP	1	PDGFRB,ENSCAFG00000014978,PIGS	down_VCAV_EC
GO:0002244	0.376	0.828	3	35	hematopoietic progenitor cell differentiation	BP	1	ANLN,REST,INHBA	down_VSAP_EC

GO:0002706	0.376	0.827	3	35	regulation of lymphocyte mediated immunity	BP	1	FAM49B,PVR,TFRC	down_VSAP_EC
GO:0014855	0.376	0.831	3	22	striated muscle cell proliferation	BP	1	FGFR2,TBX20,TBX5	up_ACOR_VSMC
GO:0046928	0.376	0.83	3	23	regulation of neurotransmitter	BP	1	FBXL20,KCNC4,PREPL	up_ACOR_VSMC
GO:0010469	0.376	0.829	3	26	regulation of signaling receptor activity	BP	1	RELN,MEF2C,HOMER3	up_VCAV_EC
GO:0042307	0.376	0.831	3	23	positive regulation of protein import into	BP	1	CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0007019	0.376	0.868	2	13	microtubule depolymerization	BP	1	FGF13,MID1	up_ACOR_VSMC
GO:0048048	0.376	0.868	2	13	embryonic eye morphogenesis	BP	1	CITED2,FRS2	up_ACOR_VSMC
GO:0000956	0.376	0.859	2	55	nuclear-transcribed mRNA catabolic process	BP	1	CTIF,SAMD4B	up_AFEM_EC
GO:0007623	0.376	0.859	2	55	circadian rhythm	BP	1	CRY2,PPARGC1A	up_AFEM_EC
GO:0031325	0.376	0.872	2	914	positive regulation of cellular metabolic process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0043044	0.376	0.867	2	14	ATP-dependent chromatin remodeling	BP	1	SMARCD2,CENPP	up_VSAP_EC
GO:0070988	0.376	0.867	2	14	demethylation	BP	1	KDM2B,KDM3B	up_VSAP_EC
GO:0000729	0.376	0.933	1	5	DNA double-strand break processing	BP	1	RBBP8	down_ACOR_VSMC
GO:2000345	0.376	0.933	1	5	regulation of hepatocyte proliferation	BP	1	GLI1	down_ACOR_VSMC
GO:0032647	0.376	0.926	1	10	regulation of interferon-alpha production	BP	1	MAVS	down_VCAV_EC
GO:0046112	0.376	0.927	1	8	nucleobase biosynthetic process	BP	1	CMPK1	down_VSAP_EC
GO:0060999	0.376	0.928	1	7	positive regulation of dendritic spine	BP	1	APOE	down_VSAP_EC
GO:2000178	0.376	0.929	1	7	negative regulation of neural precursor cell	BP	1	ILK	down_VSAP_EC
GO:0034975	0.376	0.933	1	5	protein folding in endoplasmic reticulum	BP	1	ERO1B	up_ACOR_VSMC
GO:0051000	0.376	0.933	1	5	positive regulation of nitric-oxide synthase	BP	1	HTR2B	up_ACOR_VSMC
GO:0055091	0.376	0.933	1	5	phospholipid homeostasis	BP	1	ABCA1	up_VCAV_EC
GO:0060047	0.376	0.921	1	57	heart contraction	BP	1	SEMA3A	up_VPOR_EC
GO:0098727	0.376	0.92	1	60	maintenance of cell number	BP	1	HOOK3	up_VPOR_EC
GO:0007178	0.376	0.921	1	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0007080	0.376004155	0.92254	1	18	mitotic metaphase plate congression	BP	1	CHMP4B	up_ACOR_EC
GO:0043297	0.376233639	0.92266	1	17	apical junction assembly	BP	1	FZD5	up_ACOR_EC
GO:0099518	0.376489063	0.92255	1	17	vesicle cytoskeletal trafficking	BP	1	DYNC1I1	up_ACOR_EC
GO:1903902	0.37650839	0.92231	1	18	positive regulation of viral life cycle	BP	1	CHMP4B	up_ACOR_EC
GO:0007155	0.376549026	0.74237	10	324	cell adhesion	BP	1	CDH3,ARHGAP6,DUSP26,SMAD6,ACTN2,ELMO2,FOXC2,VCAM1,NRP1,PRKCD	up_ACOR_EC
GO:0018210	0.376648562	0.85889	2	48	peptidyl-threonine modification	BP	1	DCLK2,PRKCD	up_ACOR_EC

GO:0010468	0.377	0.664	111	1270	regulation of gene expression	BP	1	ELK3,HMGB1,RNPS1,SREBF1,IRAK1,ILF3,DDX39A,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,EDC3,HNRNPD,SREBF2,HINFP,NEDD4,SRSF2,MED17,U2AF2,MTDH,HEY1,PPP1R15B,SRRT,NAB2,SLC35C2,RAN,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,EDC4,AURKB,NONO,HNRNPL,EZH2,GREM1,CDK4,SMARCC1,RNASEH2B,PLK3,DHX33,HOXA7,SMG9,SF3B4,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PPARD,YBX3,HNRNPF,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,RBM17,NOLC1,HOXA10,ERF,TCERG1,PUM3,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,ENSCAFG00000015189,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,EXOSC5,HMGN1,SIX4,SF3A1,MED16,ENSCAFG00000017103,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0006357	0.377	0.681	49	547	regulation of transcription by RNA polymerase II	BP	1	ELK3,HMGB1,SREBF1,CBX5,PPRC1,ATAD2,SREBF2,NEDD4,MED17,MTDH,INSIG1,CAV1,TIMELESS,THRAP3,AURKB,EZH2,GREM1,SMARCC1,PLK3,HOXA7,UHRF1,CKS2,BRCA1,NOC2L,E2F8,PPARD,NCL,FOSL1,SUV39H1,ZNF367,HMGB2,DMAP1,CDK2,SMARCB1,EZR,RBM14,ERF,TCERG1,SMARCAL1,ELF4,PSMC1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,CDC5L,HMGN1,ENSCAFG00000017103	down_ACOR_VSMC
GO:0042592	0.377	0.698	28	522	homeostatic process	BP	1	GPAM,DCN,NDN,PRNP,NABP2,TRPV2,ENSCAFG00000014978,LCAT,ENSCAFG00000018277,PDIA4,SLC39A6,PLCL1,THY1,ATP6V0C,PARK7,SCARA5,ZFP36L1,NCDN,CYBA,CDH2,MPV17,ORMDL3,TSC22D3,ATOX1,NAPEPLD,FOXO3,SOAT1,ANKRD54	down_VCAV_EC
GO:0051247	0.377	0.699	27	502	positive regulation of protein metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,PRNP,GLIPR2,LARP6,BMPR1A,CLIP3,AKT2,CSPG4,PARK7,EEF2,MYDGF,SASH1,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,SOAT1,PACSIN3	down_VCAV_EC
GO:0045087	0.377	0.723	15	161	innate immune response	BP	1	HMGB1,FLNB,IRAK1,SLC29A1,CAV1,TRIM35,CACTIN,HMGB2,CDC42EP4,RBM14,CORO1A,POLR3F,ELF4,ARHGEF2,PIK3CD	down_ACOR_VSMC
GO:1901137	0.377	0.722	15	232	carbohydrate derivative biosynthetic process	BP	1	PGK1,TPI1,ENSCAFG00000032470,PGAM1,UGCG,CHSY1,HIF1A,GALNT1,ALDOC,CTNNB1,PAPSS1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0016311	0.377	0.743	10	106	dephosphorylation	BP	1	PPP2R5A,MEF2C,CTTNBP2NL,ACPP,BMP2,PPP1R2,SWAP70,NCK1,IMPA1,FKBP15	up_VCAV_EC
GO:0097193	0.377	0.744	10	109	intrinsic apoptotic signaling pathway	BP	1	FIGNL1,NCK1,PTGS2,USP28,PMAIP1,SKIL,HIF1A,IVNS1ABP,ATP2A1,ARHGEF2	up_VCAV_EC
GO:0044843	0.377	0.765	7	62	cell cycle G1/S phase transition	BP	1	SKP2,NACC2,LATS2,CDKN1A,CRLF3,FAM107A,KLF11	up_ACOR_VSMC
GO:0051168	0.377	0.776	6	57	nuclear export	BP	1	DDX39A,HSPA9,RAN,NUP62,NUP188,DDX39B	down_ACOR_VSMC
GO:0050920	0.377	0.776	6	53	regulation of chemotaxis	BP	1	VEGFD,FGF18,F2RL1,NRP1,CCL5,JAM3	up_ACOR_VSMC
GO:0065007	0.377	0.828	6	3499	biological regulation	BP	1	SLITRK5,LIMK1,GATA5,CA2,LRRC17,C6	up_VCAV_VSMC
GO:0043603	0.377	0.802	4	372	cellular amide metabolic process	BP	1	RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:0033865	0.377	0.826	3	43	nucleoside bisphosphate metabolic process	BP	1	GPAM,ACSS2,ACAT1	down_VCAV_EC
GO:0033875	0.377	0.826	3	43	ribonucleoside bisphosphate metabolic	BP	1	GPAM,ACSS2,ACAT1	down_VCAV_EC
GO:0034032	0.377	0.826	3	43	purine nucleoside bisphosphate metabolic	BP	1	GPAM,ACSS2,ACAT1	down_VCAV_EC
GO:0006970	0.377	0.83	3	23	response to osmotic stress	BP	1	OSR1,ZFP36L1,SLC12A6	up_VSAP_EC
GO:1903578	0.377	0.862	2	22	regulation of ATP metabolic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0018126	0.377	0.867	2	14	protein hydroxylation	BP	1	EGLN1,P4HA1	up_ACOR_VSMC
GO:0045087	0.377	0.858	2	161	innate immune response	BP	1	ARHGEF2,ENSCAFG00000032731	up_VPOR_EC
GO:0120036	0.377	0.862	2	373	plasma membrane bounded cell projection	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0061551	0.377	0.933	1	5	trigeminal ganglion development	BP	1	SIX4	down_ACOR_VSMC

GO:0019377	0.377	0.926	1	9	glycolipid catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0021904	0.377	0.926	1	9	dorsal/ventral neural tube patterning	BP	1	GLI3	down_VCAV_EC
GO:0046479	0.377	0.926	1	9	glycosphingolipid catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0046514	0.377	0.926	1	9	ceramide catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0001662	0.377	0.928	1	7	behavioral fear response	BP	1	APOE	down_VSAP_EC
GO:0002209	0.377	0.928	1	7	behavioral defense response	BP	1	APOE	down_VSAP_EC
GO:2000403	0.377	0.928	1	7	positive regulation of lymphocyte migration	BP	1	ADAM17	down_VSAP_EC
GO:0042596	0.377	0.928	1	7	fear response	BP	1	APOE	down_VSAP_EC
GO:0046596	0.377	0.927	1	8	regulation of viral entry into host cell	BP	1	P4HB	down_VSAP_EC
GO:0002739	0.377	0.932	1	5	regulation of cytokine secretion involved in	BP	1	F2RL1	up_ACOR_VSMC
GO:0010749	0.377	0.936	1	4	regulation of nitric oxide mediated signal	BP	1	PDE5A	up_ACOR_VSMC
GO:0046688	0.377	0.932	1	5	response to copper ion	BP	1	PARK7	up_ACOR_VSMC
GO:0007267	0.377	0.925	1	332	cell-cell signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0046365	0.377	0.928	1	7	monosaccharide catabolic process	BP	1	GALE	up_VCAV_EC
GO:0045596	0.377	0.922	1	186	negative regulation of cell differentiation	BP	1	HOXA9	up_VFEM_VSMC
GO:0097435	0.377	0.923	1	230	supramolecular fiber organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0035278	0.377	0.932	1	5	miRNA mediated inhibition of translation	BP	1	TNRC6C	up_VSAP_EC
GO:0040033	0.377	0.932	1	5	negative regulation of translation, ncRNA-	BP	1	TNRC6C	up_VSAP_EC
GO:0042795	0.377	0.932	1	5	snRNA transcription by RNA polymerase II	BP	1	ICE1	up_VSAP_EC
GO:0045974	0.377	0.932	1	5	regulation of translation, ncRNA-mediated	BP	1	TNRC6C	up_VSAP_EC
GO:0032488	0.377	0.932	1	5	Cdc42 protein signal transduction	BP	1	ABL1	up_VSAP_EC
GO:0032489	0.377	0.932	1	5	regulation of Cdc42 protein signal	BP	1	ABL1	up_VSAP_EC
GO:0048752	0.377	0.932	1	5	semicircular canal morphogenesis	BP	1	ZEB1	up_VSAP_EC
GO:0006820	0.377	0.921	1	109	anion transport	BP	1	SLC16A12	up_VSAP_VSMC
GO:0060537	0.377077583	0.80056	4	117	muscle tissue development	BP	1	ACTN2,FOXC2,TBX5,C23H3orf58	up_ACOR_EC
GO:0043124	0.377548857	0.92207	1	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	up_ACOR_EC
GO:0044271	0.378	0.661	129	1501	cellular nitrogen compound biosynthetic process	BP	1	ELK3,PRPSAP1,HMGB1,SREBF1,ACLY,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,VARS,NEDD4,RRM1,MED17,SLC29A1,MTDH,HEY1,RRBP1,PPP1R15B,SRRT,POLE,NAB2,MRPS18B,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,RFC5,RFC3,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,PFAS,AURKB,NONO,TK1,EZH2,GREM1,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,ARG2,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,ELOVL1,FARSA,PPARD,POLH,YBX3,NCL,NUP62,MRPL37,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,ELOVL6,RBM14,CYC1,NOLC1,POLR3F,HOXA10,ERF,TCERG1,RARS,ATP5F1A,PUM3,SMARCAL1,PRPS1,ENSCAFG00000013366,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,PDHA1,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,MRPL18,CDC5L,NUDT1,HMGN1,CCT4,SIX4,CTPS1,MED16,EIF3M,ENSCAFG00000017103,ATP5F1D,POLR1C,NUDT3	down_ACOR_VSMC
GO:0065007	0.378	0.783	10	3499	biological regulation	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,NETO1,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0043170	0.378	0.801	7	2980	macromolecule metabolic process	BP	1	CST3,HDAC7,CITED2,RAB11B,MGAT4B,TBX15,GBGT1	down_VPOR_EC

GO:0031326	0.378	0.781	6	1176	regulation of cellular biosynthetic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0007626	0.378	0.775	6	53	locomotory behavior	BP	1	SEZ6L,FXN,CTNS,NCOA2,HTRA2,PPP3CB	up_VSAP_EC
GO:0008154	0.378	0.784	5	81	actin polymerization or depolymerization	BP	1	KIRREL1,ENSCAFG00000014978,WIPF1,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0000910	0.378	0.802	4	52	cytokinesis	BP	1	MYH9,PLK3,ANLN,CALM1	down_VSAP_EC
GO:0071219	0.378	0.803	4	50	cellular response to molecule of bacterial	BP	1	NR1H4,SERPINE1,MTDH,LYN	down_VSAP_EC
GO:0061458	0.378	0.8	4	131	reproductive system development	BP	1	HOXA9,IRX5,LEP,TNC	up_AFEM_EC
GO:0045921	0.378	0.829	3	24	positive regulation of exocytosis	BP	1	EXPH5,F2RL1,SCAMP5	up_ACOR_VSMC
GO:1902533	0.378	0.824	3	271	positive regulation of intracellular signal	BP	1	ENSCAFG00000002015,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:0090630	0.378	0.83	3	23	activation of GTPase activity	BP	1	TBC1D10C,TBC1D2B,TIAM1	up_VSAP_EC
GO:0090114	0.378	0.865	2	15	COPII-coated vesicle budding	BP	1	INSIG1,PREB	down_ACOR_VSMC
GO:0048522	0.378	0.884	2	1484	positive regulation of cellular process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0006906	0.378	0.858	2	55	vesicle fusion	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0021952	0.378	0.867	2	13	central nervous system projection neuron	BP	1	EPHB1,SPTBN4	up_VCAV_EC
GO:0030857	0.378	0.865	2	15	negative regulation of epithelial cell	BP	1	JAG1,ZEB1	up_VCAV_EC
GO:0071466	0.378	0.864	2	17	cellular response to xenobiotic stimulus	BP	1	PDGFB,AHR	up_VCAV_EC
GO:1903779	0.378	0.93	1	6	regulation of cardiac conduction	BP	1	CAV1	down_ACOR_VSMC
GO:0034643	0.378	0.932	1	5	establishment of mitochondrion localization, microtubule-	BP	1	TRAK1	down_ACOR_VSMC
GO:0047497	0.378	0.932	1	5	mitochondrion transport along microtubule	BP	1	TRAK1	down_ACOR_VSMC
GO:0097190	0.378	0.922	1	217	apoptotic signaling pathway	BP	1	IVNS1ABP	down_AFEM_EC
GO:0032940	0.378	0.923	1	231	secretion by cell	BP	1	RAB11B	down_VPOR_EC
GO:0070862	0.378	0.932	1	5	negative regulation of protein exit from	BP	1	OS9	up_ACOR_VSMC
GO:0120036	0.378	0.926	1	373	plasma membrane bounded cell projection	BP	1	WNT7A	up_AORT_VSMC
GO:2000113	0.378	0.927	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	ESR1	up_AORT_VSMC
GO:1902231	0.378	0.93	1	6	positive regulation of intrinsic apoptotic signaling pathway in	BP	1	SKIL	up_VCAV_EC
GO:0006206	0.378	0.932	1	5	pyrimidine nucleobase metabolic process	BP	1	MTOR	up_VCAV_EC
GO:0060788	0.378	0.932	1	5	ectodermal placode formation	BP	1	PROX1	up_VCAV_EC
GO:0071697	0.378	0.932	1	5	ectodermal placode morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0098869	0.378	0.93	1	6	cellular oxidant detoxification	BP	1	GCH1	up_VCAV_EC
GO:1903649	0.378	0.932	1	5	regulation of cytoplasmic transport	BP	1	DNAJC13	up_VCAV_EC
GO:0033993	0.378	0.922	1	186	response to lipid	BP	1	CYP26B1	up_VPOR_VSMC
GO:0034504	0.378	0.92	1	111	protein localization to nucleus	BP	1	SIX1	up_VFEM_EC
GO:0009607	0.378	0.923	1	232	response to biotic stimulus	BP	1	IL22RA1	up_VPUL_VSMC
GO:0001503	0.378	0.92	1	109	ossification	BP	1	SHOX2	up_VSAP_VSMC
GO:0051962	0.378	0.92	1	112	positive regulation of nervous system	BP	1	SHOX2	up_VSAP_VSMC
GO:0007528	0.378005773	0.92187	1	17	neuromuscular junction development	BP	1	LRP4	up_ACOR_EC
GO:0048015	0.378138153	0.85794	2	48	phosphatidylinositol-mediated signaling	BP	1	SOX9,C23H3orf58	up_ACOR_EC
GO:0048017	0.378138153	0.85794	2	48	inositol lipid-mediated signaling	BP	1	SOX9,C23H3orf58	up_ACOR_EC
GO:0002287	0.378590229	0.9216	1	17	alpha-beta T cell activation involved in	BP	1	PTGER4	up_ACOR_EC

GO:0002292	0.378590229	0.9216	1	17	T cell differentiation involved in immune	BP	1	PTGER4	up_ACOR_EC
GO:0002293	0.378590229	0.9216	1	17	alpha-beta T cell differentiation involved in	BP	1	PTGER4	up_ACOR_EC
GO:0002294	0.378590229	0.9216	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	PTGER4	up_ACOR_EC
GO:0042093	0.378590229	0.9216	1	17	T-helper cell differentiation	BP	1	PTGER4	up_ACOR_EC
GO:0032535	0.379	0.725	14	128	regulation of cellular component size	BP	1	ACTN2,CLCN3,F2RL1,SLC12A7,JMY,LRRC8C,NRP1,ULK2,EVL,PRKCE,CLN8,SSH3,EDN1,WASL	up_ACOR_VSMC
GO:0023057	0.379	0.736	11	409	negative regulation of signaling	BP	1	LEP,LBH,CRY2,GREM1,GREM2,CYLD,LRRC15,RAB7A,AXIN2,ADAM17,KANK1	up_AFEM_EC
GO:0044237	0.379	0.827	6	3491	cellular metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0042391	0.379	0.783	5	81	regulation of membrane potential	BP	1	DCN,FXYD1,AKT2,PARK7,TPC3	down_VCAV_EC
GO:0007162	0.379	0.785	5	66	negative regulation of cell adhesion	BP	1	SERPINE1,SOCS5,PTPN11,PTPN2,SDC4	down_VSAP_EC
GO:0008286	0.379	0.804	4	36	insulin receptor signaling pathway	BP	1	SREBF1,CDK4,SMARCC1,NCOA5	down_ACOR_VSMC
GO:0015850	0.379	0.803	4	37	organic hydroxy compound transport	BP	1	SREBF2,LIMA1,LIPC,NUS1	down_ACOR_VSMC
GO:0071166	0.379	0.803	4	36	ribonucleoprotein complex localization	BP	1	DDX39A,RAN,NUP62,DDX39B	down_ACOR_VSMC
GO:0002688	0.379	0.804	4	34	regulation of leukocyte chemotaxis	BP	1	VEGFD,F2RL1,CCL5,JAM3	up_ACOR_VSMC
GO:0021510	0.379	0.829	3	23	spinal cord development	BP	1	DLL1,HOXC10,GDPD5	up_VSAP_EC
GO:1902041	0.379	0.829	3	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	RAF1,STX4,HMOX1	up_VSAP_EC
GO:0070849	0.379	0.864	2	15	response to epidermal growth factor	BP	1	NCL,IQGAP1	down_ACOR_VSMC
GO:0042278	0.379	0.86	2	25	purine nucleoside metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:0030048	0.379	0.861	2	23	actin filament-based movement	BP	1	MYH9,MYO1C	down_VSAP_EC
GO:0046427	0.379	0.864	2	16	positive regulation of JAK-STAT cascade	BP	1	HCLS1,KIT	up_VCAV_EC
GO:0043207	0.379	0.922	1	216	response to external biotic stimulus	BP	1	IVNS1ABP	down_AFEM_EC
GO:0051707	0.379	0.922	1	216	response to other organism	BP	1	IVNS1ABP	down_AFEM_EC
GO:0006515	0.379	0.925	1	9	protein quality control for misfolded or incompletely synthesized proteins	BP	1	LONP2	down_VCAV_EC
GO:0035988	0.379	0.925	1	9	chondrocyte proliferation	BP	1	DDR2	down_VCAV_EC
GO:0006760	0.379	0.926	1	8	folic acid-containing compound metabolic	BP	1	ALDH1L2	down_VSAP_EC
GO:0030851	0.379	0.926	1	8	granulocyte differentiation	BP	1	EVI2B	down_VSAP_EC
GO:0032620	0.379	0.926	1	8	interleukin-17 production	BP	1	NR1H4	down_VSAP_EC
GO:0048643	0.379	0.927	1	7	positive regulation of skeletal muscle tissue	BP	1	CTNNB1	down_VSAP_EC
GO:0017062	0.379	0.931	1	5	respiratory chain complex III assembly	BP	1	TTC19	up_ACOR_VSMC
GO:0034551	0.379	0.931	1	5	mitochondrial respiratory chain complex III	BP	1	TTC19	up_ACOR_VSMC
GO:0061004	0.379	0.932	1	5	pattern specification involved in kidney	BP	1	BMP4	up_ACOR_VSMC
GO:0072048	0.379	0.932	1	5	renal system pattern specification	BP	1	BMP4	up_ACOR_VSMC
GO:0090153	0.379	0.932	1	5	regulation of sphingolipid biosynthetic process	BP	1	ORMDL3	up_ACOR_VSMC
GO:1905038	0.379	0.932	1	5	regulation of membrane lipid metabolic process	BP	1	ORMDL3	up_ACOR_VSMC
GO:2000303	0.379	0.932	1	5	regulation of ceramide biosynthetic process	BP	1	ORMDL3	up_ACOR_VSMC
GO:0061383	0.379	0.921	1	20	trabecula morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:0006955	0.379	0.924	1	327	immune response	BP	1	TLR2	up_AFEM_VSMC
GO:0045786	0.379	0.921	1	195	negative regulation of cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0009968	0.379	0.926	1	392	negative regulation of signal transduction	BP	1	ESR1	up_AORT_VSMC

GO:0021819	0.379	0.935	1	4	layer formation in cerebral cortex	BP	1	RELN	up_VCAV_EC
GO:0030833	0.379	0.919	1	59	regulation of actin filament polymerization	BP	1	TWF1	up_VPOR_EC
GO:1903522	0.379	0.919	1	58	regulation of blood circulation	BP	1	SEMA3A	up_VPOR_EC
GO:0045943	0.379065416	0.92139	1	17	positive regulation of transcription by RNA	BP	1	RASL11A	up_ACOR_EC
GO:0060828	0.37910475	0.82192	3	82	regulation of canonical Wnt signaling pathway	BP	1	CDH3,SOX9,LRP4	up_ACOR_EC
GO:0009615	0.379176152	0.82184	3	83	response to virus	BP	1	MAVS,IFIT2,AGBL5	up_ACOR_EC
GO:0030182	0.379342598	0.73994	10	327	neuron differentiation	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,DCLK2,MAPK8IP2,LRP4,NRP1,DBNDD2	up_ACOR_EC
GO:0071363	0.379752892	0.76975	6	188	cellular response to growth factor stimulus	BP	1	SOX9,RGMA,SMAD6,ADAMTSL2,LRP4,NRP1	up_ACOR_EC
GO:1901264	0.37997506	0.92074	1	18	carbohydrate derivative transport	BP	1	SLC25A42	up_ACOR_EC
GO:0006629	0.38	0.69	32	382	lipid metabolic process	BP	1	TEK,ADGRF5,KIT,PPP2R5A,PDGFB,TIPARP,GK5,EDN1,PTGS1,SERINC5,SPTLC2,MTOR,SAMD8,BMP2,CREM,ST3GAL6,ABCA1,GDPD5,PROX1,ENSCAFG00000010596,SH3GLB1,ELOVL7,APOD,PTGS2,PLCG2,CREB1,LIPA,LBR,IMPA1,PIP5K1B,NR1D2,ALDH1A3	up_VCAV_EC
GO:1901987	0.38	0.741	10	107	regulation of cell cycle phase transition	BP	1	RAB11A,TAOK1,BLM,RAD21,RAD17,CUL4A,ZW10,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0051170	0.38	0.762	7	69	import into nucleus	BP	1	POLA2,RAN,ENSCAFG00000011598,IPO4,NUP62,NUP188,DMAP1	down_ACOR_VSMC
GO:0071901	0.38	0.802	4	37	negative regulation of protein serine/threonine	BP	1	HMGCR,CAV1,CDKN2C,NUP62	down_ACOR_VSMC
GO:1904892	0.38	0.802	4	40	regulation of STAT cascade	BP	1	HCLS1,IL7R,KIT,CNOT7	up_VCAV_EC
GO:0045739	0.38	0.827	3	26	positive regulation of DNA repair	BP	1	HMGB1,TIMELESS,PCNA	down_ACOR_VSMC
GO:0001736	0.38	0.828	3	23	establishment of planar polarity	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0007045	0.38	0.828	3	23	cell-substrate adherens junction assembly	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0007164	0.38	0.828	3	23	establishment of tissue polarity	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0048041	0.38	0.828	3	23	focal adhesion assembly	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0006919	0.38	0.862	2	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	PDCD2,AIFM1	down_ACOR_VSMC
GO:0043648	0.38	0.859	2	26	dicarboxylic acid metabolic process	BP	1	ME3,GLS2	down_VCAV_EC
GO:0032649	0.38	0.86	2	23	regulation of interferon-gamma production	BP	1	NR1H4,FAM49B	down_VSAP_EC
GO:0045214	0.38	0.866	2	13	sarcomere organization	BP	1	ACTN2,EDN1	up_ACOR_VSMC
GO:0097009	0.38	0.865	2	13	energy homeostasis	BP	1	PRCP,NR1D2	up_VCAV_EC
GO:0002639	0.38	0.865	2	14	positive regulation of immunoglobulin	BP	1	STAT6,STX4	up_VSAP_EC
GO:0017038	0.38	0.919	1	96	protein import	BP	1	IPO7	down_ACOR_EC
GO:0019221	0.38	0.919	1	102	cytokine-mediated signaling pathway	BP	1	ASPN	down_ACOR_EC
GO:0035278	0.38	0.931	1	5	miRNA mediated inhibition of translation	BP	1	RBM14	down_ACOR_VSMC
GO:0040033	0.38	0.931	1	5	negative regulation of translation, ncRNA-	BP	1	RBM14	down_ACOR_VSMC
GO:0045974	0.38	0.931	1	5	regulation of translation, ncRNA-mediated	BP	1	RBM14	down_ACOR_VSMC
GO:0047484	0.38	0.931	1	5	regulation of response to osmotic stress	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0032897	0.38	0.925	1	9	negative regulation of viral transcription	BP	1	TRIM8	down_VCAV_EC
GO:0033233	0.38	0.925	1	9	regulation of protein sumoylation	BP	1	PARK7	down_VCAV_EC
GO:0051882	0.38	0.925	1	9	mitochondrial depolarization	BP	1	DCN	down_VCAV_EC
GO:0046131	0.38	0.926	1	8	pyrimidine ribonucleoside metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0045649	0.38	0.926	1	8	regulation of macrophage differentiation	BP	1	PTPN2	down_VSAP_EC
GO:0009583	0.38	0.931	1	5	detection of light stimulus	BP	1	GNAQ	up_ACOR_VSMC

GO:0035437	0.38	0.931	1	5	maintenance of protein localization in endoplasmic reticulum	BP	1	OS9	up_ACOR_VSMC
GO:0001816	0.38	0.921	1	194	cytokine production	BP	1	BPI	up_AORT_EC
GO:0006882	0.38	0.928	1	6	cellular zinc ion homeostasis	BP	1	SLC39A8	up_VCAV_EC
GO:0010640	0.38	0.928	1	6	regulation of platelet-derived growth factor receptor signaling	BP	1	APOD	up_VCAV_EC
GO:0021542	0.38	0.929	1	6	dentate gyrus development	BP	1	PROX1	up_VCAV_EC
GO:0055069	0.38	0.928	1	6	zinc ion homeostasis	BP	1	SLC39A8	up_VCAV_EC
GO:2001236	0.38	0.919	1	59	regulation of extrinsic apoptotic signaling	BP	1	ARHGEF2	up_VPOR_EC
GO:0044057	0.38	0.92	1	110	regulation of system process	BP	1	AVPR1A	up_VFEM_EC
GO:0006206	0.38	0.931	1	5	pyrimidine nucleobase metabolic process	BP	1	ALDH6A1	up_VSAP_EC
GO:1901626	0.38	0.931	1	5	regulation of postsynaptic membrane organization	BP	1	LRP4	up_VSAP_EC
GO:0006417	0.38	0.919	1	109	regulation of translation	BP	1	PRR16	up_VSAP_VSMC
GO:0010035	0.38	0.919	1	107	response to inorganic substance	BP	1	CAV1	up_VSAP_VSMC
GO:0042110	0.38	0.919	1	109	T cell activation	BP	1	CAV1	up_VSAP_VSMC
GO:0045661	0.380323635	0.92058	1	18	regulation of myoblast differentiation	BP	1	SOX9	up_ACOR_EC
GO:0019953	0.380596459	0.78148	5	152	sexual reproduction	BP	1	SOX9,MAPK8IP2,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0061024	0.381	0.708	19	215	membrane organization	BP	1	TIE1,ATP8A1,MX2,MALL,BAIAP2L1,RELN,MTSS1,NECTIN2,SNAP23,CAV2,ABCA1,ELMO1,SH3GLB1,STX11,TBC1D1,PMAIP1,SPTBN4,RABGAP1,USP6NL	up_VCAV_EC
GO:0055082	0.381	0.714	17	189	cellular chemical homeostasis	BP	1	CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,SWAP70,SMARCA4,PLCG2,HMGB1,MCU,HIF1A,ATP2A1	up_VCAV_EC
GO:0048598	0.381	0.721	14	207	embryonic morphogenesis	BP	1	PRICKLE1,SULF1,PRKACB,ITGA2,ENSCAFG00000032470,TMED2,HOXB7,HIF1A,CTNNB1,SDC4,EXT1,INHBA,SIX4,COL12A1	down_VSAP_EC
GO:0048732	0.381	0.735	11	116	gland development	BP	1	TNFAIP3,GATA3,NTN4,IGSF3,BMP2,HHEX,PROX1,BTBD7,CREB1,HIF1A,ALDH1A3	up_VCAV_EC
GO:0031346	0.381	0.754	8	73	positive regulation of cell projection organization	BP	1	ENPP2,CDC42EP5,FUZ,CDC42EP2,F2RL1,SHOX2,NCK1,MAP2K2	up_VSAP_EC
GO:1902905	0.381	0.754	8	72	positive regulation of supramolecular fiber	BP	1	WNT11,ARHGEF5,ABL1,CDC42EP5,CDC42EP2,F2RL1,NCK1,BAG4	up_VSAP_EC
GO:0034612	0.381	0.763	7	63	response to tumor necrosis factor	BP	1	AFF3,ANKRD1,F2RL1,NPNT,CCDC3,CCL5,INPP5K	up_ACOR_VSMC
GO:1904062	0.381	0.762	7	62	regulation of cation transmembrane transport	BP	1	AMIGO1,ABL1,KCNE3,OSR1,KLHL24,CYBA,FXYD1	up_VSAP_EC
GO:0090305	0.381	0.785	5	49	nucleic acid phosphodiester bond	BP	1	EDC3,EDC4,AIFM1,WDR33,NOB1	down_ACOR_VSMC
GO:0043086	0.381	0.781	5	170	negative regulation of catalytic activity	BP	1	CRYAB,MYO1D,LRRC15,RECK,ACACB	up_AFEM_EC
GO:0000302	0.381	0.8	4	52	response to reactive oxygen species	BP	1	PLK3,SESN2,CRYAB,KPNA4	down_VSAP_EC
GO:0001938	0.381	0.802	4	34	positive regulation of endothelial cell	BP	1	VEGFD,HTR2B,BMP4,TGFBR1	up_ACOR_VSMC
GO:0038127	0.381	0.804	4	32	ERBB signaling pathway	BP	1	SH3TC2,RASSF2,APP,PSEN1	up_ACOR_VSMC
GO:0042476	0.381	0.823	3	36	odontogenesis	BP	1	SERPINE1,CTNNB1,INHBA	down_VSAP_EC
GO:0060485	0.381	0.82	3	93	mesenchyme development	BP	1	TMEM100,GREM1,AXIN2	up_AFEM_EC
GO:0043632	0.381	0.858	2	262	modification-dependent macromolecule catabolic	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0045620	0.381	0.863	2	15	negative regulation of lymphocyte	BP	1	HMGB1,HMGB3	down_ACOR_VSMC
GO:0040014	0.381	0.858	2	27	regulation of multicellular organism growth	BP	1	GPAM,PEX5	down_VCAV_EC
GO:0045069	0.381	0.859	2	22	regulation of viral genome replication	BP	1	CNOT7,RAD23A	down_VSAP_EC
GO:1902476	0.381	0.865	2	13	chloride transmembrane transport	BP	1	SLC26A7,CLCN3	up_ACOR_VSMC
GO:0051130	0.381	0.858	2	342	positive regulation of cellular component	BP	1	SLITRK5,NTRK2	up_APUL_EC
GO:0010324	0.381	0.862	2	16	membrane invagination	BP	1	ABCA1,ELMO1	up_VCAV_EC

GO:0031328	0.381	0.862	2	512	positive regulation of cellular biosynthetic	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0043436	0.381	0.858	2	303	oxoacid metabolic process	BP	1	CYP26B1,CHST7	up_VFEM_EC
GO:0072015	0.381	0.931	1	5	glomerular visceral epithelial cell	BP	1	IQGAP1	down_ACOR_VSMC
GO:0072310	0.381	0.931	1	5	glomerular epithelial cell development	BP	1	IQGAP1	down_ACOR_VSMC
GO:0046579	0.381	0.924	1	9	positive regulation of Ras protein signal	BP	1	NOTCH2	down_VCAV_EC
GO:0097242	0.381	0.927	1	7	amyloid-beta clearance	BP	1	APOE	down_VSAP_EC
GO:0015837	0.381	0.931	1	5	amine transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0051952	0.381	0.931	1	5	regulation of amine transport	BP	1	PSEN1	up_ACOR_VSMC
GO:2000310	0.381	0.934	1	4	regulation of NMDA receptor activity	BP	1	DAPK1	up_ACOR_VSMC
GO:0016239	0.381	0.92	1	20	positive regulation of macroautophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0048708	0.381	0.92	1	20	astrocyte differentiation	BP	1	DLL1	up_AFEM_EC
GO:0061180	0.381	0.92	1	20	mammary gland epithelium development	BP	1	LBH	up_AFEM_EC
GO:1901224	0.381	0.92	1	20	positive regulation of NIK/NF-kappaB signaling	BP	1	GREM1	up_AFEM_EC
GO:1901655	0.381	0.92	1	20	cellular response to ketone	BP	1	NR3C1	up_AFEM_EC
GO:1905332	0.381	0.92	1	20	positive regulation of morphogenesis of an	BP	1	GREM1	up_AFEM_EC
GO:0010558	0.381	0.925	1	392	negative regulation of macromolecule biosynthetic process	BP	1	ESR1	up_AORT_VSMC
GO:0030030	0.381	0.925	1	377	cell projection organization	BP	1	WNT7A	up_AORT_VSMC
GO:0034762	0.381	0.919	1	122	regulation of transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0007625	0.381	0.928	1	6	grooming behavior	BP	1	HOXB8	up_VCAV_EC
GO:0032692	0.381	0.928	1	6	negative regulation of interleukin-1 production	BP	1	TNFAIP3	up_VCAV_EC
GO:0039532	0.381	0.928	1	6	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling	BP	1	RIOK3	up_VCAV_EC
GO:0003139	0.381	0.931	1	5	secondary heart field specification	BP	1	MEF2C	up_VCAV_EC
GO:0006955	0.381	0.923	1	327	immune response	BP	1	C6	up_VCAV_VSMC
GO:0051607	0.381	0.919	1	58	defense response to virus	BP	1	OAS3	up_VPOR_EC
GO:0000904	0.381	0.921	1	181	cell morphogenesis involved in differentiation	BP	1	CHL1	up_VPOR_VSMC
GO:0071679	0.381	0.931	1	5	commissural neuron axon guidance	BP	1	NFIB	up_VSAP_EC
GO:0001890	0.381026258	0.85588	2	51	placenta development	BP	1	FZD5,DLX3	up_ACOR_EC
GO:0042221	0.382	0.66	100	1012	response to chemical	BP	1	FZD1,EMX2,ENSCAFG00000009113,HNF4A,FAM107A,CD274,ACKR3,ARHGEF5,C5AR2,ACKR2,ENPP2,PTGFR,SLC8B1,PPARGC1B,FOXRED2,SLIT2,CDH1,SLC6A4,FGF7,ABL1,GOT1,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,IL17RC,PDGFD,TRAFD1,KLF15,PLXNA4,SEMA5A,CDC42EP2,HSD3B7,RARG,CCBE1,MGST1,STAT5A,STAT6,SLC25A12,F2RL1,RAB11B,NFE2L2,LPL,PDK2,ZFP36L1,MT2A,FXN,PIK3R1,GAS1,MYC,ZEB1,TBXA2R,SULF2,ABAT,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,DPYSL2,STK16,ACKR4,CASTOR1,NCEH1,FBXO7,KCNB1,CDK9,CD83,PRMT2,OSBPL7,ZFP36L2,HPGD,RAF1,PNP,NFIB,ZNF580,NCOA2,STX4,PQBP1,TIMP2,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,HMOX1,TGFBR2,CITED2,SAA1,BAG4,LBH,KEAP1,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC

GO:0032879	0.382	0.666	76	767	regulation of localization	BP	1	HOXA7,TWIST2,WNT11,HNF4A,FAM107A,CD274,ARHGEF5,C5AR2,AMIGO1,ENPP2,SLC8B1,TBC1D10C,GABRE,ACACB,SLIT2,TBC1D2B,CDH1,FGF7,ABL1,HDAC7,EMP2,KCNE3,CHRM1,DLL1,OSR1,IL17RC,CLIC5,FUZ,PDGFD,KLF15,C1QTNF2,ANXA4,PLXNA4,CCBE1,STAT5A,RECK,KLHL24,F2RL1,RAB11B,GLIS2,DDR2,ICE1,ZFP36L1,PIK3R1,TIAM1,CRACR2B,GAS1,TBXA2R,CFAP69,SASH1,FBXO4,MYD88,LRP4,PASK,AZIN2,KCNB1,FBLN1,MAPKBP1,ZNF580,CYBA,ZNF205,FXYD1,STX4,TTL,VPS11,KCNC4,ACVRL1,UBQLN2,FLOT1,PPP3CB,NCK1,MAVS,HMOX1,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0006915	0.382	0.678	46	550	apoptotic process	BP	1	PLK2,HCLS1,IL7R,PRKCH,TNFAIP3,MAP3K11,STK10,MEF2C,ATF3,GATA3,TNFAIP8,FIGNL1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,ENSCAFG00000010596,MADD,PAK2,THOC1,SH3GLB1,TLR3,NCK1,CASP10,EXOC5,PTGS2,RAPGEF2,ENSCAFG00000005099,BCL10,USP28,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ATP2A1,ARHGEF2	up_VCAV_EC
GO:0009887	0.382	0.694	28	314	animal organ morphogenesis	BP	1	EPHB1,HOXB7,FLI1,TNFAIP3,CD34,MEF2C,CHD7,TIPARP,DLL4,STC1,GATA3,EDN1,HOXB8,NTN4,MTOR,BMP2,HHEX,PROX1,MDFI,TSPAN12,BTBD7,HOXB5,JAG1,ITGA6,HIF1A,ALDH1A3,ZEB1,CDON	up_VCAV_EC
GO:1904062	0.382	0.771	6	62	regulation of cation transmembrane transport	BP	1	RELN,PDE4D,MEF2C,CHD7,APLNR,PLCG2	up_VCAV_EC
GO:0000302	0.382	0.772	6	52	response to reactive oxygen species	BP	1	PPARGC1B,ABL1,SESN1,MAP3K5,PDK2,ZNF580	up_VSAP_EC
GO:0042113	0.382	0.782	5	64	B cell activation	BP	1	PTPN2,TFRC,LYN,BTK,CDKN1A	down_VSAP_EC
GO:0021953	0.382	0.8	4	49	central nervous system neuron differentiation	BP	1	CDH11,CTNNB1,INHBA,NRP1	down_VSAP_EC
GO:0007006	0.382	0.802	4	35	mitochondrial membrane organization	BP	1	RHOT1,BNIP3,CLN8,NAIF1	up_ACOR_VSMC
GO:0098662	0.382	0.797	4	131	inorganic cation transmembrane transport	BP	1	KCNC4,ATP6V1B2,FXYD1,ATP6V0B	up_AFEM_EC
GO:0071426	0.382	0.823	3	35	ribonucleoprotein complex export from	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0070997	0.382	0.82	3	93	neuron death	BP	1	THRB,PPARGC1A,CCL5	up_AFEM_EC
GO:0048519	0.382	0.842	3	1554	negative regulation of biological process	BP	1	HOXC10,EYA1,HOXA9	up_AFEM_VSMC
GO:0001934	0.382	0.821	3	274	positive regulation of protein phosphorylation	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0051173	0.382	0.83	3	874	positive regulation of nitrogen compound	BP	1	NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0015893	0.382	0.858	2	26	drug transport	BP	1	FOLR2,PARK7	down_VCAV_EC
GO:0043967	0.382	0.86	2	21	histone H4 acetylation	BP	1	IWS1,MORF4L2	down_VSAP_EC
GO:0042108	0.382	0.863	2	14	positive regulation of cytokine biosynthetic	BP	1	TLR1,TLR3	up_ACOR_VSMC
GO:0055021	0.382	0.862	2	15	regulation of cardiac muscle tissue growth	BP	1	MEF2C,EDN1	up_VCAV_EC
GO:0031325	0.382	0.869	2	914	positive regulation of cellular metabolic process	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0030030	0.382	0.859	2	377	cell projection organization	BP	1	FLRT3,NEO1	up_VPUL_EC
GO:0010632	0.382	0.918	1	95	regulation of epithelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0009143	0.382	0.928	1	6	nucleoside triphosphate catabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0010564	0.382	0.92	1	217	regulation of cell cycle process	BP	1	GPSM2	down_AFEM_EC
GO:0098754	0.382	0.924	1	9	detoxification	BP	1	PARK7	down_VCAV_EC
GO:2000738	0.382	0.924	1	9	positive regulation of stem cell differentiation	BP	1	SEMA3C	down_VCAV_EC
GO:0009261	0.382	0.925	1	8	ribonucleotide catabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0006531	0.382	0.93	1	5	aspartate metabolic process	BP	1	NMNAT1	up_ACOR_VSMC
GO:0034162	0.382	0.93	1	5	toll-like receptor 9 signaling pathway	BP	1	PTPN22	up_ACOR_VSMC
GO:0045657	0.382	0.93	1	5	positive regulation of monocyte differentiation	BP	1	CLSTN1	up_ACOR_VSMC

GO:1902237	0.382	0.93	1	5	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	SERINC3	up_ACOR_VSMC
GO:1903071	0.382	0.93	1	5	positive regulation of ER-associated ubiquitin-dependent protein	BP	1	HERPUD1	up_ACOR_VSMC
GO:0007586	0.382	0.92	1	20	digestion	BP	1	LEP	up_AFEM_EC
GO:0021695	0.382	0.92	1	20	cerebellar cortex development	BP	1	DLL1	up_AFEM_EC
GO:0022600	0.382	0.92	1	20	digestive system process	BP	1	LEP	up_AFEM_EC
GO:0030850	0.382	0.919	1	20	prostate gland development	BP	1	TNC	up_AFEM_EC
GO:0046324	0.382	0.919	1	20	regulation of glucose import	BP	1	LEP	up_AFEM_EC
GO:0010587	0.382	0.93	1	5	miRNA catabolic process	BP	1	TENT2	up_VCAV_EC
GO:0032633	0.382	0.928	1	6	interleukin-4 production	BP	1	GATA3	up_VCAV_EC
GO:0045579	0.382	0.93	1	5	positive regulation of B cell differentiation	BP	1	ATP11C	up_VCAV_EC
GO:0072520	0.382	0.93	1	5	seminiferous tubule development	BP	1	ATRX	up_VCAV_EC
GO:0003015	0.382	0.918	1	58	heart process	BP	1	SEMA3A	up_VPOR_EC
GO:0055091	0.382	0.93	1	5	phospholipid homeostasis	BP	1	HNF4A	up_VSAP_EC
GO:0034605	0.382514285	0.91958	1	18	cellular response to heat	BP	1	PRKACA	up_ACOR_EC
GO:0042157	0.382589242	0.85487	2	51	lipoprotein metabolic process	BP	1	PORCN,PIGS	up_ACOR_EC
GO:0043069	0.383	0.694	27	262	negative regulation of programmed cell death	BP	1	SMAD6,PLCG2,BCL2,HTR2B,PRKAA2,BMP4,TM7SF3,FGFR2,SH3RF2,PPARGC1A,CITED2,AR,PLAC8B,KLHL20,LIMS2,DAPK1,BNIP3,NRP1,UNC5B,SH3RF1,FZD3,PSEN1,CLN8,OXR1,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0001816	0.383	0.732	11	194	cytokine production	BP	1	GPAM,PRNP,LUM,CHID1,RNF216,PARK7,MAST2,BPI,CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0009126	0.383	0.734	11	100	purine nucleoside monophosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,NT5C2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0009167	0.383	0.734	11	100	purine ribonucleoside monophosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,NT5C2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:2000146	0.383	0.739	10	92	negative regulation of cell motility	BP	1	HOXA7,WNT11,C5AR2,SLIT2,CDH1,FUZ,RECK,TBXA2R,FBLN1,ACVRL1	up_VSAP_EC
GO:0010769	0.383	0.753	8	69	regulation of cell morphogenesis involved	BP	1	NRP1,ULK2,PSEN1,SIPA1L1,SSH3,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:1901566	0.383	0.771	6	598	organonitrogen compound biosynthetic	BP	1	OSTC,FBP1,RSL24D1,RPL10L,PUM3,EIF5	up_VPOR_EC
GO:0035303	0.383	0.781	5	65	regulation of dephosphorylation	BP	1	NUAK1,PPP1R12A,HTT,ARFGEF3,CALM1	down_VSAP_EC
GO:0045766	0.383	0.797	4	63	positive regulation of angiogenesis	BP	1	HSPB6,MYDGF,SASH1,GREM1	down_VCAV_EC
GO:0030219	0.383	0.861	2	16	megakaryocyte differentiation	BP	1	PRMT1,HMGB2	down_ACOR_VSMC
GO:0032368	0.383	0.857	2	26	regulation of lipid transport	BP	1	AKT2,SCP2	down_VCAV_EC
GO:0032612	0.383	0.858	2	22	interleukin-1 production	BP	1	NR1H4,GBP5	down_VSAP_EC
GO:0001953	0.383	0.863	2	14	negative regulation of cell-matrix adhesion	BP	1	DUSP22,FAM107A	up_ACOR_VSMC
GO:0006023	0.383	0.86	2	17	aminoglycan biosynthetic process	BP	1	PDGFB,CHST7	up_VCAV_EC
GO:1900744	0.383	0.862	2	15	regulation of p38MAPK cascade	BP	1	MAP3K3,BMP2	up_VCAV_EC
GO:1901264	0.383	0.86	2	18	carbohydrate derivative transport	BP	1	SLC35A3,RALBP1	up_VCAV_EC
GO:0007420	0.383	0.854	2	169	brain development	BP	1	HOOK3,SEMA3A	up_VPOR_EC
GO:0006940	0.383	0.863	2	14	regulation of smooth muscle contraction	BP	1	CHRM1,TBXA2R	up_VSAP_EC
GO:0009628	0.383	0.856	2	302	response to abiotic stimulus	BP	1	NETO1,CAV1	up_VSAP_VSMC
GO:0010817	0.383	0.918	1	102	regulation of hormone levels	BP	1	STX4	down_ACOR_EC
GO:0042451	0.383	0.923	1	9	purine nucleoside biosynthetic process	BP	1	ADK	down_VCAV_EC

GO:0035337	0.383	0.923	1	9	fatty-acyl-CoA metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0046129	0.383	0.923	1	9	purine ribonucleoside biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0090022	0.383	0.923	1	9	regulation of neutrophil chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0032369	0.383	0.924	1	8	negative regulation of lipid transport	BP	1	PTPN11	down_VSAP_EC
GO:0006337	0.383	0.925	1	7	nucleosome disassembly	BP	1	SMARCA4	down_VSAP_EC
GO:0032986	0.383	0.925	1	7	protein-DNA complex disassembly	BP	1	SMARCA4	down_VSAP_EC
GO:2000515	0.383	0.924	1	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	SOCS5	down_VSAP_EC
GO:0010642	0.383	0.93	1	5	negative regulation of platelet-derived growth factor receptor signaling	BP	1	PTGIR	up_ACOR_VSMC
GO:0010714	0.383	0.93	1	5	positive regulation of collagen metabolic	BP	1	BMP4	up_ACOR_VSMC
GO:0032965	0.383	0.93	1	5	regulation of collagen biosynthetic process	BP	1	BMP4	up_ACOR_VSMC
GO:0032967	0.383	0.93	1	5	positive regulation of collagen biosynthetic	BP	1	BMP4	up_ACOR_VSMC
GO:1901722	0.383	0.93	1	5	regulation of cell proliferation involved in	BP	1	BMP4	up_ACOR_VSMC
GO:0031529	0.383	0.919	1	20	ruffle organization	BP	1	KANK1	up_AFEM_EC
GO:0003073	0.383	0.919	1	20	regulation of systemic arterial blood pressure	BP	1	AVPR1A	up_AFEM_EC
GO:0051893	0.383	0.919	1	20	regulation of focal adhesion assembly	BP	1	GREM1	up_AFEM_EC
GO:0051972	0.383	0.919	1	20	regulation of telomerase activity	BP	1	GREM1	up_AFEM_EC
GO:0070228	0.383	0.919	1	20	regulation of lymphocyte apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0090109	0.383	0.919	1	20	regulation of cell-substrate junction	BP	1	GREM1	up_AFEM_EC
GO:1903672	0.383	0.919	1	20	positive regulation of sprouting angiogenesis	BP	1	DLL1	up_AFEM_EC
GO:1902903	0.383	0.918	1	125	regulation of supramolecular fiber	BP	1	TUBB4A	up_APUL_EC
GO:0010667	0.383	0.93	1	5	negative regulation of cardiac muscle cell	BP	1	RGL2	up_VCAV_EC
GO:0035562	0.383	0.93	1	5	negative regulation of chromatin binding	BP	1	PPP3CA	up_VCAV_EC
GO:0006595	0.383	0.927	1	6	polyamine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0007616	0.383	0.93	1	5	long-term memory	BP	1	RELN	up_VCAV_EC
GO:0036491	0.383	0.93	1	5	regulation of translation initiation in response to endoplasmic reticulum	BP	1	NCK1	up_VSAP_EC
GO:0036492	0.383	0.93	1	5	eiF2alpha phosphorylation in response to endoplasmic	BP	1	NCK1	up_VSAP_EC
GO:0048146	0.383758232	0.91901	1	18	positive regulation of fibroblast proliferation	BP	1	AQP1	up_ACOR_EC
GO:0065009	0.384	0.707	19	735	regulation of molecular function	BP	1	CMKLR1,LEP,CRYAB,F3,MYO1D,GREM1,CAMK2A,GREM2,CYLD,RASGEF1B,FXYD1,LRRC15,RECK,DCUN1D3,BVES,ACACB,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0098657	0.384	0.727	12	181	import into cell	BP	1	VEGFA,MYH9,SERPINE1,ENSCAFG00000003477,CANX,PIK3C2A,TFRC,APOE,GPR107,MYO1E,LRRTM2,ICAM5	down_VSAP_EC
GO:0007169	0.384	0.735	10	178	transmembrane receptor protein tyrosine kinase	BP	1	PDGFRB,DCN,NDN,ANGPT1,IGFBP6,ENSCAFG00000014978,AKT1S1,AKT2,CSPG4,SHC1	down_VCAV_EC
GO:0048523	0.384	0.769	7	1399	negative regulation of cellular process	BP	1	EYA1,HOXA9,TRIM9,HOXA7,SIX1,CYP26B1,MTSS1	up_VFEM_EC
GO:0009952	0.384	0.769	6	66	anterior/posterior pattern specification	BP	1	HOXB7,HOXB8,BMP2,HHEX,HOXB5,CDON	up_VCAV_EC
GO:0034599	0.384	0.78	5	81	cellular response to oxidative stress	BP	1	TMEM161A,PARK7,MPV17,FUT8,FOXO3	down_VCAV_EC
GO:0042098	0.384	0.783	5	43	T cell proliferation	BP	1	LEP,BMP4,PDE5A,CD274,PTPN22	up_ACOR_VSMC
GO:0050864	0.384	0.8	4	36	regulation of B cell activation	BP	1	MNDA,MMP14,HMGB3,TFRC	down_ACOR_VSMC
GO:2000117	0.384	0.824	3	27	negative regulation of cysteine-type	BP	1	BIRC5,DHCR24,ENSCAFG00000005299	down_ACOR_VSMC

GO:0051851	0.384	0.825	3	23	modification by host of symbiont morphology or	BP	1	NAPEPLD,F2RL1,PC	up_VSAP_EC
GO:0007417	0.384	0.855	2	235	central nervous system development	BP	1	LYN,NRP2	down_ACOR_EC
GO:0070252	0.384	0.86	2	17	actin-mediated cell contraction	BP	1	CAV1,EMP2	down_ACOR_VSMC
GO:0051172	0.384	0.862	2	663	negative regulation of nitrogen compound	BP	1	CST3,HDAC7	down_VPOR_EC
GO:0007165	0.384	0.881	2	1496	signal transduction	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0007160	0.384	0.854	2	56	cell-matrix adhesion	BP	1	HOXA7,GREM1	up_AFEM_EC
GO:0010830	0.384	0.861	2	16	regulation of myotube differentiation	BP	1	MTOR,ENSCAFG00000010596	up_VCAV_EC
GO:0010604	0.384	0.867	2	919	positive regulation of macromolecule metabolic	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0006082	0.384	0.856	2	305	organic acid metabolic process	BP	1	CYP26B1,CHST7	up_VFEM_EC
GO:0035909	0.384	0.862	2	14	aorta morphogenesis	BP	1	ACVRL1,NPRL3	up_VSAP_EC
GO:0000122	0.384	0.92	1	218	negative regulation of transcription by RNA polymerase II	BP	1	GABPA	down_AFEM_EC
GO:0048522	0.384	0.954	1	1484	positive regulation of cellular process	BP	1	GATA5	down_VFEM_VSMC
GO:0000290	0.384	0.924	1	8	deadenylation-dependent decapping of nuclear-transcribed mRNA	BP	1	CNOT7	down_VSAP_EC
GO:0032331	0.384	0.924	1	8	negative regulation of chondrocyte	BP	1	CTNNB1	down_VSAP_EC
GO:0051693	0.384	0.924	1	8	actin filament capping	BP	1	CAPG	down_VSAP_EC
GO:0061037	0.384	0.924	1	8	negative regulation of cartilage development	BP	1	CTNNB1	down_VSAP_EC
GO:0023058	0.384	0.929	1	5	adaptation of signaling pathway	BP	1	HTR2B	up_ACOR_VSMC
GO:0060027	0.384	0.93	1	5	convergent extension involved in gastrulation	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0046426	0.384	0.918	1	20	negative regulation of JAK-STAT cascade	BP	1	LRRC15	up_AFEM_EC
GO:0090559	0.384	0.918	1	20	regulation of membrane permeability	BP	1	CAMK2A	up_AFEM_EC
GO:1904893	0.384	0.918	1	20	negative regulation of STAT cascade	BP	1	LRRC15	up_AFEM_EC
GO:0006811	0.384	0.922	1	330	ion transport	BP	1	SLC16A12	up_AFEM_VSMC
GO:0070168	0.384	0.927	1	6	negative regulation of biomineral tissue	BP	1	HIF1A	up_VCAV_EC
GO:0007413	0.384	0.93	1	5	axonal fasciculation	BP	1	AMIGO1	up_VSAP_EC
GO:0106030	0.384	0.93	1	5	neuron projection fasciculation	BP	1	AMIGO1	up_VSAP_EC
GO:0002534	0.384547217	0.91864	1	18	cytokine production involved in inflammatory	BP	1	NOD2	up_ACOR_EC
GO:0055085	0.385	0.695	24	284	transmembrane transport	BP	1	LRRC8D,RELN,PDE4D,MEF2C,CHD7,SLC35A3,EDN1,APLNR,SLC39A8,CTTNBP2NL,SLC49A3,SLCO2A1,YES1,SLC38A1,LRRC8C,SPNS3,RSC1A1,KCNJ3,SLC2A3,KCNJ2,SLC25A25,PLCG2,RIPK1,MCU	up_VCAV_EC
GO:0023057	0.385	0.698	22	409	negative regulation of signaling	BP	1	SLC35F6,DCN,PRNP,VASN,FBN1,BGN,KANK2,AKT1S1,CHRDL1,CLSTN1,TMEM161A,ASPN,THY1,GLI3,PARK7,CDH2,SPRED1,RAB7B,GLIS2,GREM1,NPHP4,FOXO3	down_VCAV_EC
GO:0050789	0.385	0.781	9	3295	regulation of biological process	BP	1	HOXC10,DKK2,HOXA9,LNPEP,ERC1,TAOK1,BPI,CTNNAL1,GPR155	up_AORT_EC
GO:0045088	0.385	0.75	8	81	regulation of innate immune response	BP	1	HMGB1,IRAK1,SLC29A1,CAV1,CACTIN,HMGB2,RBM14,POLR3F	down_ACOR_VSMC
GO:0002460	0.385	0.759	7	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	TP53BP1,CD274,C1S,DUSP22,B2M,MAP3K7,IL18R1	up_ACOR_VSMC
GO:0051048	0.385	0.783	5	42	negative regulation of secretion	BP	1	C5AR2,ANXA4,F2RL1,KCNB1,MAPKBP1	up_VSAP_EC
GO:0003007	0.385	0.818	3	94	heart morphogenesis	BP	1	DLL1,TMEM100,AXIN2	up_AFEM_EC
GO:1904064	0.385	0.823	3	27	positive regulation of cation transmembrane	BP	1	RELN,APLNR,PLCG2	up_VCAV_EC
GO:0042592	0.385	0.822	3	522	homeostatic process	BP	1	HOXC10,MAP2K6,CYP26B1	up_VFEM_EC

GO:0006865	0.385	0.824	3	23	amino acid transport	BP	1	OSR1,SLC25A12,CTNS	up_VSAP_EC
GO:0007009	0.385	0.856	2	27	plasma membrane organization	BP	1	AKT2,PACSIN3	down_VCAV_EC
GO:0007605	0.385	0.856	2	27	sensory perception of sound	BP	1	ENSCAFG00000017708,THRB	down_VCAV_EC
GO:0031338	0.385	0.855	2	28	regulation of vesicle fusion	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0014812	0.385	0.857	2	21	muscle cell migration	BP	1	SERPINE1,SIX4	down_VSAP_EC
GO:0007399	0.385	0.86	2	564	nervous system development	BP	1	HOXC10,TAOK1	up_AORT_EC
GO:0030516	0.385	0.861	2	15	regulation of axon extension	BP	1	IFRD1,RAB11A	up_VCAV_EC
GO:0042592	0.385	0.859	2	522	homeostatic process	BP	1	HOXC10,GATM	up_VFEM_VSMC
GO:0070266	0.385	0.862	2	14	necroptotic process	BP	1	RBCK1,ENSCAFG00000011993	up_VSAP_EC
GO:0043267	0.385	0.926	1	6	negative regulation of potassium ion transport	BP	1	CAV1	down_ACOR_VSMC
GO:1900027	0.385	0.927	1	6	regulation of ruffle assembly	BP	1	CAV1	down_ACOR_VSMC
GO:2001224	0.385	0.929	1	5	positive regulation of neuron migration	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0000338	0.385	0.922	1	9	protein deneddylation	BP	1	COPS7A	down_VCAV_EC
GO:0002446	0.385	0.923	1	8	neutrophil mediated immunity	BP	1	WDR1	down_VSAP_EC
GO:0007350	0.385	0.925	1	7	blastoderm segmentation	BP	1	NRP1	down_VSAP_EC
GO:0009083	0.385	0.929	1	5	branched-chain amino acid catabolic process	BP	1	ENSCAFG00000002977	up_ACOR_VSMC
GO:0010818	0.385	0.929	1	5	T cell chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0032402	0.385	0.929	1	5	melanosome transport	BP	1	RAB11B	up_ACOR_VSMC
GO:0048168	0.385	0.929	1	5	regulation of neuronal synaptic plasticity	BP	1	APP	up_ACOR_VSMC
GO:0051904	0.385	0.929	1	5	pigment granule transport	BP	1	RAB11B	up_ACOR_VSMC
GO:0070243	0.385	0.929	1	5	regulation of thymocyte apoptotic process	BP	1	BMP4	up_ACOR_VSMC
GO:1900102	0.385	0.929	1	5	negative regulation of endoplasmic reticulum unfolded protein	BP	1	WFS1	up_ACOR_VSMC
GO:0032387	0.385	0.918	1	20	negative regulation of intracellular transport	BP	1	CRYAB	up_AFEM_EC
GO:0007186	0.385	0.917	1	124	G protein-coupled receptor signaling	BP	1	PLCL1	up_APUL_EC
GO:0034248	0.385	0.917	1	125	regulation of cellular amide metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0008210	0.385	0.926	1	6	estrogen metabolic process	BP	1	TIPARP	up_VCAV_EC
GO:0061162	0.385	0.927	1	6	establishment of monopolar cell polarity	BP	1	FSCN1	up_VCAV_EC
GO:0061339	0.385	0.927	1	6	establishment or maintenance of	BP	1	FSCN1	up_VCAV_EC
GO:0006811	0.385	0.922	1	330	ion transport	BP	1	CA2	up_VCAV_VSMC
GO:0050767	0.385	0.919	1	184	regulation of neurogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0007417	0.385	0.919	1	235	central nervous system development	BP	1	SLIT2	up_VPUL_VSMC
GO:1903587	0.385	0.929	1	5	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	HMOX1	up_VSAP_EC
GO:0097193	0.385	0.917	1	109	intrinsic apoptotic signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0050793	0.385089029	0.70184	21	731	regulation of developmental process	BP	1	CDH3,NR1H4,BRSK1,SOX9,RHOU,AQP1,CCDC3,DIXDC1,RGMA,SMAD6,PLS1,PAK3,ARHGDIB,FOXC2,TBX5,LRP4,CLSTN1,RBM38,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0043491	0.385230998	0.85321	2	50	protein kinase B signaling	BP	1	SOX9,ENSCAFG00000004331	up_ACOR_EC
GO:0010631	0.385397661	0.79412	4	118	epithelial cell migration	BP	1	SOX9,ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC
GO:0090132	0.385397661	0.79412	4	118	epithelium migration	BP	1	SOX9,ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC

GO:0019637	0.386	0.682	35	342	organophosphate metabolic process	BP	1	NAPEPLD,ACSM3,ENPP2,ACACB,NADK,INPP5E,COQ9,NDUFS1,ENSCAFG00000004260,PLPP3,AMBRA1,PPIP5K1,PDK2,FXN,GALK1,PIK3R1,ENTPD3,PLA2G6,PIK3IP1,CTNS,NDUFS2,NT5C2,MOCOS,LCAT,ACSS2,MVK,PNPO,DCAKD,ENSCAFG00000013366,PNP,ZFYVE21,IDH1,PLPP5,NDUFV1,DDIT4	up_VSAP_EC
GO:0044092	0.386	0.714	15	270	negative regulation of molecular function	BP	1	CST3,DCN,PRNP,BGN,RECK,AKT1S1,TIMP2,CLSTN1,ASPN,LRPAP1,THY1,PARK7,SPRED1,GLIS2,FBH1	down_VCAV_EC
GO:0072659	0.386	0.742	9	82	protein localization to plasma membrane	BP	1	PLEKHF1,CDH1,EMP2,RILPL2,PIK3R1,TSPAN5,STX4,FLOT1,BAG4	up_VSAP_EC
GO:0051239	0.386	0.751	8	859	regulation of multicellular organismal process	BP	1	C3AR1,HOOK3,ARHGEF2,SEMA3A,ASPN,ACVR2A,MTDH,RNF6	up_VPOR_EC
GO:1903311	0.386	0.75	8	72	regulation of mRNA metabolic process	BP	1	AXIN2,TENT5C,ZFP36L1,NUP98,CDK9,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0045089	0.386	0.757	7	70	positive regulation of innate immune response	BP	1	HMGB1,IRAK1,CAV1,CACTIN,HMGB2,RBM14,POLR3F	down_ACOR_VSMC
GO:0051170	0.386	0.757	7	69	import into nucleus	BP	1	HCLS1,TMEM173,FERMT1,PPP3CA,APOD,NUP133,IPO11	up_VCAV_EC
GO:2000027	0.386	0.758	7	72	regulation of animal organ morphogenesis	BP	1	HOXB7,TNFAIP3,CD34,GATA3,NTN4,BMP2,BTBD7	up_VCAV_EC
GO:1990845	0.386	0.769	6	51	adaptive thermogenesis	BP	1	LEP,PLCL1,GJA1,PPARGC1A,PLAC8B,IL18R1	up_ACOR_VSMC
GO:0006643	0.386	0.767	6	68	membrane lipid metabolic process	BP	1	KIT,SERINC5,SPTLC2,SAMD8,CREM,ST3GAL6	up_VCAV_EC
GO:0099504	0.386	0.782	5	42	synaptic vesicle cycle	BP	1	DNAJC6,FBXL20,STX11,PSEN1,PREPL	up_ACOR_VSMC
GO:0003279	0.386	0.781	5	48	cardiac septum development	BP	1	CHD7,GATA3,PROX1,JAG1,LUZP1	up_VCAV_EC
GO:0043039	0.386	0.799	4	33	tRNA aminoacylation	BP	1	WARS2,FARS2,QARS,LARS2	up_VSAP_EC
GO:0044344	0.386	0.799	4	33	cellular response to fibroblast growth factor	BP	1	FGF7,ZFP36L1,SULF2,ZFP36L2	up_VSAP_EC
GO:0071774	0.386	0.799	4	33	response to fibroblast growth factor	BP	1	FGF7,ZFP36L1,SULF2,ZFP36L2	up_VSAP_EC
GO:0072078	0.386	0.799	4	33	nephron tubule morphogenesis	BP	1	HOXA11,WNT11,OSR1,IRX3	up_VSAP_EC
GO:0055076	0.386	0.819	3	44	transition metal ion homeostasis	BP	1	SLC39A6,SCARA5,ATOX1	down_VCAV_EC
GO:0002768	0.386	0.82	3	37	immune response-regulating cell surface receptor signaling	BP	1	PTPN2,EIF2B1,LYN	down_VSAP_EC
GO:0014068	0.386	0.824	3	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	LEP,F2RL1,UNC5B	up_ACOR_VSMC
GO:0008219	0.386	0.86	2	611	cell death	BP	1	IVNS1ABP,SRSF6	down_AFEM_EC
GO:0050852	0.386	0.856	2	26	T cell receptor signaling pathway	BP	1	PRNP,THY1	down_VCAV_EC
GO:0007565	0.386	0.856	2	23	female pregnancy	BP	1	TMED2,PTGS2	down_VSAP_EC
GO:0030097	0.386	0.919	1	244	hemopoiesis	BP	1	CITED2	down_VPOR_EC
GO:0032770	0.386	0.923	1	8	positive regulation of monooxygenase activity	BP	1	APOE	down_VSAP_EC
GO:0060074	0.386	0.924	1	7	synapse maturation	BP	1	DISC1	down_VSAP_EC
GO:0006044	0.386	0.929	1	5	N-acetylglucosamine metabolic process	BP	1	EXTL2	up_ACOR_VSMC
GO:0006977	0.386	0.929	1	5	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BP	1	CDKN1A	up_ACOR_VSMC
GO:0072431	0.386	0.929	1	5	signal transduction involved in mitotic G1	BP	1	CDKN1A	up_ACOR_VSMC
GO:1902400	0.386	0.929	1	5	DNA damage checkpoint intracellular signal transduction involved in G1 DNA damage	BP	1	CDKN1A	up_ACOR_VSMC
GO:0001906	0.386	0.918	1	20	cell killing	BP	1	LEP	up_AFEM_EC
GO:0035336	0.386	0.924	1	7	long-chain fatty-acyl-CoA metabolic process	BP	1	ELOVL7	up_VCAV_EC
GO:0032906	0.386	0.926	1	6	transforming growth factor beta2 production	BP	1	HIF1A	up_VCAV_EC
GO:0032909	0.386	0.926	1	6	regulation of transforming growth factor beta2	BP	1	HIF1A	up_VCAV_EC
GO:0001816	0.386	0.918	1	194	cytokine production	BP	1	C3AR1	up_VPOR_VSMC

GO:0032956	0.386	0.916	1	116	regulation of actin cytoskeleton organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0002327	0.386	0.929	1	5	immature B cell differentiation	BP	1	ABL1	up_VSAP_EC
GO:0021953	0.386367904	0.85253	2	49	central nervous system neuron differentiation	BP	1	DCLK2,NRP1	up_ACOR_EC
GO:0018105	0.386466935	0.79333	4	116	peptidyl-serine phosphorylation	BP	1	PLCL1,DCLK2,STK32C,PRKCD	up_ACOR_EC
GO:0045444	0.38648857	0.81648	3	84	fat cell differentiation	BP	1	CCDC3,SMAD6,PIAS1	up_ACOR_EC
GO:0006096	0.386507548	0.91773	1	18	glycolytic process	BP	1	ALDOC	up_ACOR_EC
GO:0006165	0.386507548	0.91773	1	18	nucleoside diphosphate phosphorylation	BP	1	ALDOC	up_ACOR_EC
GO:0006757	0.386507548	0.91773	1	18	ATP generation from ADP	BP	1	ALDOC	up_ACOR_EC
GO:0042866	0.386507548	0.91773	1	18	pyruvate biosynthetic process	BP	1	ALDOC	up_ACOR_EC
GO:0006687	0.386746349	0.91762	1	18	glycosphingolipid metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0002521	0.387	0.712	16	149	leukocyte differentiation	BP	1	TMEM176B,TMEM176A,PLCG2,LEP,CD83,RASSF2,BMP4,CITED2,F2RL1,CLSTN1,PTPN22,APP,PSEN1,CHD7,B2M,IL18R1	up_ACOR_VSMC
GO:0050778	0.387	0.715	15	141	positive regulation of immune response	BP	1	CD274,ABL1,STAT6,F2RL1,RBCK1,MYD88,CFD,NLRX1,TKFC,CYBA,STX4,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0098660	0.387	0.714	15	141	inorganic ion transmembrane transport	BP	1	AMIGO1,SLC8B1,ABL1,KCNE3,OSR1,KLHL24,SLC25A28,SCARA5,CLCN2,STEAP3,KCNB1,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0051259	0.387	0.721	13	140	protein complex oligomerization	BP	1	IRAK1,HMGCR,RRM1,C1QTNF6,PRMT1,CAV1,TK1,RCC1,B4GALT1,FARSA,SIGMAR1,CTH,PDSS1	down_ACOR_VSMC
GO:0000904	0.387	0.733	10	181	cell morphogenesis involved in differentiation	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,ENSCAFG00000017708,UST,BRSK1	down_VCAV_EC
GO:0010876	0.387	0.741	9	92	lipid localization	BP	1	ACSL3,SREBF2,PRELID1,CAV1,LIMA1,ABHD5,PPARD,LIPC,NUS1	down_ACOR_VSMC
GO:0034504	0.387	0.747	8	111	protein localization to nucleus	BP	1	PRICKLE1,SESN2,ZPR1,KPNB1,KPNA4,KPNA1,SIX4,CDKN1A	down_VSAP_EC
GO:0051336	0.387	0.754	7	251	regulation of hydrolase activity	BP	1	CRYAB,F3,MYO1D,RASGEF1B,RECK,BVES,CCL5	up_AFEM_EC
GO:0043523	0.387	0.768	6	52	regulation of neuron apoptotic process	BP	1	PPARGC1A,NRP1,UNC5B,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0044839	0.387	0.767	6	61	cell cycle G2/M phase transition	BP	1	RAB11A,TAOK1,BLM,RAD21,RAD17,TOPBP1	up_VCAV_EC
GO:0001657	0.387	0.782	5	42	ureteric bud development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NPNT	up_ACOR_VSMC
GO:0072163	0.387	0.782	5	42	mesonephric epithelium development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NPNT	up_ACOR_VSMC
GO:0072164	0.387	0.782	5	42	mesonephric tubule development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NPNT	up_ACOR_VSMC
GO:0046474	0.387	0.818	3	44	glycerophospholipid biosynthetic process	BP	1	GPAM,LCAT,PIGS	down_VCAV_EC
GO:0009987	0.387	1	3	5086	cellular process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0015908	0.387	0.823	3	23	fatty acid transport	BP	1	LEP,PLIN2,CFI	up_ACOR_VSMC
GO:1905818	0.387	0.821	3	28	regulation of chromosome separation	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0002312	0.387	0.822	3	24	B cell activation involved in immune response	BP	1	ABL1,DLL1,STAT6	up_VSAP_EC
GO:0072527	0.387	0.856	2	23	pyrimidine-containing compound metabolic	BP	1	ENTPD4,CMPK1	down_VSAP_EC
GO:0006636	0.387	0.86	2	14	unsaturated fatty acid biosynthetic process	BP	1	EDN1,ELOVL7	up_ACOR_VSMC
GO:0009411	0.387	0.852	2	56	response to UV	BP	1	MFAP4,DCUN1D3	up_AFEM_EC
GO:0043270	0.387	0.852	2	56	positive regulation of ion transport	BP	1	CAMK2A,FXYD1	up_AFEM_EC
GO:0090174	0.387	0.852	2	56	organelle membrane fusion	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0002682	0.387	0.854	2	343	regulation of immune system process	BP	1	NR1H4,BPI	up_APUL_EC
GO:0070830	0.387	0.86	2	14	bicellular tight junction assembly	BP	1	WNT11,CLDN1	up_VSAP_EC
GO:0120192	0.387	0.86	2	14	tight junction assembly	BP	1	WNT11,CLDN1	up_VSAP_EC
GO:0043010	0.387	0.916	1	96	camera-type eye development	BP	1	ACVRL1	down_ACOR_EC
GO:0046006	0.387	0.926	1	6	regulation of activated T cell proliferation	BP	1	HMGB1	down_ACOR_VSMC

GO:0019432	0.387	0.921	1	10	triglyceride biosynthetic process	BP	1	GPAM	down_VCAV_EC
GO:0046460	0.387	0.921	1	10	neutral lipid biosynthetic process	BP	1	GPAM	down_VCAV_EC
GO:0046463	0.387	0.921	1	10	acylglycerol biosynthetic process	BP	1	GPAM	down_VCAV_EC
GO:0051252	0.387	0.939	1	1051	regulation of RNA metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0070296	0.387	0.923	1	8	sarcoplasmic reticulum calcium ion transport	BP	1	CALM1	down_VSAP_EC
GO:0048668	0.387	0.924	1	7	collateral sprouting	BP	1	IFRD1	down_VSAP_EC
GO:0019430	0.387	0.928	1	5	removal of superoxide radicals	BP	1	PARK7	up_ACOR_VSMC
GO:0071450	0.387	0.928	1	5	cellular response to oxygen radical	BP	1	PARK7	up_ACOR_VSMC
GO:0071451	0.387	0.928	1	5	cellular response to superoxide	BP	1	PARK7	up_ACOR_VSMC
GO:0072178	0.387	0.928	1	5	nephric duct morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0010749	0.387	0.932	1	4	regulation of nitric oxide mediated signal	BP	1	GUCY1A1	up_VCAV_EC
GO:0044342	0.387	0.924	1	7	type B pancreatic cell proliferation	BP	1	NR4A1	up_VCAV_EC
GO:0070920	0.387	0.926	1	6	regulation of production of small RNA involved in gene silencing by RNA	BP	1	PPP3CA	up_VCAV_EC
GO:1903798	0.387	0.926	1	6	regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	PPP3CA	up_VCAV_EC
GO:0010810	0.387	0.916	1	60	regulation of cell-substrate adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0007616	0.387	0.928	1	5	long-term memory	BP	1	CTNS	up_VSAP_EC
GO:0034390	0.387	0.928	1	5	smooth muscle cell apoptotic process	BP	1	MFN2	up_VSAP_EC
GO:0034391	0.387	0.928	1	5	regulation of smooth muscle cell apoptotic	BP	1	MFN2	up_VSAP_EC
GO:0035330	0.387	0.928	1	5	regulation of hippo signaling	BP	1	LIMD1	up_VSAP_EC
GO:0042743	0.387	0.928	1	5	hydrogen peroxide metabolic process	BP	1	ZNF205	up_VSAP_EC
GO:0071340	0.387	0.928	1	5	skeletal muscle acetylcholine-gated	BP	1	LRP4	up_VSAP_EC
GO:0072641	0.387	0.928	1	5	type I interferon secretion	BP	1	MAVS	up_VSAP_EC
GO:0072642	0.387	0.928	1	5	interferon-alpha secretion	BP	1	MAVS	up_VSAP_EC
GO:1902739	0.387	0.928	1	5	regulation of interferon-alpha secretion	BP	1	MAVS	up_VSAP_EC
GO:1902741	0.387	0.928	1	5	positive regulation of interferon-alpha secretion	BP	1	MAVS	up_VSAP_EC
GO:0032456	0.387128196	0.91722	1	19	endocytic recycling	BP	1	ACTN2	up_ACOR_EC
GO:0034766	0.387231548	0.91718	1	19	negative regulation of ion transmembrane transport	BP	1	ACTN2	up_ACOR_EC
GO:0050732	0.387393594	0.91732	1	18	negative regulation of peptidyl-tyrosine	BP	1	PRKCD	up_ACOR_EC
GO:0043603	0.388	0.683	32	372	cellular amide metabolic process	BP	1	ACLY,ILF3,EIF4A3,HNRNPD,VARS,THOP1,RRBP1,PPP1R15B,MRPS18B,TRUB2,PLK3,DHX33,ARG2,MVD,FASTKD3,EIF5A,ELOVL1,FARSA,NCL,MRPL37,GSTO1,ELOVL6,RBM14,SGPL1,NOLC1,RARS,PUM3,ENSCAFG00000006478,PDHA1,GGH,MRPL18,EIF3M	down_ACOR_VSMC
GO:0006886	0.388	0.704	18	332	intracellular protein transport	BP	1	PRNP,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,CLTB,SSR3,PEX5,GLI3,PARK7,MAVS,TOM1,SEC61B,HM13,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0009150	0.388	0.708	17	161	purine ribonucleotide metabolic process	BP	1	ACSM3,ACACB,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0098662	0.388	0.717	14	131	inorganic cation transmembrane transport	BP	1	AMIGO1,SLC8B1,ABL1,KCNE3,OSR1,KLHL24,SLC25A28,SCARA5,STEAP3,KCNB1,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0048562	0.388	0.729	11	102	embryonic organ morphogenesis	BP	1	BMP4,FGFR2,GJA1,SEC24B,CITED2,TBX20,FZD3,FRS2,PSEN1,CHD7,EDN1	up_ACOR_VSMC
GO:0016032	0.388	0.74	9	94	viral process	BP	1	ILF3,NEDD4,SLC29A1,CAV1,TRIM35,TFRC,SMC3,RAD23A,PPIH	down_ACOR_VSMC

GO:0045930	0.388	0.74	9	97	negative regulation of mitotic cell cycle	BP	1	PLK2,TAOK1,BLM,RAD21,RAD17,ZW10,ATRX,TOPBP1,FBXO5	up_VCAV_EC
GO:0010038	0.388	0.793	4	62	response to metal ion	BP	1	PRNP,MT2A,ANXA11,PARK7	down_VCAV_EC
GO:0010950	0.388	0.795	4	44	positive regulation of endopeptidase activity	BP	1	CASP8,BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:1904589	0.388	0.798	4	33	regulation of protein import	BP	1	ARHGEF5,CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0097164	0.388	0.817	3	44	ammonium ion metabolic process	BP	1	MAOA,LCAT,PARK7	down_VCAV_EC
GO:0006865	0.388	0.822	3	23	amino acid transport	BP	1	PSEN1,CLN8,SLC25A12	up_ACOR_VSMC
GO:0036473	0.388	0.821	3	27	cell death in response to oxidative stress	BP	1	TLR4,RIPK1,HIF1A	up_VCAV_EC
GO:0015748	0.388	0.858	2	16	organophosphate ester transport	BP	1	PRELID1,SLC25A19	down_ACOR_VSMC
GO:1902743	0.388	0.858	2	16	regulation of lamellipodium	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:1900024	0.388	0.858	2	16	regulation of substrate adhesion-dependent cell	BP	1	NEDD9,ENSCAFG00000002015	up_VCAV_EC
GO:2000142	0.388	0.857	2	17	regulation of DNA-templated transcription,	BP	1	IRF8,HMGB1	up_VCAV_EC
GO:0009150	0.388	0.851	2	161	purine ribonucleotide metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0009891	0.388	0.857	2	521	positive regulation of biosynthetic process	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0001916	0.388	0.925	1	6	positive regulation of T cell mediated cytotoxicity	BP	1	FAM49B	down_ACOR_VSMC
GO:0010523	0.388	0.925	1	6	negative regulation of calcium ion transport into	BP	1	GSTO1	down_ACOR_VSMC
GO:0007165	0.388	0.953	1	1496	signal transduction	BP	1	GATA5	down_VFEM_VSMC
GO:0051570	0.388	0.924	1	7	regulation of histone H3-K9 methylation	BP	1	KDM3A	down_VSAP_EC
GO:0035743	0.388	0.928	1	5	CD4-positive, alpha-beta T cell cytokine production	BP	1	IL18R1	up_ACOR_VSMC
GO:0060429	0.388	0.92	1	341	epithelium development	BP	1	EYA1	up_AFEM_VSMC
GO:0050801	0.388	0.917	1	200	ion homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0033572	0.388	0.928	1	5	transferrin transport	BP	1	LMTK2	up_VCAV_EC
GO:0051491	0.388	0.925	1	6	positive regulation of filopodium assembly	BP	1	FSCN1	up_VCAV_EC
GO:0030029	0.388	0.918	1	239	actin filament-based process	BP	1	SLIT2	up_VPUL_VSMC
GO:0015740	0.388	0.928	1	5	C4-dicarboxylate transport	BP	1	SLC25A12	up_VSAP_EC
GO:0018105	0.388	0.915	1	116	peptidyl-serine phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0034394	0.388062512	0.91679	1	19	protein localization to cell surface	BP	1	ACTN2	up_ACOR_EC
GO:0061387	0.388273586	0.91691	1	18	regulation of extent of cell growth	BP	1	NRP1	up_ACOR_EC
GO:0048666	0.388545982	0.74446	8	258	neuron development	BP	1	BRSK1,RGMA,PAK3,DCLK2,MAPK8IP2,LRP4,NRP1,DBNDD2	up_ACOR_EC
GO:1901565	0.38860663	0.71867	13	442	organonitrogen compound catabolic process	BP	1	THNSL2,SARDH,EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,AZIN2,HM13,PRKCD	up_ACOR_EC
GO:0051252	0.389	0.656	92	1051	regulation of RNA metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,HNRNPD,SREBF2,HINFP,NEDD4,SRSF2,MED17,U2AF2,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,HNRNPL,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,SF3B4,UHRF1,CKS2,GMNN,BRCA1,FASTKD3,NOC2L,E2F8,PPARD,YBX3,HNRNPF,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,RBM17,HOXA10,ERF,TCERG1,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,SF3A1,MED16,ENSCAFG00000017103	down_ACOR_VSMC

GO:0051172	0.389	0.679	35	663	negative regulation of nitrogen compound metabolic process	BP	1	CST3,KIRREL1,DCN,NAB2,PRNP,BGN,KANK2,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,ASPN,THY1,CC2D1A,GLI3,PARK7,ZFP36L1,CLEC16A,LOXL3,ORMDL3,SPRED1,A2M,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0009607	0.389	0.718	13	232	response to biotic stimulus	BP	1	GPAM,CFD,ENSCAFG00000013404,WIPF1,FKBP5,RNF216,SASH1,BPI,CYBA,MAVS,GSDME,SHC1,FBH1	down_VCAV_EC
GO:0044772	0.389	0.719	13	144	mitotic cell cycle phase transition	BP	1	PLK2,RAB11A,PPP3CA,TAOK1,BLM,RAD21,RAD17,USP37,CUL4A,ZW10,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0120036	0.389	0.732	10	373	plasma membrane bounded cell projection	BP	1	PLXNA4,NEFH,CAMK2A,CYLD,DNAL1,SPATA6,CDC42EP5,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0098542	0.389	0.763	6	100	defense response to other organism	BP	1	GPAM,RNF216,BPI,CYBA,MAVS,SHC1	down_VCAV_EC
GO:0007292	0.389	0.797	4	32	female gamete generation	BP	1	PDE5A,MARF1,HPGD,DMC1	up_ACOR_VSMC
GO:0072525	0.389	0.821	3	24	pyridine-containing compound biosynthetic	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0019079	0.389	0.82	3	29	viral genome replication	BP	1	CXCL8,PROX1,CNOT7	up_VCAV_EC
GO:0071230	0.389	0.821	3	23	cellular response to amino acid stimulus	BP	1	MTOR,PDGFD,ZEB1	up_VCAV_EC
GO:0072665	0.389	0.821	3	25	protein localization to vacuole	BP	1	TNFAIP3,SH3GLB1,GCC2	up_VCAV_EC
GO:0048519	0.389	0.837	3	1554	negative regulation of biological process	BP	1	LIMK1,GATA5,LRRC17	up_VCAV_VSMC
GO:0033365	0.389	0.815	3	276	protein localization to organelle	BP	1	HOOK3,GCC2,SRP54	up_VPOR_EC
GO:2001238	0.389	0.821	3	23	positive regulation of extrinsic apoptotic	BP	1	RBCK1,HTRA2,DEDD2	up_VSAP_EC
GO:0033077	0.389	0.855	2	22	T cell differentiation in thymus	BP	1	PTPN2,CTNNB1	down_VSAP_EC
GO:0043687	0.389	0.859	2	14	post-translational protein modification	BP	1	SUMF1,STT3B	up_ACOR_VSMC
GO:1903556	0.389	0.859	2	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	CD274,PTPN22	up_ACOR_VSMC
GO:0060147	0.389	0.859	2	14	regulation of posttranscriptional gene	BP	1	ZC3H10,LIMD1	up_VSAP_EC
GO:0060966	0.389	0.859	2	14	regulation of gene silencing by RNA	BP	1	ZC3H10,LIMD1	up_VSAP_EC
GO:0046834	0.389	0.859	2	14	lipid phosphorylation	BP	1	PIK3R1,ZFYVE21	up_VSAP_EC
GO:0030036	0.389	0.917	1	223	actin cytoskeleton organization	BP	1	FSCN1	down_AFEM_EC
GO:0009312	0.389	0.92	1	9	oligosaccharide biosynthetic process	BP	1	B4GALT1	down_VCAV_EC
GO:0065008	0.389	0.938	1	1056	regulation of biological quality	BP	1	PLCL1	down_VFEM_EC
GO:0002115	0.389	0.922	1	8	store-operated calcium entry	BP	1	HOMER1	down_VSAP_EC
GO:0014003	0.389	0.928	1	5	oligodendrocyte development	BP	1	WASF3	up_ACOR_VSMC
GO:0032048	0.389	0.927	1	5	cardiolipin metabolic process	BP	1	CRLS1	up_ACOR_VSMC
GO:0032049	0.389	0.927	1	5	cardiolipin biosynthetic process	BP	1	CRLS1	up_ACOR_VSMC
GO:0032673	0.389	0.927	1	5	regulation of interleukin-4 production	BP	1	CD83	up_ACOR_VSMC
GO:0046838	0.389	0.928	1	5	phosphorylated carbohydrate	BP	1	INPP5K	up_ACOR_VSMC
GO:0046855	0.389	0.928	1	5	inositol phosphate dephosphorylation	BP	1	INPP5K	up_ACOR_VSMC
GO:0048147	0.389	0.928	1	5	negative regulation of fibroblast proliferation	BP	1	TP53INP1	up_ACOR_VSMC
GO:0071600	0.389	0.928	1	5	otic vesicle morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0002694	0.389	0.916	1	126	regulation of leukocyte activation	BP	1	BPI	up_APUL_EC
GO:0051447	0.389	0.925	1	6	negative regulation of meiotic cell cycle	BP	1	FBXO5	up_VCAV_EC
GO:0036491	0.389	0.927	1	5	regulation of translation initiation in response to endoplasmic reticulum	BP	1	NCK1	up_VCAV_EC
GO:0036492	0.389	0.927	1	5	eiF2alpha phosphorylation in response to endoplasmic	BP	1	NCK1	up_VCAV_EC

GO:0003008	0.389	0.92	1	336	system process	BP	1	GATA5	up_VCAV_VSMC
GO:0007369	0.389	0.915	1	63	gastrulation	BP	1	ACVR2A	up_VPOR_EC
GO:0071216	0.389	0.915	1	61	cellular response to biotic stimulus	BP	1	MTDH	up_VPOR_EC
GO:0045321	0.389	0.917	1	191	leukocyte activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0005975	0.389	0.917	1	183	carbohydrate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0034220	0.389	0.917	1	188	ion transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0050778	0.389	0.916	1	141	positive regulation of immune response	BP	1	NR1H4	up_VPUL_EC
GO:0010243	0.389	0.918	1	238	response to organonitrogen	BP	1	SLIT2	up_VPUL_VSMC
GO:0048812	0.389030311	0.77471	5	151	neuron projection morphogenesis	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1	up_ACOR_EC
GO:0006821	0.389161008	0.91649	1	18	chloride transport	BP	1	CLIC3	up_ACOR_EC
GO:0007422	0.389432834	0.91636	1	18	peripheral nervous system development	BP	1	SH3TC2	up_ACOR_EC
GO:0055006	0.38955966	0.9163	1	18	cardiac cell development	BP	1	ACTN2	up_ACOR_EC
GO:0060563	0.389645211	0.91626	1	18	neuroepithelial cell differentiation	BP	1	DLX3	up_ACOR_EC
GO:0048194	0.389661082	0.91625	1	18	Golgi vesicle budding	BP	1	PREB	up_ACOR_EC
GO:0032615	0.38974946	0.91621	1	18	interleukin-12 production	BP	1	PRKCD	up_ACOR_EC
GO:0070372	0.389751679	0.81405	3	85	regulation of ERK1 and ERK2 cascade	BP	1	NDRG2,DUSP26,NRP1	up_ACOR_EC
GO:0008150	0.39	0.788	23	5646	biological_process	BP	1	NR1H4,TBX5,HOXA2,MAPK10,BPI,HTR7,HOXA3,PLCL1,TUBB4A,PCSK1N,GALNT17,ARHGEF26,LZTS1,ZDHHC16,SLITRK5,WIF1,NPNT,NTRK2,HOXA1,ENSCAFG00000002230,ENSCAFG00000028814,PDE1A,PDLIM3	up_APUL_EC
GO:0000209	0.39	0.745	8	83	protein polyubiquitination	BP	1	UBE2S,UBE2T,RNF152,BRCA1,UBE2J2,DTL,UBE2K,UBE2C	down_ACOR_VSMC
GO:0046434	0.39	0.765	6	52	organophosphate catabolic process	BP	1	ENPP2,INPP5E,GALK1,ENTPD3,IDH1,DDIT4	up_VSAP_EC
GO:0030001	0.39	0.774	5	172	metal ion transport	BP	1	KCNC4,CAMK2A,FXYD1,NIPAL1,DMPK	up_AFEM_EC
GO:0065007	0.39	0.839	5	3499	biological regulation	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0006694	0.39	0.779	5	42	steroid biosynthetic process	BP	1	INSIG2,HSD3B7,HSD17B8,MVK,CYB5R3	up_VSAP_EC
GO:0051606	0.39	0.796	4	33	detection of stimulus	BP	1	TLR1,JUP,NOD2,GNAQ	up_ACOR_VSMC
GO:0009968	0.39	0.792	4	392	negative regulation of signal transduction	BP	1	BARX1,ARHGEF2,ASPN,FBP1	up_VPOR_EC
GO:0046849	0.39	0.821	3	23	bone remodeling	BP	1	LEP,RASSF2,GJA1	up_ACOR_VSMC
GO:0006366	0.39	0.819	3	583	transcription by RNA polymerase II	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0006278	0.39	0.819	3	26	RNA-dependent DNA biosynthetic process	BP	1	HMBOX1,SMG7,DCP2	up_VCAV_EC
GO:0007004	0.39	0.819	3	26	telomere maintenance via telomerase	BP	1	HMBOX1,SMG7,DCP2	up_VCAV_EC
GO:0044255	0.39	0.851	2	293	cellular lipid metabolic process	BP	1	LYN,ACSL3	down_ACOR_EC
GO:0072132	0.39	0.853	2	23	mesenchyme morphogenesis	BP	1	ACTG2,ACTA2	down_VSAP_EC
GO:0002347	0.39	0.925	1	6	response to tumor cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0031061	0.39	0.919	1	10	negative regulation of histone methylation	BP	1	PRMT6	down_VCAV_EC
GO:0051894	0.39	0.919	1	10	positive regulation of focal adhesion assembly	BP	1	THY1	down_VCAV_EC
GO:0006357	0.39	0.924	1	547	regulation of transcription by RNA polymerase II	BP	1	GATA5	down_VSAP_VSMC
GO:0001886	0.39	0.927	1	5	endothelial cell morphogenesis	BP	1	ARHGEF26	up_ACOR_VSMC
GO:0043922	0.39	0.927	1	5	negative regulation by host of viral transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0006259	0.39	0.919	1	354	DNA metabolic process	BP	1	EYA1	up_AFEM_VSMC
GO:0010648	0.39	0.921	1	407	negative regulation of cell communication	BP	1	ESR1	up_AORT_VSMC

GO:0034622	0.39	0.921	1	421	cellular protein-containing complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0010639	0.39	0.915	1	128	negative regulation of organelle organization	BP	1	TUBB4A	up_APUL_EC
GO:0031649	0.39	0.927	1	5	heat generation	BP	1	PTGS2	up_VCAV_EC
GO:1901658	0.39	0.923	1	7	glycosyl compound catabolic process	BP	1	CDA	up_VCAV_EC
GO:2000679	0.39	0.925	1	6	positive regulation of transcription regulatory region DNA binding	BP	1	GATA3	up_VCAV_EC
GO:0046475	0.39	0.927	1	5	glycerophospholipid catabolic process	BP	1	ENPP2	up_VSAP_EC
GO:0046532	0.39	0.927	1	5	regulation of photoreceptor cell	BP	1	THRB	up_VSAP_EC
GO:1904469	0.39	0.927	1	5	positive regulation of tumor necrosis factor	BP	1	MAVS	up_VSAP_EC
GO:0008015	0.3908462	0.78983	4	120	blood circulation	BP	1	GNAO1,RNLS,FOXC2,CLSTN1	up_ACOR_EC
GO:0009607	0.391	0.691	24	232	response to biotic stimulus	BP	1	CD274,MAP3K14,PTGFR,ABL1,IL17RC,F2RL1,BATF2,PLA2G6,TBXA2R,SASH1,MYD88,WIPF1,CFD,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,CA5B,PQBP1,NCK1,MAVS,JCHAIN,DDIT4	up_VSAP_EC
GO:0008380	0.391	0.731	10	149	RNA splicing	BP	1	CELF1,ZPR1,SNRPB2,PRPF3,DDX39B,STRAP,REST,ENSCAFG00000015065,RTCB,SNRPA1	down_VSAP_EC
GO:0060249	0.391	0.744	8	110	anatomical structure homeostasis	BP	1	PTPN11,EXOC5,HIF1A,SMG7,CTNNB1,TFRC,STRAP,HOMER1	down_VSAP_EC
GO:0065003	0.391	0.764	6	616	protein-containing complex assembly	BP	1	MZT1,FBP1,RSL24D1,RPL10L,TWF1,SRP54	up_VPOR_EC
GO:0009889	0.391	0.771	6	1190	regulation of biosynthetic process	BP	1	EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0010646	0.391	0.781	5	945	regulation of cell communication	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0030177	0.391	0.792	4	51	positive regulation of Wnt signaling pathway	BP	1	SULF1,ILK,SMARCA4,DISC1	down_VSAP_EC
GO:1902806	0.391	0.795	4	33	regulation of cell cycle G1/S phase transition	BP	1	FAM107A,CRADD,FBXO7,LSM10	up_VSAP_EC
GO:0050793	0.391	0.796	4	731	regulation of developmental process	BP	1	HOXA11,HOXA9,CAV1,SHOX2	up_VSAP_VSMC
GO:0009894	0.391	0.814	3	277	regulation of catabolic process	BP	1	FBP1,MTDH,ABHD5	up_VPOR_EC
GO:0002520	0.391	0.814	3	279	immune system development	BP	1	BARX1,HOXA3,ACVR2A	up_VPOR_EC
GO:0006998	0.391	0.856	2	16	nuclear envelope organization	BP	1	CTDNEP1,REEP4	down_ACOR_VSMC
GO:0031076	0.391	0.858	2	14	embryonic camera-type eye development	BP	1	CITED2,FRS2	up_ACOR_VSMC
GO:0050994	0.391	0.858	2	14	regulation of lipid catabolic process	BP	1	PRKCE,ENSCAFG00000029553	up_ACOR_VSMC
GO:2001023	0.391	0.857	2	14	regulation of response to drug	BP	1	PSEN1,PARK7	up_ACOR_VSMC
GO:0009605	0.391	0.855	2	538	response to external stimulus	BP	1	CHL1,C3AR1	up_VPOR_VSMC
GO:0009394	0.391	0.924	1	6	2'-deoxyribonucleotide metabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:0019692	0.391	0.924	1	6	deoxyribose phosphate metabolic process	BP	1	NUDT1	down_ACOR_VSMC
GO:2001024	0.391	0.921	1	8	negative regulation of response to drug	BP	1	PTPN11	down_VSAP_EC
GO:0015872	0.391	0.927	1	5	dopamine transport	BP	1	PARK7	up_ACOR_VSMC
GO:0046033	0.391	0.927	1	5	AMP metabolic process	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0051937	0.391	0.927	1	5	catecholamine transport	BP	1	PARK7	up_ACOR_VSMC
GO:0002683	0.391	0.914	1	126	negative regulation of immune system process	BP	1	BPI	up_APUL_EC
GO:0045981	0.391	0.924	1	6	positive regulation of nucleotide metabolic	BP	1	NOS2	up_VCAV_EC
GO:1900544	0.391	0.924	1	6	positive regulation of purine nucleotide	BP	1	NOS2	up_VCAV_EC
GO:1903011	0.391	0.927	1	5	negative regulation of bone development	BP	1	TJP2	up_VCAV_EC
GO:0032488	0.391	0.927	1	5	Cdc42 protein signal transduction	BP	1	ABCA1	up_VCAV_EC
GO:0032489	0.391	0.927	1	5	regulation of Cdc42 protein signal	BP	1	ABCA1	up_VCAV_EC
GO:0035774	0.391	0.924	1	6	positive regulation of insulin secretion involved in cellular response to	BP	1	HIF1A	up_VCAV_EC

GO:0045773	0.391	0.924	1	6	positive regulation of axon extension	BP	1	RAB11A	up_VCAV_EC
GO:0051051	0.391	0.914	1	112	negative regulation of transport	BP	1	TRIM9	up_VFEM_EC
GO:0032963	0.391445716	0.91541	1	18	collagen metabolic process	BP	1	MFAP4	up_ACOR_EC
GO:0006357	0.391654997	0.70663	16	547	regulation of transcription by RNA polymerase II	BP	1	NR1H4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,NOD2,RGMA,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,GMEB2	up_ACOR_EC
GO:0031324	0.391700199	0.69579	21	735	negative regulation of cellular metabolic process	BP	1	NR1H4,TRPS1,PKIB,SOX9,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,ZMYND8,CST3,PIAS1,FOXC2,LRRC15,CLSTN1,LRRC4,CHMP4B,RIOX2,PRKCD,PPP1R26,DBNDD2	up_ACOR_EC
GO:0007568	0.391861304	0.84885	2	50	aging	BP	1	PRELP,PRKCD	up_ACOR_EC
GO:0045597	0.392	0.687	26	253	positive regulation of cell differentiation	BP	1	GATA5,CD83,FNDC5,BMP4,GJA1,PDE5A,ISG15,ZNF365,FGF18,FAM210B,CLSTN1,NRP1,NPNT,SMARCD3,TBX5,CCDC3,FZD3,DKKL1,APP,PSEN1,DDR2,EDN1,DISC1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0006163	0.392	0.729	10	174	purine nucleotide metabolic process	BP	1	GPAM,ADCY6,NT5C2,ATP5MC1,UQCR10,ADK,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0070661	0.392	0.753	7	63	leukocyte proliferation	BP	1	LEP,BMP4,PDE5A,CD274,F2RL1,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0050818	0.392	0.819	3	24	regulation of coagulation	BP	1	F2RL1,ENPP4,PSEN1	up_ACOR_VSMC
GO:0002183	0.392	0.856	2	16	cytoplasmic translational initiation	BP	1	RBM14,EIF3M	down_ACOR_VSMC
GO:0010646	0.392	0.863	2	945	regulation of cell communication	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0021879	0.392	0.856	2	15	forebrain neuron differentiation	BP	1	PROX1,RAPGEF2	up_VCAV_EC
GO:0050795	0.392	0.857	2	15	regulation of behavior	BP	1	RELN,MEF2C	up_VCAV_EC
GO:0005978	0.392	0.857	2	14	glycogen biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0009250	0.392	0.857	2	14	glucan biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:0043436	0.392	0.851	2	303	oxoacid metabolic process	BP	1	GATM,CAV1	up_VSAP_VSMC
GO:0006536	0.392	0.918	1	10	glutamate metabolic process	BP	1	GLS2	down_VCAV_EC
GO:0019725	0.392	0.916	1	245	cellular homeostasis	BP	1	RAB11B	down_VPOR_EC
GO:2001028	0.392	0.92	1	8	positive regulation of endothelial cell	BP	1	VEGFA	down_VSAP_EC
GO:0002827	0.392	0.926	1	5	positive regulation of T-helper 1 type immune	BP	1	IL18R1	up_ACOR_VSMC
GO:2001032	0.392	0.926	1	5	regulation of double-strand break repair via nonhomologous end	BP	1	PARP9	up_ACOR_VSMC
GO:0030812	0.392	0.926	1	5	negative regulation of nucleotide catabolic	BP	1	DDIT4	up_ACOR_VSMC
GO:0045820	0.392	0.926	1	5	negative regulation of glycolytic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0045986	0.392	0.93	1	4	negative regulation of smooth muscle	BP	1	DOCK5	up_ACOR_VSMC
GO:0051195	0.392	0.926	1	5	negative regulation of cofactor metabolic	BP	1	DDIT4	up_ACOR_VSMC
GO:0051198	0.392	0.926	1	5	negative regulation of coenzyme metabolic	BP	1	DDIT4	up_ACOR_VSMC
GO:0021545	0.392	0.914	1	21	cranial nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0048646	0.392	0.918	1	349	anatomical structure formation involved in	BP	1	EYA1	up_AFEM_VSMC
GO:0023057	0.392	0.92	1	409	negative regulation of signaling	BP	1	ESR1	up_AORT_VSMC
GO:1900016	0.392	0.921	1	7	negative regulation of cytokine production involved in inflammatory	BP	1	APOD	up_VCAV_EC
GO:0051895	0.392	0.922	1	7	negative regulation of focal adhesion assembly	BP	1	APOD	up_VCAV_EC
GO:0071542	0.392	0.924	1	6	dopaminergic neuron differentiation	BP	1	HIF1A	up_VCAV_EC
GO:1903392	0.392	0.922	1	7	negative regulation of adherens junction	BP	1	APOD	up_VCAV_EC
GO:0007507	0.392	0.915	1	194	heart development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0045657	0.392	0.926	1	5	positive regulation of monocyte differentiation	BP	1	ZFP36L1	up_VSAP_EC

GO:0061564	0.392	0.914	1	119	axon development	BP	1	SHOX2	up_VSAP_VSMC
GO:0002063	0.392035139	0.91513	1	18	chondrocyte development	BP	1	SOX9	up_ACOR_EC
GO:0090303	0.392423847	0.91495	1	18	positive regulation of wound healing	BP	1	FOXC2	up_ACOR_EC
GO:0007435	0.39249874	0.91491	1	18	salivary gland morphogenesis	BP	1	NRP1	up_ACOR_EC
GO:0010972	0.3925456	0.91489	1	18	negative regulation of G2/M transition of mitotic	BP	1	BRSK1	up_ACOR_EC
GO:0008361	0.392745823	0.84827	2	50	regulation of cell size	BP	1	AQP1,NRP1	up_ACOR_EC
GO:0051240	0.393	0.686	26	489	positive regulation of multicellular organismal process	BP	1	GPAM,HSPB6,LRP1,LUM,GLIPR2,BMPR1A,TRPV2,NUMBL,SYDE1,CLSTN1,SEMA3C,PEX5,B4GALT1,GLI3,PARK7,ZFP36L1,MYDGF,SASH1,CYBA,MAVS,RAB7B,DDR2,GREM1,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0048598	0.393	0.698	19	207	embryonic morphogenesis	BP	1	EIF4A3,HOXA3,INSIG1,NF2,MMP14,GREM1,MAP3K20,HOXA7,HOXC10,HOXB7,UGDH,HOXB5,HOXC4,PHACTR4,TBX15,ITGA2,HOXA9,GLI1,SIX4	down_ACOR_VSMC
GO:0008154	0.393	0.737	9	81	actin polymerization or depolymerization	BP	1	ACTN2,F2RL1,JMY,EVL,PRKCE,TTC17,SSH3,FAM107A,WASL	up_ACOR_VSMC
GO:0071560	0.393	0.743	8	72	cellular response to transforming growth	BP	1	ZFP36L1,ZEB1,STK16,ZFP36L2,HPGD,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0006109	0.393	0.775	5	51	regulation of carbohydrate metabolic	BP	1	PDGFB,FAM3C,ENSCAFG00000010596,PMAIP1,HIF1A	up_VCAV_EC
GO:0060759	0.393	0.793	4	37	regulation of response to cytokine stimulus	BP	1	IRAK1,SLC29A1,CAV1,CACTIN	down_ACOR_VSMC
GO:0001959	0.393	0.794	4	33	regulation of cytokine-mediated signaling	BP	1	F2RL1,CREBRF,CCDC3,PARP9	up_ACOR_VSMC
GO:0031325	0.393	0.798	4	914	positive regulation of cellular metabolic process	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:1900182	0.393	0.794	4	33	positive regulation of protein localization to	BP	1	CDH1,GLIS2,PIK3R1,MAVS	up_VSAP_EC
GO:0048232	0.393	0.811	3	95	male gamete generation	BP	1	HOXA9,OVOL1,SPATA6	up_AFEM_EC
GO:1901570	0.393	0.855	2	16	fatty acid derivative biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0003143	0.393	0.852	2	22	embryonic heart tube morphogenesis	BP	1	TMED2,HIF1A	down_VSAP_EC
GO:0008406	0.393	0.848	2	57	gonad development	BP	1	HOXA9,IRX5	up_AFEM_EC
GO:0045137	0.393	0.848	2	57	development of primary sexual characteristics	BP	1	HOXA9,IRX5	up_AFEM_EC
GO:0035019	0.393	0.855	2	16	somatic stem cell population maintenance	BP	1	LDB2,CUL4A	up_VCAV_EC
GO:0007155	0.393	0.85	2	324	cell adhesion	BP	1	CAV1,HAPLN1	up_VSAP_VSMC
GO:0045907	0.393	0.923	1	6	positive regulation of vasoconstriction	BP	1	CAV1	down_ACOR_VSMC
GO:0031670	0.393	0.918	1	10	cellular response to nutrient	BP	1	KANK2	down_VCAV_EC
GO:0033144	0.393	0.918	1	10	negative regulation of intracellular steroid hormone receptor	BP	1	KANK2	down_VCAV_EC
GO:0006351	0.393	0.937	1	1069	transcription, DNA-templated	BP	1	MOSPD1	down_VFEM_EC
GO:0000244	0.393	0.921	1	7	spliceosomal tri-snRNP complex assembly	BP	1	PRPF3	down_VSAP_EC
GO:0035641	0.393	0.926	1	5	locomotory exploration behavior	BP	1	PRKCE	up_ACOR_VSMC
GO:0072161	0.393	0.926	1	5	mesenchymal cell differentiation involved in	BP	1	BMP4	up_ACOR_VSMC
GO:2001012	0.393	0.926	1	5	mesenchymal cell differentiation involved in renal system	BP	1	BMP4	up_ACOR_VSMC
GO:0051058	0.393	0.914	1	21	negative regulation of small GTPase mediated signal transduction	BP	1	KANK1	up_AFEM_EC
GO:0045934	0.393	0.92	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	ESR1	up_AORT_VSMC
GO:0010793	0.393	0.93	1	4	regulation of mRNA export from nucleus	BP	1	IWS1	up_VCAV_EC
GO:0033561	0.393	0.923	1	6	regulation of water loss via skin	BP	1	STMN1	up_VCAV_EC
GO:0048484	0.393	0.923	1	6	enteric nervous system development	BP	1	EDNRB	up_VCAV_EC

GO:0032787	0.393	0.914	1	144	monocarboxylic acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0010692	0.393	0.926	1	5	regulation of alkaline phosphatase activity	BP	1	PPARGC1B	up_VSAP_EC
GO:0033572	0.393	0.926	1	5	transferrin transport	BP	1	RAB11B	up_VSAP_EC
GO:0048570	0.393	0.926	1	5	notochord morphogenesis	BP	1	WNT11	up_VSAP_EC
GO:0090177	0.393	0.926	1	5	establishment of planar polarity involved in neural	BP	1	FZD1	up_VSAP_EC
GO:0090178	0.393	0.926	1	5	regulation of establishment of planar polarity involved in neural	BP	1	FZD1	up_VSAP_EC
GO:0006520	0.393	0.913	1	114	cellular amino acid metabolic process	BP	1	GATM	up_VSAP_VSMC
GO:0001944	0.393574099	0.74011	8	263	vasculature development	BP	1	AQP1,ENSCAFG00000004331,FZD5,SMAD6,ESM1,DLX3,FOXC2,NRP1	up_ACOR_EC
GO:0040007	0.394	0.707	15	276	growth	BP	1	GPAM,NOTCH2,NDN,MT2A,THBS3,BMPR1A,EVC,IGFBP6,TRPV2,PEX5,GLI3,ZFP36L1,DDR2,RDH10,FOXO3	down_VCAV_EC
GO:0006869	0.394	0.76	6	81	lipid transport	BP	1	PTPN11,OSBPL9,APOE,OSBPL6,INHBA,ESYT3	down_VSAP_EC
GO:0016073	0.394	0.817	3	26	snRNA metabolic process	BP	1	INTS7,ENSCAFG00000019620,EXOSC5	down_ACOR_VSMC
GO:0043902	0.394	0.813	3	45	positive regulation of multi-organism process	BP	1	SYDE1,SASH1,CYBA	down_VCAV_EC
GO:0061035	0.394	0.817	3	24	regulation of cartilage development	BP	1	BMP4,LNPK,FGF18	up_ACOR_VSMC
GO:0010632	0.394	0.811	3	95	regulation of epithelial cell migration	BP	1	ANGPT4,TBXA2R,ADAM17	up_AFEM_EC
GO:0043550	0.394	0.852	2	21	regulation of lipid kinase activity	BP	1	LYN,SH3GLB1	down_VSAP_EC
GO:0043112	0.394	0.847	2	57	receptor metabolic process	BP	1	GREM1,BVES	up_AFEM_EC
GO:0050886	0.394	0.853	2	17	endocrine process	BP	1	GATA3,EDN1	up_VCAV_EC
GO:0010677	0.394	0.856	2	14	negative regulation of cellular carbohydrate	BP	1	PASK,DDIT4	up_VSAP_EC
GO:0060191	0.394	0.856	2	14	regulation of lipase activity	BP	1	ABL1,LMF1	up_VSAP_EC
GO:0061028	0.394	0.856	2	14	establishment of endothelial barrier	BP	1	F2RL1,MYD88	up_VSAP_EC
GO:0060394	0.394	0.923	1	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	GREM1	down_ACOR_VSMC
GO:0021680	0.394	0.917	1	10	cerebellar Purkinje cell layer development	BP	1	NAGLU	down_VCAV_EC
GO:0050931	0.394	0.917	1	10	pigment cell differentiation	BP	1	GLI3	down_VCAV_EC
GO:0032774	0.394	0.936	1	1073	RNA biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0097659	0.394	0.937	1	1072	nucleic acid-templated transcription	BP	1	MOSPD1	down_VFEM_EC
GO:0006677	0.394	0.919	1	8	glycosylceramide metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0032703	0.394	0.92	1	8	negative regulation of interleukin-2 production	BP	1	NR1H4	down_VSAP_EC
GO:0035313	0.394	0.921	1	7	wound healing, spreading of epidermal cells	BP	1	ADAM17	down_VSAP_EC
GO:0070886	0.394	0.925	1	5	positive regulation of calcineurin-NFAT signaling	BP	1	C28H10orf71	up_ACOR_VSMC
GO:0106058	0.394	0.925	1	5	positive regulation of calcineurin-mediated	BP	1	C28H10orf71	up_ACOR_VSMC
GO:1905939	0.394	0.925	1	5	regulation of gonad development	BP	1	CITED2	up_ACOR_VSMC
GO:0010771	0.394	0.914	1	21	negative regulation of cell morphogenesis involved in differentiation	BP	1	KANK1	up_AFEM_EC
GO:0030199	0.394	0.913	1	21	collagen fibril organization	BP	1	GREM1	up_AFEM_EC
GO:0009306	0.394	0.913	1	127	protein secretion	BP	1	NR1H4	up_APUL_EC
GO:1901615	0.394	0.913	1	128	organic hydroxy compound metabolic	BP	1	NR1H4	up_APUL_EC
GO:0032070	0.394	0.923	1	6	regulation of deoxyribonuclease	BP	1	HMGB1	up_VCAV_EC
GO:0003180	0.394	0.921	1	7	aortic valve morphogenesis	BP	1	GATA3	up_VCAV_EC
GO:0060841	0.394	0.923	1	6	venous blood vessel development	BP	1	PROX1	up_VCAV_EC

GO:0006290	0.394	0.925	1	5	pyrimidine dimer repair	BP	1	DDB2	up_VSAP_EC
GO:0060346	0.394	0.925	1	5	bone trabecula formation	BP	1	PPARGC1B	up_VSAP_EC
GO:0060644	0.394	0.926	1	5	mammary gland epithelial cell differentiation	BP	1	LBH	up_VSAP_EC
GO:0061436	0.394	0.925	1	5	establishment of skin barrier	BP	1	CLDN1	up_VSAP_EC
GO:0071447	0.394	0.926	1	5	cellular response to hydroperoxide	BP	1	MGST1	up_VSAP_EC
GO:1903078	0.394042933	0.91395	1	19	positive regulation of protein localization to	BP	1	PLS1	up_ACOR_EC
GO:0048523	0.395	0.677	35	1399	negative regulation of cellular process	BP	1	HOXA9,IRX3,LEP,LBH,CRY2,GAS1,ANGPT4,HOXA7,DLL1,CRYAB,BPI,GPAM,LMCD1,TWIST2,THRB,MYO1D,GREM1,OVOL1,TENT5C,GREM2,CLEC16A,CYLD,LRRC15,RECK,NR3C1,TBXA2R,DCUN1D3,RAB7A,AXIN2,ACACB,PPARGC1A,FAP,ADAM17,SAMD4B,KANK1	up_AFEM_EC
GO:0043410	0.395	0.727	10	144	positive regulation of MAPK cascade	BP	1	VEGFA,JCAD,PTPN11,TNIK,MAGED1,CTNNB1,NRP1,SH3RF3,MADD,MID1	down_VSAP_EC
GO:0060041	0.395	0.775	5	41	retina development in camera-type eye	BP	1	NRP1,GPM6A,SMARCD3,CHD7,CLN8	up_ACOR_VSMC
GO:0001101	0.395	0.788	4	65	response to acid chemical	BP	1	ADCY6,SLC10A3,COL6A1,TMEM161A	down_VCAV_EC
GO:1901292	0.395	0.792	4	34	nucleoside phosphate catabolic process	BP	1	PDE5A,ALDOC,ENTPD3,DDIT4	up_ACOR_VSMC
GO:0006081	0.395	0.815	3	27	cellular aldehyde metabolic process	BP	1	TKT,PDXP,PGD	down_ACOR_VSMC
GO:0051438	0.395	0.817	3	24	regulation of ubiquitin-protein transferase	BP	1	PSEN1,DCUN1D4,PARK7	up_ACOR_VSMC
GO:0038202	0.395	0.816	3	24	TORC1 signaling	BP	1	SESN1,CASTOR1,NPRL3	up_VSAP_EC
GO:1902533	0.395	0.848	2	271	positive regulation of intracellular signal	BP	1	LYN,NEDD4	down_ACOR_EC
GO:0019217	0.395	0.849	2	27	regulation of fatty acid metabolic process	BP	1	AKT2,LONP2	down_VCAV_EC
GO:2000243	0.395	0.855	2	14	positive regulation of reproductive process	BP	1	PDE5A,CITED2	up_ACOR_VSMC
GO:0000082	0.395	0.846	2	57	G1/S transition of mitotic cell cycle	BP	1	CAMK2A,DCUN1D3	up_AFEM_EC
GO:0044242	0.395	0.847	2	57	cellular lipid catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0006796	0.395	0.861	2	938	phosphate-containing compound metabolic	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0042326	0.395	0.846	2	163	negative regulation of phosphorylation	BP	1	ASPN,FBP1	up_VPOR_EC
GO:0009112	0.395	0.855	2	14	nucleobase metabolic process	BP	1	GDA,ALDH6A1	up_VSAP_EC
GO:0006082	0.395	0.848	2	305	organic acid metabolic process	BP	1	GATM,CAV1	up_VSAP_VSMC
GO:0009101	0.395	0.912	1	113	glycoprotein biosynthetic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0010876	0.395	0.912	1	92	lipid localization	BP	1	ACSL3	down_ACOR_EC
GO:0046486	0.395	0.912	1	102	glycerolipid metabolic process	BP	1	ACSL3	down_ACOR_EC
GO:0072503	0.395	0.912	1	97	cellular divalent inorganic cation homeostasis	BP	1	LYN	down_ACOR_EC
GO:0060314	0.395	0.922	1	6	regulation of ryanodine-sensitive calcium-release	BP	1	GSTO1	down_ACOR_VSMC
GO:0086065	0.395	0.922	1	6	cell communication involved in cardiac	BP	1	CAV1	down_ACOR_VSMC
GO:0003009	0.395	0.918	1	9	skeletal muscle contraction	BP	1	HOMER1	down_VSAP_EC
GO:0072074	0.395	0.919	1	8	kidney mesenchyme development	BP	1	SIX4	down_VSAP_EC
GO:1900424	0.395	0.925	1	5	regulation of defense response to bacterium	BP	1	F2RL1	up_ACOR_VSMC
GO:0032482	0.395	0.929	1	4	Rab protein signal transduction	BP	1	MADD	up_VCAV_EC
GO:0043371	0.395	0.922	1	6	negative regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	HMGB1	up_VCAV_EC
GO:0050716	0.395	0.922	1	6	positive regulation of interleukin-1 secretion	BP	1	HMGB1	up_VCAV_EC
GO:0006006	0.395	0.912	1	61	glucose metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0030041	0.395	0.912	1	62	actin filament polymerization	BP	1	TWF1	up_VPOR_EC

GO:0070646	0.395	0.911	1	63	protein modification by small protein removal	BP	1	USP33	up_VPOR_EC
GO:0009101	0.395	0.912	1	113	glycoprotein biosynthetic process	BP	1	CHST7	up_VFEM_EC
GO:0000972	0.395	0.925	1	5	transcription-dependent tethering of RNA polymerase II gene DNA at	BP	1	NUP98	up_VSAP_EC
GO:0021895	0.395	0.925	1	5	cerebral cortex neuron differentiation	BP	1	GDPD5	up_VSAP_EC
GO:0060363	0.395	0.925	1	5	cranial suture morphogenesis	BP	1	INSIG2	up_VSAP_EC
GO:0021670	0.395	0.925	1	5	lateral ventricle development	BP	1	KDM2B	up_VSAP_EC
GO:0031175	0.395268697	0.74686	7	224	neuron projection development	BP	1	BRSK1,RGMA,PAK3,MAPK8IP2,LRP4,NRP1,DBNDD2	up_ACOR_EC
GO:0007265	0.395383191	0.78625	4	121	Ras protein signal transduction	BP	1	PAK3,ARHGDIB,NRP1,ARHGEF26	up_ACOR_EC
GO:0043367	0.395453572	0.9135	1	18	CD4-positive, alpha-beta T cell differentiation	BP	1	PTGER4	up_ACOR_EC
GO:0060420	0.395633656	0.91341	1	18	regulation of heart growth	BP	1	TBX5	up_ACOR_EC
GO:0048468	0.396	0.679	29	553	cell development	BP	1	NOTCH2,LRP1,NDN,SDC4,FBN1,BMPR1A,TRPV2,NUMBL,NAGLU,AKT2,SEMA3C,THY1,PEX5,TLX2,B4GALT1,GLI3,ADAMTSL4,NCDN,CDH2,ENSCAFG00000017708,IRX5,UST,PRKCSH,RDH10,FOXO3,THRB,ZBTB16,RGMA,BRSK1	down_VCAV_EC
GO:1902532	0.396	0.691	21	204	negative regulation of intracellular signal transduction	BP	1	ACKR3,TBC1D10C,SLIT2,ABL1,HDAC7,SESN1,F2RL1,MFN2,MYC,PIK3IP1,RTN4RL1,CASTOR1,LIMD1,NLRX1,TKFC,FBLN1,MAPKBP1,QARS,ARHGAP12,NPRL3,DDIT4	up_VSAP_EC
GO:0001525	0.396	0.698	18	173	angiogenesis	BP	1	HOXA7,ACKR3,ENPP2,SLIT2,ABL1,BTG1,HDAC7,EMP2,DLL1,EPN2,HPSE,CCBE1,TBXA2R,SASH1,ANPEP,ACVRL1,HMOX1,TGFBR2	up_VSAP_EC
GO:0046486	0.396	0.722	11	102	glycerolipid metabolic process	BP	1	NAPEPLD,LIPC,INSIG2,ENPP2,INPP5E,LMF1,PIK3R1,PLA2G6,LCAT,ABHD16A,ZFYVE21	up_VSAP_EC
GO:0008150	0.396	0.884	9	5646	biological_process	BP	1	HOXC10,TLR2,TBX15,EYA1,HOXA9,BEND2,HOXA10,SLC16A12,IRX5	up_AFEM_VSMC
GO:0044249	0.396	0.748	9	1851	cellular biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3,CHST7	up_VFEM_EC
GO:0071704	0.396	0.816	6	3535	organic substance metabolic process	BP	1	TLR2,TBX15,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0032481	0.396	0.816	3	24	positive regulation of type I interferon production	BP	1	PQBP1,FLOT1,MAVS	up_VSAP_EC
GO:0035767	0.396	0.855	2	14	endothelial cell chemotaxis	BP	1	FGF18,NRP1	up_ACOR_VSMC
GO:0006915	0.396	0.852	2	550	apoptotic process	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:2000243	0.396	0.854	2	14	positive regulation of reproductive process	BP	1	CFAP69,CITED2	up_VSAP_EC
GO:0022610	0.396	0.848	2	326	biological adhesion	BP	1	CAV1,HAPLN1	up_VSAP_VSMC
GO:0001558	0.396	0.911	1	101	regulation of cell growth	BP	1	ACVRL1	down_ACOR_EC
GO:0050808	0.396	0.912	1	93	synapse organization	BP	1	NRP2	down_ACOR_EC
GO:0000730	0.396	0.922	1	6	DNA recombinase assembly	BP	1	RAD51	down_ACOR_VSMC
GO:0045003	0.396	0.922	1	6	double-strand break repair via synthesis-dependent strand	BP	1	RAD51	down_ACOR_VSMC
GO:0051546	0.396	0.922	1	6	keratinocyte migration	BP	1	PPARD	down_ACOR_VSMC
GO:0090735	0.396	0.922	1	6	DNA repair complex assembly	BP	1	RAD51	down_ACOR_VSMC
GO:0043009	0.396	0.914	1	227	chordate embryonic development	BP	1	GABPA	down_AFEM_EC
GO:0048519	0.396	0.95	1	1554	negative regulation of biological process	BP	1	CST3	down_AORT_EC
GO:0060765	0.396	0.916	1	10	regulation of androgen receptor signaling	BP	1	PARK7	down_VCAV_EC
GO:0051336	0.396	0.915	1	251	regulation of hydrolase activity	BP	1	CST3	down_VPOR_EC
GO:0032373	0.396	0.919	1	8	positive regulation of sterol transport	BP	1	APOE	down_VSAP_EC
GO:0032376	0.396	0.919	1	8	positive regulation of cholesterol transport	BP	1	APOE	down_VSAP_EC
GO:0086010	0.396	0.918	1	8	membrane depolarization during action potential	BP	1	YWHAH	down_VSAP_EC

GO:0010614	0.396	0.924	1	5	negative regulation of cardiac muscle	BP	1	GATA5	up_ACOR_VSMC
GO:0014741	0.396	0.924	1	5	negative regulation of muscle hypertrophy	BP	1	GATA5	up_ACOR_VSMC
GO:0043217	0.396	0.924	1	5	myelin maintenance	BP	1	SH3TC2	up_ACOR_VSMC
GO:0002704	0.396	0.924	1	5	negative regulation of leukocyte mediated	BP	1	DUSP22	up_ACOR_VSMC
GO:0060736	0.396	0.924	1	5	prostate gland growth	BP	1	FGFR2	up_ACOR_VSMC
GO:0010718	0.396	0.912	1	21	positive regulation of epithelial to mesenchymal	BP	1	AXIN2	up_AFEM_EC
GO:0042136	0.396	0.913	1	21	neurotransmitter biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0043242	0.396	0.913	1	21	negative regulation of protein complex	BP	1	CLEC16A	up_AFEM_EC
GO:0043500	0.396	0.913	1	21	muscle adaptation	BP	1	LMCD1	up_AFEM_EC
GO:0072666	0.396	0.913	1	21	establishment of protein localization to vacuole	BP	1	RAB7A	up_AFEM_EC
GO:1902017	0.396	0.913	1	21	regulation of cilium assembly	BP	1	CYLD	up_AFEM_EC
GO:2000736	0.396	0.913	1	21	regulation of stem cell differentiation	BP	1	LBH	up_AFEM_EC
GO:0031327	0.396	0.919	1	412	negative regulation of cellular biosynthetic	BP	1	ESR1	up_AORT_VSMC
GO:0006999	0.396	0.922	1	6	nuclear pore organization	BP	1	NUP133	up_VCAV_EC
GO:0010692	0.396	0.924	1	5	regulation of alkaline phosphatase activity	BP	1	MEF2C	up_VCAV_EC
GO:1990000	0.396	0.922	1	6	amyloid fibril formation	BP	1	RIPK1	up_VCAV_EC
GO:0007266	0.396	0.911	1	64	Rho protein signal transduction	BP	1	ARHGEF2	up_VPOR_EC
GO:0006281	0.396	0.913	1	208	DNA repair	BP	1	EYA1	up_VFEM_VSMC
GO:0039535	0.396	0.925	1	5	regulation of RIG-I signaling pathway	BP	1	NLRX1	up_VSAP_EC
GO:0072161	0.396	0.925	1	5	mesenchymal cell differentiation involved in	BP	1	OSR1	up_VSAP_EC
GO:2001012	0.396	0.925	1	5	mesenchymal cell differentiation involved in renal system	BP	1	OSR1	up_VSAP_EC
GO:0010812	0.396010762	0.91301	1	19	negative regulation of cell-substrate adhesion	BP	1	ARHGAP6	up_ACOR_EC
GO:0043542	0.396286134	0.80917	3	86	endothelial cell migration	BP	1	ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC
GO:0060341	0.397	0.687	23	255	regulation of cellular localization	BP	1	ACSL3,SREBF1,NEDD4,SLC29A1,RAN,BIRC5,INSIG1,CAV1,CDK1,NF2,MMP14,PLK3,PREB,NDC80,NUP62,GSTO1,DMAP1,ENSCAFG00000005299,EZR,RBM14,CORO1A,NUS1,CCT4	down_ACOR_VSMC
GO:0045321	0.397	0.692	20	191	leukocyte activation	BP	1	TLR1,PLCG2,LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,F2RL1,CDKN1A,PTPN22,PRKCE,APP,PSEN1,CHD7,DUSP22,NOD2,B2M,IL18R1,PAG1	up_ACOR_VSMC
GO:0001501	0.397	0.716	12	178	skeletal system development	BP	1	SULF1,SERPINH1,SPARC,PTPN11,CHSY1,HOXB7,HIF1A,CTNNB1,PLS3,EXT1,CREB3L2,SIX4	down_VSAP_EC
GO:0098542	0.397	0.747	7	100	defense response to other organism	BP	1	NR1H4,SERPINE1,COTL1,ADAM17,CNOT7,BNIP3,DEFB124	down_VSAP_EC
GO:0043903	0.397	0.759	6	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	ILF3,CAV1,TRIM35,SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0021549	0.397	0.815	3	26	cerebellum development	BP	1	EZH2,ARCN1,GLI1	down_ACOR_VSMC
GO:0046683	0.397	0.815	3	26	response to organophosphorus	BP	1	RFC3,PDXP,EZR	down_ACOR_VSMC
GO:0021510	0.397	0.816	3	23	spinal cord development	BP	1	LMO4,TBX20,CLN8	up_ACOR_VSMC
GO:0050701	0.397	0.852	2	16	interleukin-1 secretion	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0000187	0.397	0.847	2	28	activation of MAPK activity	BP	1	CSPG4,SHC1	down_VCAV_EC
GO:0006446	0.397	0.848	2	27	regulation of translational initiation	BP	1	EIF3K,EIF4EBP1	down_VCAV_EC
GO:0045445	0.397	0.848	2	27	myoblast differentiation	BP	1	ZFP36L1,GREM1	down_VCAV_EC
GO:0006879	0.397	0.849	2	23	cellular iron ion homeostasis	BP	1	HIF1A,TFRC	down_VSAP_EC

GO:0002456	0.397	0.849	2	23	T cell mediated immunity	BP	1	FAM49B,PVR	down_VSAP_EC
GO:0010677	0.397	0.854	2	14	negative regulation of cellular carbohydrate	BP	1	DDIT4,INPP5K	up_ACOR_VSMC
GO:0043281	0.397	0.845	2	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	CRYAB,F3	up_AFEM_EC
GO:0023051	0.397	0.86	2	954	regulation of signaling	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0002090	0.397	0.854	2	14	regulation of receptor internalization	BP	1	UBQLN2,FLOT1	up_VSAP_EC
GO:0009165	0.397	0.911	1	104	nucleotide biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:1905523	0.397	0.921	1	6	positive regulation of macrophage migration	BP	1	MMP14	down_ACOR_VSMC
GO:1903053	0.397	0.916	1	10	regulation of extracellular matrix organization	BP	1	DDR2	down_VCAV_EC
GO:0002228	0.397	0.917	1	9	natural killer cell mediated immunity	BP	1	PVR	down_VSAP_EC
GO:0042267	0.397	0.917	1	9	natural killer cell mediated cytotoxicity	BP	1	PVR	down_VSAP_EC
GO:0030728	0.397	0.924	1	5	ovulation	BP	1	HPGD	up_ACOR_VSMC
GO:0072643	0.397	0.924	1	5	interferon-gamma secretion	BP	1	F2RL1	up_ACOR_VSMC
GO:1903358	0.397	0.924	1	5	regulation of Golgi organization	BP	1	USP6NL	up_ACOR_VSMC
GO:0001947	0.397	0.912	1	21	heart looping	BP	1	DLL1	up_AFEM_EC
GO:0032623	0.397	0.912	1	21	interleukin-2 production	BP	1	GPAM	up_AFEM_EC
GO:0061371	0.397	0.912	1	21	determination of heart left/right asymmetry	BP	1	DLL1	up_AFEM_EC
GO:0090049	0.397	0.912	1	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	TBXA2R	up_AFEM_EC
GO:0090183	0.397	0.912	1	21	regulation of kidney development	BP	1	GREM1	up_AFEM_EC
GO:0006825	0.397	0.921	1	6	copper ion transport	BP	1	CP	up_VCAV_EC
GO:0072521	0.397	0.913	1	185	purine-containing compound metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0001933	0.397	0.912	1	146	negative regulation of protein phosphorylation	BP	1	FLRT3	up_VPUL_EC
GO:0003139	0.397	0.924	1	5	secondary heart field specification	BP	1	AXIN2	up_VSAP_EC
GO:0045124	0.397	0.924	1	5	regulation of bone resorption	BP	1	PPARGC1B	up_VSAP_EC
GO:0090195	0.397	0.924	1	5	chemokine secretion	BP	1	F2RL1	up_VSAP_EC
GO:0003013	0.397042077	0.78495	4	121	circulatory system process	BP	1	GNAO1,RNLS,FOXC2,CLSTN1	up_ACOR_EC
GO:0060393	0.397099046	0.91248	1	19	regulation of pathway-restricted SMAD protein	BP	1	SMAD6	up_ACOR_EC
GO:0033619	0.397105339	0.91248	1	19	membrane protein proteolysis	BP	1	HM13	up_ACOR_EC
GO:0048545	0.398	0.769	5	68	response to steroid hormone	BP	1	SMARCA4,UBA5,REST,YWHAH,KDM3A	down_VSAP_EC
GO:0009206	0.398	0.788	4	39	purine ribonucleoside triphosphate biosynthetic	BP	1	CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0030217	0.398	0.786	4	65	T cell differentiation	BP	1	GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0001959	0.398	0.79	4	33	regulation of cytokine-mediated signaling	BP	1	SLIT2,F2RL1,CREBRF,MAVS	up_VSAP_EC
GO:0044782	0.398	0.807	3	96	cilium organization	BP	1	CYLD,DNAL1,SPATA6	up_AFEM_EC
GO:0051649	0.398	0.853	2	630	establishment of localization in cell	BP	1	ANKRD50,GPSM2	down_AFEM_EC
GO:0042733	0.398	0.847	2	27	embryonic digit morphogenesis	BP	1	BMPR1A,GLI3	down_VCAV_EC
GO:0045682	0.398	0.847	2	27	regulation of epidermis development	BP	1	NAB2,ZFP36L1	down_VCAV_EC
GO:0001825	0.398	0.853	2	14	blastocyst formation	BP	1	LATS2,CITED2	up_ACOR_VSMC
GO:0014910	0.398	0.854	2	13	regulation of smooth muscle cell migration	BP	1	SEMA6D,DOCK5	up_ACOR_VSMC
GO:0032413	0.398	0.853	2	15	negative regulation of ion transmembrane transporter activity	BP	1	ACTN2,KCNE3	up_ACOR_VSMC

GO:0090151	0.398	0.919	1	7	establishment of protein localization to mitochondrial membrane	BP	1	SAMM50	down_ACOR_VSMC
GO:0061162	0.398	0.921	1	6	establishment of monopolar cell polarity	BP	1	FSCN1	down_ACOR_VSMC
GO:0061339	0.398	0.921	1	6	establishment or maintenance of	BP	1	FSCN1	down_ACOR_VSMC
GO:0070230	0.398	0.921	1	6	positive regulation of lymphocyte apoptotic	BP	1	PRELID1	down_ACOR_VSMC
GO:0097435	0.398	0.913	1	230	supramolecular fiber organization	BP	1	FSCN1	down_AFEM_EC
GO:0006855	0.398	0.916	1	10	drug transmembrane transport	BP	1	FOLR2	down_VCAV_EC
GO:0048103	0.398	0.915	1	10	somatic stem cell division	BP	1	NUMBL	down_VCAV_EC
GO:0032239	0.398	0.919	1	7	regulation of nucleobase-containing compound	BP	1	IWS1	down_VSAP_EC
GO:0008207	0.398	0.918	1	8	C21-steroid hormone metabolic process	BP	1	REST	down_VSAP_EC
GO:1904262	0.398	0.918	1	8	negative regulation of TORC1 signaling	BP	1	SESN2	down_VSAP_EC
GO:0042269	0.398	0.924	1	5	regulation of natural killer cell mediated cytotoxicity	BP	1	LEP	up_ACOR_VSMC
GO:0002715	0.398	0.924	1	5	regulation of natural killer cell mediated immunity	BP	1	LEP	up_ACOR_VSMC
GO:0060513	0.398	0.923	1	5	prostatic bud formation	BP	1	BMP4	up_ACOR_VSMC
GO:0072347	0.398	0.924	1	5	response to anesthetic	BP	1	PRKCE	up_ACOR_VSMC
GO:0097366	0.398	0.924	1	5	response to bronchodilator	BP	1	EGLN1	up_ACOR_VSMC
GO:0071156	0.398	0.912	1	21	regulation of cell cycle arrest	BP	1	FAP	up_AFEM_EC
GO:1903391	0.398	0.912	1	21	regulation of adherens junction organization	BP	1	GREM1	up_AFEM_EC
GO:0007346	0.398	0.913	1	210	regulation of mitotic cell cycle	BP	1	TAOK1	up_AORT_EC
GO:2000810	0.398	0.924	1	5	regulation of bicellular tight junction assembly	BP	1	PRKCH	up_VCAV_EC
GO:0048589	0.398	0.913	1	188	developmental growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0022604	0.398	0.911	1	122	regulation of cell morphogenesis	BP	1	CDC42EP5	up_VFEM_EC
GO:0043410	0.398	0.911	1	144	positive regulation of MAPK cascade	BP	1	CCL24	up_VPUL_EC
GO:0046697	0.398	0.924	1	5	decidualization	BP	1	CITED2	up_VSAP_EC
GO:0048026	0.398	0.924	1	5	positive regulation of mRNA splicing, via	BP	1	NUP98	up_VSAP_EC
GO:0048261	0.398	0.924	1	5	negative regulation of receptor-mediated	BP	1	UBQLN2	up_VSAP_EC
GO:1905606	0.398	0.923	1	5	regulation of presynapse assembly	BP	1	FZD1	up_VSAP_EC
GO:0046513	0.398607415	0.91175	1	19	ceramide biosynthetic process	BP	1	PRKCD	up_ACOR_EC
GO:0051168	0.399	0.757	6	57	nuclear export	BP	1	IWS1,HHEX,THOC1,CTDSPL2,SMG7,NUP133	up_VCAV_EC
GO:0023051	0.399	0.775	5	954	regulation of signaling	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0016579	0.399	0.787	4	49	protein deubiquitination	BP	1	USP12,UCHL5,USP48,USP14	down_VSAP_EC
GO:0006892	0.399	0.787	4	39	post-Golgi vesicle-mediated transport	BP	1	EXOC5,VPS54,CHIC2,DOP1B	up_VCAV_EC
GO:0022008	0.399	0.785	4	406	neurogenesis	BP	1	HOOK3,ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0034101	0.399	0.809	3	45	erythrocyte homeostasis	BP	1	ZFP36L1,FOXO3,ANKRD54	down_VCAV_EC
GO:0071166	0.399	0.81	3	36	ribonucleoprotein complex localization	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0008286	0.399	0.81	3	36	insulin receptor signaling pathway	BP	1	NR1H4,ENPP1,PTPN2	down_VSAP_EC
GO:0044260	0.399	0.856	3	2593	cellular macromolecule metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0017158	0.399	0.814	3	24	regulation of calcium ion-dependent exocytosis	BP	1	FBXL20,SCAMP5,PREPL	up_ACOR_VSMC
GO:0006139	0.399	0.84	3	1909	nucleobase-containing compound metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0043506	0.399	0.814	3	25	regulation of JUN kinase activity	BP	1	MAP3K11,EDN1,RIPK1	up_VCAV_EC

GO:0010941	0.399	0.812	3	524	regulation of cell death	BP	1	EYA1,MAP2K6,SIX1	up_VFEM_EC
GO:1903409	0.399	0.814	3	24	reactive oxygen species biosynthetic process	BP	1	CYBA,ZNF205,ASS1	up_VSAP_EC
GO:0038083	0.399	0.851	2	16	peptidyl-tyrosine autophosphorylation	BP	1	CAV1,GREM1	down_ACOR_VSMC
GO:1902751	0.399	0.853	2	14	positive regulation of cell cycle G2/M phase	BP	1	CDC7,APP	up_ACOR_VSMC
GO:0010646	0.399	0.858	2	945	regulation of cell communication	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0046640	0.399	0.92	1	6	regulation of alpha-beta T cell proliferation	BP	1	ARG2	down_ACOR_VSMC
GO:0070168	0.399	0.92	1	6	negative regulation of biomineral tissue	BP	1	GREM1	down_ACOR_VSMC
GO:0003337	0.399	0.915	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	GREM1	down_VCAV_EC
GO:1903671	0.399	0.915	1	10	negative regulation of sprouting angiogenesis	BP	1	SPRED1	down_VCAV_EC
GO:0055012	0.399	0.917	1	8	ventricular cardiac muscle cell differentiation	BP	1	FHL2	down_VSAP_EC
GO:0061014	0.399	0.917	1	8	positive regulation of mRNA catabolic process	BP	1	CNOT7	down_VSAP_EC
GO:0060389	0.399	0.911	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	GREM1	up_AFEM_EC
GO:0021697	0.399	0.92	1	6	cerebellar cortex formation	BP	1	PROX1	up_VCAV_EC
GO:0016050	0.399	0.91	1	119	vesicle organization	BP	1	TRIM9	up_VFEM_EC
GO:0016570	0.399	0.911	1	143	histone modification	BP	1	NR1H4	up_VPUL_EC
GO:0045664	0.399	0.911	1	144	regulation of neuron differentiation	BP	1	ARHGEF2	up_VPUL_EC
GO:0030728	0.399	0.923	1	5	ovulation	BP	1	HPGD	up_VSAP_EC
GO:0035791	0.399	0.923	1	5	platelet-derived growth factor receptor-beta	BP	1	ABL1	up_VSAP_EC
GO:1905939	0.399	0.923	1	5	regulation of gonad development	BP	1	CITED2	up_VSAP_EC
GO:0023052	0.4	0.649	82	1602	signaling	BP	1	NOTCH2,PDGFRB,SLC35F6,SMAD9,ITGB5,DCN,NDN,ANGPT1,PRNP,VASN,FBN1,ADCY6,GLIPR2,BGN,KANK2,SH3BP1,BMPR1A,EVC,RECK,IGFBP6,NUMBL,ARHGEF25,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,AKT2,DOCK10,SYDE1,CLSTN1,PLCL1,CACNB3,CSPG4,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,SEMA3C,ASPN,GNAZ,THY1,TEAD1,ARHGAP10,ATP6V0C,GLI3,PARK7,ZMAT3,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ENSCAFG00000018194,ARL2BP,IFT57,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,RAB7B,SPNS1,GLIS2,ARHGAP1,SHC1,CRCP,FBH1,GREM1,NPHP4,RAC2,FOXO3,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:1901342	0.4	0.714	12	114	regulation of vasculature development	BP	1	VEGFD,LEP,BMP4,TLR3,SASH1,FGF18,EGLN1,NRP1,SYNJ2BP,JUP,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0010817	0.4	0.744	7	102	regulation of hormone levels	BP	1	NR1H4,PTPN11,HIF1A,REST,RAB11FIP1,INHBA,YWHAH	down_VSAP_EC
GO:0052547	0.4	0.745	7	82	regulation of peptidase activity	BP	1	CASP8,PAK2,PTGS2,BCL10,HMGB1,PMAIP1,PSMB9	up_VCAV_EC
GO:1904062	0.4	0.756	6	62	regulation of cation transmembrane transport	BP	1	NEDD4,CAV1,SLC30A1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0006790	0.4	0.754	6	99	sulfur compound metabolic process	BP	1	GPAM,DCN,HS3ST3B1,PARK7,ACSS2,ACAT1	down_VCAV_EC
GO:0021700	0.4	0.768	5	65	developmental maturation	BP	1	HIF1A,CTNNB1,DDIT3,DISC1,BTK	down_VSAP_EC
GO:0042098	0.4	0.771	5	43	T cell proliferation	BP	1	CD274,ABL1,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0045454	0.4	0.788	4	35	cell redox homeostasis	BP	1	PRDX4,TMX3,ERO1B,TXNDC5	up_ACOR_VSMC
GO:0110110	0.4	0.788	4	34	positive regulation of animal organ	BP	1	GATA5,BMP4,FGFR2,FRS2	up_ACOR_VSMC
GO:0034655	0.4	0.782	4	135	nucleobase-containing compound catabolic	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0050865	0.4	0.783	4	135	regulation of cell activation	BP	1	LEP,BPI,GPAM,CYLD	up_AFEM_EC
GO:0007569	0.4	0.81	3	36	cell aging	BP	1	SERPINE1,NUAK1,CDKN1A	down_VSAP_EC

GO:0032092	0.4	0.81	3	38	positive regulation of protein binding	BP	1	TRIB3,PLCL1,APOE	down_VSAP_EC
GO:1990138	0.4	0.81	3	35	neuron projection extension	BP	1	IFRD1,CTNNB1,NRP1	down_VSAP_EC
GO:0022407	0.4	0.806	3	96	regulation of cell-cell adhesion	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0010827	0.4	0.811	3	28	regulation of glucose transmembrane transport	BP	1	EDN1,YES1,RSC1A1	up_VCAV_EC
GO:0098876	0.4	0.811	3	29	vesicle-mediated transport to the plasma	BP	1	ANKRD50,EXOC5,CHIC2	up_VCAV_EC
GO:2000117	0.4	0.846	2	27	negative regulation of cysteine-type	BP	1	CST3,PARK7	down_VCAV_EC
GO:0042446	0.4	0.852	2	14	hormone biosynthetic process	BP	1	DKKL1,STC2	up_ACOR_VSMC
GO:0001569	0.4	0.852	2	14	branching involved in blood vessel	BP	1	ABL1,TGFBR2	up_VSAP_EC
GO:0051235	0.4	0.91	1	90	maintenance of location	BP	1	LYN	down_ACOR_EC
GO:0003016	0.4	0.915	1	10	respiratory system process	BP	1	NDN	down_VCAV_EC
GO:0033688	0.4	0.915	1	10	regulation of osteoblast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0034123	0.4	0.915	1	10	positive regulation of toll-like receptor signaling	BP	1	CYBA	down_VCAV_EC
GO:0048599	0.4	0.914	1	10	oocyte development	BP	1	FOXO3	down_VCAV_EC
GO:2000725	0.4	0.915	1	10	regulation of cardiac muscle cell differentiation	BP	1	GREM1	down_VCAV_EC
GO:0060341	0.4	0.912	1	255	regulation of cellular localization	BP	1	RAB11B	down_VPOR_EC
GO:0000470	0.4	0.916	1	9	maturation of LSU-rRNA	BP	1	MRPL1	down_VSAP_EC
GO:0010801	0.4	0.923	1	5	negative regulation of peptidyl-threonine	BP	1	INPP5K	up_ACOR_VSMC
GO:0030574	0.4	0.923	1	5	collagen catabolic process	BP	1	CTSB	up_ACOR_VSMC
GO:0050718	0.4	0.923	1	5	positive regulation of interleukin-1 beta	BP	1	NOD2	up_ACOR_VSMC
GO:0060363	0.4	0.923	1	5	cranial suture morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0033151	0.4	0.92	1	6	V(D)J recombination	BP	1	HMGB1	up_VCAV_EC
GO:0043122	0.4	0.909	1	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	MTDH	up_VPOR_EC
GO:0045945	0.4	0.92	1	6	positive regulation of transcription by RNA polymerase III	BP	1	ICE1	up_VSAP_EC
GO:0046602	0.4	0.923	1	5	regulation of mitotic centrosome separation	BP	1	CEP85	up_VSAP_EC
GO:0046653	0.4	0.923	1	5	tetrahydrofolate metabolic process	BP	1	ENSCAFG00000013986	up_VSAP_EC
GO:0070816	0.4	0.923	1	5	phosphorylation of RNA polymerase II C-terminal	BP	1	CDK9	up_VSAP_EC
GO:2000052	0.4	0.923	1	5	positive regulation of non-canonical Wnt signaling	BP	1	ABL1	up_VSAP_EC
GO:0007618	0.4	0.923	1	5	mating	BP	1	THRB	up_VSAP_EC
GO:1901017	0.4	0.923	1	5	negative regulation of potassium ion transmembrane	BP	1	KCNE3	up_VSAP_EC
GO:1901380	0.4	0.923	1	5	negative regulation of potassium ion	BP	1	KCNE3	up_VSAP_EC
GO:0043407	0.400026426	0.91106	1	19	negative regulation of MAP kinase activity	BP	1	PRKCD	up_ACOR_EC
GO:0008333	0.400034166	0.91105	1	19	endosome to lysosome transport	BP	1	VPS16	up_ACOR_EC
GO:0002440	0.400131033	0.84326	2	51	production of molecular mediator of immune	BP	1	FZD5,NOD2	up_ACOR_EC
GO:0046434	0.40016528	0.84318	2	52	organophosphate catabolic process	BP	1	ALDOC,PRKCD	up_ACOR_EC
GO:0010498	0.400569341	0.7524	6	194	proteasomal protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114,UBE2H,HM13	up_ACOR_EC
GO:0030326	0.400580148	0.84296	2	51	embryonic limb morphogenesis	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0035113	0.400580148	0.84296	2	51	embryonic appendage morphogenesis	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0001885	0.400624222	0.91076	1	19	endothelial cell development	BP	1	ARHGEF26	up_ACOR_EC
GO:0032956	0.401	0.717	11	116	regulation of actin cytoskeleton organization	BP	1	FSCN1,CAPG,LIMA1,NF2,STMN1,RAC1,PDXP, IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC

GO:0002218	0.401	0.756	6	53	activation of innate immune response	BP	1	TLR1,TLR3,F2RL1,PTPN22,PRKCE,NOD2	up_ACOR_VSMC
GO:0009260	0.401	0.766	5	83	ribonucleotide biosynthetic process	BP	1	ADCY6,ATP5MC1,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0046390	0.401	0.766	5	83	ribose phosphate biosynthetic process	BP	1	ADCY6,ATP5MC1,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:1905330	0.401	0.769	5	48	regulation of morphogenesis of an	BP	1	HOXB7,GATA3,NTN4,MTOR,BTBD7	up_VCAV_EC
GO:0006470	0.401	0.784	4	54	protein dephosphorylation	BP	1	NUAK1,PPP1R12A,HTT,CALM1	down_VSAP_EC
GO:0008593	0.401	0.787	4	33	regulation of Notch signaling pathway	BP	1	DLL1,EPN2,GDPD5,TSPAN5	up_VSAP_EC
GO:0043280	0.401	0.788	4	33	positive regulation of cysteine-type endopeptidase activity	BP	1	CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0032412	0.401	0.808	3	46	regulation of ion transmembrane	BP	1	PRNP,FXYD1,CACNB3	down_VCAV_EC
GO:0007498	0.401	0.808	3	38	mesoderm development	BP	1	ITGA2,EXT1,INHBA	down_VSAP_EC
GO:0090630	0.401	0.813	3	23	activation of GTPase activity	BP	1	USP6NL,EVI5L,SGSM2	up_ACOR_VSMC
GO:0006383	0.401	0.845	2	28	transcription by RNA polymerase III	BP	1	NAB2,CRCP	down_VCAV_EC
GO:0030203	0.401	0.845	2	27	glycosaminoglycan metabolic process	BP	1	DCN,ENSCAFG00000017708	down_VCAV_EC
GO:1904019	0.401	0.847	2	22	epithelial cell apoptotic process	BP	1	SERPINE1,EXOC5	down_VSAP_EC
GO:0034629	0.401	0.852	2	14	cellular protein-containing complex localization	BP	1	NACC2,WASL	up_ACOR_VSMC
GO:0048260	0.401	0.85	2	15	positive regulation of receptor-mediated	BP	1	PLCG2,B2M	up_ACOR_VSMC
GO:0006793	0.401	0.857	2	948	phosphorus metabolic process	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0071545	0.401	0.92	1	6	inositol phosphate catabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:0097286	0.401	0.92	1	6	iron ion import	BP	1	TFRC	down_ACOR_VSMC
GO:0016567	0.401	0.912	1	232	protein ubiquitination	BP	1	IVNS1ABP	down_AFEM_EC
GO:0015914	0.401	0.914	1	10	phospholipid transport	BP	1	SCP2	down_VCAV_EC
GO:0043616	0.401	0.914	1	10	keratinocyte proliferation	BP	1	ZFP36L1	down_VCAV_EC
GO:0070198	0.401	0.914	1	10	protein localization to chromosome, telomeric	BP	1	NABP2	down_VCAV_EC
GO:0032988	0.401	0.916	1	8	ribonucleoprotein complex disassembly	BP	1	KIF5B	down_VSAP_EC
GO:0002092	0.401	0.915	1	9	positive regulation of receptor internalization	BP	1	VEGFA	down_VSAP_EC
GO:0043201	0.401	0.917	1	7	response to leucine	BP	1	SESN2	down_VSAP_EC
GO:0071233	0.401	0.917	1	7	cellular response to leucine	BP	1	SESN2	down_VSAP_EC
GO:0061309	0.401	0.922	1	5	cardiac neural crest cell development involved in outflow tract	BP	1	BMP4	up_ACOR_VSMC
GO:0035295	0.401	0.914	1	356	tube development	BP	1	EYA1	up_AFEM_VSMC
GO:0043408	0.401	0.911	1	211	regulation of MAPK cascade	BP	1	TAOK1	up_AORT_EC
GO:0009890	0.401	0.916	1	420	negative regulation of biosynthetic process	BP	1	ESR1	up_AORT_VSMC
GO:1990253	0.401	0.923	1	5	cellular response to leucine starvation	BP	1	MTOR	up_VCAV_EC
GO:2001242	0.401	0.908	1	62	regulation of intrinsic apoptotic signaling	BP	1	ARHGEF2	up_VPOR_EC
GO:0016569	0.401	0.91	1	144	covalent chromatin modification	BP	1	NR1H4	up_VPUL_EC
GO:0006474	0.401	0.922	1	5	N-terminal protein amino acid acetylation	BP	1	NAA60	up_VSAP_EC
GO:0006977	0.401	0.922	1	5	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BP	1	CRADD	up_VSAP_EC
GO:0007501	0.401	0.922	1	5	mesodermal cell fate specification	BP	1	HOXA11	up_VSAP_EC
GO:0030812	0.401	0.922	1	5	negative regulation of nucleotide catabolic	BP	1	DDIT4	up_VSAP_EC
GO:0045820	0.401	0.922	1	5	negative regulation of glycolytic process	BP	1	DDIT4	up_VSAP_EC

GO:0046931	0.401	0.923	1	5	pore complex assembly	BP	1	NUP98	up_VSAP_EC
GO:0051195	0.401	0.922	1	5	negative regulation of cofactor metabolic	BP	1	DDIT4	up_VSAP_EC
GO:0051198	0.401	0.922	1	5	negative regulation of coenzyme metabolic	BP	1	DDIT4	up_VSAP_EC
GO:0072075	0.401	0.923	1	5	metanephric mesenchyme	BP	1	OSR1	up_VSAP_EC
GO:0072431	0.401	0.922	1	5	signal transduction involved in mitotic G1 DNA damage checkpoint	BP	1	CRADD	up_VSAP_EC
GO:0075522	0.401	0.922	1	5	IRES-dependent viral translational initiation	BP	1	EIF3D	up_VSAP_EC
GO:0086005	0.401	0.923	1	5	ventricular cardiac muscle cell action potential	BP	1	KCNE3	up_VSAP_EC
GO:1902400	0.401	0.922	1	5	intracellular signal transduction involved in G1 DNA damage	BP	1	CRADD	up_VSAP_EC
GO:0009583	0.401	0.922	1	5	detection of light stimulus	BP	1	CHRM1	up_VSAP_EC
GO:0051051	0.401	0.909	1	112	negative regulation of transport	BP	1	CAV1	up_VSAP_VSMC
GO:0002709	0.401078606	0.91054	1	19	regulation of T cell mediated immunity	BP	1	FZD5	up_ACOR_EC
GO:0030177	0.401404219	0.8424	2	51	positive regulation of Wnt signaling pathway	BP	1	CDH3,DIXDC1	up_ACOR_EC
GO:0030030	0.402	0.72	10	377	cell projection organization	BP	1	PLXNA4,NEFH,CAMK2A,CYLD,DNAL1,SPATA6,CDC42EP5,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0006066	0.402	0.735	8	89	alcohol metabolic process	BP	1	GK5,SPTLC2,BMP2,ABCA1,ITPKB,PLCG2,GCH1,IMPA1	up_VCAV_EC
GO:0010001	0.402	0.755	6	54	glial cell differentiation	BP	1	WASF3,ABL1,DLL1,KLF15,PLPP3,NFIB	up_VSAP_EC
GO:0097530	0.402	0.786	4	33	granulocyte migration	BP	1	C5AR2,SLIT2,IL17RC,MYD88	up_VSAP_EC
GO:0045682	0.402	0.811	3	27	regulation of epidermis development	BP	1	NAB2,EZH2,HOXA7	down_ACOR_VSMC
GO:0034250	0.402	0.807	3	45	positive regulation of cellular amide metabolic	BP	1	LARP6,EEF2,PYM1	down_VCAV_EC
GO:0061053	0.402	0.811	3	24	somite development	BP	1	WNT11,AXIN2,DLL1	up_VSAP_EC
GO:0009410	0.402	0.845	2	27	response to xenobiotic stimulus	BP	1	NR3C1,CYP1B1	down_VCAV_EC
GO:0046513	0.402	0.847	2	19	ceramide biosynthetic process	BP	1	SPTLC2,SAMD8	up_VCAV_EC
GO:1903035	0.402	0.85	2	14	negative regulation of response to wounding	BP	1	KLKB1,RTN4RL1	up_VSAP_EC
GO:0045862	0.402	0.909	1	112	positive regulation of proteolysis	BP	1	LYN	down_ACOR_EC
GO:0000394	0.402	0.919	1	6	RNA splicing, via endonucleolytic cleavage	BP	1	RTCB	down_ACOR_VSMC
GO:0006388	0.402	0.919	1	6	tRNA splicing, via endonucleolytic cleavage	BP	1	RTCB	down_ACOR_VSMC
GO:0045947	0.402	0.919	1	6	negative regulation of translational initiation	BP	1	RBM14	down_ACOR_VSMC
GO:0009607	0.402	0.911	1	232	response to biotic stimulus	BP	1	IVNS1ABP	down_AFEM_EC
GO:0009792	0.402	0.911	1	231	embryo development ending in birth or egg	BP	1	GABPA	down_AFEM_EC
GO:0044267	0.402	0.949	1	1583	cellular protein metabolic process	BP	1	CST3	down_AORT_EC
GO:1902692	0.402	0.913	1	11	regulation of neuroblast proliferation	BP	1	GLI3	down_VCAV_EC
GO:0043066	0.402	0.912	1	253	negative regulation of apoptotic process	BP	1	CITED2	down_VPOR_EC
GO:2000171	0.402	0.916	1	8	negative regulation of dendrite development	BP	1	YWHAH	down_VSAP_EC
GO:0034453	0.402	0.916	1	8	microtubule anchoring	BP	1	HOOK3	down_VSAP_EC
GO:0021895	0.402	0.922	1	5	cerebral cortex neuron differentiation	BP	1	PSEN1	up_ACOR_VSMC
GO:0034375	0.402	0.922	1	5	high-density lipoprotein particle remodeling	BP	1	LCAT	up_ACOR_VSMC
GO:0032148	0.402	0.919	1	6	activation of protein kinase B activity	BP	1	PDGFB	up_VCAV_EC
GO:0002902	0.402	0.919	1	6	regulation of B cell apoptotic process	BP	1	BCL10	up_VCAV_EC
GO:0018205	0.402	0.909	1	122	peptidyl-lysine modification	BP	1	EYA1	up_VFEM_EC
GO:0002190	0.402	0.922	1	5	cap-independent translational initiation	BP	1	NCK1	up_VSAP_EC

GO:0015872	0.402	0.922	1	5	dopamine transport	BP	1	SLC6A4	up_VSAP_EC
GO:0030948	0.402	0.922	1	5	negative regulation of vascular endothelial growth factor receptor	BP	1	EPN2	up_VSAP_EC
GO:0032048	0.402	0.922	1	5	cardiolipin metabolic process	BP	1	PLA2G6	up_VSAP_EC
GO:0032049	0.402	0.922	1	5	cardiolipin biosynthetic process	BP	1	PLA2G6	up_VSAP_EC
GO:0042448	0.402	0.922	1	5	progesterone metabolic process	BP	1	DHRS9	up_VSAP_EC
GO:0050951	0.402	0.922	1	5	sensory perception of temperature stimulus	BP	1	NR2F6	up_VSAP_EC
GO:0050961	0.402	0.922	1	5	detection of temperature stimulus involved in sensory perception	BP	1	NR2F6	up_VSAP_EC
GO:0050965	0.402	0.922	1	5	detection of temperature stimulus involved in sensory perception of	BP	1	NR2F6	up_VSAP_EC
GO:0051937	0.402	0.922	1	5	catecholamine transport	BP	1	SLC6A4	up_VSAP_EC
GO:0060027	0.402	0.922	1	5	convergent extension involved in gastrulation	BP	1	WNT11	up_VSAP_EC
GO:0072178	0.402	0.922	1	5	nephric duct morphogenesis	BP	1	OSR1	up_VSAP_EC
GO:0072347	0.402	0.922	1	5	response to anesthetic	BP	1	ABAT	up_VSAP_EC
GO:1900102	0.402	0.922	1	5	negative regulation of endoplasmic reticulum unfolded protein	BP	1	NCK1	up_VSAP_EC
GO:0016048	0.402	0.922	1	5	detection of temperature stimulus	BP	1	NR2F6	up_VSAP_EC
GO:0035907	0.402	0.922	1	5	dorsal aorta development	BP	1	ACVRL1	up_VSAP_EC
GO:0035912	0.402	0.922	1	5	dorsal aorta morphogenesis	BP	1	ACVRL1	up_VSAP_EC
GO:0060562	0.402	0.909	1	120	epithelial tube morphogenesis	BP	1	HOXA11	up_VSAP_VSMC
GO:1901880	0.402042229	0.91007	1	19	negative regulation of protein depolymerization	BP	1	TMOD1	up_ACOR_EC
GO:0060562	0.402683645	0.78049	4	120	epithelial tube morphogenesis	BP	1	SOX9,FOXC2,CLSTN1,NRP1	up_ACOR_EC
GO:0010595	0.402807218	0.84139	2	52	positive regulation of endothelial cell migration	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0051973	0.402990397	0.9096	1	19	positive regulation of telomerase activity	BP	1	PKIB	up_ACOR_EC
GO:0051172	0.403	0.652	58	663	negative regulation of nitrogen compound metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,SREBF2,SMC1A,NEDD4,U2AF2,SLC29A1,MTDH,PPP1R15B,PARPBP,NAB2,BIRC5,CAV1,TIMELESS,THRAP3,FAM129B,NF2,AURKB,CDKN2C,EZH2,GREM1,SMARCC1,PLK3,HOXA7,UHRF1,GMNN,DHCR24,BRCA1,NOC2L,PPARD,YWHAB,NCL,NUP62,SUV39H1,CACTIN,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:0090087	0.403	0.689	19	185	regulation of peptide transport	BP	1	HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,CDH1,ABL1,IL17RC,ANXA4,F2RL1,ICE1,PIK3R1,PASK,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:0001775	0.403	0.71	12	219	cell activation	BP	1	GPAM,LRP1,PRNP,SDC4,LMO4,THY1,GLI3,ZFP36L1,BPI,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0009895	0.403	0.722	10	94	negative regulation of catabolic process	BP	1	LEP,HTR2B,FEZ1,PTPN3,OS9,PSEN1,DDIT4,FEZ2,AZIN2,PARK7	up_ACOR_VSMC
GO:0070661	0.403	0.743	7	63	leukocyte proliferation	BP	1	CD274,ABL1,F2RL1,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0044085	0.403	0.774	5	1076	cellular component biogenesis	BP	1	NR1H4,TUBB4A,ARHGEF26,SLITRK5,NTRK2	up_APUL_EC
GO:0065009	0.403	0.787	4	735	regulation of molecular function	BP	1	NETO1,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0048008	0.403	0.811	3	24	platelet-derived growth factor receptor signaling	BP	1	ABL1,PDGFD,ZFAND5	up_VSAP_EC
GO:0033365	0.403	0.843	2	276	protein localization to organelle	BP	1	IPO7,NEDD4	down_ACOR_EC
GO:0006024	0.403	0.849	2	16	glycosaminoglycan biosynthetic process	BP	1	XYLT1,UGDH	down_ACOR_VSMC
GO:1903313	0.403	0.848	2	16	positive regulation of mRNA metabolic process	BP	1	THRAP3,SF3B4	down_ACOR_VSMC

GO:0042632	0.403	0.844	2	27	cholesterol homeostasis	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0062013	0.403	0.844	2	27	positive regulation of small molecule metabolic	BP	1	AKT2,PARK7	down_VCAV_EC
GO:0009259	0.403	0.841	2	166	ribonucleotide metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0043085	0.403	0.843	2	323	positive regulation of catalytic activity	BP	1	MAP2K6,TIAM1	up_VFEM_EC
GO:0048635	0.403	0.85	2	14	negative regulation of muscle organ	BP	1	DLL1,SAV1	up_VSAP_EC
GO:1903556	0.403	0.85	2	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	CD274,C5AR2	up_VSAP_EC
GO:1901293	0.403	0.908	1	106	nucleoside phosphate biosynthetic process	BP	1	TNRC6B	down_ACOR_EC
GO:0032570	0.403	0.919	1	6	response to progesterone	BP	1	CAV1	down_ACOR_VSMC
GO:0033689	0.403	0.919	1	6	negative regulation of osteoblast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:0051451	0.403	0.919	1	6	myoblast migration	BP	1	SIX4	down_ACOR_VSMC
GO:1904385	0.403	0.919	1	6	cellular response to angiotensin	BP	1	CAV1	down_ACOR_VSMC
GO:1990776	0.403	0.919	1	6	response to angiotensin	BP	1	CAV1	down_ACOR_VSMC
GO:0035855	0.403	0.915	1	8	megakaryocyte development	BP	1	PTPN11	down_VSAP_EC
GO:0032011	0.403	0.917	1	7	ARF protein signal transduction	BP	1	ARFGEF3	down_VSAP_EC
GO:0032012	0.403	0.917	1	7	regulation of ARF protein signal transduction	BP	1	ARFGEF3	down_VSAP_EC
GO:0060544	0.403	0.915	1	8	regulation of necroptotic process	BP	1	ARHGEF2	down_VSAP_EC
GO:0140131	0.403	0.921	1	5	positive regulation of lymphocyte chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0071404	0.403	0.921	1	5	cellular response to low-density lipoprotein	BP	1	ABCA1	up_VCAV_EC
GO:0072172	0.403	0.917	1	7	mesonephric tubule formation	BP	1	GATA3	up_VCAV_EC
GO:0002704	0.403	0.921	1	5	negative regulation of leukocyte mediated	BP	1	PPP3CB	up_VSAP_EC
GO:0010661	0.403	0.921	1	5	positive regulation of muscle cell apoptotic	BP	1	MFN2	up_VSAP_EC
GO:0010765	0.403	0.922	1	5	positive regulation of sodium ion transport	BP	1	FXYD1	up_VSAP_EC
GO:0070254	0.403	0.921	1	5	mucus secretion	BP	1	CYBA	up_VSAP_EC
GO:0070255	0.403	0.921	1	5	regulation of mucus secretion	BP	1	CYBA	up_VSAP_EC
GO:0070365	0.403	0.922	1	5	hepatocyte differentiation	BP	1	HNF4A	up_VSAP_EC
GO:1904925	0.403	0.921	1	5	positive regulation of autophagy of mitochondrion in	BP	1	MFN2	up_VSAP_EC
GO:0007530	0.403	0.921	1	5	sex determination	BP	1	CITED2	up_VSAP_EC
GO:0018904	0.403	0.922	1	5	ether metabolic process	BP	1	PEX7	up_VSAP_EC
GO:0032402	0.403	0.921	1	5	melanosome transport	BP	1	RAB11B	up_VSAP_EC
GO:0034162	0.403	0.921	1	5	toll-like receptor 9 signaling pathway	BP	1	UNC93B1	up_VSAP_EC
GO:0051904	0.403	0.921	1	5	pigment granule transport	BP	1	RAB11B	up_VSAP_EC
GO:2000010	0.403	0.922	1	5	positive regulation of protein localization to cell	BP	1	STX4	up_VSAP_EC
GO:0019083	0.403031378	0.90958	1	19	viral transcription	BP	1	TRIM8	up_ACOR_EC
GO:0046939	0.403211581	0.90949	1	19	nucleotide phosphorylation	BP	1	ALDOC	up_ACOR_EC
GO:0043331	0.403347445	0.90921	1	20	response to dsRNA	BP	1	MAVS	up_ACOR_EC
GO:0090130	0.403627371	0.77972	4	121	tissue migration	BP	1	SOX9,ENSCAFG00000004331,FOXC2,NRP1	up_ACOR_EC
GO:0010243	0.404	0.678	25	238	response to organonitrogen compound	BP	1	ACTN2,LEP,ABCA1,CASTOR1,GLRB,ADCY6,AKAP6,P2RX7,UBR1,PTPN22,OS9,STT3B,APLP1,SESN3,PRKCE,APP,PSEN1,JUP,NOD2,HERPUD1,INPP5K,FAF2,WFS1,DZIP3,SH3BP4	up_ACOR_VSMC

GO:0043069	0.404	0.68	23	262	negative regulation of programmed cell death	BP	1	PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,MEF2C,GATA3,FIGNL1,PELI1,ARG2,ITPKB,PAK2,PTGS2,PLCG2,BCL10,CTNNA1,RIPK1,ITGA6,HIF1A,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0006164	0.404	0.751	6	86	purine nucleotide biosynthetic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1	down_VSAP_EC
GO:0042063	0.404	0.765	5	67	gliogenesis	BP	1	PTPN11,ILK,SLC45A3,EIF2B1,CTNNB1	down_VSAP_EC
GO:0090313	0.404	0.849	2	14	regulation of protein targeting to membrane	BP	1	TCAF1,INPP5K	up_ACOR_VSMC
GO:0071478	0.404	0.841	2	58	cellular response to radiation	BP	1	CRYAB,MFAP4	up_AFEM_EC
GO:0043502	0.404	0.848	2	16	regulation of muscle adaptation	BP	1	EDN1,PPP3CA	up_VCAV_EC
GO:0023051	0.404	0.855	2	954	regulation of signaling	BP	1	GATA5,CA2	up_VCAV_VSMC
GO:0044703	0.404	0.841	2	172	multi-organism reproductive process	BP	1	ACVR2A,RPL10L	up_VPOR_EC
GO:0072523	0.404	0.849	2	14	purine-containing compound catabolic	BP	1	GDA,PNP	up_VSAP_EC
GO:1901862	0.404	0.85	2	14	negative regulation of muscle tissue	BP	1	DLL1,SAV1	up_VSAP_EC
GO:0031953	0.404	0.918	1	6	negative regulation of protein	BP	1	CAV1	down_ACOR_VSMC
GO:0072413	0.404	0.918	1	6	signal transduction involved in mitotic cell	BP	1	CASP2	down_ACOR_VSMC
GO:1902402	0.404	0.918	1	6	signal transduction involved in mitotic DNA	BP	1	CASP2	down_ACOR_VSMC
GO:1902403	0.404	0.918	1	6	signal transduction involved in mitotic DNA	BP	1	CASP2	down_ACOR_VSMC
GO:0034113	0.404	0.913	1	10	heterotypic cell-cell adhesion	BP	1	THY1	down_VCAV_EC
GO:0002279	0.404	0.913	1	10	mast cell activation involved in immune	BP	1	RAC2	down_VCAV_EC
GO:0002448	0.404	0.913	1	10	mast cell mediated immunity	BP	1	RAC2	down_VCAV_EC
GO:0043303	0.404	0.913	1	10	mast cell degranulation	BP	1	RAC2	down_VCAV_EC
GO:0051281	0.404	0.913	1	10	positive regulation of release of sequestered calcium ion into cytosol	BP	1	THY1	down_VCAV_EC
GO:0071108	0.404	0.912	1	11	protein K48-linked deubiquitination	BP	1	PARK7	down_VCAV_EC
GO:0090140	0.404	0.913	1	10	regulation of mitochondrial fission	BP	1	DCN	down_VCAV_EC
GO:0071225	0.404	0.915	1	8	cellular response to muramyl dipeptide	BP	1	ARHGEF2	down_VSAP_EC
GO:0072012	0.404	0.914	1	9	glomerulus vasculature development	BP	1	ACTA2	down_VSAP_EC
GO:1990126	0.404	0.915	1	8	retrograde transport, endosome to plasma	BP	1	ANKRD50	down_VSAP_EC
GO:0060644	0.404	0.921	1	5	mammary gland epithelial cell differentiation	BP	1	LBH	up_ACOR_VSMC
GO:2000052	0.404	0.921	1	5	positive regulation of non-canonical Wnt signaling	BP	1	MLLT3	up_ACOR_VSMC
GO:0000303	0.404	0.918	1	6	response to superoxide	BP	1	GCH1	up_VCAV_EC
GO:0000305	0.404	0.918	1	6	response to oxygen radical	BP	1	GCH1	up_VCAV_EC
GO:0010566	0.404	0.918	1	6	regulation of ketone biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0060306	0.404	0.916	1	7	regulation of membrane repolarization	BP	1	KCNJ2	up_VCAV_EC
GO:0086009	0.404	0.916	1	7	membrane repolarization	BP	1	KCNJ2	up_VCAV_EC
GO:0048568	0.404	0.908	1	148	embryonic organ development	BP	1	HOXA3	up_VPUL_EC
GO:0002739	0.404	0.921	1	5	regulation of cytokine secretion involved in	BP	1	F2RL1	up_VSAP_EC
GO:0014003	0.404	0.921	1	5	oligodendrocyte development	BP	1	WASF3	up_VSAP_EC
GO:0023058	0.404	0.921	1	5	adaptation of signaling pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0032673	0.404	0.921	1	5	regulation of interleukin-4 production	BP	1	CD83	up_VSAP_EC
GO:0033127	0.404	0.921	1	5	regulation of histone phosphorylation	BP	1	CDK9	up_VSAP_EC
GO:0045725	0.404	0.921	1	5	positive regulation of glycogen biosynthetic	BP	1	C1QTNF2	up_VSAP_EC

GO:0046838	0.404	0.921	1	5	phosphorylated carbohydrate	BP	1	INPP5E	up_VSAP_EC
GO:0046855	0.404	0.921	1	5	inositol phosphate dephosphorylation	BP	1	INPP5E	up_VSAP_EC
GO:0051045	0.404	0.921	1	5	negative regulation of membrane protein	BP	1	TIMP2	up_VSAP_EC
GO:0070875	0.404	0.921	1	5	positive regulation of glycogen metabolic	BP	1	C1QTNF2	up_VSAP_EC
GO:1902237	0.404	0.921	1	5	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	NCK1	up_VSAP_EC
GO:1903071	0.404	0.921	1	5	positive regulation of ER-associated ubiquitin-dependent protein	BP	1	UBQLN2	up_VSAP_EC
GO:0007213	0.404	0.921	1	5	G protein-coupled acetylcholine receptor	BP	1	CHRM1	up_VSAP_EC
GO:0048535	0.404	0.921	1	5	lymph node development	BP	1	TOX	up_VSAP_EC
GO:0090153	0.404	0.921	1	5	regulation of sphingolipid biosynthetic process	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:1905038	0.404	0.921	1	5	regulation of membrane lipid metabolic process	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:2000303	0.404	0.921	1	5	regulation of ceramide biosynthetic process	BP	1	ENSCAFG00000000071	up_VSAP_EC
GO:1903706	0.404	0.908	1	119	regulation of hemopoiesis	BP	1	HOXA9	up_VSAP_VSMC
GO:0032663	0.404659837	0.90878	1	19	regulation of interleukin-2 production	BP	1	NR1H4	up_ACOR_EC
GO:0097006	0.404826336	0.90869	1	19	regulation of plasma lipoprotein particle levels	BP	1	NR1H4	up_ACOR_EC
GO:1903036	0.404844995	0.90868	1	19	positive regulation of response to wounding	BP	1	FOXC2	up_ACOR_EC
GO:0051247	0.405	0.654	50	502	positive regulation of protein metabolic process	BP	1	ADRA1B,TLR1,LEP,MAP3K8,MID1,HTR2B,RASSF2,MBP,SKP2,PRKAA2,BMP4,FGFR2,TLR3,SH3RF2,PDE5A,SASH1,FGF18,F2RL1,FAM129A,DAPK1,NRP1,PTPN22,NPNT,SMPD1,PRKCE,CCNT1,FRS2,RNF19A,PARP9,APP,PSEN1,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,MAP3K7,WFS1,ENSCAFG00000029553,PARK7,NGRN,CRKL	up_ACOR_VSMC
GO:0055085	0.405	0.67	29	284	transmembrane transport	BP	1	SLC43A1,PEX7,AMIGO1,CALHM2,SLC8B1,SLC43A3,MFSD3,ABL1,PEX2,KCNE3,OSR1,CLIC5,KLF15,C1QTNF2,KLHL24,SLC25A12,PIK3R1,SLC25A28,SCARA5,AZIN2,CLCN2,STEAP3,KCNB1,LONP2,ENSCAFG00000013366,CYBA,FXYD1,KCNC4,PEX6	up_VSAP_EC
GO:0019725	0.405	0.676	25	245	cellular homeostasis	BP	1	C5AR2,SLC8B1,ABL1,PTGES2,ENSCAFG00000000071,F2RL1,RAB11B,FXN,PIK3R1,MYC,DLD,SCARA5,FBXO4,E2F4,KCNB1,TXNDC16,FTL,RAF1,CYBA,STX4,PPP3CB,HMOX1,ENSCAFG00000006478,NCOA4,RAB11FIP2	up_VSAP_EC
GO:0070925	0.405	0.686	19	293	organelle assembly	BP	1	ACTN1,EXOC5,FSCN1,MZT1,WDR1,MSN,RPGR,DYNLL1,TUBB,CNOT7,KPNB1,SH3GLB1,SDC4,HTT,EIF2S1,DISC1,SIX4,RSL24D1,MYBPC2	down_VSAP_EC
GO:1901564	0.405	0.743	9	2053	organonitrogen compound metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,ENSCAFG00000028814	up_APUL_EC
GO:0030518	0.405	0.766	5	42	intracellular steroid hormone receptor	BP	1	LBH,SKP2,MED14,AR,PARK7	up_ACOR_VSMC
GO:0045667	0.405	0.784	4	38	regulation of osteoblast differentiation	BP	1	FBXO5,GREM1,TWIST2,GLI1	down_ACOR_VSMC
GO:0048468	0.405	0.807	3	553	cell development	BP	1	EYA1,SIX1,RADIL	up_VFEM_EC
GO:0007584	0.405	0.81	3	24	response to nutrient	BP	1	PDK2,CASTOR1,BGLAP	up_VSAP_EC
GO:0032722	0.405	0.849	2	14	positive regulation of chemokine production	BP	1	MBP,TLR3	up_ACOR_VSMC
GO:0008654	0.405	0.839	2	58	phospholipid biosynthetic process	BP	1	GPAM,AGPAT2	up_AFEM_EC
GO:1904035	0.405	0.847	2	16	regulation of epithelial cell apoptotic process	BP	1	TNFAIP3,GATA3	up_VCAV_EC
GO:0050858	0.405	0.918	1	6	negative regulation of antigen receptor-mediated signaling	BP	1	EZR	down_ACOR_VSMC
GO:0050860	0.405	0.918	1	6	negative regulation of T cell receptor signaling	BP	1	EZR	down_ACOR_VSMC

GO:0002886	0.405	0.912	1	10	regulation of myeloid leukocyte mediated	BP	1	RAC2	down_VCAV_EC
GO:0090185	0.405	0.912	1	10	negative regulation of kidney development	BP	1	GREM1	down_VCAV_EC
GO:0072215	0.405	0.914	1	8	regulation of metanephros	BP	1	CTNNB1	down_VSAP_EC
GO:2000696	0.405	0.915	1	8	regulation of epithelial cell differentiation involved in kidney	BP	1	CTNNB1	down_VSAP_EC
GO:0001840	0.405	0.921	1	5	neural plate development	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0043517	0.405	0.918	1	6	positive regulation of DNA damage response, signal transduction by p53 class mediator	BP	1	ANKRD1	up_ACOR_VSMC
GO:0048710	0.405	0.921	1	5	regulation of astrocyte differentiation	BP	1	APP	up_ACOR_VSMC
GO:1901700	0.405	0.912	1	364	response to oxygen-containing compound	BP	1	TLR2	up_AFEM_VSMC
GO:0009967	0.405	0.914	1	435	positive regulation of signal transduction	BP	1	WNT7A	up_AORT_VSMC
GO:0048857	0.405	0.918	1	6	neural nucleus development	BP	1	ALDH1A3	up_VCAV_EC
GO:1902532	0.405	0.909	1	204	negative regulation of intracellular signal	BP	1	FBP1	up_VFEM_VSMC
GO:0002418	0.405	0.92	1	5	immune response to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0002834	0.405	0.92	1	5	regulation of response to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0002837	0.405	0.92	1	5	regulation of immune response to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0009164	0.405	0.921	1	5	nucleoside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0010714	0.405	0.92	1	5	positive regulation of collagen metabolic	BP	1	LARP6	up_VSAP_EC
GO:0015837	0.405	0.921	1	5	amine transport	BP	1	OSR1	up_VSAP_EC
GO:0032461	0.405	0.92	1	5	positive regulation of protein oligomerization	BP	1	JCHAIN	up_VSAP_EC
GO:0032965	0.405	0.92	1	5	regulation of collagen biosynthetic process	BP	1	LARP6	up_VSAP_EC
GO:0032967	0.405	0.92	1	5	positive regulation of collagen biosynthetic	BP	1	LARP6	up_VSAP_EC
GO:0034114	0.405	0.92	1	5	regulation of heterotypic cell-cell adhesion	BP	1	FLOT1	up_VSAP_EC
GO:0035268	0.405	0.92	1	5	protein mannosylation	BP	1	FKRP	up_VSAP_EC
GO:0035458	0.405	0.921	1	5	cellular response to interferon-beta	BP	1	HTRA2	up_VSAP_EC
GO:0042454	0.405	0.921	1	5	ribonucleoside catabolic process	BP	1	PNP	up_VSAP_EC
GO:0042572	0.405	0.921	1	5	retinol metabolic process	BP	1	RETSAT	up_VSAP_EC
GO:0046085	0.405	0.92	1	5	adenosine metabolic process	BP	1	NT5C2	up_VSAP_EC
GO:0051482	0.405	0.921	1	5	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-	BP	1	F2RL1	up_VSAP_EC
GO:0051952	0.405	0.921	1	5	regulation of amine transport	BP	1	OSR1	up_VSAP_EC
GO:0060501	0.405	0.921	1	5	positive regulation of epithelial cell proliferation involved in lung	BP	1	FGF7	up_VSAP_EC
GO:0070234	0.405	0.92	1	5	positive regulation of T cell apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0097502	0.405	0.92	1	5	mannosylation	BP	1	FKRP	up_VSAP_EC
GO:1900103	0.405	0.921	1	5	positive regulation of endoplasmic reticulum unfolded protein	BP	1	PIK3R1	up_VSAP_EC
GO:0048341	0.405	0.92	1	5	paraxial mesoderm formation	BP	1	WNT11	up_VSAP_EC
GO:0061042	0.405	0.921	1	5	vascular wound healing	BP	1	HPSE	up_VSAP_EC
GO:0031529	0.405448669	0.90817	1	20	ruffle organization	BP	1	ARHGEF26	up_ACOR_EC
GO:0032526	0.405800892	0.90821	1	19	response to retinoic acid	BP	1	AQP1	up_ACOR_EC

GO:0048523	0.406	0.646	72	1399	negative regulation of cellular process	BP	1	CST3,GPAM,NOTCH2,SLC35F6,KIRREL1,DCN,NAB2,NDN,PRNP,SDC4,VASN,FBN1,BGN,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,AKT1S1,CHRDL1,TIMP2,AKT2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,TMEM161A,CXXC5,ASPN,POLDIP2,LRPAP1,THY1,ARHGAP10,TLX2,CC2D1A,B4GALT1,GLI3,PARK7,ZFP36L1,MYDGF,CLEC16A,BPI,CYBA,IFT57,CDH2,LOXL3,ORMDL3,GSDME,SPRED1,RAB7B,A2M,TSC22D3,GLIS2,TWIST2,ARHGAP1,PRKCSH,SHC1,FBH1,GREM1,PLEKHH2,NPHP4,EVI5L,FOXO3,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA,BRSK1	down_VCAV_EC
GO:0007268	0.406	0.723	9	130	chemical synaptic transmission	BP	1	KIF5B,HTR7,PLCL1,CDH11,CTNNB1,APOE,GSK3B,LRRTM2,USP14	down_VSAP_EC
GO:0098916	0.406	0.723	9	130	anterograde trans-synaptic signaling	BP	1	KIF5B,HTR7,PLCL1,CDH11,CTNNB1,APOE,GSK3B,LRRTM2,USP14	down_VSAP_EC
GO:0051099	0.406	0.762	5	70	positive regulation of binding	BP	1	TRIB3,PLCL1,CTNNB1,APOE,CALM1	down_VSAP_EC
GO:0007224	0.406	0.764	5	50	smoothened signaling pathway	BP	1	PTCHD1,HHAT,CTNNA1,IQUB,CDON	up_VCAV_EC
GO:0009892	0.406	0.786	4	835	negative regulation of metabolic process	BP	1	NR1H4,PLCL1,PCSK1N,LZTS1	up_APUL_EC
GO:0051246	0.406	0.786	4	832	regulation of protein metabolic process	BP	1	PLCL1,PCSK1N,NPNT,NTRK2	up_APUL_EC
GO:0070936	0.406	0.807	3	28	protein K48-linked ubiquitination	BP	1	UBE2T,RNF152,UBE2C	down_ACOR_VSMC
GO:0051172	0.406	0.809	3	663	negative regulation of nitrogen compound	BP	1	NR1H4,PTGER2,FLRT3	up_VPUL_EC
GO:0032655	0.406	0.846	2	16	regulation of interleukin-12 production	BP	1	HMGB1,MAST2	down_ACOR_VSMC
GO:0009408	0.406	0.842	2	27	response to heat	BP	1	TRPV2,SCARA5	down_VCAV_EC
GO:0051209	0.406	0.842	2	28	release of sequestered calcium ion into cytosol	BP	1	THY1,CYBA	down_VCAV_EC
GO:0051283	0.406	0.842	2	28	negative regulation of sequestering of calcium	BP	1	THY1,CYBA	down_VCAV_EC
GO:0032677	0.406	0.843	2	22	regulation of interleukin-8 production	BP	1	SERPINE1,DDIT3	down_VSAP_EC
GO:0008299	0.406	0.848	2	14	isoprenoid biosynthetic process	BP	1	DHRS9,MVK	up_VSAP_EC
GO:0060359	0.406	0.848	2	14	response to ammonium ion	BP	1	CHRM1,ABAT	up_VSAP_EC
GO:0033561	0.406	0.917	1	6	regulation of water loss via skin	BP	1	STMN1	down_ACOR_VSMC
GO:1901385	0.406	0.917	1	6	regulation of voltage-gated calcium channel	BP	1	REM1	down_ACOR_VSMC
GO:0042551	0.406	0.912	1	10	neuron maturation	BP	1	IRX5	down_VCAV_EC
GO:1904031	0.406	0.912	1	10	positive regulation of cyclin-dependent protein	BP	1	MAPRE3	down_VCAV_EC
GO:0006213	0.406	0.912	1	9	pyrimidine nucleoside metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0019674	0.406	0.913	1	9	NAD metabolic process	BP	1	NMNAT2	down_VSAP_EC
GO:0003264	0.406	0.92	1	5	regulation of cardioblast proliferation	BP	1	TBX5	up_ACOR_VSMC
GO:0030540	0.406	0.92	1	5	female genitalia development	BP	1	CHD7	up_ACOR_VSMC
GO:0032957	0.406	0.92	1	5	inositol trisphosphate metabolic process	BP	1	PLCG2	up_ACOR_VSMC
GO:0003266	0.406	0.92	1	5	regulation of secondary heart field cardioblast	BP	1	TBX5	up_ACOR_VSMC
GO:0070816	0.406	0.92	1	5	phosphorylation of RNA polymerase II C-terminal	BP	1	CCNT1	up_ACOR_VSMC
GO:0071396	0.406	0.907	1	134	cellular response to lipid	BP	1	NR1H4	up_APUL_EC
GO:0010863	0.406	0.92	1	5	positive regulation of phospholipase C activity	BP	1	SELE	up_VCAV_EC
GO:0006000	0.406	0.92	1	5	fructose metabolic process	BP	1	KHK	up_VSAP_EC
GO:0006086	0.406	0.92	1	5	acetyl-CoA biosynthetic process from pyruvate	BP	1	PDK2	up_VSAP_EC
GO:0006688	0.406	0.92	1	5	glycosphingolipid biosynthetic process	BP	1	B3GALT4	up_VSAP_EC
GO:0034475	0.406	0.92	1	5	U4 snRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0050927	0.406	0.92	1	5	positive regulation of positive chemotaxis	BP	1	F2RL1	up_VSAP_EC

GO:0060263	0.406	0.92	1	5	regulation of respiratory burst	BP	1	JCHAIN	up_VSAP_EC
GO:0071636	0.406	0.92	1	5	positive regulation of transforming growth factor beta production	BP	1	WNT11	up_VSAP_EC
GO:1903897	0.406	0.92	1	5	regulation of PERK-mediated unfolded	BP	1	NCK1	up_VSAP_EC
GO:0072007	0.406	0.92	1	5	mesangial cell differentiation	BP	1	OSR1	up_VSAP_EC
GO:0072143	0.406	0.92	1	5	mesangial cell development	BP	1	OSR1	up_VSAP_EC
GO:1904238	0.406	0.92	1	5	pericyte cell differentiation	BP	1	OSR1	up_VSAP_EC
GO:0009101	0.406	0.907	1	113	glycoprotein biosynthetic process	BP	1	GALNT17	up_VSAP_VSMC
GO:0070534	0.406177324	0.90802	1	19	protein K63-linked ubiquitination	BP	1	NOD2	up_ACOR_EC
GO:0009790	0.406190462	0.71637	10	335	embryo development	BP	1	SOX9,FZD5,SMAD6,FOXC2,TBX5,LRP4,RARRES2,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0022603	0.406238924	0.72221	9	301	regulation of anatomical structure morphogenesis	BP	1	BRSK1,SOX9,RHOU,AQP1,PAK3,FOXC2,TBX5,LRP4,NRP1	up_ACOR_EC
GO:1905954	0.406632663	0.90779	1	19	positive regulation of lipid localization	BP	1	PRKCD	up_ACOR_EC
GO:0080090	0.407	0.631	149	1734	regulation of primary metabolic process	BP	1	ELK3,ACSL3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,ILF3,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,MED17,U2AF2,PSMD3,SLC29A1,MTDH,HEY1,PPP1R15B,SF1,PARPBP,SRRT,CTDNEP1,NAB2,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,AURKB,NONO,HNRNPL,CDKN2C,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,CDK4,SMARCC1,PLK3,PCNA,DHX33,HOXA7,SF3B4,UHRF1,CKS2,PDCD2,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,TFRC,PPARD,RAP2C,YBX3,HNRNPF,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,RBM14,RBM17,RAD23A,NOLC1,CDC20,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,DELE1,CCNB3,MIS18A,HMGN1,CCT4,SIX4,MTBP,NECAB3,SF3A1,MED16,ENSCAFG00000017103,AMER1,DCUN1D5	down_ACOR_VSMC
GO:1901700	0.407	0.675	24	364	response to oxygen-containing compound	BP	1	ARHGEF2,NR1H4,PLK3,SERPINE1,ENPP1,PTPN11,TRIB3,SMARCA4,SESN2,MYO1C,MSN,HIF1A,PTPN2,YES1,MTDH,ADAM17,AGRN,GNAQ,CTNNB1,CRYAB,KPNA4,LYN,NR4A1,HOMER1	down_VSAP_EC
GO:0048514	0.407	0.68	22	214	blood vessel morphogenesis	BP	1	VEGFD,LEP,ANGPT1,BMP4,FGFR2,GJA1,TLR3,SEC24B,CITED2,SASH1,FGF18,EGLN1,NRP1,TBX20,SYNJ2BP,CHD7,JUP,EDN1,HPGD,JAM3,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0046649	0.407	0.696	15	162	lymphocyte activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,TXLNA,MMP14,HMGB3,ARG2,TFRC,FAM49B,TOX,CORO1A,ELF4,JMJD6,CTPS1	down_ACOR_VSMC
GO:0006935	0.407	0.696	15	143	chemotaxis	BP	1	VEGFD,SEMA5A,FEZ1,HRH1,FGF18,F2RL1,NRP1,UNC5B,FZD3,DAG1,APP,CCL5,JAM3,FEZ2,ENSCAFG00000029553	up_ACOR_VSMC
GO:0042330	0.407	0.696	15	143	taxis	BP	1	VEGFD,SEMA5A,FEZ1,HRH1,FGF18,F2RL1,NRP1,UNC5B,FZD3,DAG1,APP,CCL5,JAM3,FEZ2,ENSCAFG00000029553	up_ACOR_VSMC
GO:0006869	0.407	0.724	9	81	lipid transport	BP	1	LEP,LCAT,ABCA1,APOL6,ABCA4,SCP2,OSBPL1A,PLIN2,CFI	up_ACOR_VSMC
GO:0050867	0.407	0.724	9	83	positive regulation of cell activation	BP	1	LEP,CD83,TP53BP1,CD274,F2RL1,CDKN1A,PTPN22,APP,NOD2	up_ACOR_VSMC
GO:0003205	0.407	0.762	5	67	cardiac chamber development	BP	1	LTBP1,FHL2,HIF1A,ADAMTS6,NRP1	down_VSAP_EC
GO:0002449	0.407	0.78	4	53	lymphocyte mediated immunity	BP	1	FAM49B,PVR,TFRC,BTK	down_VSAP_EC
GO:0010468	0.407	0.793	4	1270	regulation of gene expression	BP	1	BARX1,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0006383	0.407	0.806	3	28	transcription by RNA polymerase III	BP	1	NAB2,POLR3F,POLR1C	down_ACOR_VSMC

GO:0002065	0.407	0.804	3	37	columnar/cuboidal epithelial cell	BP	1	SERPINE1,HIF1A,KLF5	down_VSAP_EC
GO:0030330	0.407	0.808	3	25	DNA damage response, signal transduction by p53 class mediator	BP	1	ATRX,ANKRD1,CDKN1A	up_ACOR_VSMC
GO:0001934	0.407	0.84	2	274	positive regulation of protein phosphorylation	BP	1	ACVRL1,LYN	down_ACOR_EC
GO:0045621	0.407	0.841	2	28	positive regulation of lymphocyte	BP	1	GLI3,ZBTB16	down_VCAV_EC
GO:0010799	0.407	0.847	2	14	regulation of peptidyl-threonine	BP	1	APP,INPP5K	up_ACOR_VSMC
GO:0043954	0.407	0.847	2	14	cellular component maintenance	BP	1	LNPK,F2RL1	up_ACOR_VSMC
GO:0031401	0.407	0.841	2	358	positive regulation of protein modification	BP	1	NPNT,NTRK2	up_APUL_EC
GO:0006687	0.407	0.844	2	18	glycosphingolipid metabolic process	BP	1	KIT,CREM	up_VCAV_EC
GO:0007064	0.407	0.847	2	15	mitotic sister chromatid cohesion	BP	1	SMC5,ATRX	up_VCAV_EC
GO:0032945	0.407	0.845	2	17	negative regulation of mononuclear cell	BP	1	PELI1,ARG2	up_VCAV_EC
GO:0050672	0.407	0.845	2	17	negative regulation of lymphocyte proliferation	BP	1	PELI1,ARG2	up_VCAV_EC
GO:0045892	0.407	0.84	2	328	negative regulation of transcription, DNA-	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0015695	0.407	0.917	1	6	organic cation transport	BP	1	SLC25A19	down_ACOR_VSMC
GO:0070262	0.407	0.917	1	6	peptidyl-serine dephosphorylation	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0043370	0.407	0.911	1	10	regulation of CD4-positive, alpha-beta T cell	BP	1	LOXL3	down_VCAV_EC
GO:0048678	0.407	0.911	1	10	response to axon injury	BP	1	RGMA	down_VCAV_EC
GO:0060338	0.407	0.912	1	10	regulation of type I interferon-mediated	BP	1	MAVS	down_VCAV_EC
GO:0009988	0.407	0.913	1	8	cell-cell recognition	BP	1	MSN	down_VSAP_EC
GO:1900117	0.407	0.913	1	8	regulation of execution phase of apoptosis	BP	1	PAK2	down_VSAP_EC
GO:0060479	0.407	0.913	1	8	lung cell differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0006591	0.407	0.92	1	5	ornithine metabolic process	BP	1	AZIN2	up_ACOR_VSMC
GO:0007618	0.407	0.92	1	5	mating	BP	1	APP	up_ACOR_VSMC
GO:0048268	0.407	0.92	1	5	clathrin coat assembly	BP	1	SNAP91	up_ACOR_VSMC
GO:0090085	0.407	0.92	1	5	regulation of protein deubiquitination	BP	1	PARK7	up_ACOR_VSMC
GO:0010564	0.407	0.908	1	217	regulation of cell cycle process	BP	1	TAOK1	up_AORT_EC
GO:0002790	0.407	0.906	1	133	peptide secretion	BP	1	NR1H4	up_APUL_EC
GO:0006829	0.407	0.915	1	7	zinc ion transport	BP	1	SLC39A8	up_VCAV_EC
GO:0030497	0.407	0.913	1	8	fatty acid elongation	BP	1	ELOVL7	up_VCAV_EC
GO:0071577	0.407	0.915	1	7	zinc ion transmembrane transport	BP	1	SLC39A8	up_VCAV_EC
GO:0086002	0.407	0.915	1	7	cardiac muscle cell action potential involved in	BP	1	KCNJ2	up_VCAV_EC
GO:0010038	0.407	0.906	1	62	response to metal ion	BP	1	FBP1	up_VPOR_EC
GO:0044403	0.407	0.906	1	116	symbiont process	BP	1	CAV1	up_VSAP_VSMC
GO:0022604	0.407	0.906	1	122	regulation of cell morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0006575	0.407296918	0.83827	2	53	cellular modified amino acid metabolic process	BP	1	SARDH,ENSCAFG00000028814	up_ACOR_EC
GO:1902893	0.407500481	0.90736	1	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6	up_ACOR_EC
GO:0043068	0.408	0.685	19	190	positive regulation of programmed cell death	BP	1	RASSF2,NACC2,ITM2C,BMP4,LATS2,TP53INP1,CD274,ANKRD1,DAPK1,BNIP3,CDKN1A,JMY,DKKL1,PSEN1,SPINK2,SIAH1,SERINC3,KLF11,PARK7	up_ACOR_VSMC
GO:0000377	0.408	0.728	8	119	RNA splicing, via transesterification reactions with bulged	BP	1	CELF1,SNRPB2,PRPF3,DDX39B,STRAP,REST,ENSCAFG00000015065,SNRPA1	down_VSAP_EC

GO:0000398	0.408	0.728	8	119	mRNA splicing, via spliceosome	BP	1	CELF1,SNRPB2,PRPF3,DDX39B,STRAP,REST,ENSCAFG00000015065,SNRPA1	down_VSAP_EC
GO:0042113	0.408	0.739	7	64	B cell activation	BP	1	TBC1D10C,ABL1,DLL1,STAT6,ZFP36L1,PIK3R1,ZFP36L2	up_VSAP_EC
GO:0046486	0.408	0.747	6	102	glycerolipid metabolic process	BP	1	GPAM,PDGFRB,ENSCAFG00000014978,LCAT,PIGS,NAPEPLD	down_VCAV_EC
GO:0055080	0.408	0.759	5	176	cation homeostasis	BP	1	RAB20,CNNM4,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0051053	0.408	0.764	5	45	negative regulation of DNA metabolic process	BP	1	GATA3,THOC1,BLM,RAD17,DCP2	up_VCAV_EC
GO:0071229	0.408	0.779	4	51	cellular response to acid chemical	BP	1	NR1H4,SESN2,YES1,LYN	down_VSAP_EC
GO:0045667	0.408	0.781	4	38	regulation of osteoblast differentiation	BP	1	MEF2C,BMP2,JAG1,FBXO5	up_VCAV_EC
GO:0050868	0.408	0.806	3	28	negative regulation of T cell activation	BP	1	PELI1,ARG2,HMGB1	up_VCAV_EC
GO:0048878	0.408	0.802	3	283	chemical homeostasis	BP	1	C3AR1,HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0051702	0.408	0.807	3	24	interaction with symbiont	BP	1	NAPEPLD,F2RL1,PC	up_VSAP_EC
GO:0032728	0.408	0.845	2	16	positive regulation of interferon-beta	BP	1	HMGB2,POLR3F	down_ACOR_VSMC
GO:0032784	0.408	0.842	2	21	regulation of DNA-templated transcription,	BP	1	IWS1,DDX39B	down_VSAP_EC
GO:0046888	0.408	0.847	2	14	negative regulation of hormone secretion	BP	1	LEP,PFKL	up_ACOR_VSMC
GO:0060997	0.408	0.847	2	14	dendritic spine morphogenesis	BP	1	ZNF365,WASL	up_ACOR_VSMC
GO:0019827	0.408	0.838	2	59	stem cell population maintenance	BP	1	LBH,DLL1	up_AFEM_EC
GO:0045910	0.408	0.847	2	14	negative regulation of DNA recombination	BP	1	THOC1,BLM	up_VCAV_EC
GO:0008284	0.408	0.908	1	238	positive regulation of cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0046903	0.408	0.909	1	255	secretion	BP	1	RAB11B	down_VPOR_EC
GO:2000112	0.408	0.931	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0048490	0.408	0.912	1	9	anterograde synaptic vesicle transport	BP	1	AP3S1	down_VSAP_EC
GO:0099514	0.408	0.912	1	9	synaptic vesicle cytoskeletal transport	BP	1	AP3S1	down_VSAP_EC
GO:0099517	0.408	0.912	1	9	synaptic vesicle transport along microtubule	BP	1	AP3S1	down_VSAP_EC
GO:1902043	0.408	0.912	1	9	positive regulation of extrinsic apoptotic signaling pathway via	BP	1	ATF3	down_VSAP_EC
GO:0007141	0.408	0.919	1	5	male meiosis I	BP	1	DMC1	up_ACOR_VSMC
GO:1905606	0.408	0.919	1	5	regulation of presynapse assembly	BP	1	APP	up_ACOR_VSMC
GO:0007189	0.408	0.906	1	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	PTHLH	up_AFEM_EC
GO:0014068	0.408	0.906	1	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	LEP	up_AFEM_EC
GO:0019400	0.408	0.914	1	7	alditol metabolic process	BP	1	GK5	up_VCAV_EC
GO:0039529	0.408	0.916	1	6	RIG-I signaling pathway	BP	1	LSM14A	up_VCAV_EC
GO:1901028	0.408	0.914	1	7	regulation of mitochondrial outer membrane permeabilization involved	BP	1	SH3GLB1	up_VCAV_EC
GO:1903055	0.408	0.916	1	6	positive regulation of extracellular matrix	BP	1	FSCN1	up_VCAV_EC
GO:0016050	0.408	0.906	1	119	vesicle organization	BP	1	CAV1	up_VSAP_VSMC
GO:0002027	0.4083015	0.90674	1	20	regulation of heart rate	BP	1	RNLS	up_ACOR_EC
GO:0050900	0.408417457	0.79994	3	89	leukocyte migration	BP	1	MMP28,PTGER4,RARRES2	up_ACOR_EC
GO:0120036	0.408544495	0.70916	11	373	plasma membrane bounded cell projection	BP	1	BRSK1,RGMA,PLS1,ACTN2,PAK3,MAPK8IP2,LRP4,NRP1,ARHGEF26,PRKCD,DBNDD2	up_ACOR_EC
GO:0010975	0.409	0.716	10	103	regulation of neuron projection development	BP	1	IFRD1,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,NCK1,FES,RAPGEF2	up_VCAV_EC
GO:0055114	0.409	0.72	9	157	oxidation-reduction process	BP	1	AKT2,ACAA1,UQCR10,PEX5,PARK7,LOXL3,MTFR1L,LONP2,ACAT1	down_VCAV_EC

GO:0006913	0.409	0.736	7	124	nucleocytoplasmic transport	BP	1	ENSCAFG00000014978,SNUPN,GLI3,PARK7, MAVS,SEC61B,ANKRD54	down_VCAV_EC
GO:0051169	0.409	0.736	7	124	nuclear transport	BP	1	ENSCAFG00000014978,SNUPN,GLI3,PARK7, MAVS,SEC61B,ANKRD54	down_VCAV_EC
GO:0001101	0.409	0.739	7	65	response to acid chemical	BP	1	PTGFR,OSR1,PDGFD,RARG,ZEB1,CASTOR1,HT RA2	up_VSAP_EC
GO:0007548	0.409	0.76	5	68	sex differentiation	BP	1	PTPN11,CTNNB1,INHBA,SIX4,SPINK2	down_VSAP_EC
GO:0045165	0.409	0.777	4	65	cell fate commitment	BP	1	BMPR1A,LMO4,GLI3,LOXL3	down_VCAV_EC
GO:0007229	0.409	0.782	4	32	integrin-mediated signaling pathway	BP	1	FERMT1,LIMS2,NRP1,FUT8	up_ACOR_VSMC
GO:0043038	0.409	0.781	4	34	amino acid activation	BP	1	WARS2,FARS2,QARS,LARS2	up_VSAP_EC
GO:0031333	0.409	0.802	3	46	negative regulation of protein complex assembly	BP	1	LMO4,CLIP3,CLSTN1	down_VCAV_EC
GO:0001658	0.409	0.806	3	24	branching involved in ureteric bud	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0022404	0.409	0.805	3	28	molting cycle process	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:0022405	0.409	0.805	3	28	hair cycle process	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:0001942	0.409	0.805	3	28	hair follicle development	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:0002009	0.409	0.837	2	177	morphogenesis of an epithelium	BP	1	PTK7,SEMA3A	up_VPOR_EC
GO:1902679	0.409	0.839	2	329	negative regulation of RNA biosynthetic process	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:1903507	0.409	0.839	2	329	negative regulation of nucleic acid-templated	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0097193	0.409	0.905	1	109	intrinsic apoptotic signaling pathway	BP	1	USP28	down_ACOR_EC
GO:0006999	0.409	0.916	1	6	nuclear pore organization	BP	1	NDC1	down_ACOR_VSMC
GO:0008210	0.409	0.916	1	6	estrogen metabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0030903	0.409	0.916	1	6	notochord development	BP	1	GLI1	down_ACOR_VSMC
GO:0030029	0.409	0.908	1	239	actin filament-based process	BP	1	FSCN1	down_AFEM_EC
GO:0006195	0.409	0.91	1	10	purine nucleotide catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0015936	0.409	0.91	1	10	coenzyme A metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0032607	0.409	0.91	1	11	interferon-alpha production	BP	1	MAVS	down_VCAV_EC
GO:0032941	0.409	0.91	1	10	secretion by tissue	BP	1	CYBA	down_VCAV_EC
GO:0034381	0.409	0.911	1	10	plasma lipoprotein particle clearance	BP	1	LRPAP1	down_VCAV_EC
GO:0071604	0.409	0.91	1	10	transforming growth factor beta production	BP	1	LUM	down_VCAV_EC
GO:0071634	0.409	0.91	1	10	regulation of transforming growth factor beta	BP	1	LUM	down_VCAV_EC
GO:0002830	0.409	0.919	1	5	positive regulation of type 2 immune response	BP	1	NOD2	up_ACOR_VSMC
GO:0030517	0.409	0.919	1	5	negative regulation of axon extension	BP	1	NRP1	up_ACOR_VSMC
GO:0032760	0.409	0.906	1	22	positive regulation of tumor necrosis factor	BP	1	LEP	up_AFEM_EC
GO:0060419	0.409	0.906	1	22	heart growth	BP	1	ACACB	up_AFEM_EC
GO:1903557	0.409	0.906	1	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	LEP	up_AFEM_EC
GO:0071243	0.409	0.914	1	7	cellular response to arsenic-containing	BP	1	MAPK13	up_VCAV_EC
GO:0002521	0.409	0.906	1	149	leukocyte differentiation	BP	1	EVI2B	up_VPUL_EC
GO:0019438	0.409262139	0.66311	35	1258	aromatic compound biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX 9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RAS L11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND 8,GUCY1B1,PIAS1,MAVS,FOXC2,LRP4,CLSTN1 ,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2, GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0007031	0.409334199	0.90622	1	20	peroxisome organization	BP	1	MAVS	up_ACOR_EC
GO:0007431	0.409676477	0.90627	1	19	salivary gland development	BP	1	NRP1	up_ACOR_EC

GO:0048483	0.409973494	0.90612	1	19	autonomic nervous system development	BP	1	NRP1	up_ACOR_EC
GO:0008219	0.41	0.644	60	611	cell death	BP	1	RHOT1,SMAD6,PLCG2,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,TM7SF3,TLR3,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,USP53,ITPR1,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,EGLN1,CDKN1A,JMY,NRP1,LRPAP1,DMPK,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,APP,PSEN1,SPINK2,CCL5,CLN8,PERP,SIAH1,OXR1,NOD2,DDIT4,SERINC3,TNFRSF11B,KLF11,HERPUD1,MAP3K7,WFS1,NAIF1,PARK7,ZMAT3	up_ACOR_VSMC
GO:0043254	0.41	0.693	15	164	regulation of protein complex assembly	BP	1	FSCN1,HMGB1,STXBP6,CAPG,INSIG1,STMN1,DHX33,PREB,RAC1,FOSL1,IQGAP2,CDC42EP4,CORO1A,ARPC1B,PSMC1	down_ACOR_VSMC
GO:0043207	0.41	0.703	12	216	response to external biotic stimulus	BP	1	GPAM,CFD,ENSCAFG00000013404,WIPF1,FKBP5,RNF216,SASH1,BPI,CYBA,MAVS,GSDME,SHC1	down_VCAV_EC
GO:0051707	0.41	0.703	12	216	response to other organism	BP	1	GPAM,CFD,ENSCAFG00000013404,WIPF1,FKBP5,RNF216,SASH1,BPI,CYBA,MAVS,GSDME,SHC1	down_VCAV_EC
GO:0050778	0.41	0.726	8	141	positive regulation of immune response	BP	1	CFD,PRNP,THY1,PARK7,CYBA,MAVS,RAB7B,A2M	down_VCAV_EC
GO:0007005	0.41	0.758	5	175	mitochondrion organization	BP	1	MLLT11,CAMK2A,CLEC16A,CHCHD10,PPARGC1A	up_AFEM_EC
GO:0007286	0.41	0.78	4	34	spermatid development	BP	1	AFF4,SPINK2,DMC1,JAM3	up_ACOR_VSMC
GO:0032635	0.41	0.802	3	37	interleukin-6 production	BP	1	ARHGEF2,NR1H4,SOCS5	down_VSAP_EC
GO:0031325	0.41	0.81	3	914	positive regulation of cellular metabolic process	BP	1	NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0034314	0.41	0.844	2	16	Arp2/3 complex-mediated actin nucleation	BP	1	IQGAP2,ARPC1B	down_ACOR_VSMC
GO:0043488	0.41	0.839	2	28	regulation of mRNA stability	BP	1	SAMD4B,ZFP36L1	down_VCAV_EC
GO:0060998	0.41	0.846	2	14	regulation of dendritic spine development	BP	1	PSEN1,ASAP1	up_ACOR_VSMC
GO:0098661	0.41	0.845	2	14	inorganic anion transmembrane transport	BP	1	SLC26A7,CLCN3	up_ACOR_VSMC
GO:0030833	0.41	0.836	2	59	regulation of actin filament polymerization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0060632	0.41	0.916	1	6	regulation of microtubule-based movement	BP	1	CFAP298	down_ACOR_VSMC
GO:0003352	0.41	0.916	1	6	regulation of cilium movement	BP	1	CFAP298	down_ACOR_VSMC
GO:0007595	0.41	0.916	1	6	lactation	BP	1	CAV1	down_ACOR_VSMC
GO:0009081	0.41	0.916	1	6	branched-chain amino acid metabolic process	BP	1	BCAT1	down_ACOR_VSMC
GO:0006576	0.41	0.91	1	10	cellular biogenic amine metabolic process	BP	1	NAPEPLD	down_VCAV_EC
GO:1903541	0.41	0.91	1	10	regulation of exosomal secretion	BP	1	SDC4	down_VCAV_EC
GO:1903543	0.41	0.91	1	10	positive regulation of exosomal secretion	BP	1	SDC4	down_VCAV_EC
GO:0048534	0.41	0.908	1	262	hematopoietic or lymphoid organ	BP	1	CITED2	down_VPOR_EC
GO:0033081	0.41	0.912	1	8	regulation of T cell differentiation in thymus	BP	1	PTPN2	down_VSAP_EC
GO:0060716	0.41	0.911	1	9	labyrinthine layer blood vessel development	BP	1	TMED2	down_VSAP_EC
GO:0019369	0.41	0.919	1	5	arachidonic acid metabolic process	BP	1	CYP2J2	up_ACOR_VSMC
GO:0009880	0.41	0.905	1	22	embryonic pattern specification	BP	1	DLL1	up_AFEM_EC
GO:0072359	0.41	0.91	1	368	circulatory system development	BP	1	EYA1	up_AFEM_VSMC
GO:0050865	0.41	0.905	1	135	regulation of cell activation	BP	1	BPI	up_APUL_EC
GO:0051090	0.41	0.905	1	134	regulation of DNA-binding transcription factor	BP	1	NR1H4	up_APUL_EC
GO:0051573	0.41	0.918	1	5	negative regulation of histone H3-K9	BP	1	KDM3A	up_VCAV_EC
GO:0016051	0.41	0.904	1	63	carbohydrate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:1902903	0.41	0.905	1	125	regulation of supramolecular fiber	BP	1	CDC42EP5	up_VFEM_EC
GO:0044419	0.41	0.905	1	117	interspecies interaction between organisms	BP	1	CAV1	up_VSAP_VSMC

GO:0051301	0.41	0.905	1	117	cell division	BP	1	FGF5	up_VSAP_VSMC
GO:0042100	0.410225957	0.90599	1	19	B cell proliferation	BP	1	PRKCD	up_ACOR_EC
GO:0035567	0.410229447	0.90599	1	19	non-canonical Wnt signaling pathway	BP	1	FZD5	up_ACOR_EC
GO:2000379	0.410568194	0.9056	1	20	positive regulation of reactive oxygen species	BP	1	PRKCD	up_ACOR_EC
GO:0042127	0.410618255	0.69887	13	452	regulation of cell proliferation	BP	1	CDH3,SOX9,PTH1R,NDRG2,AQP1,FZD5,PTGIR,SMAD6,ESM1,PIAS1,TBX5,CLSTN1,PYGO2	up_ACOR_EC
GO:0009611	0.410788202	0.77397	4	122	response to wounding	BP	1	AQP1,RGMA,FOXC2,PRKCD	up_ACOR_EC
GO:0019953	0.411	0.69	16	152	sexual reproduction	BP	1	LEP,PRDX4,BMP4,ATRX,PDE5A,GLRB,MARF1,AFF4,DKKL1,APP,SPINK2,HPGD,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0017038	0.411	0.72	9	96	protein import	BP	1	TIMM44,POLA2,RAN,ENSCAFG00000011598,IPO4,NUP62,NUP188,SAMM50,DMAP1	down_ACOR_VSMC
GO:0033674	0.411	0.725	8	144	positive regulation of kinase activity	BP	1	PDGFRB,PRNP,LMO4,CSPG4,SASH1,MAPRE3,DDR2,SHC1	down_VCAV_EC
GO:0006869	0.411	0.727	8	81	lipid transport	BP	1	OSBPL9,ATP8A1,PDZD8,ABCA1,OSBPL6,SLCO3A1,APOD,NOS2	up_VCAV_EC
GO:0051250	0.411	0.779	4	38	negative regulation of lymphocyte activation	BP	1	HMGB1,MNDA,HMGB3,ARG2	down_ACOR_VSMC
GO:0023052	0.411	0.795	4	1602	signaling	BP	1	TBX5,GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0007204	0.411	0.8	3	46	positive regulation of cytosolic calcium ion	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0031110	0.411	0.805	3	24	regulation of microtubule polymerization or depolymerization	BP	1	FGF13,MID1,TUBB4A	up_ACOR_VSMC
GO:0001954	0.411	0.842	2	17	positive regulation of cell-matrix adhesion	BP	1	RAC1,EMP2	down_ACOR_VSMC
GO:0050794	0.411	0.914	2	3075	regulation of cellular process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:1901700	0.411	0.839	2	364	response to oxygen-containing compound	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0035563	0.411	0.915	1	6	positive regulation of chromatin binding	BP	1	GMNN	down_ACOR_VSMC
GO:0051491	0.411	0.915	1	6	positive regulation of filopodium assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0050771	0.411	0.908	1	11	negative regulation of axonogenesis	BP	1	THY1	down_VCAV_EC
GO:0090190	0.411	0.91	1	10	positive regulation of branching involved in ureteric bud	BP	1	GREM1	down_VCAV_EC
GO:0002931	0.411	0.91	1	9	response to ischemia	BP	1	HYOU1	down_VSAP_EC
GO:0021544	0.411	0.911	1	8	subpallium development	BP	1	INHBA	down_VSAP_EC
GO:0014044	0.411	0.912	1	8	Schwann cell development	BP	1	ILK	down_VSAP_EC
GO:0014829	0.411	0.912	1	8	vascular smooth muscle contraction	BP	1	ACTA2	down_VSAP_EC
GO:0022011	0.411	0.912	1	8	myelination in peripheral nervous system	BP	1	ILK	down_VSAP_EC
GO:0032292	0.411	0.912	1	8	peripheral nervous system axon	BP	1	ILK	down_VSAP_EC
GO:1904467	0.411	0.912	1	8	regulation of tumor necrosis factor secretion	BP	1	NR1H4	down_VSAP_EC
GO:2000352	0.411	0.911	1	8	negative regulation of endothelial cell apoptotic	BP	1	SERPINE1	down_VSAP_EC
GO:0006366	0.411	0.915	1	583	transcription by RNA polymerase II	BP	1	GATA5	down_VSAP_VSMC
GO:0032230	0.411	0.918	1	5	positive regulation of synaptic transmission,	BP	1	PRKCE	up_ACOR_VSMC
GO:0060788	0.411	0.918	1	5	ectodermal placode formation	BP	1	FRS2	up_ACOR_VSMC
GO:0071697	0.411	0.918	1	5	ectodermal placode morphogenesis	BP	1	FRS2	up_ACOR_VSMC
GO:0032677	0.411	0.905	1	22	regulation of interleukin-8 production	BP	1	BPI	up_AFEM_EC
GO:0033627	0.411	0.905	1	22	cell adhesion mediated by integrin	BP	1	ADAM17	up_AFEM_EC
GO:0045582	0.411	0.905	1	22	positive regulation of T cell differentiation	BP	1	CYLD	up_AFEM_EC
GO:0051341	0.411	0.905	1	22	regulation of oxidoreductase activity	BP	1	LEP	up_AFEM_EC
GO:0043269	0.411	0.904	1	135	regulation of ion transport	BP	1	HOXA3	up_APUL_EC

GO:1900112	0.411	0.918	1	5	regulation of histone H3-K9 trimethylation	BP	1	ATRX	up_VCAV_EC
GO:0006089	0.411	0.913	1	7	lactate metabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0001990	0.411	0.915	1	6	regulation of systemic arterial blood pressure by	BP	1	EDN1	up_VCAV_EC
GO:0034643	0.411	0.918	1	5	establishment of mitochondrion localization, microtubule-	BP	1	HIF1A	up_VCAV_EC
GO:0043950	0.411	0.915	1	6	positive regulation of cAMP-mediated signaling	BP	1	RAPGEF2	up_VCAV_EC
GO:0047497	0.411	0.918	1	5	mitochondrion transport along microtubule	BP	1	HIF1A	up_VCAV_EC
GO:2000345	0.411	0.918	1	5	regulation of hepatocyte proliferation	BP	1	TNFAIP3	up_VCAV_EC
GO:0045165	0.411	0.904	1	65	cell fate commitment	BP	1	ARHGEF2	up_VPOR_EC
GO:0051345	0.411	0.905	1	151	positive regulation of hydrolase activity	BP	1	CCL24	up_VPUL_EC
GO:0050678	0.411	0.904	1	117	regulation of epithelial cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0002449	0.411629028	0.83529	2	53	lymphocyte mediated immunity	BP	1	FZD5,PRKCD	up_ACOR_EC
GO:0009605	0.412	0.658	34	538	response to external stimulus	BP	1	VEGFA,ASNS,NR1H4,HSPA5,SERPINE1,SOCS5,COTL1,BHLHE40,SESN2,PTGS2,KIF5B,PTPN2,NEO1,MTDH,ADAM17,ACTA2,CNOT7,GNAQ,APOE,MMP28,LYN,BNIP3,DDIT3,ATF3,GBP5,HTT,EIF2S1,RDH11,EXT1,A2M,CDKN1A,NRP1,USP14,DEFB124	down_VSAP_EC
GO:0046649	0.412	0.686	17	162	lymphocyte activation	BP	1	PLCG2,LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,F2RL1,CDKN1A,PTPN22,PSEN1,CHD7,DUSP22,NOD2,B2M,IL18R1,PAG1	up_ACOR_VSMC
GO:0032870	0.412	0.718	9	162	cellular response to hormone stimulus	BP	1	ADCY6,KANK2,ENSCAFG00000014978,AKT2,NR3C1,PARK7,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0009615	0.412	0.72	9	83	response to virus	BP	1	MAP3K14,F2RL1,MYD88,NLRX1,TKFC,RNF216,PQBP1,MAVS,DDIT4	up_VSAP_EC
GO:0098727	0.412	0.746	6	60	maintenance of cell number	BP	1	SMC1A,MED17,SRRT,EZH2,SMC3,ASPM	down_ACOR_VSMC
GO:0002250	0.412	0.758	5	68	adaptive immune response	BP	1	SOCS5,FAM49B,PVR,TFRC,BTK	down_VSAP_EC
GO:0032879	0.412	0.78	4	767	regulation of localization	BP	1	TRIM9,HOXA7,SIX1,TIAM1	up_VFEM_EC
GO:0046483	0.412	0.831	3	1948	heterocycle metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0042509	0.412	0.842	2	17	regulation of tyrosine phosphorylation of STAT	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0010463	0.412	0.837	2	28	mesenchymal cell proliferation	BP	1	BMPR1A,CLSTN1	down_VCAV_EC
GO:0030001	0.412	0.835	2	172	metal ion transport	BP	1	HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0007018	0.412	0.904	1	82	microtubule-based movement	BP	1	SPG11	down_ACOR_EC
GO:0050769	0.412	0.904	1	95	positive regulation of neurogenesis	BP	1	LYN	down_ACOR_EC
GO:0009109	0.412	0.915	1	6	coenzyme catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0048484	0.412	0.914	1	6	enteric nervous system development	BP	1	PHACTR4	down_ACOR_VSMC
GO:0060379	0.412	0.915	1	6	cardiac muscle cell myoblast differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0043069	0.412	0.907	1	262	negative regulation of programmed cell death	BP	1	CITED2	down_VPOR_EC
GO:0001945	0.412	0.91	1	9	lymph vessel development	BP	1	PTPN14	down_VSAP_EC
GO:0001946	0.412	0.91	1	9	lymphangiogenesis	BP	1	PTPN14	down_VSAP_EC
GO:0036303	0.412	0.91	1	9	lymph vessel morphogenesis	BP	1	PTPN14	down_VSAP_EC
GO:0048246	0.412	0.91	1	9	macrophage chemotaxis	BP	1	MMP28	down_VSAP_EC
GO:0055091	0.412	0.918	1	5	phospholipid homeostasis	BP	1	ABCA1	up_ACOR_VSMC
GO:0003143	0.412	0.905	1	22	embryonic heart tube morphogenesis	BP	1	DLL1	up_AFEM_EC
GO:1903510	0.412	0.905	1	22	mucopolysaccharide metabolic process	BP	1	XYLT1	up_AFEM_EC
GO:0061024	0.412	0.906	1	215	membrane organization	BP	1	SGCD	up_AORT_EC
GO:0044093	0.412	0.911	1	437	positive regulation of molecular function	BP	1	ESR1	up_AORT_VSMC

GO:0007020	0.412	0.915	1	6	microtubule nucleation	BP	1	MZT1	up_VCAV_EC
GO:0046827	0.412	0.915	1	6	positive regulation of protein export from	BP	1	CTDSPL2	up_VCAV_EC
GO:0048012	0.412	0.912	1	7	hepatocyte growth factor receptor signaling	BP	1	STMN1	up_VCAV_EC
GO:0003181	0.412	0.913	1	7	atrioventricular valve morphogenesis	BP	1	BMP2	up_VCAV_EC
GO:0060065	0.412	0.913	1	7	uterus development	BP	1	GATA3	up_VCAV_EC
GO:1905809	0.412	0.913	1	7	negative regulation of synapse organization	BP	1	ARHGEF15	up_VCAV_EC
GO:1901700	0.412	0.909	1	364	response to oxygen-containing compound	BP	1	CA2	up_VCAV_VSMC
GO:0001819	0.412	0.904	1	120	positive regulation of cytokine production	BP	1	TLR2	up_VSAP_VSMC
GO:0051091	0.412478452	0.7969	3	87	positive regulation of DNA-binding transcription factor activity	BP	1	NOD2,MAVS,CLU	up_ACOR_EC
GO:2000112	0.413	0.717	10	1119	regulation of cellular macromolecule biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:0030879	0.413	0.778	4	34	mammary gland development	BP	1	HOXA9,STAT6,TGFBR2,LBH	up_VSAP_EC
GO:2000177	0.413	0.803	3	26	regulation of neural precursor cell	BP	1	NF2,ASPM,GLI1	down_ACOR_VSMC
GO:0008217	0.413	0.799	3	38	regulation of blood pressure	BP	1	PRCP,PTGS2,ACTA2	down_VSAP_EC
GO:0046634	0.413	0.804	3	24	regulation of alpha-beta T cell activation	BP	1	CD83,CD274,PTPN22	up_ACOR_VSMC
GO:0042327	0.413	0.798	3	289	positive regulation of phosphorylation	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0009566	0.413	0.803	3	24	fertilization	BP	1	HOXA11,HOXA9,CFAP69	up_VSAP_EC
GO:0035329	0.413	0.842	2	16	hippo signaling	BP	1	NF2,AMOTL1	down_ACOR_VSMC
GO:0030901	0.413	0.844	2	14	midbrain development	BP	1	FGFR2,FZD3	up_ACOR_VSMC
GO:0035773	0.413	0.843	2	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	PRKCE,RAB11B	up_ACOR_VSMC
GO:0006471	0.413	0.841	2	17	protein ADP-ribosylation	BP	1	TIPARP,PARP4	up_VCAV_EC
GO:0022607	0.413	0.849	2	969	cellular component assembly	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0006952	0.413	0.836	2	319	defense response	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0006882	0.413	0.914	1	6	cellular zinc ion homeostasis	BP	1	SLC30A1	down_ACOR_VSMC
GO:0001539	0.413	0.914	1	6	cilium or flagellum-dependent cell motility	BP	1	TTLL1	down_ACOR_VSMC
GO:0043276	0.413	0.914	1	6	anoikis	BP	1	CAV1	down_ACOR_VSMC
GO:0045981	0.413	0.914	1	6	positive regulation of nucleotide metabolic	BP	1	CDK1	down_ACOR_VSMC
GO:0055069	0.413	0.914	1	6	zinc ion homeostasis	BP	1	SLC30A1	down_ACOR_VSMC
GO:0060285	0.413	0.914	1	6	cilium-dependent cell motility	BP	1	TTLL1	down_ACOR_VSMC
GO:1900544	0.413	0.914	1	6	positive regulation of purine nucleotide	BP	1	CDK1	down_ACOR_VSMC
GO:0010907	0.413	0.908	1	10	positive regulation of glucose metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0030334	0.413	0.906	1	267	regulation of cell migration	BP	1	HDAC7	down_VPOR_EC
GO:1901701	0.413	0.906	1	271	cellular response to oxygen-containing	BP	1	RAB11B	down_VPOR_EC
GO:0010556	0.413	0.929	1	1137	regulation of macromolecule	BP	1	MOSPD1	down_VFEM_EC
GO:0014912	0.413	0.911	1	8	negative regulation of smooth muscle cell	BP	1	SERPINE1	down_VSAP_EC
GO:0033158	0.413	0.911	1	8	regulation of protein import into nucleus,	BP	1	CDKN1A	down_VSAP_EC
GO:0032642	0.413	0.904	1	22	regulation of chemokine production	BP	1	ADAM17	up_AFEM_EC
GO:0033866	0.413	0.904	1	22	nucleoside bisphosphate biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0034030	0.413	0.904	1	22	ribonucleoside bisphosphate biosynthetic	BP	1	ACACB	up_AFEM_EC

GO:0034033	0.413	0.904	1	22	purine nucleoside bisphosphate biosynthetic	BP	1	ACACB	up_AFEM_EC
GO:1903578	0.413	0.904	1	22	regulation of ATP metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0016477	0.413	0.911	1	426	cell migration	BP	1	WNT7A	up_AORT_VSMC
GO:0048667	0.413	0.904	1	140	cell morphogenesis involved in neuron	BP	1	SLITRK5	up_APUL_EC
GO:0051127	0.413	0.917	1	5	positive regulation of actin nucleation	BP	1	NCKAP1	up_VCAV_EC
GO:0070486	0.413	0.914	1	6	leukocyte aggregation	BP	1	STK10	up_VCAV_EC
GO:0009416	0.413833038	0.79583	3	88	response to light stimulus	BP	1	BRSK1,AQP1,MFAP4	up_ACOR_EC
GO:0048518	0.414	0.623	164	1676	positive regulation of biological process	BP	1	SYNPO2L,EXPH5,ADRA1B,VEGFD,TLR1,SMAD6,ACTN2,LGR6,PLCG2,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CD83,CDC7,PCGF5,HTR2B,RASSF2,TCAF1,FNDC5,MBP,ZRANB1,C28H10orf71,LIPT2,SKP2,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,LNPK,SYNPO2,TM7SF3,FGFR2,TP53BP1,ABCA1,GJA1,ELF1,ATRX,MED14,HRH1,TLR3,SH3RF2,WASF3,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,PKP4,ISG15,CD274,ZNF365,MARCKSL1,AR,SASH1,LMO4,TMEM108,FGF18,FAM210B,CDKN2B,PLAC8B,LIMS2,ANKRD1,F2RL1,HRH2,FAM129A,MARCH5,ENPP4,DAPK1,RBM4B,BNIP3,EGLN1,AKAP6,CDKN1A,JMY,C1S,CRLF3,CLSTN1,CREBRF,NRP1,PTPN22,NPNT,UNC5B,ATP7A,SCP2,SMARCD3,EVL,SMPD1,SLITRK5,TBX20,C7,TBX5,CCDC3,PRKCE,CCNT1,FZD3,DKKL1,FRS2,RNF19A,CCPG1,DAG1,PARP9,CHD6,APP,ECM2,PSEN1,SEMA6D,TGFBR1,CHD7,JUP,SPINK2,CCL5,DDR2,FOSL2,PERP,DUSP22,SIAH1,EDN1,NID1,AKTIP,DUSP26,NOD2,ARID5B,ASAP1,FAM107A,B2M,DISC1,SH3RF3,SERINC3,FXYD1,DCUN1D4,SCAMP5,KLF11,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,AZIN2,WDR48,WASL,CAT,DOCK5,ZKSCAN1,SH3BP4,ERAP1,ENSCAFG00000029553,PARK7,SLC8A1,TEAD1,NG	up_ACOR_VSMC
GO:0051234	0.414	0.662	32	1283	establishment of localization	BP	1	TRAPPC3L,LEP,KCNC4,CRY2,VPS26C,RAB20,GAS1,DLL1,CRYAB,KCND1,GPAM,CHRM2,SLC17A5,MYO1D,ATP6V1B2,SLC6A6,GREM1,CAMK2A,FXYD1,ICAM5,REEP2,BVES,RAB7A,ATP6V0B,NIPAL1,SLC46A2,CCL5,DMPK,SLC43A1,CLIC4,KXD1,ANXA11	up_AFEM_EC
GO:0034654	0.414	0.712	11	1236	nucleobase-containing compound biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0046649	0.414	0.716	9	162	lymphocyte activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,ZFP36L1,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0002790	0.414	0.716	9	133	peptide secretion	BP	1	NR1H4,PTPN11,SEL1L,HIF1A,LYN,GBP5,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0033500	0.414	0.744	6	64	carbohydrate homeostasis	BP	1	ADGRF5,PRCP,SMARCA4,ADIPOR2,MCU,HIF1A	up_VCAV_EC
GO:0042593	0.414	0.744	6	64	glucose homeostasis	BP	1	ADGRF5,PRCP,SMARCA4,ADIPOR2,MCU,HIF1A	up_VCAV_EC
GO:0090288	0.414	0.759	5	44	negative regulation of cellular response to growth factor stimulus	BP	1	FZD1,SLIT2,ABL1,EPN2,SULF2	up_VSAP_EC
GO:0001649	0.414	0.773	4	54	osteoblast differentiation	BP	1	ILK,FHL2,CTNNB1,REST	down_VSAP_EC
GO:0006928	0.414	0.8	3	557	movement of cell or subcellular component	BP	1	HOXA7,SIX1,TIAM1	up_VFEM_EC
GO:0010823	0.414	0.841	2	17	negative regulation of mitochondrion	BP	1	SLC25A5,PRELID1	down_ACOR_VSMC
GO:0010633	0.414	0.836	2	28	negative regulation of epithelial cell migration	BP	1	DCN,SPRED1	down_VCAV_EC
GO:1901799	0.414	0.837	2	24	negative regulation of proteasomal protein catabolic process	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0030330	0.414	0.837	2	25	DNA damage response, signal transduction by p53 class mediator	BP	1	SESN2,CDKN1A	down_VSAP_EC
GO:2000242	0.414	0.842	2	15	negative regulation of reproductive process	BP	1	PRDX4,BMP4	up_ACOR_VSMC
GO:0032387	0.414	0.838	2	20	negative regulation of intracellular transport	BP	1	FERMT1,APOD	up_VCAV_EC
GO:0006357	0.414	0.841	2	547	regulation of transcription by RNA polymerase II	BP	1	BARX1,NKX2-5	up_VPOR_VSMC

GO:0006801	0.414	0.842	2	15	superoxide metabolic process	BP	1	F2RL1,CYBA	up_VSAP_EC
GO:0000083	0.414	0.914	1	6	regulation of transcription involved in G1/S transition of mitotic cell	BP	1	HINFP	down_ACOR_VSMC
GO:0051220	0.414	0.914	1	6	cytoplasmic sequestering of protein	BP	1	YWHAB	down_ACOR_VSMC
GO:0055090	0.414	0.914	1	6	acylglycerol homeostasis	BP	1	LIPC	down_ACOR_VSMC
GO:0070328	0.414	0.914	1	6	triglyceride homeostasis	BP	1	LIPC	down_ACOR_VSMC
GO:0010243	0.414	0.905	1	238	response to organonitrogen	BP	1	GABPA	down_AFEM_EC
GO:0035751	0.414	0.908	1	10	regulation of lysosomal lumen pH	BP	1	ATP6V0C	down_VCAV_EC
GO:2000104	0.414	0.907	1	11	negative regulation of DNA-dependent DNA	BP	1	FBH1	down_VCAV_EC
GO:0007095	0.414	0.907	1	11	mitotic G2 DNA damage checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:0043552	0.414	0.907	1	11	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0090218	0.414	0.907	1	11	positive regulation of lipid kinase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0032880	0.414	0.906	1	266	regulation of protein localization	BP	1	RAB11B	down_VPOR_EC
GO:1905521	0.414	0.909	1	9	regulation of macrophage migration	BP	1	MMP28	down_VSAP_EC
GO:0048584	0.414	0.914	1	592	positive regulation of response to stimulus	BP	1	GATA5	down_VSAP_VSMC
GO:0007616	0.414	0.917	1	5	long-term memory	BP	1	LRRN4	up_ACOR_VSMC
GO:0051899	0.414	0.903	1	22	membrane depolarization	BP	1	MLLT11	up_AFEM_EC
GO:0018193	0.414	0.908	1	368	peptidyl-amino acid modification	BP	1	EYA1	up_AFEM_VSMC
GO:0097119	0.414	0.917	1	5	postsynaptic density protein 95 clustering	BP	1	RELN	up_VCAV_EC
GO:0048666	0.414	0.906	1	258	neuron development	BP	1	SLIT2	up_VPUL_VSMC
GO:0018209	0.414	0.903	1	125	peptidyl-serine modification	BP	1	CAV1	up_VSAP_VSMC
GO:0009628	0.414274042	0.71511	9	302	response to abiotic stimulus	BP	1	BRSK1,SOX9,PCSK1N,AQP1,PTGER4,USP53,FIGNL1,PRKACA,MFAP4	up_ACOR_EC
GO:0043436	0.414457483	0.71494	9	303	oxoacid metabolic process	BP	1	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,PTGDS,ALDOC,AZIN2,PM20D1	up_ACOR_EC
GO:0072358	0.414550949	0.72185	8	268	cardiovascular system development	BP	1	AQP1,ENSCAFG00000004331,FZD5,SMAD6,ESM1,DLX3,FOXC2,NRP1	up_ACOR_EC
GO:0042981	0.415	0.652	39	471	regulation of apoptotic process	BP	1	PLK2,HCLS1,IL7R,PRKCH,TNFAIP3,MAP3K11,STK10,MEF2C,ATF3,GATA3,TNFAIP8,FIGNL1,ARG2,CASP8,MAP3K3,BMP2,SLK,ITPKB,MADD,PAK2,SH3GLB1,NCK1,CASP10,PTGS2,RAPGEF2,BCL10,TAOK1,CTNNA1,HMGB1,PMAIP1,RIPK1,APAF1,ITGA6,SKIL,HIF1A,ALDH1A3,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0007507	0.415	0.695	13	194	heart development	BP	1	PRICKLE1,LTBP1,PTPN11,TMED2,ILK,FHL2,TGFBR1,HIF1A,ADAMTS6,CTNNB1,NEXN,REST,NRP1	down_VSAP_EC
GO:0006820	0.415	0.71	10	109	anion transport	BP	1	ATP8A1,LRRC8D,SLC35A3,STC1,SLC38A1,LRRC8C,ABCA1,SLCO3A1,NOS2,RIPK1	up_VCAV_EC
GO:1901576	0.415	0.731	9	1877	organic substance biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3,CHST7	up_VFEM_EC
GO:0009952	0.415	0.733	7	66	anterior/posterior pattern specification	BP	1	MLLT3,BMP4,CLSTN1,FRS2,PSEN1,PCSK6,CRKL	up_ACOR_VSMC
GO:0019221	0.415	0.741	6	102	cytokine-mediated signaling pathway	BP	1	DCN,BGN,NUMBL,ASPN,MAVS,FOXO3	down_VCAV_EC
GO:0009893	0.415	0.762	5	995	positive regulation of metabolic process	BP	1	EYA1,HOXA9,MAP2K6,SIX1,CYP26B1	up_VFEM_EC
GO:0045934	0.415	0.772	4	407	negative regulation of nucleobase-containing compound metabolic	BP	1	CXHXorf57,ENSCAFG00000002015,FBP1,MTDH	up_VPOR_EC
GO:0006725	0.415	0.829	3	1956	cellular aromatic compound metabolic	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0021761	0.415	0.801	3	27	limbic system development	BP	1	RELN,PROX1,ALDH1A3	up_VCAV_EC
GO:0051306	0.415	0.8	3	29	mitotic sister chromatid separation	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0060688	0.415	0.8	3	29	regulation of morphogenesis of a	BP	1	HOXB7,NTN4,BTBD7	up_VCAV_EC

GO:1901575	0.415	0.841	2	643	organic substance catabolic process	BP	1	ETFA,USP33	down_AFEM_EC
GO:0072676	0.415	0.837	2	25	lymphocyte migration	BP	1	MSN,ADAM17	down_VSAP_EC
GO:0071364	0.415	0.842	2	14	cellular response to epidermal growth factor	BP	1	DUSP22,INPP5K	up_ACOR_VSMC
GO:0042102	0.415	0.838	2	19	positive regulation of T cell proliferation	BP	1	NCK1,HMGB1	up_VCAV_EC
GO:0050873	0.415	0.839	2	18	brown fat cell differentiation	BP	1	PTGS2,ITGA6	up_VCAV_EC
GO:0016311	0.415	0.902	1	106	dephosphorylation	BP	1	MYO1D	down_ACOR_EC
GO:0009220	0.415	0.913	1	6	pyrimidine ribonucleotide biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0046132	0.415	0.913	1	6	pyrimidine ribonucleoside biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0046134	0.415	0.913	1	6	pyrimidine nucleoside biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0046184	0.415	0.913	1	6	aldehyde biosynthetic process	BP	1	TKT	down_ACOR_VSMC
GO:2000679	0.415	0.913	1	6	positive regulation of transcription regulatory region DNA binding	BP	1	FAM129B	down_ACOR_VSMC
GO:2000780	0.415	0.907	1	11	negative regulation of double-strand break	BP	1	FBH1	down_VCAV_EC
GO:0001502	0.415	0.91	1	8	cartilage condensation	BP	1	SULF1	down_VSAP_EC
GO:0046621	0.415	0.91	1	8	negative regulation of organ growth	BP	1	WWC3	down_VSAP_EC
GO:0098743	0.415	0.91	1	8	cell aggregation	BP	1	SULF1	down_VSAP_EC
GO:0051129	0.415	0.904	1	221	negative regulation of cellular component	BP	1	TAOK1	up_AORT_EC
GO:0006265	0.415	0.916	1	5	DNA topological change	BP	1	TOP1	up_VCAV_EC
GO:0007218	0.415	0.911	1	7	neuropeptide signaling pathway	BP	1	RAPGEF2	up_VCAV_EC
GO:0030522	0.415	0.901	1	67	intracellular receptor signaling pathway	BP	1	RNF6	up_VPOR_EC
GO:1903708	0.415	0.902	1	65	positive regulation of hemopoiesis	BP	1	ACVR2A	up_VPOR_EC
GO:0010605	0.416	0.638	64	745	negative regulation of macromolecule metabolic process	BP	1	EDNRB,HCLS1,TNFAIP3,TNIP1,PDGFB,PDE4D,MOV10,MEF2C,FERMT1,ATF3,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,GATA3,EDN1,HOXB8,SOX18,PPP3CA,TENT2,BMP2,CDYL,HMG20A,HHEX,CREM,PREX2,TUT7,SH3BP5,CNOT6,ENC1,PROX1,UHRF2,MDFI,HMBOX1,PAK2,THOC1,SWAP70,SMARCA4,APOD,NCK1,TIMELESS,PTGS2,TCERG1,CREB1,BASP1,PAN3,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,BLM,RAD17,MTA2,KDM5A,HIF1A,KDM3A,ATRX,HIST2H2AC,ARID5A,ENSCAFG00000002015,DCP2,IVNS1ABP,ELK3	up_VCAV_EC
GO:1901137	0.416	0.677	19	232	carbohydrate derivative biosynthetic process	BP	1	NPR1,ST8SIA6,PANK3,TNIP1,PDGFB,ST6GAL1,GK5,ADSS,GUCY1A1,B3GNT5,CHST7,ST3GAL6,GALNT18,ELOVL7,MFNG,ENSCAFG00000024323,GUCY1B1,HIF1A,TET2	up_VCAV_EC
GO:0048589	0.416	0.68	18	188	developmental growth	BP	1	IFRD1,PDE4D,MEF2C,CHD7,STC1,GATA3,EDN1,RAB11A,MTOR,HHEX,PROX1,APOD,SLC25A25,CREB1,SPTBN4,ATRX,RBBP6,GINS4	up_VCAV_EC
GO:0032970	0.416	0.699	12	130	regulation of actin filament-based process	BP	1	FSCN1,CAPG,CAV1,LIMA1,NF2,STMN1,RAC1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0045765	0.416	0.705	11	105	regulation of angiogenesis	BP	1	VEGFD,LEP,TLR3,SASH1,FGF18,EGLN1,NRP1,SYNJ2BP,JUP,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0071417	0.416	0.708	10	142	cellular response to organonitrogen	BP	1	ARHGEF2,NR1H4,ENPP1,PTPN11,TRIB3,SESN2,MYO1C,PTPN2,CTNNB1,NR4A1	down_VSAP_EC
GO:0071496	0.416	0.716	9	97	cellular response to external stimulus	BP	1	ATF3,RALB,TMEM150C,CASP8,MTOR,TLR3,BCL10,PMAIP1,ITGA6	up_VCAV_EC
GO:0046777	0.416	0.716	9	86	protein autophosphorylation	BP	1	EEF2K,ABL1,PDGFD,CAMKK2,TNKS1BP1,DDR2,PASK,STK16,ULK1	up_VSAP_EC
GO:0071704	0.416	0.772	8	3535	organic substance metabolic process	BP	1	CST3,HDAC7,CITED2,RAB11B,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0032271	0.416	0.731	7	73	regulation of protein polymerization	BP	1	CAPG,STMN1,RAC1,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0002377	0.416	0.8	3	26	immunoglobulin production	BP	1	IL7R,THOC1,SWAP70	up_VCAV_EC
GO:0034754	0.416	0.801	3	24	cellular hormone metabolic process	BP	1	HSD17B8,RETSAT,DHRS9	up_VSAP_EC

GO:0050777	0.416	0.835	2	28	negative regulation of immune response	BP	1	LOXL3,A2M	down_VCAV_EC
GO:0051153	0.416	0.835	2	28	regulation of striated muscle cell differentiation	BP	1	RBM38,GREM1	down_VCAV_EC
GO:0051928	0.416	0.835	2	28	positive regulation of calcium ion transport	BP	1	TRPV2,THY1	down_VCAV_EC
GO:0098727	0.416	0.832	2	60	maintenance of cell number	BP	1	LBH,DLL1	up_AFEM_EC
GO:0050810	0.416	0.839	2	17	regulation of steroid biosynthetic process	BP	1	BMP2,PROX1	up_VCAV_EC
GO:0043516	0.416	0.907	1	10	regulation of DNA damage response, signal transduction by p53 class	BP	1	SPRED1	down_VCAV_EC
GO:0090162	0.416	0.908	1	9	establishment of epithelial cell polarity	BP	1	MSN	down_VSAP_EC
GO:0045717	0.416	0.908	1	9	negative regulation of fatty acid biosynthetic	BP	1	TRIB3	down_VSAP_EC
GO:0046456	0.416	0.909	1	8	icosanoid biosynthetic process	BP	1	PTGS2	down_VSAP_EC
GO:0050857	0.416	0.908	1	9	positive regulation of antigen receptor-mediated signaling	BP	1	LYN	down_VSAP_EC
GO:0043207	0.416	0.904	1	216	response to external biotic stimulus	BP	1	BPI	up_AORT_EC
GO:0051707	0.416	0.904	1	216	response to other organism	BP	1	BPI	up_AORT_EC
GO:0050882	0.416	0.916	1	5	voluntary musculoskeletal movement	BP	1	MTOR	up_VCAV_EC
GO:0003417	0.416	0.913	1	6	growth plate cartilage development	BP	1	STC1	up_VCAV_EC
GO:0009620	0.416	0.909	1	8	response to fungus	BP	1	BCL10	up_VCAV_EC
GO:0021871	0.416	0.913	1	6	forebrain regionalization	BP	1	BMP2	up_VCAV_EC
GO:0046716	0.416	0.913	1	6	muscle cell cellular homeostasis	BP	1	HIF1A	up_VCAV_EC
GO:0090051	0.416	0.913	1	6	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	DLL4	up_VCAV_EC
GO:0032535	0.416	0.902	1	128	regulation of cellular component size	BP	1	CDC42EP5	up_VFEM_EC
GO:0044255	0.417	0.66	29	293	cellular lipid metabolic process	BP	1	PIP5K1B,PLCG2,LEP,HTR2B,LCAT,CHPT1,PPARGC1A,PIGN,PIGS,UGCG,PLPP2,PIGG,ACAD11,GGPS1,CYP2J2,ORMDL3,SMPD1,CRLS1,CLN8,EDN1,HPGD,SERINC3,NEU3,SERINC1,CFI,INPP5K,ENSCAFG00000029553,ELOVL7,LMF1	up_ACOR_VSMC
GO:0045860	0.417	0.691	14	132	positive regulation of protein kinase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,PDE5A,SASH1,FGF18,CCNT1,FRS2,PSEN1,DDR2,EDN1,MAP3K7	up_ACOR_VSMC
GO:0099537	0.417	0.714	9	131	trans-synaptic signaling	BP	1	KIF5B,HTR7,PLCL1,CDH11,CTNNB1,APOE,GSK3B,LRRTM2,USP14	down_VSAP_EC
GO:0008064	0.417	0.731	7	72	regulation of actin polymerization or	BP	1	CAPG,LIMA1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0030832	0.417	0.731	7	72	regulation of actin filament length	BP	1	CAPG,LIMA1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0008610	0.417	0.752	5	177	lipid biosynthetic process	BP	1	LEP,GPAM,SDR42E1,ACACB,AGPAT2	up_AFEM_EC
GO:0007162	0.417	0.771	4	66	negative regulation of cell adhesion	BP	1	PRNP,SDC4,GLI3,LOXL3	down_VCAV_EC
GO:0003151	0.417	0.775	4	34	outflow tract morphogenesis	BP	1	FZD1,WNT11,TGFBR2,CITED2	up_VSAP_EC
GO:1990823	0.417	0.796	3	39	response to leukemia inhibitory factor	BP	1	TFRC,KLF5,KDM3A	down_VSAP_EC
GO:1990830	0.417	0.796	3	39	cellular response to leukemia inhibitory factor	BP	1	TFRC,KLF5,KDM3A	down_VSAP_EC
GO:0042246	0.417	0.839	2	17	tissue regeneration	BP	1	EZH2,PPARD	down_ACOR_VSMC
GO:1903426	0.417	0.839	2	17	regulation of reactive oxygen species	BP	1	CAV1,ARG2	down_ACOR_VSMC
GO:0038083	0.417	0.839	2	16	peptidyl-tyrosine autophosphorylation	BP	1	FES,BMX	up_VCAV_EC
GO:0009886	0.417	0.912	1	6	post-embryonic animal morphogenesis	BP	1	HMGN1	down_ACOR_VSMC
GO:0010960	0.417	0.912	1	6	magnesium ion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:0048308	0.417	0.912	1	6	organelle inheritance	BP	1	PLK3	down_ACOR_VSMC
GO:0050996	0.417	0.912	1	6	positive regulation of lipid catabolic process	BP	1	ABHD5	down_ACOR_VSMC

GO:0042987	0.417	0.907	1	10	amyloid precursor protein catabolic process	BP	1	PRNP	down_VCAV_EC
GO:0060713	0.417	0.906	1	10	labyrinthine layer morphogenesis	BP	1	ZFP36L1	down_VCAV_EC
GO:0097345	0.417	0.907	1	10	mitochondrial outer membrane	BP	1	SLC35F6	down_VCAV_EC
GO:2001014	0.417	0.908	1	8	regulation of skeletal muscle cell differentiation	BP	1	SIX4	down_VSAP_EC
GO:0071711	0.417	0.909	1	8	basement membrane organization	BP	1	PLOD3	down_VSAP_EC
GO:0043584	0.417	0.915	1	5	nose development	BP	1	CHD7	up_ACOR_VSMC
GO:0060218	0.417	0.915	1	5	hematopoietic stem cell differentiation	BP	1	CHD2	up_ACOR_VSMC
GO:0090128	0.417	0.915	1	5	regulation of synapse maturation	BP	1	DISC1	up_ACOR_VSMC
GO:0090177	0.417	0.915	1	5	establishment of planar polarity involved in neural	BP	1	SEC24B	up_ACOR_VSMC
GO:0090178	0.417	0.915	1	5	regulation of establishment of planar polarity involved in neural	BP	1	SEC24B	up_ACOR_VSMC
GO:0016192	0.417	0.909	1	452	vesicle-mediated transport	BP	1	WNT7A	up_AORT_VSMC
GO:0009636	0.417	0.9	1	66	response to toxic substance	BP	1	SLC7A11	up_VPOR_EC
GO:0021766	0.417039291	0.90228	1	20	hippocampus development	BP	1	DCLK2	up_ACOR_EC
GO:0051603	0.417402462	0.71231	9	305	proteolysis involved in cellular protein catabolic	BP	1	EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,HM13	up_ACOR_EC
GO:0051247	0.418	0.641	50	502	positive regulation of protein metabolic process	BP	1	FZD1,PRR16,CDON,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,IL6R,CRADD,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CCBE1,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,TRAF7,MYC,EEF2,SASH1,FBXO4,LARP6,MYD88,LRP4,PHF1,RNF166,RPUSD4,CDK9,OSBPL7,RAF1,EIF3D,ACVRL1,UBQLN2,HTRA2,FLOT1,NCK1,MAVS,MAP2K2,TGFBR2,BAG4,SOAT1	up_VSAP_EC
GO:0006412	0.418	0.664	25	245	translation	BP	1	PRR16,MRPL37,WARS2,PYM1,ZFP36L1,EEF2,LARP6,RPL13,ANKHD1,FARS2,UBA52,RPUSD4,RPL15,EIF3G,SAMD4B,ZFP36L2,EIF3K,EIF3L,QARS,EIF3D,TNRC6C,COA1,NCK1,MRPL4,LARS2	up_VSAP_EC
GO:0031330	0.418	0.714	9	85	negative regulation of cellular catabolic process	BP	1	LEP,HTR2B,FEZ1,PTPN3,OS9,PSEN1,DDIT4,FEZ2,PARK7	up_ACOR_VSMC
GO:0045665	0.418	0.742	6	55	negative regulation of neuron differentiation	BP	1	THRB,SLIT2,DLL1,IRX3,RTN4RL1,LRP4	up_VSAP_EC
GO:0051147	0.418	0.756	5	44	regulation of muscle cell differentiation	BP	1	DLL1,ZEB1,SHOX2,CDK9,FLOT1	up_VSAP_EC
GO:0009145	0.418	0.772	4	40	purine nucleoside triphosphate biosynthetic	BP	1	CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0035148	0.418	0.769	4	66	tube formation	BP	1	SDC4,LMO4,IFT57,GREM1	down_VCAV_EC
GO:0010648	0.418	0.77	4	407	negative regulation of cell communication	BP	1	BARX1,ARHGEF2,ASPN,FBP1	up_VPOR_EC
GO:0045667	0.418	0.796	3	38	regulation of osteoblast differentiation	BP	1	ILK,CTNNB1,REST	down_VSAP_EC
GO:1903900	0.418	0.796	3	40	regulation of viral life cycle	BP	1	P4HB,CNOT7,RAD23A	down_VSAP_EC
GO:0008585	0.418	0.8	3	24	female gonad development	BP	1	ARID5B,DMC1,LHX9	up_ACOR_VSMC
GO:0035306	0.418	0.8	3	24	positive regulation of dephosphorylation	BP	1	NPNT,SMPD1,DUSP26	up_ACOR_VSMC
GO:0043507	0.418	0.8	3	23	positive regulation of JUN kinase activity	BP	1	SASH1,EDN1,MAP3K7	up_ACOR_VSMC
GO:0046545	0.418	0.8	3	24	development of primary female sexual	BP	1	ARID5B,DMC1,LHX9	up_ACOR_VSMC
GO:0120034	0.418	0.798	3	28	positive regulation of plasma membrane bounded cell projection	BP	1	MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0050818	0.418	0.8	3	24	regulation of coagulation	BP	1	KLKB1,HPSE,F2RL1	up_VSAP_EC
GO:0000245	0.418	0.834	2	24	spliceosomal complex assembly	BP	1	CELF1,DDX39B	down_VSAP_EC
GO:0001776	0.418	0.835	2	23	leukocyte homeostasis	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0001941	0.418	0.84	2	14	postsynaptic membrane organization	BP	1	GLRB,LRRC4	up_ACOR_VSMC
GO:0006096	0.418	0.837	2	18	glycolytic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC

GO:0006165	0.418	0.837	2	18	nucleoside diphosphate phosphorylation	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0006757	0.418	0.837	2	18	ATP generation from ADP	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0042866	0.418	0.837	2	18	pyruvate biosynthetic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0001501	0.418	0.83	2	178	skeletal system development	BP	1	HOXA3,ACVR2A	up_VPOR_EC
GO:0032101	0.418	0.831	2	173	regulation of response to external stimulus	BP	1	C3AR1,SEMA3A	up_VPOR_EC
GO:0048468	0.418	0.838	2	553	cell development	BP	1	CHL1,NKX2-5	up_VPOR_VSMC
GO:0030836	0.418	0.912	1	6	positive regulation of actin filament	BP	1	PDXP	down_ACOR_VSMC
GO:0032688	0.418	0.912	1	6	negative regulation of interferon-beta	BP	1	CACTIN	down_ACOR_VSMC
GO:0043371	0.418	0.912	1	6	negative regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0050716	0.418	0.912	1	6	positive regulation of interleukin-1 secretion	BP	1	HMGB1	down_ACOR_VSMC
GO:0003171	0.418	0.906	1	10	atrioventricular valve development	BP	1	BMPR1A	down_VCAV_EC
GO:0019219	0.418	0.927	1	1151	regulation of nucleobase-containing compound metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0050999	0.418	0.907	1	9	regulation of nitric-oxide synthase activity	BP	1	APOE	down_VSAP_EC
GO:0045616	0.418	0.907	1	9	regulation of keratinocyte differentiation	BP	1	ERRFI1	down_VSAP_EC
GO:0033079	0.418	0.915	1	5	immature T cell proliferation	BP	1	BMP4	up_ACOR_VSMC
GO:0033083	0.418	0.915	1	5	regulation of immature T cell proliferation	BP	1	BMP4	up_ACOR_VSMC
GO:0010692	0.418	0.915	1	5	regulation of alkaline phosphatase activity	BP	1	NPNT	up_ACOR_VSMC
GO:0044321	0.418	0.915	1	5	response to leptin	BP	1	LEP	up_ACOR_VSMC
GO:0097186	0.418	0.912	1	6	amelogenesis	BP	1	ITGA6	up_VCAV_EC
GO:0021756	0.418	0.912	1	6	striatum development	BP	1	ALDH1A3	up_VCAV_EC
GO:0030278	0.418	0.9	1	66	regulation of ossification	BP	1	ACVR2A	up_VPOR_EC
GO:0050730	0.418	0.9	1	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	ARHGEF2	up_VPOR_EC
GO:0010639	0.418	0.9	1	128	negative regulation of organelle organization	BP	1	TRIM9	up_VFEM_EC
GO:0009607	0.419	0.684	15	232	response to biotic stimulus	BP	1	NR1H4,HSPA5,SERPINE1,COTL1,PVR,MTDH,ADAM17,ACTA2,CNOT7,LYN,BNIP3,DDIT3,GSK3B,GBP5,DEFB124	down_VSAP_EC
GO:0034655	0.419	0.689	14	135	nucleobase-containing compound catabolic process	BP	1	AXIN2,TENT5C,EXOSC7,PYM1,DFFB,ZFP36L1,GALK1,ENTPD3,SMG9,SAMD4B,ZFP36L2,PNP,TNRC6C,DDIT4	up_VSAP_EC
GO:0060326	0.419	0.713	9	84	cell chemotaxis	BP	1	ARHGEF5,C5AR2,SLC8B1,SLIT2,IL17RC,HSD3B7,F2RL1,ZNF580,SAA1	up_VSAP_EC
GO:0000375	0.419	0.718	8	120	RNA splicing, via transesterification	BP	1	CELF1,SNRPB2,PRPF3,DDX39B,STRAP,REST,ENSCAFG00000015065,SNRPA1	down_VSAP_EC
GO:0050708	0.419	0.728	7	101	regulation of protein secretion	BP	1	NR1H4,PTPN11,HIF1A,LYN,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0002697	0.419	0.739	6	85	regulation of immune effector process	BP	1	SOCS5,FAM49B,PVR,TFRC,LYN,A2M	down_VSAP_EC
GO:0002697	0.419	0.751	5	85	regulation of immune effector process	BP	1	RNF216,MAVS,LOXL3,A2M,RAC2	down_VCAV_EC
GO:0001656	0.419	0.773	4	35	metanephros development	BP	1	HOXA11,OSR2,OSR1,IRX3	up_VSAP_EC
GO:0072676	0.419	0.798	3	25	lymphocyte migration	BP	1	APP,CCL5,WASL	up_ACOR_VSMC
GO:0071479	0.419	0.797	3	29	cellular response to ionizing radiation	BP	1	GATA3,FIGNL1,BLM	up_VCAV_EC
GO:1990266	0.419	0.799	3	24	neutrophil migration	BP	1	C5AR2,SLIT2,MYD88	up_VSAP_EC
GO:0055092	0.419	0.833	2	28	sterol homeostasis	BP	1	LCAT,SOAT1	down_VCAV_EC
GO:0017158	0.419	0.834	2	24	regulation of calcium ion-dependent exocytosis	BP	1	GSK3B,REST	down_VSAP_EC
GO:0010212	0.419	0.83	2	60	response to ionizing radiation	BP	1	CRYAB,DCUN1D3	up_AFEM_EC
GO:0009311	0.419	0.835	2	21	oligosaccharide metabolic process	BP	1	ST6GAL1,ST3GAL6	up_VCAV_EC

GO:0016072	0.419	0.9	1	102	rRNA metabolic process	BP	1	WDR12	down_ACOR_EC
GO:0000054	0.419	0.911	1	6	ribosomal subunit export from nucleus	BP	1	RAN	down_ACOR_VSMC
GO:0033750	0.419	0.911	1	6	ribosome localization	BP	1	RAN	down_ACOR_VSMC
GO:0071428	0.419	0.911	1	6	rRNA-containing ribonucleoprotein complex export from	BP	1	RAN	down_ACOR_VSMC
GO:0010884	0.419	0.911	1	6	positive regulation of lipid storage	BP	1	SREBF2	down_ACOR_VSMC
GO:0032486	0.419	0.911	1	6	Rap protein signal transduction	BP	1	RAP2C	down_ACOR_VSMC
GO:0033151	0.419	0.911	1	6	V(D)J recombination	BP	1	HMGB1	down_ACOR_VSMC
GO:0044546	0.419	0.911	1	6	NLRP3 inflammasome complex assembly	BP	1	DHX33	down_ACOR_VSMC
GO:0045776	0.419	0.911	1	6	negative regulation of blood pressure	BP	1	PRCP	down_ACOR_VSMC
GO:0046827	0.419	0.911	1	6	positive regulation of protein export from	BP	1	RAN	down_ACOR_VSMC
GO:0048665	0.419	0.911	1	6	neuron fate specification	BP	1	HOXC10	down_ACOR_VSMC
GO:1900225	0.419	0.911	1	6	regulation of NLRP3 inflammasome complex	BP	1	DHX33	down_ACOR_VSMC
GO:1902624	0.419	0.909	1	7	positive regulation of neutrophil migration	BP	1	RAC1	down_ACOR_VSMC
GO:0045671	0.419	0.908	1	8	negative regulation of osteoclast differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0090141	0.419	0.906	1	9	positive regulation of mitochondrial fission	BP	1	BNIP3	down_VSAP_EC
GO:0007413	0.419	0.915	1	5	axonal fasciculation	BP	1	NRP1	up_ACOR_VSMC
GO:0106030	0.419	0.915	1	5	neuron projection fasciculation	BP	1	NRP1	up_ACOR_VSMC
GO:0050793	0.419	0.915	1	731	regulation of developmental process	BP	1	TBX5	up_APUL_VSMC
GO:0000729	0.419	0.914	1	5	DNA double-strand break processing	BP	1	BLM	up_VCAV_EC
GO:0006448	0.419	0.909	1	7	regulation of translational elongation	BP	1	DPH5	up_VCAV_EC
GO:0010563	0.419	0.902	1	203	negative regulation of phosphorus metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0031175	0.419	0.902	1	224	neuron projection development	BP	1	SHOX2	up_VFEM_VSMC
GO:0045936	0.419	0.902	1	203	negative regulation of phosphate metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0003156	0.419206754	0.90116	1	20	regulation of animal organ formation	BP	1	TBX5	up_ACOR_EC
GO:0051972	0.419355026	0.90108	1	20	regulation of telomerase activity	BP	1	PKIB	up_ACOR_EC
GO:2000026	0.419513498	0.68116	16	560	regulation of multicellular organismal development	BP	1	CDH3,NR1H4,BRSK1,SOX9,AQP1,DIXDC1,RGMA,PAK3,ARHGDIB,FOXC2,TBX5,LRP4,CLSTN1,NRP1,PYGO2,EFEMP1	up_ACOR_EC
GO:0098739	0.419574126	0.90097	1	20	import across plasma membrane	BP	1	SLC9A9	up_ACOR_EC
GO:0050688	0.419798134	0.90085	1	20	regulation of defense response to virus	BP	1	MAVS	up_ACOR_EC
GO:0022603	0.42	0.68	16	301	regulation of anatomical structure morphogenesis	BP	1	HSPB6,DCN,BMPR1A,TRPV2,SEMA3C,ASPN,THY1,TLX2,B4GALT1,MYDGF,SASH1,SPRED1,UST,GREM1,THRB,BRSK1	down_VCAV_EC
GO:0001817	0.42	0.695	12	182	regulation of cytokine production	BP	1	ARHGEF2,SULF1,NR1H4,SERPINE1,SOCS5,FAM49B,HIF1A,ADAM17,LYN,DDIT3,GBP5,BTK	down_VSAP_EC
GO:0019220	0.42	0.752	5	525	regulation of phosphate metabolic process	BP	1	ARHGEF2,ASPN,ACVR2A,FBP1,ENSCAFG00000032731	up_VPOR_EC
GO:0051174	0.42	0.752	5	525	regulation of phosphorus metabolic process	BP	1	ARHGEF2,ASPN,ACVR2A,FBP1,ENSCAFG00000032731	up_VPOR_EC
GO:0061041	0.42	0.772	4	34	regulation of wound healing	BP	1	F2RL1,ENPP4,PRKCE,RREB1	up_ACOR_VSMC
GO:1903169	0.42	0.772	4	34	regulation of calcium ion transmembrane transport	BP	1	PLCG2,CACNB3,PRKCE,CHD7	up_ACOR_VSMC
GO:0071346	0.42	0.771	4	41	cellular response to interferon-gamma	BP	1	GBP5,NLRC5,IRF8,FLNB	up_VCAV_EC
GO:0035304	0.42	0.796	3	29	regulation of protein dephosphorylation	BP	1	PPP2R5A,PPP1R2,SWAP70	up_VCAV_EC
GO:0045604	0.42	0.836	2	17	regulation of epidermal cell differentiation	BP	1	EZH2,HOXA7	down_ACOR_VSMC
GO:0021782	0.42	0.833	2	23	glial cell development	BP	1	ILK,EIF2B1	down_VSAP_EC

GO:0032943	0.42	0.829	2	60	mononuclear cell proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0046651	0.42	0.829	2	60	lymphocyte proliferation	BP	1	LEP,GPAM	up_AFEM_EC
GO:0000737	0.42	0.911	1	6	DNA catabolic process, endonucleolytic	BP	1	AIFM1	down_ACOR_VSMC
GO:0003417	0.42	0.911	1	6	growth plate cartilage development	BP	1	POC1A	down_ACOR_VSMC
GO:0072348	0.42	0.911	1	6	sulfur compound transport	BP	1	SLC25A19	down_ACOR_VSMC
GO:0030097	0.42	0.902	1	244	hemopoiesis	BP	1	GABPA	down_AFEM_EC
GO:0035024	0.42	0.907	1	8	negative regulation of Rho protein signal	BP	1	TNFAIP1	down_VSAP_EC
GO:0021561	0.42	0.907	1	8	facial nerve development	BP	1	NRP1	down_VSAP_EC
GO:0021610	0.42	0.907	1	8	facial nerve morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0061551	0.42	0.914	1	5	trigeminal ganglion development	BP	1	NRP1	up_ACOR_VSMC
GO:0016570	0.42	0.9	1	143	histone modification	BP	1	NR1H4	up_APUL_EC
GO:0001556	0.42	0.909	1	7	oocyte maturation	BP	1	FBXO5	up_VCAV_EC
GO:2000463	0.42	0.914	1	5	positive regulation of excitatory postsynaptic	BP	1	RELN	up_VCAV_EC
GO:0015740	0.42	0.914	1	5	C4-dicarboxylate transport	BP	1	LRRC8D	up_VCAV_EC
GO:0043408	0.42	0.901	1	211	regulation of MAPK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0048514	0.42	0.901	1	214	blood vessel morphogenesis	BP	1	EYA1	up_VFEM_VSMC
GO:0006470	0.420202989	0.82924	2	54	protein dephosphorylation	BP	1	DUSP26,PRKCD	up_ACOR_EC
GO:1901224	0.420485545	0.90049	1	20	positive regulation of NIK/NF-kappaB signaling	BP	1	NOD2	up_ACOR_EC
GO:0061180	0.420635196	0.90041	1	20	mammary gland epithelium development	BP	1	PYGO2	up_ACOR_EC
GO:0051056	0.420802579	0.79048	3	87	regulation of small GTPase mediated signal	BP	1	ARHGDIB,NRP1,ARHGEF26	up_ACOR_EC
GO:0045087	0.420978873	0.7482	5	161	innate immune response	BP	1	NR1H4,NOD2,TRIM8,MAVS,RARRES2	up_ACOR_EC
GO:0010769	0.421	0.727	7	69	regulation of cell morphogenesis involved	BP	1	IFRD1,RELN,RAB11A,NEDD9,PPP3CA,RAPGEF2,ENSCAFG00000002015	up_VCAV_EC
GO:0016573	0.421	0.752	5	50	histone acetylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:0050680	0.421	0.753	5	44	negative regulation of epithelial cell proliferation	BP	1	LIMS2,PEX2,SAV1,NFIB,ACVRL1	up_VSAP_EC
GO:0023057	0.421	0.767	4	409	negative regulation of signaling	BP	1	BARX1,ARHGEF2,ASPN,FBP1	up_VPOR_EC
GO:0007154	0.421	0.788	4	1622	cell communication	BP	1	TBX5,GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0051704	0.421	0.794	3	476	multi-organism process	BP	1	LYN,ACSL4,NEDD4	down_ACOR_EC
GO:0007399	0.421	0.795	3	564	nervous system development	BP	1	HOXC10,EYA1,SIX1	up_VFEM_EC
GO:0002526	0.421	0.836	2	17	acute inflammatory response	BP	1	B4GALT1,PRCP	down_ACOR_VSMC
GO:0023052	0.421	0.859	2	1602	signaling	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0001960	0.421	0.837	2	15	negative regulation of cytokine-mediated	BP	1	F2RL1,CCDC3	up_ACOR_VSMC
GO:0051898	0.421	0.837	2	15	negative regulation of protein kinase B signaling	BP	1	DAG1,INPP5K	up_ACOR_VSMC
GO:0060761	0.421	0.837	2	15	negative regulation of response to cytokine	BP	1	F2RL1,CCDC3	up_ACOR_VSMC
GO:0019693	0.421	0.829	2	172	ribose phosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0016180	0.421	0.837	2	15	snRNA processing	BP	1	EXOSC7,INTS12	up_VSAP_EC
GO:0010998	0.421	0.91	1	6	regulation of translational initiation by eIF2 alpha phosphorylation	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0017185	0.421	0.911	1	6	peptidyl-lysine hydroxylation	BP	1	JMJD6	down_ACOR_VSMC
GO:0036490	0.421	0.91	1	6	regulation of translation in response to endoplasmic reticulum	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0044550	0.421	0.91	1	6	secondary metabolite biosynthetic process	BP	1	CTH	down_ACOR_VSMC

GO:0044788	0.421	0.91	1	6	modulation by host of viral process	BP	1	SMC3	down_ACOR_VSMC
GO:0046784	0.421	0.91	1	6	viral mRNA export from host cell nucleus	BP	1	DDX39B	down_ACOR_VSMC
GO:0098901	0.421	0.908	1	7	regulation of cardiac muscle cell action	BP	1	CAV1	down_ACOR_VSMC
GO:1990089	0.421	0.91	1	6	response to nerve growth factor	BP	1	CORO1A	down_ACOR_VSMC
GO:1990090	0.421	0.91	1	6	cellular response to nerve growth factor stimulus	BP	1	CORO1A	down_ACOR_VSMC
GO:0060045	0.421	0.903	1	11	positive regulation of cardiac muscle cell	BP	1	BMPR1A	down_VCAV_EC
GO:0001916	0.421	0.91	1	6	positive regulation of T cell mediated cytotoxicity	BP	1	B2M	up_ACOR_VSMC
GO:0097435	0.421	0.901	1	230	supramolecular fiber organization	BP	1	TAOK1	up_AORT_EC
GO:0010647	0.421	0.906	1	460	positive regulation of cell communication	BP	1	WNT7A	up_AORT_VSMC
GO:0050974	0.421	0.911	1	6	detection of mechanical stimulus involved in	BP	1	KIT	up_VCAV_EC
GO:0019934	0.421	0.91	1	6	cGMP-mediated signaling	BP	1	GUCY1B1	up_VCAV_EC
GO:0043276	0.421	0.91	1	6	anoikis	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0043486	0.421	0.908	1	7	histone exchange	BP	1	PSME4	up_VCAV_EC
GO:0007051	0.421	0.898	1	70	spindle organization	BP	1	MZT1	up_VPOR_EC
GO:0090150	0.421	0.898	1	64	establishment of protein localization to membrane	BP	1	SRP54	up_VPOR_EC
GO:0032535	0.421	0.899	1	128	regulation of cellular component size	BP	1	PRR16	up_VSAP_VSMC
GO:1905332	0.42123755	0.90009	1	20	positive regulation of morphogenesis of an	BP	1	SOX9	up_ACOR_EC
GO:0061614	0.421367867	0.90003	1	20	pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6	up_ACOR_EC
GO:0018958	0.42170688	0.89985	1	20	phenol-containing compound metabolic	BP	1	CDH3	up_ACOR_EC
GO:0006082	0.42184883	0.70835	9	305	organic acid metabolic process	BP	1	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,PTGDS,ALDOC,AZIN2,PM20D1	up_ACOR_EC
GO:0009161	0.422	0.699	11	103	ribonucleoside monophosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,NT5C2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0007015	0.422	0.716	8	144	actin filament organization	BP	1	KIRREL1,RHOD,ENSCAFG00000014978,WIPF1,MYO1B,ACTR3B,PLEKHH2,RAC2	down_VCAV_EC
GO:0045765	0.422	0.735	6	105	regulation of angiogenesis	BP	1	HSPB6,DCN,MYDGF,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0006950	0.422	0.758	5	1102	response to stress	BP	1	NR1H4,MAPK10,BPI,PCSK1N,ZDHHC16	up_APUL_EC
GO:0050730	0.422	0.767	4	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	PRNP,CSPG4,ARL2BP,GREM1	down_VCAV_EC
GO:0006508	0.422	0.794	3	483	proteolysis	BP	1	LYN,USP28,NEDD4	down_ACOR_EC
GO:0022037	0.422	0.795	3	27	metencephalon development	BP	1	EZH2,ARCN1,GLI1	down_ACOR_VSMC
GO:0019935	0.422	0.793	3	38	cyclic-nucleotide-mediated signaling	BP	1	GNAQ,APOE,CALM1	down_VSAP_EC
GO:0002286	0.422	0.797	3	24	T cell activation involved in immune response	BP	1	F2RL1,PSEN1,IL18R1	up_ACOR_VSMC
GO:0002690	0.422	0.796	3	26	positive regulation of leukocyte chemotaxis	BP	1	VEGFD,F2RL1,CCL5	up_ACOR_VSMC
GO:0022414	0.422	0.79	3	294	reproductive process	BP	1	SEMA3A,ACVR2A,RPL10L	up_VPOR_EC
GO:0070925	0.422	0.791	3	293	organelle assembly	BP	1	MZT1,RSL24D1,RPL10L	up_VPOR_EC
GO:0048468	0.422	0.794	3	553	cell development	BP	1	HOXA11,IRX5,SHOX2	up_VSAP_VSMC
GO:0032945	0.422	0.835	2	17	negative regulation of mononuclear cell	BP	1	MNDA,ARG2	down_ACOR_VSMC
GO:0050672	0.422	0.835	2	17	negative regulation of lymphocyte proliferation	BP	1	MNDA,ARG2	down_ACOR_VSMC
GO:0002042	0.422	0.83	2	29	cell migration involved in sprouting angiogenesis	BP	1	SPRED1,GREM1	down_VCAV_EC
GO:0032609	0.422	0.831	2	25	interferon-gamma production	BP	1	NR1H4,FAM49B	down_VSAP_EC
GO:0010390	0.422	0.837	2	15	histone monoubiquitination	BP	1	DDB2,KDM2B	up_VSAP_EC
GO:0006955	0.422	0.83	2	327	immune response	BP	1	TLR2,CAV1	up_VSAP_VSMC

GO:0036119	0.422	0.91	1	6	response to platelet-derived growth factor	BP	1	IQGAP1	down_ACOR_VSMC
GO:0036120	0.422	0.91	1	6	cellular response to platelet-derived growth	BP	1	IQGAP1	down_ACOR_VSMC
GO:0045815	0.422	0.91	1	6	positive regulation of gene expression,	BP	1	ATAD2	down_ACOR_VSMC
GO:0014002	0.422	0.903	1	11	astrocyte development	BP	1	LRP1	down_VCAV_EC
GO:0044458	0.422	0.905	1	9	motile cilium assembly	BP	1	DYNLL1	down_VSAP_EC
GO:0010762	0.422	0.905	1	9	regulation of fibroblast migration	BP	1	SDC4	down_VSAP_EC
GO:1902745	0.422	0.905	1	9	positive regulation of lamellipodium	BP	1	FSCN1	down_VSAP_EC
GO:0046949	0.422	0.91	1	6	fatty-acyl-CoA biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0007417	0.422	0.901	1	235	central nervous system development	BP	1	HOXC10	up_AORT_EC
GO:0006914	0.422	0.898	1	141	autophagy	BP	1	LZTS1	up_APUL_EC
GO:0016569	0.422	0.899	1	144	covalent chromatin modification	BP	1	NR1H4	up_APUL_EC
GO:0061919	0.422	0.898	1	141	process utilizing autophagic mechanism	BP	1	LZTS1	up_APUL_EC
GO:0021794	0.422	0.91	1	6	thalamus development	BP	1	PTCHD1	up_VCAV_EC
GO:0003128	0.422	0.91	1	6	heart field specification	BP	1	MEF2C	up_VCAV_EC
GO:1900271	0.422	0.91	1	6	regulation of long-term synaptic potentiation	BP	1	RELN	up_VCAV_EC
GO:1904706	0.422	0.908	1	7	negative regulation of vascular smooth muscle	BP	1	MEF2C	up_VCAV_EC
GO:0045666	0.422	0.897	1	68	positive regulation of neuron differentiation	BP	1	ARHGEF2	up_VPOR_EC
GO:0010256	0.422	0.899	1	129	endomembrane system organization	BP	1	MTSS1	up_VFEM_EC
GO:0051186	0.422	0.899	1	159	cofactor metabolic process	BP	1	ENSCAFG00000028814	up_VPUL_EC
GO:0002694	0.422	0.898	1	126	regulation of leukocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:1901184	0.422121047	0.89963	1	20	regulation of ERBB signaling pathway	BP	1	SH3TC2	up_ACOR_EC
GO:0030850	0.422496105	0.89943	1	20	prostate gland development	BP	1	SOX9	up_ACOR_EC
GO:0001708	0.422799379	0.89927	1	20	cell fate specification	BP	1	SOX9	up_ACOR_EC
GO:0030030	0.422834333	0.69628	11	377	cell projection organization	BP	1	BRSK1,RGMA,PLS1,ACTN2,PAK3,MAPK8IP2,LRP4,NRP1,ARHGEF26,PRKCD,DBNDD2	up_ACOR_EC
GO:0016236	0.423	0.735	6	88	macroautophagy	BP	1	SESN2,HIF1A,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:2001252	0.423	0.736	6	61	positive regulation of chromosome organization	BP	1	GATA3,HMBOX1,PRKD2,SMC5,RAD21,ATRX	up_VCAV_EC
GO:0042752	0.423	0.77	4	34	regulation of circadian rhythm	BP	1	PRKAA2,PPARGC1A,RBM4B,GNAQ	up_ACOR_VSMC
GO:0006887	0.423	0.789	3	99	exocytosis	BP	1	CHRM2,CAMK2A,RAB7A	up_AFEM_EC
GO:0050728	0.423	0.793	3	31	negative regulation of inflammatory response	BP	1	TNFAIP3,GATA3,APOD	up_VCAV_EC
GO:0060548	0.423	0.829	2	294	negative regulation of cell death	BP	1	IGF1R,PDPN	down_ACOR_EC
GO:1900076	0.423	0.83	2	29	regulation of cellular response to insulin	BP	1	ENSCAFG00000014978,AKT2	down_VCAV_EC
GO:0031110	0.423	0.831	2	24	regulation of microtubule polymerization or depolymerization	BP	1	ARHGEF2,MID1	down_VSAP_EC
GO:0070227	0.423	0.831	2	25	lymphocyte apoptotic process	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0030520	0.423	0.836	2	15	intracellular estrogen receptor signaling	BP	1	LBH,SKP2	up_ACOR_VSMC
GO:0043547	0.423	0.827	2	61	positive regulation of GTPase activity	BP	1	RASGEF1B,CCL5	up_AFEM_EC
GO:0120193	0.423	0.835	2	15	tight junction organization	BP	1	WNT11,CLDN1	up_VSAP_EC
GO:0010043	0.423	0.907	1	7	response to zinc ion	BP	1	SLC30A1	down_ACOR_VSMC
GO:0010559	0.423	0.909	1	6	regulation of glycoprotein biosynthetic process	BP	1	NECAB3	down_ACOR_VSMC
GO:0045876	0.423	0.909	1	6	positive regulation of sister chromatid cohesion	BP	1	FEN1	down_ACOR_VSMC

GO:0051450	0.423	0.91	1	6	myoblast proliferation	BP	1	PPARD	down_ACOR_VSMC
GO:0055083	0.423	0.909	1	6	monovalent inorganic anion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:1903018	0.423	0.909	1	6	regulation of glycoprotein metabolic process	BP	1	NECAB3	down_ACOR_VSMC
GO:1904357	0.423	0.909	1	6	negative regulation of telomere maintenance via telomere lengthening	BP	1	TINF2	down_ACOR_VSMC
GO:1904424	0.423	0.909	1	6	regulation of GTP binding	BP	1	STMN1	down_ACOR_VSMC
GO:0016071	0.423	0.9	1	248	mRNA metabolic process	BP	1	SRSF6	down_AFEM_EC
GO:1903393	0.423	0.903	1	11	positive regulation of adherens junction	BP	1	THY1	down_VCAV_EC
GO:0051093	0.423	0.901	1	273	negative regulation of developmental process	BP	1	HDAC7	down_VPOR_EC
GO:0061318	0.423	0.906	1	8	renal filtration cell differentiation	BP	1	MYO1E	down_VSAP_EC
GO:0072010	0.423	0.906	1	8	glomerular epithelium development	BP	1	MYO1E	down_VSAP_EC
GO:0072112	0.423	0.906	1	8	glomerular visceral epithelial cell	BP	1	MYO1E	down_VSAP_EC
GO:0072311	0.423	0.906	1	8	glomerular epithelial cell differentiation	BP	1	MYO1E	down_VSAP_EC
GO:0006995	0.423	0.909	1	6	cellular response to nitrogen starvation	BP	1	GABARAPL1	up_ACOR_VSMC
GO:0034643	0.423	0.912	1	5	establishment of mitochondrion localization, microtubule-	BP	1	RHOT1	up_ACOR_VSMC
GO:0034656	0.423	0.91	1	6	nucleobase-containing small molecule catabolic	BP	1	ENPP4	up_ACOR_VSMC
GO:0043562	0.423	0.909	1	6	cellular response to nitrogen levels	BP	1	GABARAPL1	up_ACOR_VSMC
GO:0047497	0.423	0.912	1	5	mitochondrion transport along microtubule	BP	1	RHOT1	up_ACOR_VSMC
GO:0071404	0.423	0.912	1	5	cellular response to low-density lipoprotein	BP	1	ABCA1	up_ACOR_VSMC
GO:2000345	0.423	0.912	1	5	regulation of hepatocyte proliferation	BP	1	LIMS2	up_ACOR_VSMC
GO:2001267	0.423	0.909	1	6	regulation of cysteine-type endopeptidase activity involved in	BP	1	PARK7	up_ACOR_VSMC
GO:0001578	0.423	0.899	1	23	microtubule bundle formation	BP	1	DNAL1	up_AFEM_EC
GO:0042307	0.423	0.898	1	23	positive regulation of protein import into	BP	1	LEP	up_AFEM_EC
GO:0023056	0.423	0.906	1	462	positive regulation of signaling	BP	1	WNT7A	up_AORT_VSMC
GO:0009100	0.423	0.898	1	139	glycoprotein metabolic process	BP	1	GALNT17	up_APUL_EC
GO:0065009	0.423	0.912	1	735	regulation of molecular function	BP	1	HOXA3	up_APUL_VSMC
GO:0034498	0.423	0.909	1	6	early endosome to Golgi transport	BP	1	SNX2	up_VCAV_EC
GO:0001775	0.423	0.9	1	219	cell activation	BP	1	HOXA9	up_VFEM_VSMC
GO:0071407	0.423	0.898	1	129	cellular response to organic cyclic compound	BP	1	CAV1	up_VSAP_VSMC
GO:0010605	0.423127026	0.66667	21	745	negative regulation of macromolecule metabolic process	BP	1	NR1H4,TRPS1,PKIB,SOX9,PCSK1N,NDRG2,IFI6,DUSP26,SMAD6,ZMYND8,CST3,PIAS1,FOXC2,LRRC15,CLSTN1,LRRC4,SFMBT2,RIOX2,AZIN2,PRKCD,DBNDD2	up_ACOR_EC
GO:0032210	0.423211	0.89906	1	20	regulation of telomere maintenance via	BP	1	PKIB	up_ACOR_EC
GO:1904356	0.423211	0.89906	1	20	regulation of telomere maintenance via telomere lengthening	BP	1	PKIB	up_ACOR_EC
GO:0003007	0.424	0.708	9	94	heart morphogenesis	BP	1	MEF2C,CHD7,DLL4,GATA3,MTOR,BMP2,PROX1,JAG1,HIF1A	up_VCAV_EC
GO:0003205	0.424	0.764	4	67	cardiac chamber development	BP	1	NOTCH2,BMPR1A,LMO4,SEMA3C	down_VCAV_EC
GO:0010952	0.424	0.766	4	46	positive regulation of peptidase activity	BP	1	CASP8,BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:0048525	0.424	0.795	3	25	negative regulation of viral process	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0071466	0.424	0.834	2	17	cellular response to xenobiotic stimulus	BP	1	MCM7,GSTO1	down_ACOR_VSMC
GO:0070664	0.424	0.833	2	18	negative regulation of leukocyte proliferation	BP	1	PELI1,ARG2	up_VCAV_EC

GO:0044403	0.424	0.897	1	116	symbiont process	BP	1	NEDD4	down_ACOR_EC
GO:1905564	0.424	0.909	1	6	positive regulation of vascular endothelial cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0010517	0.424	0.902	1	11	regulation of phospholipase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0022617	0.424	0.902	1	11	extracellular matrix disassembly	BP	1	DDR2	down_VCAV_EC
GO:0045824	0.424	0.902	1	11	negative regulation of innate immune response	BP	1	A2M	down_VCAV_EC
GO:0007167	0.424	0.9	1	274	enzyme linked receptor protein signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:1902236	0.424	0.904	1	9	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	HYOU1	down_VSAP_EC
GO:0006956	0.424	0.905	1	8	complement activation	BP	1	A2M	down_VSAP_EC
GO:0032897	0.424	0.904	1	9	negative regulation of viral transcription	BP	1	REST	down_VSAP_EC
GO:0045003	0.424	0.909	1	6	double-strand break repair via synthesis-dependent strand	BP	1	DMC1	up_ACOR_VSMC
GO:0090735	0.424	0.909	1	6	DNA repair complex assembly	BP	1	DMC1	up_ACOR_VSMC
GO:0000730	0.424	0.909	1	6	DNA recombinase assembly	BP	1	DMC1	up_ACOR_VSMC
GO:0010863	0.424	0.912	1	5	positive regulation of phospholipase C activity	BP	1	HTR2B	up_ACOR_VSMC
GO:0043496	0.424	0.909	1	6	regulation of protein homodimerization activity	BP	1	PARK7	up_ACOR_VSMC
GO:1900112	0.424	0.912	1	5	regulation of histone H3-K9 trimethylation	BP	1	ATRX	up_ACOR_VSMC
GO:0097194	0.424	0.898	1	23	execution phase of apoptosis	BP	1	FAP	up_AFEM_EC
GO:1904357	0.424	0.909	1	6	negative regulation of telomere maintenance via telomere lengthening	BP	1	DCP2	up_VCAV_EC
GO:0034770	0.424	0.912	1	5	histone H4-K20 methylation	BP	1	ARID4B	up_VCAV_EC
GO:0034773	0.424	0.912	1	5	histone H4-K20 trimethylation	BP	1	ARID4B	up_VCAV_EC
GO:0045652	0.424	0.907	1	7	regulation of megakaryocyte	BP	1	MEF2C	up_VCAV_EC
GO:0048545	0.424	0.897	1	68	response to steroid hormone	BP	1	RNF6	up_VPOR_EC
GO:0000902	0.424	0.901	1	266	cell morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:1901698	0.424	0.901	1	266	response to nitrogen compound	BP	1	SLIT2	up_VPUL_VSMC
GO:0046677	0.424117795	0.82648	2	54	response to antibiotic	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:2001020	0.424185294	0.78781	3	88	regulation of response to DNA damage stimulus	BP	1	FIGNL1,CLU,PRKCD	up_ACOR_EC
GO:0045184	0.424375324	0.67954	15	532	establishment of protein localization	BP	1	SH3TC2,NR1H4,KCNB1,EDEM2,FZD5,NOD2,PTGER4,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD,ENSCAFG00000010493	up_ACOR_EC
GO:0051055	0.424530231	0.89815	1	21	negative regulation of lipid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:0046822	0.424587447	0.82621	2	53	regulation of nucleocytoplasmic	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0042440	0.424728093	0.89804	1	21	pigment metabolic process	BP	1	CDH3	up_ACOR_EC
GO:1901652	0.425	0.701	10	105	response to peptide	BP	1	TNFAIP3,PPARG,BAIAP2L1,MTOR,NCK1,TIMELESS,JAG1,CREB1,NR4A1,ARHGEF2	up_VCAV_EC
GO:0006732	0.425	0.722	7	107	coenzyme metabolic process	BP	1	PGK1,TPI1,PGAM1,ALDH1L2,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0032388	0.425	0.725	7	62	positive regulation of intracellular transport	BP	1	ACTN2,LEP,TCAF1,PTPN22,SCP2,PSEN1,JUP	up_ACOR_VSMC
GO:0032879	0.425	0.726	7	767	regulation of localization	BP	1	C3AR1,HOXA3,ARHGEF2,SEMA3A,GCC2,ABHD5,CCAR1	up_VPOR_EC
GO:0000904	0.425	0.745	5	181	cell morphogenesis involved in differentiation	BP	1	PLXNA4,CAMK2A,BVES,LRRN2,KANK1	up_AFEM_EC
GO:0030856	0.425	0.767	4	41	regulation of epithelial cell differentiation	BP	1	PRKCH,GATA3,JAG1,ZEB1	up_VCAV_EC
GO:0000045	0.425	0.79	3	46	autophagosome assembly	BP	1	GABARAP,WDR45,EMC6	down_VCAV_EC
GO:0072009	0.425	0.789	3	48	nephron epithelium development	BP	1	CLSTN1,GLI3,GREM1	down_VCAV_EC

GO:0007584	0.425	0.794	3	24	response to nutrient	BP	1	CASTOR1,CDKN2B,P2RX7	up_ACOR_VSMC
GO:0000003	0.425	0.788	3	295	reproduction	BP	1	SEMA3A,ACVR2A,RPL10L	up_VPOR_EC
GO:0035904	0.425	0.794	3	25	aorta development	BP	1	LOX,ACVRL1,NPRL3	up_VSAP_EC
GO:0043271	0.425	0.829	2	28	negative regulation of ion transport	BP	1	AKT2,PACSIN3	down_VCAV_EC
GO:0051208	0.425	0.829	2	29	sequestering of calcium ion	BP	1	THY1,CYBA	down_VCAV_EC
GO:0051282	0.425	0.829	2	29	regulation of sequestering of calcium ion	BP	1	THY1,CYBA	down_VCAV_EC
GO:0032729	0.425	0.835	2	15	positive regulation of interferon-gamma	BP	1	TLR3,IL18R1	up_ACOR_VSMC
GO:0048584	0.425	0.833	2	592	positive regulation of response to stimulus	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0002712	0.425	0.835	2	15	regulation of B cell mediated immunity	BP	1	NECTIN2,THOC1	up_VCAV_EC
GO:0002889	0.425	0.835	2	15	regulation of immunoglobulin	BP	1	NECTIN2,THOC1	up_VCAV_EC
GO:0021575	0.425	0.834	2	15	hindbrain morphogenesis	BP	1	ABL1,DLL1	up_VSAP_EC
GO:0021587	0.425	0.834	2	15	cerebellum morphogenesis	BP	1	ABL1,DLL1	up_VSAP_EC
GO:0060330	0.425	0.908	1	6	regulation of response to interferon-gamma	BP	1	SLC29A1	down_ACOR_VSMC
GO:0060334	0.425	0.908	1	6	regulation of interferon-gamma-mediated	BP	1	SLC29A1	down_ACOR_VSMC
GO:1900120	0.425	0.906	1	7	regulation of receptor binding	BP	1	HOXA3	down_ACOR_VSMC
GO:0008206	0.425	0.902	1	11	bile acid metabolic process	BP	1	ACAA1	down_VCAV_EC
GO:1902230	0.425	0.902	1	11	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	TMEM161A	down_VCAV_EC
GO:0044092	0.425	0.9	1	270	negative regulation of molecular function	BP	1	CST3	down_VPOR_EC
GO:0031326	0.425	0.924	1	1176	regulation of cellular biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0010939	0.425	0.903	1	9	regulation of necrotic cell death	BP	1	ARHGEF2	down_VSAP_EC
GO:0032506	0.425	0.905	1	8	cytokinetic process	BP	1	MYH9	down_VSAP_EC
GO:0035330	0.425	0.911	1	5	regulation of hippo signaling	BP	1	WWC2	up_ACOR_VSMC
GO:0048752	0.425	0.911	1	5	semicircular canal morphogenesis	BP	1	CHD7	up_ACOR_VSMC
GO:0097119	0.425	0.912	1	5	postsynaptic density protein 95 clustering	BP	1	LRRC4	up_ACOR_VSMC
GO:0006865	0.425	0.897	1	23	amino acid transport	BP	1	SLC6A6	up_AFEM_EC
GO:0015908	0.425	0.897	1	23	fatty acid transport	BP	1	LEP	up_AFEM_EC
GO:0006812	0.425	0.899	1	222	cation transport	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0045664	0.425	0.897	1	144	regulation of neuron differentiation	BP	1	NTRK2	up_APUL_EC
GO:0042119	0.425	0.906	1	7	neutrophil activation	BP	1	CXCL8	up_VCAV_EC
GO:0046784	0.425	0.909	1	6	viral mRNA export from host cell nucleus	BP	1	THOC1	up_VCAV_EC
GO:1905564	0.425	0.908	1	6	positive regulation of vascular endothelial cell	BP	1	HMGB1	up_VCAV_EC
GO:0043603	0.425	0.902	1	372	cellular amide metabolic process	BP	1	ENSCAFG00000028814	up_VCAV_VSMC
GO:0032970	0.425	0.897	1	130	regulation of actin filament-based process	BP	1	CDC42EP5	up_VFEM_EC
GO:0048608	0.425	0.897	1	129	reproductive structure development	BP	1	HOXA9	up_VFEM_EC
GO:0000122	0.425	0.898	1	218	negative regulation of transcription by RNA polymerase II	BP	1	SHOX2	up_VFEM_VSMC
GO:1990778	0.425141518	0.78697	3	91	protein localization to cell periphery	BP	1	PLS1,ACTN2,LRRC15	up_ACOR_EC
GO:0045600	0.425524514	0.89762	1	21	positive regulation of fat cell differentiation	BP	1	CCDC3	up_ACOR_EC

GO:0048699	0.426	0.642	38	371	generation of neurons	BP	1	VEGFD,LEP,EPYC,FEZ1,ITM2C,BMP4,FGFR2,GJA1,SEC24B,ACSL6,ZNF365,LMO4,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SMARCD3,SLITRK5,TBX20,FZD3,FRS2,RND1,DAG1,POMK,APP,PSEN1,CHD7,SIPA1L1,CLN8,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,WASL,CRKL	up_ACOR_VSMC
GO:0071310	0.426	0.646	33	634	cellular response to organic substance	BP	1	PCOLCE,PDGFRB,SMAD9,LRP1,DCN,NDN,PRNP,VASN,FBN1,ADCY6,BGN,KANK2,COL6A1,NUMBL,ENSCAFG00000014978,AKT1S1,CHRDL1,AKT2,NR3C1,GFPT2,ASPN,PARK7,ZFP36L1,SASH1,MAVS,GSDME,FUT8,RAB7B,RAB31,SHC1,GREM1,FOXO3,RGMA	down_VCAV_EC
GO:0060627	0.426	0.681	14	165	regulation of vesicle-mediated transport	BP	1	SELE,RAB11A,RAB27A,PPP3CA,BMP2K,RSC1A1,FES,HIST1H1A,PLCG2,HMGB1,TBC1D1,DNAJC13,RABGAP1,USP6NL	up_VCAV_EC
GO:0031330	0.426	0.745	5	85	negative regulation of cellular catabolic process	BP	1	TIMP2,PSMF1,POLDIP2,PARK7,CLEC16A	down_VCAV_EC
GO:0035270	0.426	0.767	4	35	endocrine system development	BP	1	BMP4,CITED2,ARID5B,CRKL	up_ACOR_VSMC
GO:0001938	0.426	0.768	4	34	positive regulation of endothelial cell	BP	1	STAT5A,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:0050709	0.426	0.792	3	28	negative regulation of protein secretion	BP	1	SREBF1,ARG2,EZR	down_ACOR_VSMC
GO:0007009	0.426	0.792	3	27	plasma membrane organization	BP	1	BAIAP2L1,MTSS1,CAV2	up_VCAV_EC
GO:0043506	0.426	0.793	3	25	regulation of JUN kinase activity	BP	1	ARHGEF5,MAP3K5,SASH1	up_VSAP_EC
GO:1902882	0.426	0.828	2	29	regulation of response to oxidative stress	BP	1	PARK7,FUT8	down_VCAV_EC
GO:0021510	0.426	0.83	2	23	spinal cord development	BP	1	ZPR1,VLDLR	down_VSAP_EC
GO:0032411	0.426	0.829	2	24	positive regulation of transporter activity	BP	1	HTT,CALM1	down_VSAP_EC
GO:0003407	0.426	0.834	2	15	neural retina development	BP	1	GPM6A,SMARCD3	up_ACOR_VSMC
GO:0009893	0.426	0.841	2	995	positive regulation of metabolic process	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0044419	0.426	0.896	1	117	interspecies interaction between organisms	BP	1	NEDD4	down_ACOR_EC
GO:0051249	0.426	0.896	1	107	regulation of lymphocyte activation	BP	1	LYN	down_ACOR_EC
GO:0006925	0.426	0.908	1	6	inflammatory cell apoptotic process	BP	1	PIK3CD	down_ACOR_VSMC
GO:0043586	0.426	0.908	1	6	tongue development	BP	1	SIX4	down_ACOR_VSMC
GO:0071312	0.426	0.908	1	6	cellular response to alkaloid	BP	1	RAD51	down_ACOR_VSMC
GO:0060914	0.426	0.901	1	11	heart formation	BP	1	BMPR1A	down_VCAV_EC
GO:0002437	0.426	0.908	1	6	inflammatory response to antigenic stimulus	BP	1	PARK7	up_ACOR_VSMC
GO:0046006	0.426	0.908	1	6	regulation of activated T cell proliferation	BP	1	CD274	up_ACOR_VSMC
GO:0060122	0.426	0.911	1	5	inner ear receptor cell stereocilium organization	BP	1	SEC24B	up_ACOR_VSMC
GO:0072641	0.426	0.911	1	5	type I interferon secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:0072642	0.426	0.911	1	5	interferon-alpha secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:1902739	0.426	0.911	1	5	regulation of interferon-alpha secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:1902741	0.426	0.911	1	5	positive regulation of interferon-alpha secretion	BP	1	PTPN22	up_ACOR_VSMC
GO:0007045	0.426	0.897	1	23	cell-substrate adherens junction assembly	BP	1	GREM1	up_AFEM_EC
GO:0001776	0.426	0.897	1	23	leukocyte homeostasis	BP	1	GPAM	up_AFEM_EC
GO:0032602	0.426	0.897	1	23	chemokine production	BP	1	ADAM17	up_AFEM_EC
GO:0043154	0.426	0.897	1	23	negative regulation of cysteine-type endopeptidase activity	BP	1	CRYAB	up_AFEM_EC
GO:0048041	0.426	0.897	1	23	focal adhesion assembly	BP	1	GREM1	up_AFEM_EC
GO:0060350	0.426	0.897	1	23	endochondral bone morphogenesis	BP	1	AXIN2	up_AFEM_EC
GO:0051450	0.426	0.908	1	6	myoblast proliferation	BP	1	ZNF609	up_VCAV_EC

GO:0061307	0.426	0.906	1	7	cardiac neural crest cell differentiation involved in heart development	BP	1	JAG1	up_VCAV_EC
GO:0061308	0.426	0.906	1	7	cardiac neural crest cell development involved in heart development	BP	1	JAG1	up_VCAV_EC
GO:0097201	0.426	0.904	1	8	negative regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	NCK1	up_VCAV_EC
GO:0060284	0.426	0.898	1	212	regulation of cell development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0120039	0.426178294	0.74384	5	158	plasma membrane bounded cell projection	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1	up_ACOR_EC
GO:0035924	0.426510753	0.89709	1	21	cellular response to vascular endothelial growth factor stimulus	BP	1	NRP1	up_ACOR_EC
GO:1903533	0.426860648	0.8969	1	21	regulation of protein targeting	BP	1	KCNB1	up_ACOR_EC
GO:0043067	0.427	0.634	47	479	regulation of programmed cell death	BP	1	SMAD6,PLCG2,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,TM7SF3,FGFR2,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,CDKN1A,JMY,NRP1,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,PSEN1,SPINK2,CLN8,SIAH1,OXR1,NOD2,SERINC3,TNFRSF11B,KLF11,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0008285	0.427	0.692	11	201	negative regulation of cell proliferation	BP	1	NDN,PRNP,SDC4,KANK2,CLSTN1,B4GALT1,GLI3,IFT57,GSDME,GREM1,ZBTB16	down_VCAV_EC
GO:0048872	0.427	0.706	9	85	homeostasis of number of cells	BP	1	RASSF2,BMP4,CITED2,ISG15,FAM210B,P4HTM,JAM3,B2M,WDR48	up_ACOR_VSMC
GO:0051147	0.427	0.748	5	44	regulation of muscle cell differentiation	BP	1	BMP4,FGFR2,DMPK,FRS2,EDN1	up_ACOR_VSMC
GO:0098771	0.427	0.743	5	180	inorganic ion homeostasis	BP	1	RAB20,CNNM4,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0006470	0.427	0.746	5	54	protein dephosphorylation	BP	1	PPP2R5A,CTTNBP2NL,PPP1R2,SWAP70,NCK1	up_VCAV_EC
GO:0043281	0.427	0.746	5	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	PAK2,PTGS2,BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:0040014	0.427	0.791	3	27	regulation of multicellular organism growth	BP	1	CDK4,EZR,SGPL1	down_ACOR_VSMC
GO:0021543	0.427	0.787	3	49	pallium development	BP	1	PEX5,GLI3,CDH2	down_VCAV_EC
GO:0003231	0.427	0.787	3	48	cardiac ventricle development	BP	1	BMPR1A,LMO4,SEMA3C	down_VCAV_EC
GO:0062012	0.427	0.785	3	100	regulation of small molecule metabolic	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC
GO:0098542	0.427	0.785	3	100	defense response to other organism	BP	1	BPI,GPAM,ADAM17	up_AFEM_EC
GO:0043255	0.427	0.791	3	29	regulation of carbohydrate biosynthetic	BP	1	PDGFB,FAM3C,ENSCAFG00000010596	up_VCAV_EC
GO:0035909	0.427	0.834	2	14	aorta morphogenesis	BP	1	SEC24B,CHD7	up_ACOR_VSMC
GO:0006163	0.427	0.824	2	174	purine nucleotide metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0034622	0.427	0.828	2	421	cellular protein-containing complex assembly	BP	1	MYBPC2,CCL24	up_VPUL_EC
GO:0060677	0.427	0.907	1	6	ureteric bud elongation	BP	1	SIX4	down_ACOR_VSMC
GO:0071803	0.427	0.908	1	6	positive regulation of podosome assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0051171	0.427	0.941	1	1697	regulation of nitrogen compound metabolic	BP	1	CST3	down_AORT_EC
GO:0006336	0.427	0.901	1	11	DNA replication-independent nucleosome	BP	1	CABIN1	down_VCAV_EC
GO:0021799	0.427	0.9	1	11	cerebral cortex radially oriented cell migration	BP	1	GLI3	down_VCAV_EC
GO:0031111	0.427	0.901	1	11	negative regulation of microtubule polymerization or	BP	1	CLIP3	down_VCAV_EC
GO:0036475	0.427	0.901	1	11	neuron death in response to oxidative stress	BP	1	PARK7	down_VCAV_EC
GO:1901984	0.427	0.901	1	11	negative regulation of protein acetylation	BP	1	PARK7	down_VCAV_EC
GO:1902042	0.427	0.9	1	11	negative regulation of extrinsic apoptotic signaling pathway via	BP	1	PARK7	down_VCAV_EC

GO:1902914	0.427	0.901	1	11	regulation of protein polyubiquitination	BP	1	SASH1	down_VCAV_EC
GO:1903203	0.427	0.901	1	11	regulation of oxidative stress-induced neuron	BP	1	PARK7	down_VCAV_EC
GO:2000145	0.427	0.899	1	279	regulation of cell motility	BP	1	HDAC7	down_VPOR_EC
GO:0044766	0.427	0.902	1	9	multi-organism transport	BP	1	DDX39B	down_VSAP_EC
GO:0101023	0.427	0.904	1	8	vascular endothelial cell proliferation	BP	1	ADAM17	down_VSAP_EC
GO:1902579	0.427	0.902	1	9	multi-organism localization	BP	1	DDX39B	down_VSAP_EC
GO:1905562	0.427	0.904	1	8	regulation of vascular endothelial cell	BP	1	ADAM17	down_VSAP_EC
GO:0002347	0.427	0.908	1	6	response to tumor cell	BP	1	CD274	up_ACOR_VSMC
GO:0050882	0.427	0.911	1	5	voluntary musculoskeletal movement	BP	1	ITPR1	up_ACOR_VSMC
GO:0051127	0.427	0.911	1	5	positive regulation of actin nucleation	BP	1	WASL	up_ACOR_VSMC
GO:1900027	0.427	0.908	1	6	regulation of ruffle assembly	BP	1	EVL	up_ACOR_VSMC
GO:0007565	0.427	0.897	1	23	female pregnancy	BP	1	RECK	up_AFEM_EC
GO:0048144	0.427	0.897	1	23	fibroblast proliferation	BP	1	FOSL2	up_AFEM_EC
GO:0048145	0.427	0.897	1	23	regulation of fibroblast proliferation	BP	1	FOSL2	up_AFEM_EC
GO:0051851	0.427	0.897	1	23	modification by host of symbiont morphology or	BP	1	NAPEPLD	up_AFEM_EC
GO:0072527	0.427	0.897	1	23	pyrimidine-containing compound metabolic	BP	1	GPAM	up_AFEM_EC
GO:2001238	0.427	0.896	1	23	positive regulation of extrinsic apoptotic	BP	1	CYLD	up_AFEM_EC
GO:0021513	0.427	0.907	1	6	spinal cord dorsal/ventral patterning	BP	1	DLL4	up_VCAV_EC
GO:0061003	0.427	0.911	1	5	positive regulation of dendritic spine	BP	1	RELN	up_VCAV_EC
GO:1903427	0.427	0.905	1	7	negative regulation of reactive oxygen species biosynthetic process	BP	1	CD34	up_VCAV_EC
GO:1901615	0.427	0.896	1	128	organic hydroxy compound metabolic	BP	1	CYP26B1	up_VFEM_EC
GO:0034248	0.427	0.896	1	125	regulation of cellular amide metabolic process	BP	1	PRR16	up_VSAP_VSMC
GO:0051240	0.427078184	0.68028	14	489	positive regulation of multicellular organismal process	BP	1	NR1H4,SOX9,AQP1,FZD5,NOD2,IL33,PLS1,PTGER4,MAVS,FOXC2,TBX5,CLSTN1,NRP1,AGPAT2	up_ACOR_EC
GO:1904377	0.427188687	0.89673	1	21	positive regulation of protein localization to cell	BP	1	PLS1	up_ACOR_EC
GO:0007611	0.42734026	0.82418	2	54	learning or memory	BP	1	BRSK1,MAPK8IP2	up_ACOR_EC
GO:0032414	0.427493774	0.89657	1	21	positive regulation of ion transmembrane transporter activity	BP	1	ACTN2	up_ACOR_EC
GO:0006356	0.427818767	0.89661	1	20	regulation of transcription by RNA polymerase I	BP	1	RASL11A	up_ACOR_EC
GO:0002682	0.42788995	0.6969	10	343	regulation of immune system process	BP	1	C7,NR1H4,SOX9,FZD5,NOD2,MMP28,PTGER4,MAVS,CLSTN1,RARRES2	up_ACOR_EC
GO:0006357	0.428	0.629	55	547	regulation of transcription by RNA polymerase II	BP	1	SMAD6,LEP,GATA5,PCGF5,NACC2,BMP4,FGFR2,TP53BP1,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,AR,LMO4,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,TBX20,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,MXI1,CHD7,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,NOD2,ENSCAFG00000018360,KLF11,RPRD1B,WFS1,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0048284	0.428	0.731	6	66	organelle fusion	BP	1	SNAP23,CAV2,STX11,TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0043409	0.428	0.733	6	54	negative regulation of MAPK cascade	BP	1	TBC1D10C,ABL1,F2RL1,MYC,FBLN1,QARS	up_VSAP_EC
GO:0070372	0.428	0.744	5	85	regulation of ERK1 and ERK2 cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,SPRED1,SHC1	down_VCAV_EC
GO:0051259	0.428	0.76	4	140	protein complex oligomerization	BP	1	KCNC4,CRYAB,KCND1,ACACB	up_AFEM_EC
GO:0021953	0.428	0.786	3	49	central nervous system neuron differentiation	BP	1	LMO4,PEX5,GLI3	down_VCAV_EC

GO:0048008	0.428	0.792	3	24	platelet-derived growth factor receptor signaling	BP	1	PTGIR,NRP1,ARID5B	up_ACOR_VSMC
GO:0051289	0.428	0.792	3	25	protein homotetramerization	BP	1	ACTN2,PCBD1,EVL	up_ACOR_VSMC
GO:0043280	0.428	0.789	3	33	positive regulation of cysteine-type endopeptidase activity	BP	1	BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:2000045	0.428	0.827	2	29	regulation of G1/S transition of mitotic cell	BP	1	KANK2,LSM10	down_VCAV_EC
GO:0007154	0.428	0.855	2	1622	cell communication	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0090050	0.428	0.832	2	15	positive regulation of cell migration involved in sprouting angiogenesis	BP	1	NRP1,PIK3C2A	up_ACOR_VSMC
GO:0006006	0.428	0.823	2	61	glucose metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0016054	0.428	0.823	2	61	organic acid catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0046395	0.428	0.823	2	61	carboxylic acid catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0003006	0.428	0.823	2	180	developmental process involved in reproduction	BP	1	SEMA3A,ACVR2A	up_VPOR_EC
GO:0060969	0.428	0.907	1	6	negative regulation of gene silencing	BP	1	ATAD2	down_ACOR_VSMC
GO:0000578	0.428	0.9	1	11	embryonic axis specification	BP	1	PCSK6	down_VCAV_EC
GO:0007628	0.428	0.9	1	11	adult walking behavior	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0032715	0.428	0.9	1	11	negative regulation of interleukin-6 production	BP	1	BPI	down_VCAV_EC
GO:0010586	0.428	0.903	1	8	miRNA metabolic process	BP	1	SND1	down_VSAP_EC
GO:0002021	0.428	0.902	1	9	response to dietary excess	BP	1	APOE	down_VSAP_EC
GO:0002279	0.428	0.901	1	10	mast cell activation involved in immune	BP	1	LYN	down_VSAP_EC
GO:0002448	0.428	0.901	1	10	mast cell mediated immunity	BP	1	LYN	down_VSAP_EC
GO:0043303	0.428	0.901	1	10	mast cell degranulation	BP	1	LYN	down_VSAP_EC
GO:0044281	0.428	0.907	1	622	small molecule metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0015740	0.428	0.91	1	5	C4-dicarboxylate transport	BP	1	SLC25A12	up_ACOR_VSMC
GO:0042795	0.428	0.91	1	5	snRNA transcription by RNA polymerase II	BP	1	ELL2	up_ACOR_VSMC
GO:0072132	0.428	0.896	1	23	mesenchyme morphogenesis	BP	1	TMEM100	up_AFEM_EC
GO:0051276	0.428	0.901	1	398	chromosome organization	BP	1	EYA1	up_AFEM_VSMC
GO:0007015	0.428	0.896	1	144	actin filament organization	BP	1	PDLIM3	up_APUL_EC
GO:0050778	0.428	0.895	1	141	positive regulation of immune response	BP	1	NR1H4	up_APUL_EC
GO:0045292	0.428	0.905	1	7	mRNA cis splicing, via spliceosome	BP	1	PRPF39	up_VCAV_EC
GO:0033006	0.428	0.905	1	7	regulation of mast cell activation involved in	BP	1	FES	up_VCAV_EC
GO:0043304	0.428	0.905	1	7	regulation of mast cell degranulation	BP	1	FES	up_VCAV_EC
GO:0050766	0.428	0.903	1	8	positive regulation of phagocytosis	BP	1	RAB27A	up_VCAV_EC
GO:0032102	0.428	0.895	1	67	negative regulation of response to external	BP	1	SEMA3A	up_VPOR_EC
GO:0051098	0.428	0.895	1	129	regulation of binding	BP	1	TIAM1	up_VFEM_EC
GO:0002683	0.428	0.895	1	126	negative regulation of immune system process	BP	1	HOXA9	up_VSAP_VSMC
GO:0030193	0.428200813	0.89619	1	21	regulation of blood coagulation	BP	1	PRKCD	up_ACOR_EC
GO:1900046	0.428200813	0.89619	1	21	regulation of hemostasis	BP	1	PRKCD	up_ACOR_EC
GO:0007626	0.428408764	0.82348	2	53	locomotory behavior	BP	1	TMOD1,GNAO1	up_ACOR_EC
GO:0007034	0.428782332	0.82309	2	55	vacuolar transport	BP	1	CHMP4B,VPS16	up_ACOR_EC

GO:0050896	0.429	0.677	20	2346	response to stimulus	BP	1	C3AR1,BARX1,CXHXorf57,ARHGEF2,ENSCAFG00000002015,OAS3,SLC7A11,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,SEMA3D,PDE1C,SRP54,STK17B,ENSCAFG00000032731,NAALADL2,GNPNAT1,RNF6	up_VPOR_EC
GO:0072521	0.429	0.665	19	185	purine-containing compound metabolic process	BP	1	ACSM3,ACACB,GDA,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,PNP,NDUFV1,DDIT4	up_VSAP_EC
GO:0022604	0.429	0.684	13	122	regulation of cell morphogenesis	BP	1	CDC7,ZRANB1,WASF3,ZMYM2,NRP1,ULK2,PSEN1,SIPA1L1,SSH3,DOCK5,BVES,RREB1,CRKL	up_ACOR_VSMC
GO:0016043	0.429	0.768	5	1973	cellular component organization	BP	1	GPSM2,EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:2000060	0.429	0.746	5	45	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	SH3RF2,RNF19A,PSEN1,DISC1,HERPUD1	up_ACOR_VSMC
GO:0008584	0.429	0.764	4	39	male gonad development	BP	1	KIT,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:0046546	0.429	0.764	4	39	development of primary male sexual	BP	1	KIT,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:1903034	0.429	0.787	3	40	regulation of response to wounding	BP	1	SERPINE1,APOE,LYN	down_VSAP_EC
GO:0042180	0.429	0.822	2	61	cellular ketone metabolic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0030808	0.429	0.831	2	15	regulation of nucleotide biosynthetic process	BP	1	PDK2,DDIT4	up_VSAP_EC
GO:0045912	0.429	0.831	2	15	negative regulation of carbohydrate metabolic	BP	1	PASK,DDIT4	up_VSAP_EC
GO:1900371	0.429	0.831	2	15	regulation of purine nucleotide biosynthetic	BP	1	PDK2,DDIT4	up_VSAP_EC
GO:0051241	0.429	0.825	2	336	negative regulation of multicellular organismal	BP	1	HOXA9,HOXC10	up_VSAP_VSMC
GO:0070525	0.429	0.904	1	7	tRNA threonylcarbamoyladenosine metabolic process	BP	1	OSGEP	down_ACOR_VSMC
GO:0071696	0.429	0.907	1	6	ectodermal placode development	BP	1	SIX4	down_ACOR_VSMC
GO:0006511	0.429	0.897	1	253	ubiquitin-dependent protein catabolic process	BP	1	USP33	down_AFEM_EC
GO:0043170	0.429	1	1	2980	macromolecule metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0002520	0.429	0.898	1	279	immune system development	BP	1	CITED2	down_VPOR_EC
GO:0009889	0.429	0.923	1	1190	regulation of biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0031498	0.429	0.903	1	8	chromatin disassembly	BP	1	SMARCA4	down_VSAP_EC
GO:1903747	0.429	0.902	1	9	regulation of establishment of protein localization to	BP	1	SH3GLB1	down_VSAP_EC
GO:0048870	0.429	0.903	1	451	cell motility	BP	1	WNT7A	up_AORT_VSMC
GO:0051674	0.429	0.903	1	451	localization of cell	BP	1	WNT7A	up_AORT_VSMC
GO:0003344	0.429	0.906	1	6	pericardium morphogenesis	BP	1	DLL4	up_VCAV_EC
GO:0001832	0.429	0.904	1	7	blastocyst growth	BP	1	GINS4	up_VCAV_EC
GO:0044550	0.429	0.907	1	6	secondary metabolite biosynthetic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0048713	0.429	0.907	1	6	regulation of oligodendrocyte	BP	1	MTOR	up_VCAV_EC
GO:0045860	0.429	0.895	1	132	positive regulation of protein kinase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0061458	0.429	0.895	1	131	reproductive system development	BP	1	HOXA9	up_VFEM_EC
GO:0009301	0.429	0.907	1	6	snRNA transcription	BP	1	ICE1	up_VSAP_EC
GO:0009306	0.429	0.895	1	127	protein secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0060711	0.42924321	0.89562	1	21	labyrinthine layer development	BP	1	FZD5	up_ACOR_EC
GO:0030595	0.429482483	0.82247	2	57	leukocyte chemotaxis	BP	1	MMP28,RARRES2	up_ACOR_EC
GO:0034220	0.43	0.671	16	188	ion transmembrane transport	BP	1	LRRC8D,RELN,PDE4D,MEF2C,CHD7,SLC35A3,APLNR,SLC39A8,SLC38A1,LRRC8C,KCNJ3,KCNJ2,SLC25A25,PLCG2,RIPK1,MCU	up_VCAV_EC

GO:0007165	0.43	0.69	13	1496	signal transduction	BP	1	C3AR1,BARX1,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,PDE1C,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0071559	0.43	0.711	8	75	response to transforming growth factor beta	BP	1	ZFP36L1,ZEB1,STK16,ZFP36L2,HPGD,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0016458	0.43	0.731	6	59	gene silencing	BP	1	MOV10,PPP3CA,TUT7,UHRF2,CNOT7,HIST2H2AC	up_VCAV_EC
GO:0071219	0.43	0.744	5	50	cellular response to molecule of bacterial	BP	1	IRAK1,MTDH,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0043901	0.43	0.746	5	44	negative regulation of multi-organism process	BP	1	MYD88,NLRX1,TKFC,MAPKBP1,MAVS	up_VSAP_EC
GO:0061333	0.43	0.764	4	35	renal tubule morphogenesis	BP	1	HOXA11,WNT11,OSR1,IRX3	up_VSAP_EC
GO:0042274	0.43	0.785	3	47	ribosomal small subunit biogenesis	BP	1	RPS10,MRPS11,RPS27	down_VCAV_EC
GO:0010950	0.43	0.786	3	44	positive regulation of endopeptidase activity	BP	1	LYN,FAM162A,REST	down_VSAP_EC
GO:0044773	0.43	0.789	3	28	mitotic DNA damage checkpoint	BP	1	TAOK1,BLM,TOPBP1	up_VCAV_EC
GO:0006915	0.43	0.788	3	550	apoptotic process	BP	1	EYA1,MAP2K6,SIX1	up_VFEM_EC
GO:0021954	0.43	0.79	3	26	central nervous system neuron development	BP	1	SLIT2,PLXNA4,NFIB	up_VSAP_EC
GO:2000106	0.43	0.825	2	29	regulation of leukocyte apoptotic process	BP	1	GPAM,TSC22D3	down_VCAV_EC
GO:0050793	0.43	0.832	2	731	regulation of developmental process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0051289	0.43	0.826	2	25	protein homotetramerization	BP	1	VASP,GBP5	down_VSAP_EC
GO:0045912	0.43	0.831	2	15	negative regulation of carbohydrate metabolic	BP	1	DDIT4,INPP5K	up_ACOR_VSMC
GO:0045661	0.43	0.829	2	18	regulation of myoblast differentiation	BP	1	MEF2C,CDON	up_VCAV_EC
GO:0060306	0.43	0.904	1	7	regulation of membrane repolarization	BP	1	CAV1	down_ACOR_VSMC
GO:0086002	0.43	0.904	1	7	cardiac muscle cell action potential involved in	BP	1	CAV1	down_ACOR_VSMC
GO:0086009	0.43	0.904	1	7	membrane repolarization	BP	1	CAV1	down_ACOR_VSMC
GO:0032446	0.43	0.897	1	255	protein modification by small protein conjugation	BP	1	IVNS1ABP	down_AFEM_EC
GO:0043066	0.43	0.897	1	253	negative regulation of apoptotic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0007212	0.43	0.899	1	11	dopamine receptor signaling pathway	BP	1	ADCY6	down_VCAV_EC
GO:0043457	0.43	0.899	1	11	regulation of cellular respiration	BP	1	PARK7	down_VCAV_EC
GO:0060193	0.43	0.899	1	11	positive regulation of lipase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0036444	0.43	0.906	1	6	calcium import into the mitochondrion	BP	1	MICU2	up_ACOR_VSMC
GO:0043410	0.43	0.894	1	144	positive regulation of MAPK cascade	BP	1	NPNT	up_APUL_EC
GO:0042403	0.43	0.906	1	6	thyroid hormone metabolic process	BP	1	GATA3	up_VCAV_EC
GO:0021537	0.43	0.893	1	73	telencephalon development	BP	1	SEMA3A	up_VPOR_EC
GO:1901701	0.43	0.897	1	271	cellular response to oxygen-containing	BP	1	SLIT2	up_VPUL_VSMC
GO:0002360	0.43	0.906	1	6	T cell lineage commitment	BP	1	STAT6	up_VSAP_EC
GO:0043369	0.43	0.906	1	6	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BP	1	STAT6	up_VSAP_EC
GO:0009950	0.43	0.906	1	6	dorsal/ventral axis specification	BP	1	LRP4	up_VSAP_EC
GO:0060872	0.43	0.906	1	6	semicircular canal development	BP	1	ZEB1	up_VSAP_EC
GO:0060389	0.430090424	0.89517	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	SMAD6	up_ACOR_EC
GO:0006810	0.430101707	0.64415	34	1244	transport	BP	1	SH3TC2,CA4,CDH3,NR1H4,CLIC3,BRSK1,CALY,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,NOD2,DYNC1I1,PLS1,ACTN2,CFI,PTGER4,PREB,SLC25A42,MAPK8IP2,MAVS,SLC9A9,CHMP4B,RARRES2,VPS16,ABCB9,NRP1,AZIN2,HM13,PRKCD,PM20D1,ENSCAFG00000010493,ATP7B	up_ACOR_EC
GO:0043270	0.430278826	0.82196	2	56	positive regulation of ion transport	BP	1	ACTN2,PRKCD	up_ACOR_EC

GO:0090183	0.430434624	0.89498	1	21	regulation of kidney development	BP	1	SOX9	up_ACOR_EC
GO:0007283	0.43080107	0.78252	3	91	spermatogenesis	BP	1	SOX9,PYGO2,CCNYL1	up_ACOR_EC
GO:0065008	0.431	0.613	103	1056	regulation of biological quality	BP	1	FZD1,PRR16,THRB,NAPEPLD,HNF4A,FAM107A,AXIN2,C5AR2,LIPC,WASF3,AMIGO1,LRRN3,SLC8B1,PPARGC1B,RNPEP,ACACB,TPCN2,IRX5,SLIT2,SLC6A4,ABL1,PEX2,GOT1,EBF2,KLKB1,EMP2,KCNE3,CHRM1,DLL1,CDC42EP5,TENT5C,PDGFD,SAV1,HPSE,PLXNA4,ANKRD54,CLDN1,CDC42EP2,PTGES2,STAT6,HSD17B8,PLPP3,ENSCAFG00000000071,F2RL1,RAB11B,MORC3,PDK2,MFN2,ZFP36L1,FXN,RETSAT,PIK3R1,SLC25A28,MYC,DLD,SCARA5,TBXA2R,ABAT,CIZ1,AGTR1,FBXO4,HOXC10,LRP4,PASK,DPYSL2,DAGLB,HPS4,E2F4,PRKAB1,FBXO7,KCNB1,LCAT,LIMD1,DHRS9,FBLN1,TXNDC16,FTL,SAMD4B,ZFP36L2,RAF1,TAF8,CYBA,ZNF205,XKR8,FXYD1,STX4,TTL,KCNC4,ACVRL1,ALDH9A1,ASS1,FLOT1,PPP3CB,PEX6,NCK1,HMOX1,CITED2,BAG4,ENSCAFG00000006478,NCOA4,KEAP1,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0008284	0.431	0.658	21	238	positive regulation of cell proliferation	BP	1	HMGB1,HOXA3,SLC25A5,CDCA7L,PRMT1,EZH2,GREM1,CDK4,RNASEH2B,PDCD2,MVD,B4GALT1,TFRC,NRAS,PPARD,EMP2,HMGB2,CDK2,CORO1A,ASPM,GLI1	down_ACOR_VSMC
GO:1903706	0.431	0.69	11	119	regulation of hemopoiesis	BP	1	HMGB1,HSPA9,PRELID1,PRMT1,MMP14,HMGB3,HOXA7,PDCD2,HMGB2,TOX,HOXA9	down_ACOR_VSMC
GO:0051961	0.431	0.711	8	73	negative regulation of nervous system	BP	1	ITM2C,ZNF365,NRP1,ULK2,APP,PSEN1,ASAP1,B2M	up_ACOR_VSMC
GO:0032879	0.431	0.764	4	767	regulation of localization	BP	1	NETO1,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0048565	0.431	0.785	3	38	digestive tract development	BP	1	HIF1A,CTNNB1,KLF5	down_VSAP_EC
GO:0071333	0.431	0.789	3	25	cellular response to glucose stimulus	BP	1	PRKAA2,PRKCE,RAB11B	up_ACOR_VSMC
GO:0097327	0.431	0.789	3	25	response to antineoplastic agent	BP	1	CDH1,HMOX1,DDIT4	up_VSAP_EC
GO:0006471	0.431	0.829	2	17	protein ADP-ribosylation	BP	1	PUM3,TINF2	down_ACOR_VSMC
GO:0051496	0.431	0.829	2	17	positive regulation of stress fiber assembly	BP	1	NF2,RAC1	down_ACOR_VSMC
GO:1903825	0.431	0.829	2	17	organic acid transmembrane transport	BP	1	LRRC8D,SLC38A1	up_VCAV_EC
GO:1905039	0.431	0.829	2	17	carboxylic acid transmembrane transport	BP	1	LRRC8D,SLC38A1	up_VCAV_EC
GO:0090407	0.431	0.821	2	177	organophosphate biosynthetic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0030520	0.431	0.831	2	15	intracellular estrogen receptor signaling	BP	1	PPARGC1B,LBH	up_VSAP_EC
GO:1900408	0.431	0.83	2	15	negative regulation of cellular response to	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:1903202	0.431	0.83	2	15	negative regulation of oxidative stress-induced	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:0021801	0.431	0.906	1	6	cerebral cortex radial glia guided migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0022030	0.431	0.906	1	6	telencephalon glial cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0051654	0.431	0.906	1	6	establishment of mitochondrion	BP	1	TRAK1	down_ACOR_VSMC
GO:0072574	0.431	0.905	1	6	hepatocyte proliferation	BP	1	GLI1	down_ACOR_VSMC
GO:0072575	0.431	0.905	1	6	epithelial cell proliferation involved in liver	BP	1	GLI1	down_ACOR_VSMC
GO:0072576	0.431	0.905	1	6	liver morphogenesis	BP	1	GLI1	down_ACOR_VSMC
GO:0060341	0.431	0.896	1	255	regulation of cellular localization	BP	1	GPSM2	down_AFEM_EC
GO:0019538	0.431	0.94	1	1713	protein metabolic process	BP	1	CST3	down_AORT_EC
GO:0032881	0.431	0.898	1	11	regulation of polysaccharide metabolic	BP	1	AKT2	down_VCAV_EC
GO:0032885	0.431	0.898	1	11	regulation of polysaccharide	BP	1	AKT2	down_VCAV_EC
GO:0043300	0.431	0.898	1	11	regulation of leukocyte degranulation	BP	1	RAC2	down_VCAV_EC
GO:0002886	0.431	0.899	1	10	regulation of myeloid leukocyte mediated	BP	1	LYN	down_VSAP_EC

GO:0009143	0.431	0.905	1	6	nucleoside triphosphate catabolic process	BP	1	ENTPD3	up_ACOR_VSMC
GO:0060390	0.431	0.906	1	6	regulation of SMAD protein signal	BP	1	BMP4	up_ACOR_VSMC
GO:0072109	0.431	0.905	1	6	glomerular mesangium development	BP	1	BMP4	up_ACOR_VSMC
GO:0007268	0.431	0.894	1	130	chemical synaptic transmission	BP	1	NETO1	up_VSAP_VSMC
GO:0098916	0.431	0.894	1	130	anterograde trans-synaptic signaling	BP	1	NETO1	up_VSAP_VSMC
GO:0001659	0.431037263	0.82153	2	54	temperature homeostasis	BP	1	PLCL1,FOXC2	up_ACOR_EC
GO:0048858	0.431189102	0.73957	5	159	cell projection morphogenesis	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1	up_ACOR_EC
GO:0033559	0.431284567	0.89452	1	21	unsaturated fatty acid metabolic process	BP	1	PTGDS	up_ACOR_EC
GO:0038034	0.431485315	0.89441	1	21	signal transduction in absence of ligand	BP	1	IFI6	up_ACOR_EC
GO:0097192	0.431485315	0.89441	1	21	extrinsic apoptotic signaling pathway in	BP	1	IFI6	up_ACOR_EC
GO:0044248	0.432	0.62	68	691	cellular catabolic process	BP	1	PEX7,AXIN2,LIPC,ENPP2,PLEKHF1,RNPEP,ACAA1,FOXRED2,ACACB,TPCN2,RETREG1,GDA,ABTB1,PEX2,GOT1,CTSS,TENT5C,ADHFE1,HPSE,ALDH6A1,VPS36,EXOSC7,FAAH,PYM1,AMBRA1,DFFB,MFN2,ZFP36L1,GALK1,RBCK1,ENTPD3,RNF24,FBXW4,GCDH,BCKDHB,FBXO4,RMND5A,POLDIP2,ATG2A,FBXW5,SMG9,FBXO7,UBA7,EHHADH,RNF166,LONP2,ABHD16A,PIP4K2B,RNF216,OSBPL7,ENSCAFG00000002977,SAMD4B,ZFP36L2,PNP,TIMP2,IDH1,UBQLN2,CTSF,CDC26,HTRA2,TNRC6C,ULK1,HMOX1,NPRL3,KEAP1,FUNDC2,DDIT4,IDO2	up_VSAP_EC
GO:0034613	0.432	0.628	50	576	cellular protein localization	BP	1	ACSL3,SREBF1,RPA1,DDX39A,STXBP6,USP4,NEDD4,ZW10,CENPA,SLC29A1,NDC1,TIMM44,POLA2,CTDNEP1,HSPA9,RAN,HM13,INSIG1,CAV1,CDK1,NF2,AURKB,MMP14,EZH2,PLK3,ENSCAFG00000011598,PREB,TRAM1,NDC80,IPO4,YWHAB,NUP62,EMP2,NUP188,HASPIN,TOMM34,SAMM50,DMAP1,DDX39B,SNX15,RAB35,EZR,MIOS,TTK,KNL1,PMPCA,TINF2,CCT4,SIX4,MTBP	down_ACOR_VSMC
GO:0050865	0.432	0.677	14	135	regulation of cell activation	BP	1	LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,LMO4,F2RL1,CDKN1A,PTPN22,APP,DUSP22,NOD2,PAG1	up_ACOR_VSMC
GO:0009150	0.432	0.699	9	161	purine ribonucleotide metabolic process	BP	1	GPAM,ADCY6,NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0002697	0.432	0.702	9	85	regulation of immune effector process	BP	1	STAT6,F2RL1,NLRX1,TKFC,RNF216,STX4,PQBP1,PPP3CB,MAVS	up_VSAP_EC
GO:0050794	0.432	0.759	7	3075	regulation of cellular process	BP	1	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0051091	0.432	0.74	5	87	positive regulation of DNA-binding transcription factor activity	BP	1	PARK7,MAVS,RAB7B,DDR2,GREM1	down_VCAV_EC
GO:0008643	0.432	0.743	5	45	carbohydrate transport	BP	1	LEP,SLC2A5,EDN1,INPP5K,SLC2A12	up_ACOR_VSMC
GO:0008152	0.432	0.812	5	3714	metabolic process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0050792	0.432	0.742	5	55	regulation of viral process	BP	1	CXCL8,NECTIN2,PROX1,SMARCA4,CNOT7	up_VCAV_EC
GO:0018107	0.432	0.743	5	45	peptidyl-threonine phosphorylation	BP	1	OSR1,CAMKK2,TNKS1BP1,ULK1,TGFBR2	up_VSAP_EC
GO:0043524	0.432	0.761	4	39	negative regulation of neuron apoptotic process	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIX4	down_ACOR_VSMC
GO:0001659	0.432	0.759	4	54	temperature homeostasis	BP	1	PTGS2,PLCL1,DDIT3,KDM3A	down_VSAP_EC
GO:0002687	0.432	0.762	4	36	positive regulation of leukocyte migration	BP	1	VEGFD,F2RL1,APP,CCL5	up_ACOR_VSMC
GO:0051153	0.432	0.787	3	28	regulation of striated muscle cell differentiation	BP	1	MMP14,EZH2,GREM1	down_ACOR_VSMC
GO:1900407	0.432	0.789	3	24	regulation of cellular response to oxidative	BP	1	FUT8,OXR1,PARK7	up_ACOR_VSMC
GO:0019216	0.432	0.781	3	101	regulation of lipid metabolic process	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC
GO:0003281	0.432	0.787	3	30	ventricular septum development	BP	1	GATA3,PROX1,LUZP1	up_VCAV_EC
GO:0043200	0.432	0.788	3	26	response to amino acid	BP	1	PDGFD,ZEB1,CASTOR1	up_VSAP_EC
GO:2001021	0.432	0.823	2	30	negative regulation of response to DNA damage	BP	1	TMEM161A,FBH1	down_VCAV_EC

GO:0031929	0.432	0.82	2	62	TOR signaling	BP	1	LEP,CLEC16A	up_AFEM_EC
GO:0048589	0.432	0.821	2	188	developmental growth	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0000460	0.432	0.83	2	15	maturation of 5.8S rRNA	BP	1	EXOSC7,RCL1	up_VSAP_EC
GO:0007398	0.432	0.905	1	6	ectoderm development	BP	1	NF2	down_ACOR_VSMC
GO:0051057	0.432	0.898	1	11	positive regulation of small GTPase mediated signal transduction	BP	1	NOTCH2	down_VCAV_EC
GO:0045944	0.432	0.896	1	287	positive regulation of transcription by RNA polymerase II	BP	1	CITED2	down_VPOR_EC
GO:0008053	0.432	0.899	1	10	mitochondrial fusion	BP	1	BNIP3	down_VSAP_EC
GO:0009314	0.432	0.894	1	143	response to radiation	BP	1	HOXA1	up_APUL_EC
GO:0044772	0.432	0.893	1	144	mitotic cell cycle phase transition	BP	1	LZTS1	up_APUL_EC
GO:0036119	0.432	0.905	1	6	response to platelet-derived growth factor	BP	1	YES1	up_VCAV_EC
GO:0036120	0.432	0.905	1	6	cellular response to platelet-derived growth	BP	1	YES1	up_VCAV_EC
GO:0060004	0.432	0.905	1	6	reflex	BP	1	ALDH1A3	up_VCAV_EC
GO:0090025	0.432	0.903	1	7	regulation of monocyte chemotaxis	BP	1	HMGB1	up_VCAV_EC
GO:0006629	0.432	0.899	1	382	lipid metabolic process	BP	1	CYP1A1	up_VCAV_VSMC
GO:0072330	0.432	0.892	1	68	monocarboxylic acid biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0000122	0.432	0.895	1	218	negative regulation of transcription by RNA polymerase II	BP	1	NKX2-5	up_VPOR_VSMC
GO:0042326	0.432	0.894	1	163	negative regulation of phosphorylation	BP	1	FLRT3	up_VPUL_EC
GO:0021800	0.432	0.905	1	6	cerebral cortex tangential migration	BP	1	SLIT2	up_VSAP_EC
GO:0007186	0.432	0.893	1	124	G protein-coupled receptor signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0010256	0.432	0.893	1	129	endomembrane system organization	BP	1	CAV1	up_VSAP_VSMC
GO:0032970	0.432	0.893	1	130	regulation of actin filament-based process	BP	1	CAV1	up_VSAP_VSMC
GO:0099537	0.432	0.893	1	131	trans-synaptic signaling	BP	1	NETO1	up_VSAP_VSMC
GO:0099175	0.432786574	0.8937	1	21	regulation of postsynapse organization	BP	1	LRP4	up_ACOR_EC
GO:0008306	0.432922177	0.89363	1	21	associative learning	BP	1	BRSK1	up_ACOR_EC
GO:0031325	0.433	0.616	79	914	positive regulation of cellular metabolic process	BP	1	ACSL3,HMGB1,SREBF1,IRAK1,ILF3,PPRC1,AAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,U2AF2,SLC29A1,MTDH,CTDNEP1,PRELID1,RFC2,INSIG1,CAV1,CDK1,RFC5,RFC3,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,AURKB,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,SF3B4,CKS2,PDCD2,RNF152,BRCA1,FASTKD3,EIF5A,E2F8,TFRC,PPARD,RAP2C,CYCS,NCL,RAC1,NUP62,EMP2,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,EZR,CLSPN,RBM14,RAD23A,CDC20,PSMC1,AIFM1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0048878	0.433	0.651	24	283	chemical homeostasis	BP	1	EDNRB,ADGRF5,PRCP,CP,ATP2B1,PDE4D,CHD7,GPR4,STC1,EDN1,APLNR,SLC39A8,PDZD8,ABCA1,STMN1,SWAP70,SMARCA4,PLCG2,ADIPOR2,HMGB1,MCU,NR1D2,HIF1A,ATP2A1	up_VCAV_EC
GO:0060429	0.433	0.663	18	341	epithelium development	BP	1	SMAD9,SDC4,KANK2,BMPR1A,LMO4,CLSTN1,SEMA3C,B4GALT1,GLI3,ADAMTSL4,ZFP36L1,IFT57,CDH2,LOXL3,RDH10,GREM1,THRB,BRSK1	down_VCAV_EC
GO:0000904	0.433	0.663	18	181	cell morphogenesis involved in differentiation	BP	1	RADIL,SLIT2,ABL1,PLXNA4,RILPL2,SHOX2,LRP4,DPYSL2,FRMD6,FBLN1,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN,LATS2	up_VSAP_EC
GO:0050790	0.433	0.741	5	532	regulation of catalytic activity	BP	1	ENSCAFG00000002015,ASPN,ACVR2A,ABHD5,ENSCAFG00000032731	up_VPOR_EC

GO:0010565	0.433	0.76	4	40	regulation of cellular ketone metabolic process	BP	1	SREBF1,INSIG1,CAV1,BRCA1	down_ACOR_VSMC
GO:0008584	0.433	0.784	3	39	male gonad development	BP	1	INHBA,SIX4,SPINK2	down_VSAP_EC
GO:0046546	0.433	0.784	3	39	development of primary male sexual	BP	1	INHBA,SIX4,SPINK2	down_VSAP_EC
GO:0097479	0.433	0.784	3	41	synaptic vesicle localization	BP	1	CTNNB1,GSK3B,AP3S1	down_VSAP_EC
GO:0001558	0.433	0.781	3	101	regulation of cell growth	BP	1	PLXNA4,DCUN1D3,ADAM17	up_AFEM_EC
GO:0050708	0.433	0.781	3	101	regulation of protein secretion	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:0034333	0.433	0.788	3	25	adherens junction assembly	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0097300	0.433	0.827	2	17	programmed necrotic cell death	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:1900408	0.433	0.829	2	15	negative regulation of cellular response to	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:1902895	0.433	0.829	2	15	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:1903202	0.433	0.829	2	15	negative regulation of oxidative stress-induced	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0001960	0.433	0.829	2	15	negative regulation of cytokine-mediated	BP	1	SLIT2,F2RL1	up_VSAP_EC
GO:0003407	0.433	0.829	2	15	neural retina development	BP	1	THRB,IRX5	up_VSAP_EC
GO:1902369	0.433	0.829	2	15	negative regulation of RNA catabolic process	BP	1	AXIN2,TENT5C	up_VSAP_EC
GO:2000772	0.433	0.829	2	15	regulation of cellular senescence	BP	1	ABL1,YPEL3	up_VSAP_EC
GO:0043537	0.433	0.829	2	15	negative regulation of blood vessel endothelial	BP	1	TBXA2R,ACVRL1	up_VSAP_EC
GO:0060761	0.433	0.829	2	15	negative regulation of response to cytokine	BP	1	SLIT2,F2RL1	up_VSAP_EC
GO:0010975	0.433	0.892	1	103	regulation of neuron projection development	BP	1	LYN	down_ACOR_EC
GO:0034504	0.433	0.892	1	111	protein localization to nucleus	BP	1	IPO7	down_ACOR_EC
GO:0006448	0.433	0.902	1	7	regulation of translational elongation	BP	1	EIF5A	down_ACOR_VSMC
GO:1903047	0.433	0.895	1	257	mitotic cell cycle process	BP	1	GPSM2	down_AFEM_EC
GO:0009994	0.433	0.898	1	11	oocyte differentiation	BP	1	FOXO3	down_VCAV_EC
GO:0030835	0.433	0.897	1	11	negative regulation of actin filament	BP	1	PLEKHH2	down_VCAV_EC
GO:0001958	0.433	0.898	1	11	endochondral ossification	BP	1	NAB2	down_VCAV_EC
GO:0036075	0.433	0.898	1	11	replacement ossification	BP	1	NAB2	down_VCAV_EC
GO:0060351	0.433	0.898	1	11	cartilage development involved in endochondral bone morphogenesis	BP	1	THBS3	down_VCAV_EC
GO:0071526	0.433	0.897	1	12	semaphorin-plexin signaling pathway	BP	1	SEMA3C	down_VCAV_EC
GO:0021904	0.433	0.899	1	9	dorsal/ventral neural tube patterning	BP	1	PRKACB	down_VSAP_EC
GO:0042023	0.433	0.901	1	8	DNA endoreduplication	BP	1	ZPR1	down_VSAP_EC
GO:0045920	0.433	0.899	1	9	negative regulation of exocytosis	BP	1	REST	down_VSAP_EC
GO:0034122	0.433	0.899	1	9	negative regulation of toll-like receptor signaling	BP	1	LYN	down_VSAP_EC
GO:0043302	0.433	0.904	1	6	positive regulation of leukocyte degranulation	BP	1	F2RL1	up_ACOR_VSMC
GO:0060009	0.433	0.908	1	5	Sertoli cell development	BP	1	ATRX	up_ACOR_VSMC
GO:0060394	0.433	0.905	1	6	negative regulation of pathway-restricted SMAD protein phosphorylation	BP	1	SMAD6	up_ACOR_VSMC
GO:0055065	0.433	0.893	1	145	metal ion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0010934	0.433	0.903	1	7	macrophage cytokine production	BP	1	TLR4	up_VCAV_EC
GO:0034105	0.433	0.905	1	6	positive regulation of tissue remodeling	BP	1	PPP3CA	up_VCAV_EC
GO:0051764	0.433	0.905	1	6	actin crosslink formation	BP	1	BAIAP2L1	up_VCAV_EC

GO:0072348	0.433	0.904	1	6	sulfur compound transport	BP	1	LRRC8D	up_VCAV_EC
GO:0080134	0.433	0.898	1	386	regulation of response to stress	BP	1	C6	up_VCAV_VSMC
GO:0032984	0.433	0.892	1	70	protein-containing complex disassembly	BP	1	ARHGEF2	up_VPOR_EC
GO:0001775	0.433	0.894	1	219	cell activation	BP	1	CYP26B1	up_VPOR_VSMC
GO:0071396	0.433	0.892	1	134	cellular response to lipid	BP	1	CYP26B1	up_VFEM_EC
GO:0009117	0.433	0.894	1	208	nucleotide metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0031641	0.433	0.904	1	6	regulation of myelination	BP	1	WASF3	up_VSAP_EC
GO:0036336	0.433	0.905	1	6	dendritic cell migration	BP	1	ARHGEF5	up_VSAP_EC
GO:0051899	0.433210682	0.89327	1	22	membrane depolarization	BP	1	IFI6	up_ACOR_EC
GO:0051291	0.433226373	0.89346	1	21	protein heterooligomerization	BP	1	TRPS1	up_ACOR_EC
GO:0010647	0.433407462	0.67801	13	460	positive regulation of cell communication	BP	1	CDH3,NR1H4,SOX9,FZD5,DIXDC1,NOD2,ESM1,TNFRSF19,MAVS,SH3RF3,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0048523	0.434	0.608	120	1399	negative regulation of cellular process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,SREBF2,SMC1A,HINFP,NEDD4,WDR76,U2AF2,ZW10,INTS7,MNDA,CAPG,SLC29A1,MTDH,PPM1G,TRIP13,SLC25A5,PPP1R15B,PARPBP,FBXO5,HSPA9,NAB2,PRELID1,BIRC5,INSIG1,PRMT1,CAV1,CDK1,CASP2,FANCI,TIMELESS,THRAP3,LIMA1,FAM129B,NF2,AURKB,MMP14,CDKN2C,TOPBP1,EZH2,STMN1,GREM1,MAP3K20,NEK2,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,HMGB3,HOXA7,ARG2,UHRF1,RNF152,GMNN,DHCR24,BRCA1,NOC2L,E2F8,B4GALT1,PPARD,NDC80,RAP2C,YWHAB,NCL,NUP62,DTL,PRR11,IQGAP1,SUV39H1,CACTIN,HMGB2,GSTO1,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,ENSCAFG00000005299,EZR,CLSPN,BUB1,RBM14,CORO1A,BEND6,PHACTR4,TTK,ERF,ASPM,TCERG1,ENSCAFG00000010224,TXNDC12,CTH,NCOA5,ARHGEF2,KNL1,TWIST2,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,H2AFX,CDC5L,ATRIP,CDKN3,SIX4,MTBP,ZWINT,GEN1,AMER1	down_ACOR_VSMC
GO:0043043	0.434	0.648	25	247	peptide biosynthetic process	BP	1	PRR16,MRPL37,WARS2,PYM1,ZFP36L1,EEF2,LARP6,RPL13,ANKHD1,FARS2,UBA52,RPUSD4,RPL15,EIF3G,SAMD4B,ZFP36L2,EIF3K,EIF3L,QARS,EIF3D,TNRC6C,COA1,NCK1,MRPL4,LARS2	up_VSAP_EC
GO:0040007	0.434	0.662	18	276	growth	BP	1	CELF1,ENPP1,PTPN11,IFRD1,TMED2,SMARCA4,SESN2,HIF1A,ZPR1,ESM1,ADAM17,CTNNB1,WWC3,IGFBP7,INHBA,SIX4,CDKN1A,NRP1	down_VSAP_EC
GO:0010556	0.434	0.698	10	1137	regulation of macromolecule biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:1902275	0.434	0.728	6	60	regulation of chromatin organization	BP	1	SREBF1,ATAD2,UHRF1,BRCA1,NOC2L,TADA2A	down_ACOR_VSMC
GO:0043902	0.434	0.742	5	45	positive regulation of multi-organism process	BP	1	F2RL1,CFAP69,SASH1,PC,CYBA	up_VSAP_EC
GO:0033002	0.434	0.757	4	55	muscle cell proliferation	BP	1	SULF1,CTNNB1,ENSCAFG00000017326,CDKN1A	down_VSAP_EC
GO:2001022	0.434	0.759	4	42	positive regulation of response to DNA damage	BP	1	TIMELESS,HMGB1,PMAIP1,SKIL	up_VCAV_EC
GO:0051492	0.434	0.786	3	28	regulation of stress fiber assembly	BP	1	NF2,STMN1,RAC1	down_ACOR_VSMC
GO:0032481	0.434	0.788	3	24	positive regulation of type I interferon production	BP	1	PLCG2,TLR3,PTPN22	up_ACOR_VSMC
GO:0010822	0.434	0.785	3	31	positive regulation of mitochondrion	BP	1	SH3GLB1,PMAIP1,HIF1A	up_VCAV_EC
GO:0035239	0.434	0.781	3	299	tube morphogenesis	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:1903312	0.434	0.787	3	25	negative regulation of mRNA metabolic process	BP	1	AXIN2,TENT5C,CDK9	up_VSAP_EC
GO:0070301	0.434	0.787	3	25	cellular response to hydrogen peroxide	BP	1	ABL1,MAP3K5,ZNF580	up_VSAP_EC
GO:0006904	0.434	0.828	2	15	vesicle docking involved in exocytosis	BP	1	SCFD2,VPS11	up_VSAP_EC

GO:0002260	0.434	0.828	2	15	lymphocyte homeostasis	BP	1	ABL1,PPP3CB	up_VSAP_EC
GO:0030194	0.434	0.899	1	9	positive regulation of blood coagulation	BP	1	SERPINE1	down_VSAP_EC
GO:1900048	0.434	0.899	1	9	positive regulation of hemostasis	BP	1	SERPINE1	down_VSAP_EC
GO:0009968	0.434	0.898	1	392	negative regulation of signal transduction	BP	1	EYA1	up_AFEM_VSMC
GO:0032787	0.434	0.892	1	144	monocarboxylic acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0010664	0.434	0.904	1	6	negative regulation of striated muscle cell	BP	1	RGL2	up_VCAV_EC
GO:0036490	0.434	0.904	1	6	regulation of translation in response to endoplasmic reticulum	BP	1	NCK1	up_VCAV_EC
GO:0044848	0.434	0.904	1	6	biological phase	BP	1	FERMT1	up_VCAV_EC
GO:0044851	0.434	0.904	1	6	hair cycle phase	BP	1	FERMT1	up_VCAV_EC
GO:0048819	0.434	0.904	1	6	regulation of hair follicle maturation	BP	1	FERMT1	up_VCAV_EC
GO:0006325	0.434	0.893	1	234	chromatin organization	BP	1	EYA1	up_VFEM_VSMC
GO:0097190	0.434	0.893	1	217	apoptotic signaling pathway	BP	1	EYA1	up_VFEM_VSMC
GO:0010884	0.434	0.904	1	6	positive regulation of lipid storage	BP	1	ACACB	up_VSAP_EC
GO:0002718	0.434002272	0.89304	1	21	regulation of cytokine production involved in	BP	1	FZD5	up_ACOR_EC
GO:0097061	0.434226037	0.89292	1	21	dendritic spine organization	BP	1	PAK3	up_ACOR_EC
GO:0021536	0.43449454	0.89277	1	21	diencephalon development	BP	1	NRP1	up_ACOR_EC
GO:0051338	0.435	0.643	29	288	regulation of transferase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,EIF4A2,LATS2,PDE5A,SASH1,LMO4,FGF18,CDKN2B,CDKN1A,SMPD1,CCNT1,FRS2,APP,PSEN1,DDR2,DUSP22,EDN1,DUSP26,LRRC4,PRKAG3,DCUN1D4,MAP3K7,INPP5K,PARK7,HMBOX1	up_ACOR_VSMC
GO:0045944	0.435	0.658	19	287	positive regulation of transcription by RNA polymerase II	BP	1	ARHGEF2,VEGFA,PPP1R12A,SMARCA4,SESN2,HIF1A,YES1,PEG3,CNOT7,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,KDM3A	down_VSAP_EC
GO:0007420	0.435	0.667	16	169	brain development	BP	1	PTCHD1,RELN,CHD7,HOOK3,BMP2,HHEX,GDPD5,PROX1,ENSCAFG00000010224,APOD,RAPGEF2,CREB1,HIF1A,ATRX,ALDH1A3,CDON	up_VCAV_EC
GO:0032787	0.435	0.678	13	144	monocarboxylic acid metabolic process	BP	1	SCD,SREBF1,INSIG1,CAV1,BRCA1,ELOVL1,PPARD,ELOVL6,SGPL1,PDHA1,LIPC,PGD,ACADL	down_ACOR_VSMC
GO:0065007	0.435	0.716	13	3499	biological regulation	BP	1	TBX5,HOXA3,NR1H4,EVI2B,RGS1,STK32B,WIF1,CCL24,HTR7,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0010942	0.435	0.685	11	200	positive regulation of cell death	BP	1	LRP1,PRNP,CLIP3,B4GALT1,PARK7,ADAMTSL4,IFT57,GSDME,FBH1,FOXO3,ZBTB16	down_VCAV_EC
GO:0009123	0.435	0.687	11	104	nucleoside monophosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,NT5C2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0071559	0.435	0.715	7	75	response to transforming growth factor beta	BP	1	MEF2C,FERMT1,SMAD1,YES1,SKIL,ENSCAFG00000002015,ZEB1	up_VCAV_EC
GO:1903037	0.435	0.716	7	65	regulation of leukocyte cell-cell adhesion	BP	1	CD274,ZBTB16,CD83,PNP,ASS1,NCK1,TGFBR2	up_VSAP_EC
GO:0048638	0.435	0.724	6	82	regulation of developmental growth	BP	1	CELF1,PTPN11,IFRD1,WWC3,SIX4,NRP1	down_VSAP_EC
GO:0009966	0.435	0.763	4	868	regulation of signal transduction	BP	1	NR1H4,ARHGEF26,NPNT,NTRK2	up_APUL_EC
GO:0022607	0.435	0.765	4	969	cellular component assembly	BP	1	NR1H4,MYBPC2,CCL24,FLRT3	up_VPUL_EC
GO:0071621	0.435	0.785	3	27	granulocyte chemotaxis	BP	1	HRH1,CCL5,JAM3	up_ACOR_VSMC
GO:0098773	0.435	0.785	3	29	skin epidermis development	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:2000177	0.435	0.785	3	26	regulation of neural precursor cell	BP	1	CDON,LIMS2,KDM2B	up_VSAP_EC
GO:0044728	0.435	0.826	2	17	DNA methylation or demethylation	BP	1	EZH2,MIS18A	down_ACOR_VSMC
GO:0016575	0.435	0.823	2	23	histone deacetylation	BP	1	MORF4L2,REST	down_VSAP_EC
GO:1905898	0.435	0.827	2	16	positive regulation of response to endoplasmic	BP	1	SERINC3,HERPUD1	up_ACOR_VSMC

GO:0030041	0.435	0.818	2	62	actin filament polymerization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0001654	0.435	0.891	1	110	eye development	BP	1	ACVRL1	down_ACOR_EC
GO:0048880	0.435	0.891	1	110	sensory system development	BP	1	ACVRL1	down_ACOR_EC
GO:0150063	0.435	0.891	1	110	visual system development	BP	1	ACVRL1	down_ACOR_EC
GO:0061550	0.435	0.904	1	6	cranial ganglion development	BP	1	SIX4	down_ACOR_VSMC
GO:0019941	0.435	0.894	1	258	modification-dependent protein catabolic process	BP	1	USP33	down_AFEM_EC
GO:0080090	0.435	0.938	1	1734	regulation of primary metabolic process	BP	1	CST3	down_AORT_EC
GO:0021983	0.435	0.896	1	11	pituitary gland development	BP	1	BMPR1A	down_VCAV_EC
GO:0043243	0.435	0.896	1	11	positive regulation of protein complex	BP	1	CLEC16A	down_VCAV_EC
GO:0060441	0.435	0.896	1	11	epithelial tube branching involved in lung	BP	1	RDH10	down_VCAV_EC
GO:0070233	0.435	0.898	1	9	negative regulation of T cell apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:0021873	0.435	0.907	1	5	forebrain neuroblast division	BP	1	FGFR2	up_ACOR_VSMC
GO:0002312	0.435	0.892	1	24	B cell activation involved in immune response	BP	1	DLL1	up_AFEM_EC
GO:0032270	0.435	0.9	1	479	positive regulation of cellular protein metabolic	BP	1	WNT7A	up_AORT_VSMC
GO:0031347	0.435	0.891	1	144	regulation of defense response	BP	1	NR1H4	up_APUL_EC
GO:0010998	0.435	0.904	1	6	regulation of translational initiation by eIF2 alpha phosphorylation	BP	1	NCK1	up_VCAV_EC
GO:0035728	0.435	0.904	1	6	response to hepatocyte growth factor	BP	1	CREB1	up_VCAV_EC
GO:0035729	0.435	0.904	1	6	cellular response to hepatocyte growth factor	BP	1	CREB1	up_VCAV_EC
GO:0060330	0.435	0.904	1	6	regulation of response to interferon-gamma	BP	1	NLRC5	up_VCAV_EC
GO:0060334	0.435	0.904	1	6	regulation of interferon-gamma-mediated	BP	1	NLRC5	up_VCAV_EC
GO:0070741	0.435	0.904	1	6	response to interleukin-6	BP	1	ST3GAL6	up_VCAV_EC
GO:0071354	0.435	0.904	1	6	cellular response to interleukin-6	BP	1	ST3GAL6	up_VCAV_EC
GO:0048863	0.435	0.891	1	70	stem cell differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0071900	0.435	0.891	1	131	regulation of protein serine/threonine kinase	BP	1	CAV1	up_VSAP_VSMC
GO:0043242	0.435268604	0.89235	1	21	negative regulation of protein complex	BP	1	TMOD1	up_ACOR_EC
GO:0006900	0.435417703	0.89226	1	21	vesicle budding from membrane	BP	1	PREB	up_ACOR_EC
GO:0006325	0.4356781	0.71169	7	234	chromatin organization	BP	1	NR1H4,SOX9,PHF20,ZMYND8,RIOX2,PRKCD,PYGO2	up_ACOR_EC
GO:0080090	0.436	0.679	15	1734	regulation of primary metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ABHD5,PUM3,EIF5,CCAR1,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0031347	0.436	0.703	8	144	regulation of defense response	BP	1	CHID1,RNF216,PARK7,CYBA,MAVS,RAB7B,A2M,NAPEPLD	down_VCAV_EC
GO:0010721	0.436	0.706	8	73	negative regulation of cell development	BP	1	ITM2C,ZNF365,NRP1,ULK2,APP,PSEN1,ASAP1,B2M	up_ACOR_VSMC
GO:0031175	0.436	0.722	6	224	neuron projection development	BP	1	PLXNA4,NEFH,CAMK2A,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0019722	0.436	0.74	5	45	calcium-mediated signaling	BP	1	PTGFR,TBC1D10C,CAMKK2,PDK2,PPP3CB	up_VSAP_EC
GO:0019079	0.436	0.784	3	29	viral genome replication	BP	1	ILF3,RAD23A,PPIH	down_ACOR_VSMC
GO:1901888	0.436	0.784	3	29	regulation of cell junction assembly	BP	1	CAV1,GREM1,RAC1	down_ACOR_VSMC
GO:2000045	0.436	0.784	3	29	regulation of G1/S transition of mitotic cell	BP	1	CASP2,EZH2,MTBP	down_ACOR_VSMC
GO:1903725	0.436	0.821	2	30	regulation of phospholipid metabolic process	BP	1	PDGFRB,ENSCAFG00000014978	down_VCAV_EC
GO:0006801	0.436	0.827	2	15	superoxide metabolic process	BP	1	F2RL1,PARK7	up_ACOR_VSMC
GO:0030808	0.436	0.827	2	15	regulation of nucleotide biosynthetic process	BP	1	PPARGC1A,DDIT4	up_ACOR_VSMC

GO:1900371	0.436	0.827	2	15	regulation of purine nucleotide biosynthetic	BP	1	PPARGC1A,DDIT4	up_ACOR_VSMC
GO:1902743	0.436	0.826	2	16	regulation of lamellipodium	BP	1	ENPP2,SLIT2	up_VSAP_EC
GO:0035542	0.436	0.903	1	6	regulation of SNARE complex assembly	BP	1	STXBP6	down_ACOR_VSMC
GO:0018195	0.436	0.903	1	6	peptidyl-arginine modification	BP	1	PARK7	up_ACOR_VSMC
GO:0071786	0.436	0.903	1	6	endoplasmic reticulum tubular network	BP	1	LNPK	up_ACOR_VSMC
GO:0072091	0.436	0.891	1	24	regulation of stem cell proliferation	BP	1	OVOL1	up_AFEM_EC
GO:0080135	0.436	0.893	1	240	regulation of cellular response to stress	BP	1	TAOK1	up_AORT_EC
GO:0030277	0.436	0.901	1	7	maintenance of gastrointestinal	BP	1	TLR4	up_VCAV_EC
GO:0048009	0.436	0.899	1	8	insulin-like growth factor receptor signaling	BP	1	BMP2	up_VCAV_EC
GO:0051216	0.436	0.89	1	70	cartilage development	BP	1	HOXA3	up_VPOR_EC
GO:0051960	0.436	0.893	1	216	regulation of nervous system development	BP	1	NKX2-5	up_VPOR_VSMC
GO:0033160	0.436	0.903	1	6	positive regulation of protein import into	BP	1	MAVS	up_VSAP_EC
GO:0032623	0.436075199	0.8919	1	21	interleukin-2 production	BP	1	NR1H4	up_ACOR_EC
GO:0014812	0.436353816	0.89175	1	21	muscle cell migration	BP	1	SEMA6D	up_ACOR_EC
GO:0048583	0.437	0.621	56	1095	regulation of response to stimulus	BP	1	NOTCH2,PDGFRB,SLC35F6,DCN,CFD,PRNP,VASN,FBN1,GLIPR2,BGN,KANK2,BMPR1A,EVC,RECK,IGFBP6,CHID1,ARHGEF25,ENSCAFG00000014978,AKT1S1,CHRDL1,AKT2,CLSTN1,CSPG4,PRMT6,TMEM161A,ASPN,THY1,RNF216,ATP6V0C,GLI3,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,FUT8,NCLN,SPRED1,RAB7B,A2M,GLIS2,SHC1,FBH1,GREM1,NPHP4,RAC2,NAPEPLD,FOXO3,ANKRD54,RGMA,CDK14	down_VCAV_EC
GO:0007005	0.437	0.66	18	175	mitochondrion organization	BP	1	DDHD1,NDUFS7,AMBRA1,MFN2,FXN,DMAC2,POLDIP2,NDUFAF3,NDUFB10,FBXO7,MTFR1L,ZNF205,SMIM20,HTRA2,COA1,BAG4,FUNDC2,CLUH	up_VSAP_EC
GO:0001659	0.437	0.725	6	54	temperature homeostasis	BP	1	LEP,PLCL1,GJA1,PPARGC1A,PLAC8B,IL18R1	up_ACOR_VSMC
GO:0017157	0.437	0.755	4	58	regulation of exocytosis	BP	1	LYN,GSK3B,SDC4,REST	down_VSAP_EC
GO:0001932	0.437	0.755	4	416	regulation of protein phosphorylation	BP	1	ARHGEF2,ASPN,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0051017	0.437	0.779	3	49	actin filament bundle assembly	BP	1	RHOD,ENSCAFG00000014978,MYO1B	down_VCAV_EC
GO:0019218	0.437	0.784	3	25	regulation of steroid metabolic process	BP	1	LEP,DKKL1,LMF1	up_ACOR_VSMC
GO:0048518	0.437	0.804	3	1676	positive regulation of biological process	BP	1	TLR2,EYA1,HOXA9	up_AFEM_VSMC
GO:1901360	0.437	0.814	3	2016	organic cyclic compound metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0043933	0.437	0.785	3	698	protein-containing complex subunit	BP	1	MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0055025	0.437	0.824	2	17	positive regulation of cardiac muscle tissue	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0031324	0.437	0.827	2	735	negative regulation of cellular metabolic process	BP	1	CST3,HDAC7	down_VPOR_EC
GO:0002532	0.437	0.821	2	25	production of molecular mediator involved in inflammatory response	BP	1	SERPINE1,GBP5	down_VSAP_EC
GO:0032495	0.437	0.826	2	15	response to muramyl dipeptide	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0044843	0.437	0.817	2	62	cell cycle G1/S phase transition	BP	1	CAMK2A,DCUN1D3	up_AFEM_EC
GO:2001242	0.437	0.817	2	62	regulation of intrinsic apoptotic signaling	BP	1	PLAGL2,CYLD	up_AFEM_EC
GO:0001822	0.437	0.89	1	98	kidney development	BP	1	SULF1	down_ACOR_EC
GO:1901652	0.437	0.89	1	105	response to peptide	BP	1	IGF1R	down_ACOR_EC
GO:0006353	0.437	0.9	1	7	DNA-templated transcription, termination	BP	1	PRMT5	down_ACOR_VSMC
GO:0060572	0.437	0.895	1	11	morphogenesis of an epithelial bud	BP	1	RDH10	down_VCAV_EC

GO:0071359	0.437	0.895	1	11	cellular response to dsRNA	BP	1	MAVS	down_VCAV_EC
GO:0010224	0.437	0.897	1	9	response to UV-B	BP	1	CDKN1A	down_VSAP_EC
GO:0071545	0.437	0.903	1	6	inositol phosphate catabolic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0097286	0.437	0.902	1	6	iron ion import	BP	1	B2M	up_ACOR_VSMC
GO:0038202	0.437	0.891	1	24	TORC1 signaling	BP	1	CLEC16A	up_AFEM_EC
GO:0048008	0.437	0.891	1	24	platelet-derived growth factor receptor signaling	BP	1	F3	up_AFEM_EC
GO:0048812	0.437	0.89	1	151	neuron projection morphogenesis	BP	1	SLITRK5	up_APUL_EC
GO:0016926	0.437	0.903	1	6	protein desumoylation	BP	1	SENP6	up_VCAV_EC
GO:0031268	0.437	0.897	1	9	pseudopodium organization	BP	1	ENSCAFG00000010224	up_VCAV_EC
GO:0031269	0.437	0.897	1	9	pseudopodium assembly	BP	1	ENSCAFG00000010224	up_VCAV_EC
GO:1903307	0.437	0.899	1	8	positive regulation of regulated secretory	BP	1	RAB27A	up_VCAV_EC
GO:0008064	0.437	0.889	1	72	regulation of actin polymerization or	BP	1	TWF1	up_VPOR_EC
GO:0030832	0.437	0.889	1	72	regulation of actin filament length	BP	1	TWF1	up_VPOR_EC
GO:0032103	0.437	0.889	1	69	positive regulation of response to external	BP	1	C3AR1	up_VPOR_EC
GO:0099536	0.437	0.89	1	133	synaptic signaling	BP	1	NETO1	up_VSAP_VSMC
GO:0043967	0.43740937	0.89117	1	21	histone H4 acetylation	BP	1	PHF20	up_ACOR_EC
GO:0043550	0.437944594	0.89087	1	21	regulation of lipid kinase activity	BP	1	ENSCAFG00000004331	up_ACOR_EC
GO:0051641	0.438	0.627	44	858	cellular localization	BP	1	SNX18,LRP1,PRNP,TMEM230,TLN2,NABP2,CLIP3,RHOD,ENSCAFG00000014978,ERGIC1,AKT2,MICALL2,SNUPN,SSR2,SCP2,TRIM8,THY1,CLTB,SSR3,WDR45,PEX5,GLI3,PARK7,YIF1A,ZFP36L1,CYBA,ARL2BP,IFT57,MAVS,CDH2,TOM1,MGARP,RAB7B,SEC61B,GLIS2,RAB31,HM13,ARHGAP1,EVI5L,LONP2,RAC2,ANKRD54,SEC61A1,BRSK1	down_VCAV_EC
GO:0006811	0.438	0.635	33	330	ion transport	BP	1	AMIGO1,CALHM2,SLC8B1,GABRE,TPCN2,NIPAL3,SLC6A4,ABL1,SLC16A12,KCNE3,CHRM1,OSR1,CLIC5,ABCB11,CCS,KLHL24,SLC25A12,RAB11B,SLC25A28,CRACR2B,SLC27A6,CTNS,SCARA5,SLC10A6,NIPAL1,CLCN2,STEAP3,KCNB1,FTL,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0045860	0.438	0.694	9	132	positive regulation of protein kinase activity	BP	1	VEGFA,PTPN11,TNIK,ADAM17,MAGED1,MMD,VLDLR,PAK2,MADD	down_VSAP_EC
GO:0030336	0.438	0.696	9	86	negative regulation of cell migration	BP	1	HOXA7,WNT11,C5AR2,SLIT2,CDH1,FUZ,RECK,TBXA2R,ACVRL1	up_VSAP_EC
GO:0033036	0.438	0.741	5	852	macromolecule localization	BP	1	LYN,IPO7,ACSL3,STX4,NEDD4	down_ACOR_EC
GO:0018393	0.438	0.738	5	51	internal peptidyl-lysine acetylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:0061005	0.438	0.782	3	28	cell differentiation involved in kidney	BP	1	GREM1,IQGAP1,AMER1	down_ACOR_VSMC
GO:0030856	0.438	0.78	3	41	regulation of epithelial cell differentiation	BP	1	SERPINE1,ERRFI1,CTNNB1	down_VSAP_EC
GO:0050871	0.438	0.785	3	24	positive regulation of B cell activation	BP	1	TP53BP1,CDKN1A,NOD2	up_ACOR_VSMC
GO:0050954	0.438	0.819	2	30	sensory perception of mechanical stimulus	BP	1	ENSCAFG00000017708,THRB	down_VCAV_EC
GO:0060425	0.438	0.82	2	25	lung morphogenesis	BP	1	CTNNB1,PLOD3	down_VSAP_EC
GO:2000785	0.438	0.825	2	16	regulation of autophagosome assembly	BP	1	FEZ1,FEZ2	up_ACOR_VSMC
GO:0050679	0.438	0.816	2	62	positive regulation of epithelial cell proliferation	BP	1	F3,ADAM17	up_AFEM_EC
GO:0098900	0.438	0.825	2	15	regulation of action potential	BP	1	KCNE3,KCNB1	up_VSAP_EC
GO:0022618	0.438	0.89	1	111	ribonucleoprotein complex assembly	BP	1	RPSA	down_ACOR_EC
GO:0051179	0.438	0.937	1	1747	localization	BP	1	SCAMP4	down_AORT_EC
GO:2000649	0.438	0.895	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	FXYD1	down_VCAV_EC

GO:0007263	0.438	0.898	1	8	nitric oxide mediated signal transduction	BP	1	APOE	down_VSAP_EC
GO:0045683	0.438	0.897	1	9	negative regulation of epidermis development	BP	1	INHBA	down_VSAP_EC
GO:0046068	0.438	0.905	1	5	cGMP metabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:0007584	0.438	0.89	1	24	response to nutrient	BP	1	POSTN	up_AFEM_EC
GO:0015698	0.438	0.89	1	24	inorganic anion transport	BP	1	CLIC4	up_AFEM_EC
GO:0030512	0.438	0.89	1	24	negative regulation of transforming growth factor beta receptor	BP	1	ADAM17	up_AFEM_EC
GO:1903845	0.438	0.89	1	24	negative regulation of cellular response to transforming growth	BP	1	ADAM17	up_AFEM_EC
GO:0009607	0.438	0.892	1	232	response to biotic stimulus	BP	1	BPI	up_AORT_EC
GO:0090322	0.438	0.9	1	7	regulation of superoxide metabolic process	BP	1	GCH1	up_VCAV_EC
GO:2001044	0.438	0.898	1	8	regulation of integrin-mediated signaling	BP	1	CTNNA1	up_VCAV_EC
GO:0030036	0.438	0.892	1	223	actin cytoskeleton organization	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006753	0.438	0.892	1	211	nucleoside phosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0043254	0.438	0.891	1	164	regulation of protein complex assembly	BP	1	CCL24	up_VPUL_EC
GO:1903530	0.438	0.89	1	165	regulation of secretion by cell	BP	1	NR1H4	up_VPUL_EC
GO:0051090	0.438	0.889	1	134	regulation of DNA-binding transcription factor	BP	1	TLR2	up_VSAP_VSMC
GO:0009247	0.438416735	0.8904	1	22	glycolipid biosynthetic process	BP	1	PIGS	up_ACOR_EC
GO:0018209	0.438876901	0.75084	4	125	peptidyl-serine modification	BP	1	PLCL1,DCLK2,STK32C,PRKCD	up_ACOR_EC
GO:0051276	0.439	0.631	36	398	chromosome organization	BP	1	IWS1,CHD7,GATA3,RAB11A,PSME4,NASP,HHEX,UHRF2,ARID4B,HMBOX1,BAZ1A,PRKD2,SMARCA4,CENPC,ESCO1,NSD1,HIST1H1A,TOP1,SENP6,SMG7,ASF1A,HMGB1,BLM,NUP133,SMC5,RAD21,ZW10,KDM5A,KDM3A,ATRX,HIST2H2AC,HP1BP3,DCP2,TET2,FBXO5,GINS4	up_VCAV_EC
GO:0009259	0.439	0.661	17	166	ribonucleotide metabolic process	BP	1	ACSM3,ACACB,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0009058	0.439	0.711	9	1910	biosynthetic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3,CHST7	up_VFEM_EC
GO:2001235	0.439	0.712	7	69	positive regulation of apoptotic signaling	BP	1	NACC2,ITM2C,TP53INP1,BNIP3,SIAH1,SERINC3,PARK7	up_ACOR_VSMC
GO:0009416	0.439	0.721	6	88	response to light stimulus	BP	1	BHLHE40,HIF1A,GNAQ,EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0046907	0.439	0.736	5	536	intracellular transport	BP	1	HOOK3,XPOT,GCC2,SRP54,TMEM87B	up_VPOR_EC
GO:1903305	0.439	0.757	4	36	regulation of regulated secretory pathway	BP	1	FBXL20,F2RL1,SCAMP5,PREPL	up_ACOR_VSMC
GO:0045807	0.439	0.756	4	35	positive regulation of endocytosis	BP	1	DLL1,F2RL1,CYBA,FLOT1	up_VSAP_EC
GO:0042773	0.439	0.781	3	32	ATP synthesis coupled electron transport	BP	1	CDK1,CYCS,CYC1	down_ACOR_VSMC
GO:0045598	0.439	0.778	3	47	regulation of fat cell differentiation	BP	1	ZFP36L1,NAPEPLD,ZBTB16	down_VCAV_EC
GO:1905037	0.439	0.778	3	47	autophagosome organization	BP	1	GABARAP,WDR45,EMC6	down_VCAV_EC
GO:0046486	0.439	0.776	3	102	glycerolipid metabolic process	BP	1	GPAM,NAPEPLD,AGPAT2	up_AFEM_EC
GO:0002376	0.439	0.783	3	622	immune system process	BP	1	NR1H4,BPI,HOXA3	up_APUL_EC
GO:0042327	0.439	0.817	2	289	positive regulation of phosphorylation	BP	1	ACVRL1,LYN	down_ACOR_EC
GO:0045599	0.439	0.822	2	19	negative regulation of fat cell differentiation	BP	1	GATA3,JAG1	up_VCAV_EC
GO:0032413	0.439	0.825	2	15	negative regulation of ion transmembrane transporter activity	BP	1	KCNE3,OSR1	up_VSAP_EC
GO:0045123	0.439	0.894	1	11	cellular extravasation	BP	1	THY1	down_VCAV_EC
GO:0048878	0.439	0.892	1	283	chemical homeostasis	BP	1	RAB11B	down_VPOR_EC

GO:0005979	0.439	0.896	1	9	regulation of glycogen biosynthetic process	BP	1	ENPP1	down_VSAP_EC
GO:0010962	0.439	0.896	1	9	regulation of glucan biosynthetic process	BP	1	ENPP1	down_VSAP_EC
GO:0070873	0.439	0.896	1	9	regulation of glycogen metabolic process	BP	1	ENPP1	down_VSAP_EC
GO:0086065	0.439	0.902	1	6	cell communication involved in cardiac	BP	1	JUP	up_ACOR_VSMC
GO:0009081	0.439	0.902	1	6	branched-chain amino acid metabolic process	BP	1	ENSCAFG00000002977	up_ACOR_VSMC
GO:0042159	0.439	0.901	1	6	lipoprotein catabolic process	BP	1	LYPLAL1	up_ACOR_VSMC
GO:0001658	0.439	0.89	1	24	branching involved in ureteric bud	BP	1	GREM1	up_AFEM_EC
GO:0000165	0.439	0.891	1	236	MAPK cascade	BP	1	TAOK1	up_AORT_EC
GO:0009108	0.439	0.888	1	68	coenzyme biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0070914	0.439	0.902	1	6	UV-damage excision repair	BP	1	DDB2	up_VSAP_EC
GO:0051098	0.439	0.889	1	129	regulation of binding	BP	1	CAV1	up_VSAP_VSMC
GO:0060047	0.439668421	0.81508	2	57	heart contraction	BP	1	GNAO1,RNLS	up_ACOR_EC
GO:0023056	0.439755036	0.67214	13	462	positive regulation of signaling	BP	1	CDH3,NR1H4,SOX9,FZD5,DIXDC1,NOD2,ESM1,TNFRSF19,MAVS,SH3RF3,CLU,NRP1,PRKCD	up_ACOR_EC
GO:0044770	0.44	0.669	14	161	cell cycle phase transition	BP	1	PLK2,RAB11A,PPP3CA,TIMELESS,TAOK1,BLM,RAD21,RAD17,USP37,CUL4A,ZW10,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0019438	0.44	0.689	11	1258	aromatic compound biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0044403	0.44	0.687	10	116	symbiont process	BP	1	CXCL8,TNIP1,IRF8,GUCY1A1,NECTIN2,PROX1,THOC1,SMARCA4,CNOT7,USP6NL	up_VCAV_EC
GO:0023061	0.44	0.688	10	95	signal release	BP	1	HNF4A,SLC8B1,RAB11B,PASK,KCNB1,RAF1,STX4,KCNC4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0000902	0.44	0.708	7	266	cell morphogenesis	BP	1	PLXNA4,GREM1,CAMK2A,BVES,CDC42EP5,LRRN2,KANK1	up_AFEM_EC
GO:0006261	0.44	0.711	7	68	DNA-dependent DNA replication	BP	1	BAZ1A,THOC1,ETAA1,BLM,ATRX,TOPBP1,GINS4	up_VCAV_EC
GO:0051494	0.44	0.737	5	44	negative regulation of cytoskeleton organization	BP	1	FGF13,ARHGAP28,MID1,TUBB4A,INPP5K	up_ACOR_VSMC
GO:0007548	0.44	0.752	4	68	sex differentiation	BP	1	BMPR1A,IRX5,RDH10,FOXO3	down_VCAV_EC
GO:0048523	0.44	0.768	4	1399	negative regulation of cellular process	BP	1	DKK2,HOXA9,TAOK1,BPI	up_AORT_EC
GO:0051173	0.44	0.759	4	874	positive regulation of nitrogen compound	BP	1	NR1H4,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0031058	0.44	0.781	3	28	positive regulation of histone modification	BP	1	SREBF1,BRCA1,TADA2A	down_ACOR_VSMC
GO:0000041	0.44	0.78	3	31	transition metal ion transport	BP	1	CP,SLC39A8,LMTK2	up_VCAV_EC
GO:0060675	0.44	0.781	3	29	ureteric bud morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:0034637	0.44	0.782	3	25	cellular carbohydrate biosynthetic process	BP	1	GOT1,C1QTNF2,PASK	up_VSAP_EC
GO:0051238	0.44	0.899	1	7	sequestering of metal ion	BP	1	SLC30A1	down_ACOR_VSMC
GO:0043632	0.44	0.891	1	262	modification-dependent macromolecule catabolic	BP	1	USP33	down_AFEM_EC
GO:0046854	0.44	0.894	1	11	phosphatidylinositol phosphorylation	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0033120	0.44	0.896	1	9	positive regulation of RNA splicing	BP	1	ZPR1	down_VSAP_EC
GO:0072015	0.44	0.904	1	5	glomerular visceral epithelial cell	BP	1	BMP4	up_ACOR_VSMC
GO:0072310	0.44	0.904	1	5	glomerular epithelial cell development	BP	1	BMP4	up_ACOR_VSMC
GO:1902667	0.44	0.904	1	5	regulation of axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1903069	0.44	0.901	1	6	regulation of ER-associated ubiquitin-dependent protein	BP	1	HERPUD1	up_ACOR_VSMC
GO:2000794	0.44	0.901	1	6	regulation of epithelial cell proliferation involved in lung morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0006094	0.44	0.889	1	24	gluconeogenesis	BP	1	LEP	up_AFEM_EC

GO:0009566	0.44	0.889	1	24	fertilization	BP	1	HOXA9	up_AFEM_EC
GO:0051702	0.44	0.889	1	24	interaction with symbiont	BP	1	NAPEPLD	up_AFEM_EC
GO:1901799	0.44	0.889	1	24	negative regulation of proteasomal protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0008608	0.44	0.899	1	7	attachment of spindle microtubules to	BP	1	CENPC	up_VCAV_EC
GO:0071312	0.44	0.901	1	6	cellular response to alkaloid	BP	1	BLM	up_VCAV_EC
GO:0033622	0.44	0.901	1	6	integrin activation	BP	1	SELP	up_VCAV_EC
GO:0002673	0.44	0.901	1	6	regulation of acute inflammatory response	BP	1	PTGS2	up_VCAV_EC
GO:0046174	0.44	0.897	1	8	polyol catabolic process	BP	1	IMPA1	up_VCAV_EC
GO:0051099	0.44	0.888	1	70	positive regulation of binding	BP	1	HOXA3	up_VPOR_EC
GO:0000737	0.44	0.901	1	6	DNA catabolic process, endonucleolytic	BP	1	DFFB	up_VSAP_EC
GO:0021604	0.44	0.901	1	6	cranial nerve structural organization	BP	1	PLXNA4	up_VSAP_EC
GO:0021612	0.44	0.901	1	6	facial nerve structural organization	BP	1	PLXNA4	up_VSAP_EC
GO:0048667	0.44	0.888	1	140	cell morphogenesis involved in neuron	BP	1	SHOX2	up_VSAP_VSMC
GO:0098662	0.440088035	0.74971	4	131	inorganic cation transmembrane transport	BP	1	KCNB1,ACTN2,SLC9A9,PM20D1	up_ACOR_EC
GO:0051341	0.440137147	0.88944	1	22	regulation of oxidoreductase activity	BP	1	CDH3	up_ACOR_EC
GO:0009058	0.441	0.597	156	1910	biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,ADGRF5,ST8SIA6,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,ST6GAL1,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NOS3,NLRC5,QKI,GK5,GATA3,EDN1,HOXB8,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,PTGS1,ENSCAFG00000017103,ZDHHC22,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,FAM3C,GUCY1A1,ODC1,SPTLC2,ARG2,B3GNT5,TARSL2,MTOR,SAMD8,ELF4,HHAT,BMP2,HMG20A,HHEX,CHST7,CREM,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,AADAT,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,GALNT18,PRKD2,THOC1,SH3GLB1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,MRRF,PTGS2,TOP1,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,LBR,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,RAD17,IMPA1,SKIL,GPBP1,USP37,PIP5K1B,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,BCAT1,ZNF146,ATRX,NR4A1,ALDH1A3,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZDH	up_VCAV_EC
GO:0001819	0.441	0.7	8	120	positive regulation of cytokine production	BP	1	ARHGEF2,SULF1,SERPINE1,FAM49B,HIF1A,ADAM17,DDIT3,GBP5	down_VSAP_EC
GO:0009108	0.441	0.71	7	68	coenzyme biosynthetic process	BP	1	MAT2B,PCBD1,ALDOC,DDIT4,PTS,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0016070	0.441	0.721	7	1479	RNA metabolic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0048545	0.441	0.751	4	68	response to steroid hormone	BP	1	KANK2,NR3C1,PARK7,ZFP36L1	down_VCAV_EC
GO:0098655	0.441	0.749	4	142	cation transmembrane transport	BP	1	KCNC4,ATP6V1B2,FXYD1,ATP6V0B	up_AFEM_EC
GO:0006997	0.441	0.753	4	42	nucleus organization	BP	1	PSME4,NECTIN2,NUP133,KDM3A	up_VCAV_EC
GO:0006513	0.441	0.78	3	28	protein monoubiquitination	BP	1	UBE2T,UHRF1,DTL	down_ACOR_VSMC
GO:0060675	0.441	0.78	3	29	ureteric bud morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0010569	0.441	0.822	2	17	regulation of double-strand break repair via homologous	BP	1	PARPBP,RAD51	down_ACOR_VSMC
GO:0010605	0.441	0.824	2	745	negative regulation of macromolecule metabolic	BP	1	CST3,HDAC7	down_VPOR_EC
GO:0070646	0.441	0.814	2	63	protein modification by small protein removal	BP	1	USP54,CYLD	up_AFEM_EC

GO:0048709	0.441	0.822	2	17	oligodendrocyte differentiation	BP	1	EIF2B2,MTOR	up_VCAV_EC
GO:0051181	0.441	0.893	1	11	cofactor transport	BP	1	FOLR2	down_VCAV_EC
GO:0010518	0.441	0.895	1	9	positive regulation of phospholipase activity	BP	1	ARF4	down_VSAP_EC
GO:0010984	0.441	0.901	1	6	regulation of lipoprotein particle clearance	BP	1	LRPAP1	up_ACOR_VSMC
GO:0036010	0.441	0.901	1	6	protein localization to endosome	BP	1	NRP1	up_ACOR_VSMC
GO:0043653	0.441	0.901	1	6	mitochondrial fragmentation involved in	BP	1	BNIP3	up_ACOR_VSMC
GO:0070230	0.441	0.901	1	6	positive regulation of lymphocyte apoptotic	BP	1	CD274	up_ACOR_VSMC
GO:0072176	0.441	0.901	1	6	nephric duct development	BP	1	BMP4	up_ACOR_VSMC
GO:0072711	0.441	0.904	1	5	cellular response to hydroxyurea	BP	1	ATRX	up_ACOR_VSMC
GO:1901071	0.441	0.9	1	6	glucosamine-containing compound metabolic	BP	1	EXTL2	up_ACOR_VSMC
GO:1901385	0.441	0.901	1	6	regulation of voltage-gated calcium channel	BP	1	CACNB3	up_ACOR_VSMC
GO:0048259	0.441	0.889	1	24	regulation of receptor-mediated endocytosis	BP	1	GREM1	up_AFEM_EC
GO:0051438	0.441	0.889	1	24	regulation of ubiquitin-protein transferase	BP	1	DCUN1D3	up_AFEM_EC
GO:0006954	0.441	0.889	1	147	inflammatory response	BP	1	NR1H4	up_APUL_EC
GO:0003184	0.441	0.901	1	6	pulmonary valve morphogenesis	BP	1	JAG1	up_VCAV_EC
GO:0006654	0.441	0.898	1	7	phosphatidic acid biosynthetic process	BP	1	SH3GLB1	up_VCAV_EC
GO:0009886	0.441	0.901	1	6	post-embryonic animal morphogenesis	BP	1	ATRX	up_VCAV_EC
GO:0046473	0.441	0.898	1	7	phosphatidic acid metabolic process	BP	1	SH3GLB1	up_VCAV_EC
GO:0061085	0.441	0.9	1	6	regulation of histone H3-K27 methylation	BP	1	GATA3	up_VCAV_EC
GO:0048511	0.441	0.887	1	72	rhythmic process	BP	1	HTR7	up_VPOR_EC
GO:0048878	0.441	0.891	1	283	chemical homeostasis	BP	1	HOXA3	up_VPUL_VSMC
GO:0051546	0.441	0.9	1	6	keratinocyte migration	BP	1	FGF7	up_VSAP_EC
GO:0061085	0.441	0.901	1	6	regulation of histone H3-K27 methylation	BP	1	PHF1	up_VSAP_EC
GO:0070493	0.441	0.9	1	6	thrombin-activated receptor signaling	BP	1	HPGD	up_VSAP_EC
GO:1900274	0.441	0.9	1	6	regulation of phospholipase C activity	BP	1	ABL1	up_VSAP_EC
GO:0007098	0.441051079	0.81412	2	56	centrosome cycle	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0065003	0.441156462	0.65834	17	616	protein-containing complex assembly	BP	1	TMOD1,TRPS1,KCTD12,CALY,SOX9,KCNB1,SMAD6,ACTN2,PAK3,PTGER4,PREB,CLSTN1,CLU,CHMP4B,VPS16,PRKCD,TUBB4A	up_ACOR_EC
GO:0071674	0.441550122	0.88846	1	23	mononuclear cell migration	BP	1	RARRES2	up_ACOR_EC
GO:0034654	0.441989197	0.63281	34	1236	nucleobase-containing compound biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC

GO:0051171	0.442	0.597	145	1697	regulation of nitrogen compound metabolic process	BP	1	ELK3,ACSL3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,ILF3,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,MED17,U2AF2,PSMD3,SLC29A1,MTDH,HEY1,PPP1R15B,PARPBP,SRRT,NAB2,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,AURKB,NONO,HNRNPL,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,SF3B4,UHRF1,CKS2,PDCD2,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,TFRC,PPARD,RAP2C,YBX3,HNRNPF,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,RBM14,RBM17,RAD23A,NOLC1,CDC20,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,DELE1,CCNB3,MIS18A,HMGN1,CCT4,SIX4,MTBP,NECAB3,SF3A1,MED16,ENSCAFG00000017103,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0044249	0.442	0.671	16	1851	cellular biosynthetic process	BP	1	BARX1,OSTC,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0001667	0.442	0.664	15	146	ameboidal-type cell migration	BP	1	HTR2B,FERMT1,BMP4,SASH1,FGF18,NRP1,EVL,PRKCE,SYNJ2BP,JUP,DDR2,ARID5B,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0009991	0.442	0.686	10	110	response to extracellular stimulus	BP	1	P2RX7,SELL,ATF3,RALB,MTOR,SLC25A25,BCL10,PMAIP1,ITGA6,P2RX2	up_VCAV_EC
GO:0017038	0.442	0.686	10	96	protein import	BP	1	PEX7,ARHGEF5,CDH1,PEX2,PIK3R1,NUP98,LONP2,SNUPN,PEX6,MAVS	up_VSAP_EC
GO:0001823	0.442	0.735	5	45	mesonephros development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NPNT	up_ACOR_VSMC
GO:0032640	0.442	0.753	4	39	tumor necrosis factor production	BP	1	HMGB1,ARG2,CACTIN,ARHGEF2	down_ACOR_VSMC
GO:0006360	0.442	0.779	3	28	transcription by RNA polymerase I	BP	1	DHX33,NCL,POLR1C	down_ACOR_VSMC
GO:0035304	0.442	0.78	3	29	regulation of protein dephosphorylation	BP	1	SLC29A1,PPP2R5D,YWHAB	down_ACOR_VSMC
GO:0006641	0.442	0.781	3	25	triglyceride metabolic process	BP	1	LIPC,INSIG2,LMF1	up_VSAP_EC
GO:0048701	0.442	0.781	3	25	embryonic cranial skeleton morphogenesis	BP	1	TBX15,IRX5,TGFBR2	up_VSAP_EC
GO:0050729	0.442	0.781	3	25	positive regulation of inflammatory response	BP	1	NAPEPLD,IL17RC,MYD88	up_VSAP_EC
GO:1902807	0.442	0.821	2	18	negative regulation of cell cycle G1/S phase	BP	1	CASP2,EZH2	down_ACOR_VSMC
GO:2000134	0.442	0.821	2	18	negative regulation of G1/S transition of mitotic	BP	1	CASP2,EZH2	down_ACOR_VSMC
GO:0042775	0.442	0.816	2	28	mitochondrial ATP synthesis coupled	BP	1	UQCR10,PARK7	down_VCAV_EC
GO:0038202	0.442	0.818	2	24	TORC1 signaling	BP	1	SESN2,SEC13	down_VSAP_EC
GO:0045669	0.442	0.817	2	24	positive regulation of osteoblast differentiation	BP	1	ILK,CTNNB1	down_VSAP_EC
GO:0046635	0.442	0.823	2	15	positive regulation of alpha-beta T cell	BP	1	CD83,PTPN22	up_ACOR_VSMC
GO:0050854	0.442	0.822	2	16	regulation of antigen receptor-mediated	BP	1	ELF1,DUSP22	up_ACOR_VSMC
GO:0001817	0.442	0.814	2	182	regulation of cytokine production	BP	1	C3AR1,ARHGEF2	up_VPOR_EC
GO:0051493	0.442	0.813	2	188	regulation of cytoskeleton organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0043069	0.442	0.891	1	262	negative regulation of programmed cell death	BP	1	IVNS1ABP	down_AFEM_EC
GO:0042474	0.442	0.892	1	11	middle ear morphogenesis	BP	1	NAGLU	down_VCAV_EC
GO:0061213	0.442	0.892	1	11	positive regulation of mesonephros	BP	1	GREM1	down_VCAV_EC
GO:0051179	0.442	0.936	1	1747	localization	BP	1	JUP	down_VFEM_VSMC
GO:0046850	0.442	0.894	1	9	regulation of bone remodeling	BP	1	TFRC	down_VSAP_EC

GO:0007625	0.442	0.9	1	6	grooming behavior	BP	1	SLITRK5	up_ACOR_VSMC
GO:0051561	0.442	0.9	1	6	positive regulation of mitochondrial calcium ion concentration	BP	1	MICU2	up_ACOR_VSMC
GO:1902231	0.442	0.9	1	6	positive regulation of intrinsic apoptotic signaling pathway in	BP	1	NACC2	up_ACOR_VSMC
GO:0045921	0.442	0.888	1	24	positive regulation of exocytosis	BP	1	RAB7A	up_AFEM_EC
GO:0010866	0.442	0.9	1	6	regulation of triglyceride biosynthetic process	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0033599	0.442	0.9	1	6	regulation of mammary gland epithelial cell	BP	1	GATA3	up_VCAV_EC
GO:0043923	0.442	0.898	1	7	positive regulation by host of viral transcription	BP	1	SMARCA4	up_VCAV_EC
GO:0007249	0.442	0.886	1	71	I-kappaB kinase/NF-kappaB signaling	BP	1	MTDH	up_VPOR_EC
GO:0044331	0.442	0.9	1	6	cell-cell adhesion mediated by cadherin	BP	1	FLOT1	up_VSAP_EC
GO:0072348	0.442	0.9	1	6	sulfur compound transport	BP	1	CTNS	up_VSAP_EC
GO:0001701	0.442	0.887	1	134	in utero embryonic development	BP	1	GJB5	up_VSAP_VSMC
GO:0002790	0.442	0.887	1	133	peptide secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0051656	0.442013932	0.74813	4	129	establishment of organelle localization	BP	1	CDH3,DYNC1I1,PREB,CHMP4B	up_ACOR_EC
GO:0035272	0.442074406	0.88857	1	21	exocrine system development	BP	1	NRP1	up_ACOR_EC
GO:0021545	0.442581158	0.88828	1	21	cranial nerve development	BP	1	NRP1	up_ACOR_EC
GO:0042129	0.443	0.753	4	35	regulation of T cell proliferation	BP	1	CD274,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0043488	0.443	0.779	3	28	regulation of mRNA stability	BP	1	HNRNPD,THRAP3,FASTKD3	down_ACOR_VSMC
GO:0051716	0.443	0.81	3	2001	cellular response to stimulus	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0001508	0.443	0.816	2	25	action potential	BP	1	GNAQ,YWHAH	down_VSAP_EC
GO:0061053	0.443	0.817	2	24	somite development	BP	1	TMED2,SIX4	down_VSAP_EC
GO:0006629	0.443	0.816	2	382	lipid metabolic process	BP	1	NR1H4,PLCL1	up_APUL_EC
GO:0051496	0.443	0.82	2	17	positive regulation of stress fiber assembly	BP	1	ARHGEF15,MTOR	up_VCAV_EC
GO:0042982	0.443	0.822	2	15	amyloid precursor protein metabolic process	BP	1	NECAB3,SOAT1	up_VSAP_EC
GO:0048646	0.443	0.815	2	349	anatomical structure formation involved in	BP	1	HOXA11,CAV1	up_VSAP_VSMC
GO:0030488	0.443	0.897	1	7	tRNA methylation	BP	1	THUMPD2	down_ACOR_VSMC
GO:0048534	0.443	0.89	1	262	hematopoietic or lymphoid organ	BP	1	GABPA	down_AFEM_EC
GO:0003203	0.443	0.892	1	11	endocardial cushion morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0034654	0.443	0.917	1	1236	nucleobase-containing compound biosynthetic	BP	1	MOSPD1	down_VFEM_EC
GO:0010640	0.443	0.899	1	6	regulation of platelet-derived growth factor receptor signaling	BP	1	PTGIR	up_ACOR_VSMC
GO:0050482	0.443	0.9	1	6	arachidonic acid secretion	BP	1	CFI	up_ACOR_VSMC
GO:0070262	0.443	0.9	1	6	peptidyl-serine dephosphorylation	BP	1	DUSP26	up_ACOR_VSMC
GO:1903963	0.443	0.9	1	6	arachidonate transport	BP	1	CFI	up_ACOR_VSMC
GO:1904152	0.443	0.9	1	6	regulation of retrograde protein transport, ER to	BP	1	OS9	up_ACOR_VSMC
GO:1990266	0.443	0.888	1	24	neutrophil migration	BP	1	CCL5	up_AFEM_EC
GO:0060487	0.443	0.897	1	7	lung epithelial cell differentiation	BP	1	CREB1	up_VCAV_EC
GO:0070507	0.443	0.886	1	73	regulation of microtubule cytoskeleton organization	BP	1	ARHGEF2	up_VPOR_EC
GO:0007264	0.443	0.887	1	164	small GTPase mediated signal transduction	BP	1	ARHGEF2	up_VPUL_EC
GO:0098869	0.443	0.899	1	6	cellular oxidant detoxification	BP	1	SESN1	up_VSAP_EC

GO:0009135	0.4436836	0.88745	1	22	purine nucleoside diphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0009179	0.4436836	0.88745	1	22	purine ribonucleoside diphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0046031	0.4436836	0.88745	1	22	ADP metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0051049	0.444	0.639	25	479	regulation of transport	BP	1	GPAM,SLC35F6,LRP1,PRNP,SDC4,FXYD1,TRPV2,CLIP3,ENSCAFG00000014978,AKT2,SCP2,CACNB3,LRPAP1,THY1,GLI3,PARK7,CYBA,MAVS,CDH2,ARHGAP1,GREM1,EVI5L,RAC2,CLIC4,PACSIN3	down_VCAV_EC
GO:0018130	0.444	0.685	11	1261	heterocycle biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0002521	0.444	0.682	10	149	leukocyte differentiation	BP	1	VEGFA,MYH9,SOCS5,PTPN2,EVI2B,CTNNB1,TFRC,LYN,GLO1,BTK	down_VSAP_EC
GO:0019222	0.444	0.706	9	1934	regulation of metabolic process	BP	1	HOXC10,EYA1,HOXA9,MAP2K6,HOXA10,HOXA7,SIX1,YBX3,CYP26B1	up_VFEM_EC
GO:0010959	0.444	0.706	7	79	regulation of metal ion transport	BP	1	PDGFB,PDE4D,CHD7,STC1,APLNR,PLCG2,SPTBN4	up_VCAV_EC
GO:0030177	0.444	0.732	5	51	positive regulation of Wnt signaling pathway	BP	1	CTDNEP1,CAV1,ASPM,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0051225	0.444	0.733	5	49	spindle assembly	BP	1	RAB11A,MZT1,SENP6,HAUS3,FBXO5	up_VCAV_EC
GO:0009314	0.444	0.746	4	143	response to radiation	BP	1	CRY2,CRYAB,MFAP4,DCUN1D3	up_AFEM_EC
GO:0071248	0.444	0.752	4	35	cellular response to metal ion	BP	1	ENSCAFG00000009113,CDH1,MT2A,HMOX1	up_VSAP_EC
GO:0070231	0.444	0.819	2	18	T cell apoptotic process	BP	1	PRELID1,ARG2	down_ACOR_VSMC
GO:0033260	0.444	0.821	2	15	nuclear DNA replication	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0016482	0.444	0.811	2	63	cytosolic transport	BP	1	MYO1D,RAB7A	up_AFEM_EC
GO:0032456	0.444	0.818	2	19	endocytic recycling	BP	1	EHD4,LMTK2	up_VCAV_EC
GO:0051130	0.444	0.814	2	342	positive regulation of cellular component	BP	1	CAV1,SHOX2	up_VSAP_VSMC
GO:0010874	0.444	0.896	1	7	regulation of cholesterol efflux	BP	1	SREBF2	down_ACOR_VSMC
GO:0018208	0.444	0.897	1	7	peptidyl-proline modification	BP	1	PPIB	down_ACOR_VSMC
GO:0050794	0.444	1	1	3075	regulation of cellular process	BP	1	GATA5	down_AFEM_VSMC
GO:1902808	0.444	0.891	1	12	positive regulation of cell cycle G1/S phase	BP	1	LSM10	down_VCAV_EC
GO:0000002	0.444	0.894	1	9	mitochondrial genome maintenance	BP	1	SESN2	down_VSAP_EC
GO:0060037	0.444	0.893	1	9	pharyngeal system development	BP	1	SIX4	down_VSAP_EC
GO:0045879	0.444	0.892	1	10	negative regulation of smoothened signaling	BP	1	PRKACB	down_VSAP_EC
GO:2000197	0.444	0.903	1	5	regulation of ribonucleoprotein	BP	1	IWS1	up_VCAV_EC
GO:0016570	0.444	0.886	1	143	histone modification	BP	1	EYA1	up_VFEM_EC
GO:0006812	0.444	0.888	1	222	cation transport	BP	1	NETO1	up_VFEM_VSMC
GO:0010998	0.444	0.899	1	6	regulation of translational initiation by eIF2 alpha phosphorylation	BP	1	NCK1	up_VSAP_EC
GO:0036490	0.444	0.899	1	6	regulation of translation in response to endoplasmic reticulum	BP	1	NCK1	up_VSAP_EC
GO:1901575	0.444237945	0.65302	18	643	organic substance catabolic process	BP	1	PLCL1,THNSL2,SARDH,EDEM2,KLHL25,PLCE1,CFI,PIAS1,CLU,ALDOC,CHMP4B,TP53INP2,RARRES2,RNF114,UBE2H,AZIN2,HM13,PRKCD	up_ACOR_EC
GO:0070972	0.44495261	0.88654	1	23	protein localization to endoplasmic reticulum	BP	1	CHMP4B	up_ACOR_EC
GO:0071356	0.44497355	0.81117	2	57	cellular response to tumor necrosis factor	BP	1	NR1H4,CCDC3	up_ACOR_EC
GO:0032269	0.445	0.694	8	306	negative regulation of cellular protein metabolic	BP	1	GAS1,CRYAB,GREM1,CLEC16A,CYLD,LRRC15,RECK,SAMD4B	up_AFEM_EC
GO:0071479	0.445	0.777	3	29	cellular response to ionizing radiation	BP	1	INTS7,RAD51,MAP3K20	down_ACOR_VSMC
GO:0006909	0.445	0.774	3	42	phagocytosis	BP	1	MYH9,ENSCAFG00000003477,ICAM5	down_VSAP_EC
GO:0001508	0.445	0.779	3	25	action potential	BP	1	TPCN2,KCNE3,KCNB1	up_VSAP_EC

GO:0009132	0.445	0.778	3	25	nucleoside diphosphate metabolic process	BP	1	GALK1,ENTPD3,DDIT4	up_VSAP_EC
GO:0048278	0.445	0.778	3	25	vesicle docking	BP	1	SCFD2,STX4,VPS11	up_VSAP_EC
GO:0048518	0.445	0.844	2	1676	positive regulation of biological process	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0009066	0.445	0.82	2	16	aspartate family amino acid metabolic process	BP	1	NIT2,NMNAT1	up_ACOR_VSMC
GO:1901988	0.445	0.811	2	63	negative regulation of cell cycle phase transition	BP	1	OVOL1,DCUN1D3	up_AFEM_EC
GO:0035065	0.445	0.819	2	17	regulation of histone acetylation	BP	1	IWS1,GATA3	up_VCAV_EC
GO:0046939	0.445	0.817	2	19	nucleotide phosphorylation	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0006366	0.445	0.819	2	583	transcription by RNA polymerase II	BP	1	BARX1,NKX2-5	up_VPOR_VSMC
GO:0001819	0.445	0.885	1	120	positive regulation of cytokine production	BP	1	SULF1	down_ACOR_EC
GO:0002507	0.445	0.896	1	7	tolerance induction	BP	1	HMGB1	down_ACOR_VSMC
GO:0043030	0.445	0.89	1	12	regulation of macrophage activation	BP	1	BPI	down_VCAV_EC
GO:1904355	0.445	0.891	1	11	positive regulation of telomere capping	BP	1	NABP2	down_VCAV_EC
GO:1990774	0.445	0.893	1	9	tumor necrosis factor secretion	BP	1	NR1H4	down_VSAP_EC
GO:0006595	0.445	0.898	1	6	polyamine metabolic process	BP	1	AZIN2	up_ACOR_VSMC
GO:0072413	0.445	0.898	1	6	signal transduction involved in mitotic cell	BP	1	CDKN1A	up_ACOR_VSMC
GO:1902402	0.445	0.898	1	6	signal transduction involved in mitotic DNA	BP	1	CDKN1A	up_ACOR_VSMC
GO:1902403	0.445	0.898	1	6	signal transduction involved in mitotic DNA	BP	1	CDKN1A	up_ACOR_VSMC
GO:0030097	0.445	0.888	1	244	hemopoiesis	BP	1	HOXA9	up_AORT_EC
GO:0051345	0.445	0.886	1	151	positive regulation of hydrolase activity	BP	1	NPNT	up_APUL_EC
GO:0071696	0.445	0.898	1	6	ectodermal placode development	BP	1	PROX1	up_VCAV_EC
GO:0071803	0.445	0.898	1	6	positive regulation of podosome assembly	BP	1	ARHGEF5	up_VSAP_EC
GO:0030099	0.445	0.886	1	133	myeloid cell differentiation	BP	1	HOXA9	up_VSAP_VSMC
GO:0071417	0.445	0.886	1	142	cellular response to organonitrogen	BP	1	CAV1	up_VSAP_VSMC
GO:0045069	0.445882965	0.8862	1	22	regulation of viral genome replication	BP	1	MAVS	up_ACOR_EC
GO:0060548	0.446	0.637	25	294	negative regulation of cell death	BP	1	PLK2,HCLS1,IL7R,KIT,PRKCH,TNFAIP3,CD34,MEF2C,GATA3,FIGNL1,PELI1,ARG2,ITPKB,PAK2,NCK1,PTGS2,PLCG2,BCL10,CTNNA1,RIPK1,ITGA6,HIF1A,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0043603	0.446	0.642	22	372	cellular amide metabolic process	BP	1	ASNS,CARS,NR1H4,PLK3,SARS,AARS,ENSCAFG00000028814,PGAM1,PUM3,UGCG,ALDH1L2,SESN2,MRPL1,YARS,TARS,NARS,EIF4EBP1,CNOT7,APOE,EIF5,EIF2S1,RSL24D1	down_VSAP_EC
GO:0042110	0.446	0.682	10	109	T cell activation	BP	1	HMGB1,PRELID1,CAV1,ARG2,TFRC,FAM49B,CORO1A,ELF4,JMJD6,CTPS1	down_ACOR_VSMC
GO:0032868	0.446	0.707	7	66	response to insulin	BP	1	GOT1,KLF15,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0050804	0.446	0.714	6	87	modulation of chemical synaptic transmission	BP	1	KIF5B,PLCL1,CDH11,APOE,GSK3B,LRRTM2	down_VSAP_EC
GO:0099177	0.446	0.714	6	87	regulation of trans-synaptic signaling	BP	1	KIF5B,PLCL1,CDH11,APOE,GSK3B,LRRTM2	down_VSAP_EC
GO:0042177	0.446	0.731	5	47	negative regulation of protein catabolic process	BP	1	PTPN3,OS9,PSEN1,AZIN2,PARK7	up_ACOR_VSMC
GO:0048468	0.446	0.73	5	553	cell development	BP	1	HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,RNF6	up_VPOR_EC
GO:0051251	0.446	0.746	4	69	positive regulation of lymphocyte activation	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:0050806	0.446	0.777	3	25	positive regulation of synaptic transmission	BP	1	PRKCE,APP,FAM107A	up_ACOR_VSMC
GO:0070373	0.446	0.777	3	26	negative regulation of ERK1 and ERK2 cascade	BP	1	NDRG2,SYNJ2BP,DUSP26	up_ACOR_VSMC
GO:0002698	0.446	0.777	3	25	negative regulation of immune effector process	BP	1	NLRX1,TKFC,PPP3CB	up_VSAP_EC
GO:0014066	0.446	0.777	3	26	regulation of phosphatidylinositol 3-	BP	1	PDGFD,F2RL1,PIK3IP1	up_VSAP_EC

GO:0006998	0.446	0.819	2	16	nuclear envelope organization	BP	1	DMPK,SUN1	up_ACOR_VSMC
GO:0070849	0.446	0.82	2	15	response to epidermal growth factor	BP	1	DUSP22,INPP5K	up_ACOR_VSMC
GO:0032880	0.446	0.888	1	266	regulation of protein localization	BP	1	GPSM2	down_AFEM_EC
GO:0060255	0.446	0.935	1	1782	regulation of macromolecule metabolic	BP	1	CST3	down_AORT_EC
GO:0045738	0.446	0.889	1	12	negative regulation of DNA repair	BP	1	FBH1	down_VCAV_EC
GO:1902622	0.446	0.891	1	11	regulation of neutrophil migration	BP	1	RAC2	down_VCAV_EC
GO:0000291	0.446	0.891	1	10	nuclear-transcribed mRNA catabolic process,	BP	1	CNOT7	down_VSAP_EC
GO:0045063	0.446	0.893	1	9	T-helper 1 cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0015844	0.446	0.898	1	6	monoamine transport	BP	1	PARK7	up_ACOR_VSMC
GO:0021542	0.446	0.898	1	6	dentate gyrus development	BP	1	TMEM108	up_ACOR_VSMC
GO:0045773	0.446	0.898	1	6	positive regulation of axon extension	BP	1	NRP1	up_ACOR_VSMC
GO:1904385	0.446	0.898	1	6	cellular response to angiotensin	BP	1	ACTN2	up_ACOR_VSMC
GO:1990776	0.446	0.898	1	6	response to angiotensin	BP	1	ACTN2	up_ACOR_VSMC
GO:0010648	0.446	0.891	1	407	negative regulation of cell communication	BP	1	EYA1	up_AFEM_VSMC
GO:0031065	0.446	0.896	1	7	positive regulation of histone deacetylation	BP	1	PRKD2	up_VCAV_EC
GO:0032271	0.446	0.884	1	73	regulation of protein polymerization	BP	1	TWF1	up_VPOR_EC
GO:0035542	0.446	0.898	1	6	regulation of SNARE complex assembly	BP	1	VPS11	up_VSAP_EC
GO:0050865	0.446	0.885	1	135	regulation of cell activation	BP	1	CAV1	up_VSAP_VSMC
GO:0044070	0.446556582	0.88582	1	22	regulation of anion transport	BP	1	PRKCD	up_ACOR_EC
GO:0008037	0.446983545	0.88558	1	22	cell recognition	BP	1	NRP1	up_ACOR_EC
GO:0010256	0.446987691	0.74393	4	129	endomembrane system organization	BP	1	SH3TC2,AQP1,CHMP4B,PRKCD	up_ACOR_EC
GO:0070727	0.447	0.613	50	579	cellular macromolecule localization	BP	1	ACSL3,SREBF1,RPA1,DDX39A,STXBP6,USP4,NEDD4,ZW10,CENPA,SLC29A1,NDC1,TIMM44,POLA2,CTDNEP1,HSPA9,RAN,HM13,INSIG1,CAV1,CDK1,NF2,AURKB,MMP14,EZH2,PLK3,ENSCAFG00000011598,PREB,TRAM1,NDC80,IPO4,YWHAB,NUP62,EMP2,NUP188,HASPIN,TOMM34,SAMM50,DMAP1,DDX39B,SNX15,RAB35,EZR,MIOS,TTK,KNL1,PMPCA,TINF2,CCT4,SIX4,MTBP	down_ACOR_VSMC
GO:0055082	0.447	0.648	19	189	cellular chemical homeostasis	BP	1	C5AR2,SLC8B1,ABL1,ENSCAFG00000000071,F2RL1,RAB11B,FXN,PIK3R1,MYC,SCARA5,KCNB1,FTL,RAF1,CYBA,STX4,PPP3CB,HMOX1,NCOA4,RAB11FIP2	up_VSAP_EC
GO:0006397	0.447	0.674	11	168	mRNA processing	BP	1	CELF1,IWS1,SNRPB2,PRPF3,DDX39B,PDCD11,STRAP,REST,ENSCAFG00000015065,BCAS2,SNRPA1	down_VSAP_EC
GO:0006887	0.447	0.681	10	99	exocytosis	BP	1	EXPH5,FBXL20,SYT16,STX11,F2RL1,PSEN1,RAB11B,SCAMP5,SCRN2,PREPL	up_ACOR_VSMC
GO:0050789	0.447	0.732	9	3295	regulation of biological process	BP	1	CHL1,FGF5,HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:1903706	0.447	0.694	8	119	regulation of hemopoiesis	BP	1	SOCS5,HIF1A,PTPN2,EVI2B,CTNNB1,LYN,PRMT1,INHBA	down_VSAP_EC
GO:0050878	0.447	0.696	8	75	regulation of body fluid levels	BP	1	LNPK,GJA1,F2RL1,ENPP4,PRKCE,EDN1,INPP5K,WFS1	up_ACOR_VSMC
GO:0051100	0.447	0.73	5	53	negative regulation of binding	BP	1	PDGFB,RALB,ARHGAP28,PPP3CA,STMN1	up_VCAV_EC
GO:0007204	0.447	0.73	5	46	positive regulation of cytosolic calcium ion	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:0048518	0.447	0.767	4	1676	positive regulation of biological process	BP	1	HOXA3,TBX5,GATA5,SLIT2	up_VPUL_VSMC
GO:0033143	0.447	0.777	3	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	LBH,SKP2,PARK7	up_ACOR_VSMC
GO:0016073	0.447	0.776	3	26	snRNA metabolic process	BP	1	EXOSC7,ICE1,INTS12	up_VSAP_EC
GO:0035306	0.447	0.814	2	24	positive regulation of dephosphorylation	BP	1	PPP1R12A,CALM1	down_VSAP_EC

GO:0021879	0.447	0.819	2	15	forebrain neuron differentiation	BP	1	FGFR2,NRP1	up_ACOR_VSMC
GO:0009303	0.447	0.818	2	16	rRNA transcription	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0051568	0.447	0.817	2	17	histone H3-K4 methylation	BP	1	GATA3,TET2	up_VCAV_EC
GO:0033993	0.447	0.81	2	186	response to lipid	BP	1	MTDH,RNF6	up_VPOR_EC
GO:0031323	0.447	0.934	1	1788	regulation of cellular metabolic process	BP	1	CST3	down_AORT_EC
GO:2000249	0.447	0.889	1	12	regulation of actin cytoskeleton	BP	1	RHOD	down_VCAV_EC
GO:0022414	0.447	0.888	1	294	reproductive process	BP	1	CITED2	down_VPOR_EC
GO:0030206	0.447	0.892	1	9	chondroitin sulfate biosynthetic process	BP	1	CHSY1	down_VSAP_EC
GO:0001780	0.447	0.897	1	6	neutrophil homeostasis	BP	1	JAM3	up_ACOR_VSMC
GO:0006655	0.447	0.898	1	6	phosphatidylglycerol biosynthetic process	BP	1	CRLS1	up_ACOR_VSMC
GO:0032332	0.447	0.898	1	6	positive regulation of chondrocyte	BP	1	FGF18	up_ACOR_VSMC
GO:0034497	0.447	0.898	1	6	protein localization to phagophore assembly site	BP	1	PIK3C3	up_ACOR_VSMC
GO:0035563	0.447	0.897	1	6	positive regulation of chromatin binding	BP	1	PARP9	up_ACOR_VSMC
GO:0046471	0.447	0.898	1	6	phosphatidylglycerol metabolic process	BP	1	CRLS1	up_ACOR_VSMC
GO:0019226	0.447	0.897	1	6	transmission of nerve impulse	BP	1	SPTBN4	up_VCAV_EC
GO:0007183	0.447	0.893	1	8	SMAD protein complex assembly	BP	1	SMAD1	up_VCAV_EC
GO:0060969	0.447	0.897	1	6	negative regulation of gene silencing	BP	1	PPP3CA	up_VCAV_EC
GO:0061138	0.447	0.884	1	73	morphogenesis of a branching epithelium	BP	1	SEMA3A	up_VPOR_EC
GO:2000027	0.447	0.884	1	72	regulation of animal organ morphogenesis	BP	1	ASPN	up_VPOR_EC
GO:0031175	0.447	0.887	1	224	neuron projection development	BP	1	CHL1	up_VPOR_VSMC
GO:0051050	0.447	0.887	1	235	positive regulation of transport	BP	1	NKX2-5	up_VPOR_VSMC
GO:0016569	0.447	0.885	1	144	covalent chromatin modification	BP	1	EYA1	up_VFEM_EC
GO:0021871	0.447	0.897	1	6	forebrain regionalization	BP	1	EMX2	up_VSAP_EC
GO:0002684	0.447001726	0.70155	7	239	positive regulation of immune system process	BP	1	C7,NR1H4,FZD5,NOD2,MAVS,CLSTN1,RARRES2	up_ACOR_EC
GO:0033077	0.447343059	0.88537	1	22	T cell differentiation in thymus	BP	1	FZD5	up_ACOR_EC
GO:0061640	0.447484128	0.8851	1	23	cytoskeleton-dependent cytokinesis	BP	1	CHMP4B	up_ACOR_EC
GO:0065008	0.448	0.611	54	1056	regulation of biological quality	BP	1	GPAM,SLC35F6,KIRREL1,DCN,MAOA,NDN,PRNP,FBN1,ADCY6,TLN2,VKORC1,NABP2,FXYD1,TRPV2,ENSCAFG00000014978,AKT1S1,AKT2,LCAT,SAMD4B,ENSCAFG00000018277,PDIA4,SLC39A6,CLSTN1,PLCL1,THY1,CYP1B1,ATP6V0C,RETSAT,PARK7,SCARA5,ZFP36L1,NCDN,TPC3,RNPEP,CYBA,ARL2BP,CDH2,MPV17,ORMDL3,NCLN,ENSCAFG00000017708,ACTR3B,IRX5,TSC22D3,RDH10,PCSK6,PLEKHH2,ATOX1,NAPEPLD,FOXO3,SOAT1,THRB,ANKRD54,BRSK1	down_VCAV_EC
GO:0033674	0.448	0.659	15	144	positive regulation of kinase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,PDE5A,SASH1,LMO4,FGF18,CCNT1,FRS2,PSEN1,DDR2,EDN1,MAP3K7	up_ACOR_VSMC
GO:0003002	0.448	0.68	10	118	regionalization	BP	1	HOXB7,RELN,MEF2C,DLL4,EDN1,HOXB8,BMP2,HHEX,HOXB5,CDON	up_VCAV_EC
GO:0007420	0.448	0.685	9	169	brain development	BP	1	SMAD9,BMPR1A,NUMBL,NAGLU,ENSCAFG00000018277,PEX5,GLI3,CDH2,FOXO3	down_VCAV_EC
GO:0000070	0.448	0.703	7	75	mitotic sister chromatid segregation	BP	1	RAB11A,CENPC,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0005977	0.448	0.776	3	26	glycogen metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0006073	0.448	0.776	3	26	cellular glucan metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0044042	0.448	0.776	3	26	glucan metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0051603	0.448	0.811	2	305	proteolysis involved in cellular protein catabolic	BP	1	USP28,NEDD4	down_ACOR_EC

GO:0000079	0.448	0.812	2	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CCNYL1,CDKN1A	down_VSAP_EC
GO:0019321	0.448	0.895	1	7	pentose metabolic process	BP	1	PGD	down_ACOR_VSMC
GO:0031116	0.448	0.895	1	7	positive regulation of microtubule	BP	1	RAC1	down_ACOR_VSMC
GO:0043114	0.448	0.894	1	7	regulation of vascular permeability	BP	1	TRPV4	down_ACOR_VSMC
GO:0010591	0.448	0.888	1	12	regulation of lamellipodium assembly	BP	1	RAC2	down_VCAV_EC
GO:0048333	0.448	0.889	1	12	mesodermal cell differentiation	BP	1	BMPR1A	down_VCAV_EC
GO:0000003	0.448	0.887	1	295	reproduction	BP	1	CITED2	down_VPOR_EC
GO:0051270	0.448	0.888	1	296	regulation of cellular component movement	BP	1	HDAC7	down_VPOR_EC
GO:0007379	0.448	0.897	1	6	segment specification	BP	1	MLLT3	up_ACOR_VSMC
GO:0021854	0.448	0.897	1	6	hypothalamus development	BP	1	NRP1	up_ACOR_VSMC
GO:0071542	0.448	0.897	1	6	dopaminergic neuron differentiation	BP	1	VEGFD	up_ACOR_VSMC
GO:0023057	0.448	0.89	1	409	negative regulation of signaling	BP	1	EYA1	up_AFEM_VSMC
GO:0051052	0.448	0.884	1	145	regulation of DNA metabolic process	BP	1	EYA1	up_VFEM_EC
GO:0006825	0.448	0.897	1	6	copper ion transport	BP	1	STEAP3	up_VSAP_EC
GO:0060969	0.448	0.897	1	6	negative regulation of gene silencing	BP	1	ZC3H10	up_VSAP_EC
GO:0040037	0.448	0.897	1	6	negative regulation of fibroblast growth factor receptor signaling	BP	1	SULF2	up_VSAP_EC
GO:0085029	0.448	0.897	1	6	extracellular matrix assembly	BP	1	LOX	up_VSAP_EC
GO:0003015	0.44892007	0.80817	2	58	heart process	BP	1	GNAO1,RNLS	up_ACOR_EC
GO:0043412	0.449	0.593	119	1225	macromolecule modification	BP	1	FGF13,ADRA1B,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MBP,ZRANB1,LIPT2,B3GALNT2,SKP2,PRKAA2,BMP4,B3GNT7,FGFR2,CCDC126,ABCA1,ATRX,TLR3,SH3RF2,LATS2,PIGN,PDE5A,PIGS,ISG15,SASH1,FGF18,NDRG2,TMX3,CDKN2B,USP53,GRK7,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,ERO1B,DAPK1,MAGT1,EGLN1,SUMF1,NCEH1,CDKN1A,NRP1,PTPN22,ULK2,DMPK,NPNT,OS9,STT3B,SMPD1,FUT11,UBE2H,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,FRS2,RNF19A,LYPLAL1,DAG1,FUT8,POMK,PARP9,APP,PSEN1,SYNJ2BP,SHPRH,PIK3C3,CCL5,DDR2,PSKH1,DUSP22,EDN1,OXR1,RNF141,PHF20,AKTIP,TRMT9B,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PRKAG3,SH3RF3,EOGT,DCUN1D4,RNF181,USP20,HERPUD1,RPRD1B,MAP3K7,INPP5K,CNOT4,OSGEPL1,KLHDC8B,WFS1,KLHL36,WDR48,DZIP3,ENSCAFG00000029553,PARK7,ZDHHC21,LMF1,CRKL,CDKL2	up_ACOR_VSMC
GO:1901575	0.449	0.606	63	643	organic substance catabolic process	BP	1	PLCG2,LEP,PLCL1,ENOSF1,ZRANB1,FBXL20,ENSCAFG00000002977,SKP2,PNRC1,SH3RF2,LPL,PDE5A,MAOA,ISG15,ZNRF3,CTSS,PTPN3,KLHL20,ACAD11,ENPP4,CTSB,BNIP3,EGLN1,LIPE,DCP1B,UBR1,OS9,STT3B,SMPD1,UBE2H,MOXD1,PYGM,RNF24,PRKCE,SARDH,RNF19A,LYPLAL1,PSEN1,LAMP2,CLN8,SIAH1,ALDOC,CTSF,ENTPD3,PCYOX1,DDIT4,DISC1,RNF181,NEU3,USP20,HERPUD1,CFI,GAA,INPP5K,FAF2,CNOT4,WFS1,AZIN2,CTIF,DZIP3,ERAP1,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0050673	0.449	0.668	12	135	epithelial cell proliferation	BP	1	HMGB1,BIRC5,CAV1,B4GALT1,NRAS,PPARD,HMGB2,ENSCAFG00000005299,GLI1,TINF2,HMGN1,SIX4	down_ACOR_VSMC
GO:0032496	0.449	0.694	8	77	response to lipopolysaccharide	BP	1	PLCG2,ABCA1,PTGIR,SASH1,ANKRD1,PRKCE,NOD2,TNFRSF11B	up_ACOR_VSMC
GO:1990778	0.449	0.693	8	91	protein localization to cell periphery	BP	1	PPP2R5A,TSPAN15,RAB11A,ZDHHC22,TSPAN14,EPB41,EXOC5,RAPGEF2	up_VCAV_EC
GO:0050730	0.449	0.703	7	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	ENPP2,IL6R,FGF7,ABL1,PDGFD,PLPP3,LRP4	up_VSAP_EC

GO:0072522	0.449	0.712	6	91	purine-containing compound biosynthetic	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1	down_VSAP_EC
GO:0019362	0.449	0.748	4	35	pyridine nucleotide metabolic process	BP	1	NADK,GALK1,PNP,DDIT4	up_VSAP_EC
GO:0046496	0.449	0.748	4	35	nicotinamide nucleotide metabolic process	BP	1	NADK,GALK1,PNP,DDIT4	up_VSAP_EC
GO:0050864	0.449	0.748	4	36	regulation of B cell activation	BP	1	TBC1D10C,STAT6,ZFP36L1,ZFP36L2	up_VSAP_EC
GO:0071310	0.449	0.775	3	634	cellular response to organic substance	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0008637	0.449	0.772	3	35	apoptotic mitochondrial changes	BP	1	SH3GLB1,PMAIP1,ATP2A1	up_VCAV_EC
GO:0032609	0.449	0.776	3	25	interferon-gamma production	BP	1	CD274,ABL1,F2RL1	up_VSAP_EC
GO:0000060	0.449	0.818	2	15	protein import into nucleus, translocation	BP	1	CDKN1A,PSEN1	up_ACOR_VSMC
GO:0007266	0.449	0.808	2	64	Rho protein signal transduction	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0030900	0.449	0.883	1	101	forebrain development	BP	1	NRP2	down_ACOR_EC
GO:0034367	0.449	0.894	1	7	protein-containing complex remodeling	BP	1	LIPC	down_ACOR_VSMC
GO:0034368	0.449	0.894	1	7	protein-lipid complex remodeling	BP	1	LIPC	down_ACOR_VSMC
GO:0034369	0.449	0.894	1	7	plasma lipoprotein particle remodeling	BP	1	LIPC	down_ACOR_VSMC
GO:0046365	0.449	0.894	1	7	monosaccharide catabolic process	BP	1	GALE	down_ACOR_VSMC
GO:0071025	0.449	0.894	1	7	RNA surveillance	BP	1	EXOSC5	down_ACOR_VSMC
GO:0071027	0.449	0.894	1	7	nuclear RNA surveillance	BP	1	EXOSC5	down_ACOR_VSMC
GO:0071028	0.449	0.894	1	7	nuclear mRNA surveillance	BP	1	EXOSC5	down_ACOR_VSMC
GO:0071243	0.449	0.894	1	7	cellular response to arsenic-containing	BP	1	GSTO1	down_ACOR_VSMC
GO:0009069	0.449	0.889	1	11	serine family amino acid metabolic process	BP	1	THNSL2	down_VCAV_EC
GO:0072283	0.449	0.888	1	12	metanephric renal vesicle morphogenesis	BP	1	GREM1	down_VCAV_EC
GO:0019438	0.449	0.914	1	1258	aromatic compound biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:1903541	0.449	0.889	1	10	regulation of exosomal secretion	BP	1	SDC4	down_VSAP_EC
GO:1903543	0.449	0.889	1	10	positive regulation of exosomal secretion	BP	1	SDC4	down_VSAP_EC
GO:0002828	0.449	0.891	1	9	regulation of type 2 immune response	BP	1	SOCS5	down_VSAP_EC
GO:1905517	0.449	0.889	1	10	macrophage migration	BP	1	MMP28	down_VSAP_EC
GO:0000083	0.449	0.896	1	6	regulation of transcription involved in G1/S transition of mitotic cell	BP	1	KLF11	up_ACOR_VSMC
GO:0003323	0.449	0.896	1	6	type B pancreatic cell development	BP	1	BMP4	up_ACOR_VSMC
GO:0006171	0.449	0.9	1	5	cAMP biosynthetic process	BP	1	ADCY6	up_ACOR_VSMC
GO:0006825	0.449	0.897	1	6	copper ion transport	BP	1	ATP7A	up_ACOR_VSMC
GO:0032633	0.449	0.896	1	6	interleukin-4 production	BP	1	CD83	up_ACOR_VSMC
GO:0035883	0.449	0.896	1	6	enteroendocrine cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0046058	0.449	0.9	1	5	cAMP metabolic process	BP	1	ADCY6	up_ACOR_VSMC
GO:0003309	0.449	0.896	1	6	type B pancreatic cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0033160	0.449	0.896	1	6	positive regulation of protein import into	BP	1	TMEM173	up_VCAV_EC
GO:0090335	0.449	0.894	1	7	regulation of brown fat cell differentiation	BP	1	PTGS2	up_VCAV_EC
GO:1904707	0.449	0.894	1	7	positive regulation of vascular smooth muscle	BP	1	PDGFB	up_VCAV_EC
GO:1990748	0.449	0.892	1	8	cellular detoxification	BP	1	GCH1	up_VCAV_EC
GO:0045637	0.449	0.883	1	73	regulation of myeloid cell differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0045944	0.449	0.887	1	287	positive regulation of transcription by RNA polymerase II	BP	1	GATA5	up_VPUL_VSMC

GO:0045947	0.449	0.897	1	6	negative regulation of translational initiation	BP	1	ANKHD1	up_VSAP_EC
GO:0070601	0.449	0.896	1	6	centromeric sister chromatid cohesion	BP	1	AXIN2	up_VSAP_EC
GO:2000765	0.449	0.896	1	6	regulation of cytoplasmic translation	BP	1	NCK1	up_VSAP_EC
GO:1903055	0.449	0.896	1	6	positive regulation of extracellular matrix	BP	1	DDR2	up_VSAP_EC
GO:0051310	0.449365064	0.88421	1	22	metaphase plate congression	BP	1	CHMP4B	up_ACOR_EC
GO:0007267	0.45	0.628	29	332	cell-cell signaling	BP	1	EPHB1,PLK2,PCDH12,ENSCAFG00000007112,PDGFB,RELN,MEF2C,FERMT1,CHD7,RAPGEF1,GATA3,EDN1,SNCAIP,HOMER3,PPP3CA,GUCY1A1,SNAP23,BMP2,HHEX,SLC12A7,MCC,SMARCA4,GRM8,CREB1,STX11,MCU,HIF1A,ALS2,P2RX2	up_VCAV_EC
GO:0002694	0.45	0.664	13	126	regulation of leukocyte activation	BP	1	LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,F2RL1,CDKN1A,PTPN22,APP,DUSP22,NOD2,PAG1	up_ACOR_VSMC
GO:0019219	0.45	0.684	10	1151	regulation of nucleobase-containing compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0021987	0.45	0.747	4	37	cerebral cortex development	BP	1	EMX2,CDON,SLIT2,MCPH1	up_VSAP_EC
GO:0072088	0.45	0.747	4	36	nephron epithelium morphogenesis	BP	1	HOXA11,WNT11,OSR1,IRX3	up_VSAP_EC
GO:0060688	0.45	0.773	3	29	regulation of morphogenesis of a	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0045931	0.45	0.769	3	49	positive regulation of mitotic cell cycle	BP	1	POLDIP2,LSM10,EIF4EBP1	down_VCAV_EC
GO:0072384	0.45	0.775	3	24	organelle transport along microtubule	BP	1	RHOT1,SUN1,DYNC1I1	up_ACOR_VSMC
GO:1900542	0.45	0.774	3	26	regulation of purine nucleotide metabolic	BP	1	PPARGC1A,DDIT4,PARK7	up_ACOR_VSMC
GO:0045943	0.45	0.815	2	17	positive regulation of transcription by RNA	BP	1	DHX33,NCL	down_ACOR_VSMC
GO:0008625	0.45	0.81	2	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	GABARAP,PARK7	down_VCAV_EC
GO:0031532	0.45	0.81	2	31	actin cytoskeleton reorganization	BP	1	RHOD,SHC1	down_VCAV_EC
GO:0002698	0.45	0.812	2	25	negative regulation of immune effector process	BP	1	SOCS5,A2M	down_VSAP_EC
GO:0030219	0.45	0.816	2	16	megakaryocyte differentiation	BP	1	CDKN2B,CNOT4	up_ACOR_VSMC
GO:0060322	0.45	0.808	2	193	head development	BP	1	HOOK3,SEMA3A	up_VPOR_EC
GO:0030111	0.45	0.883	1	108	regulation of Wnt signaling pathway	BP	1	SULF1	down_ACOR_EC
GO:1903427	0.45	0.893	1	7	negative regulation of reactive oxygen species biosynthetic process	BP	1	CAV1	down_ACOR_VSMC
GO:1901698	0.45	0.886	1	266	response to nitrogen compound	BP	1	GABPA	down_AFEM_EC
GO:0043001	0.45	0.888	1	11	Golgi to plasma membrane protein	BP	1	RAB31	down_VCAV_EC
GO:0045453	0.45	0.888	1	12	bone resorption	BP	1	NCDN	down_VCAV_EC
GO:0055023	0.45	0.887	1	12	positive regulation of cardiac muscle tissue	BP	1	BMPR1A	down_VCAV_EC
GO:0060561	0.45	0.888	1	11	apoptotic process involved in	BP	1	B4GALT1	down_VCAV_EC
GO:0061384	0.45	0.887	1	12	heart trabecula morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0018130	0.45	0.914	1	1261	heterocycle biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0032494	0.45	0.896	1	6	response to peptidoglycan	BP	1	NOD2	up_ACOR_VSMC
GO:0035721	0.45	0.896	1	6	intraciliary retrograde transport	BP	1	IFT43	up_ACOR_VSMC
GO:0051491	0.45	0.896	1	6	positive regulation of filopodium assembly	BP	1	NRP1	up_ACOR_VSMC
GO:1901798	0.45	0.893	1	7	positive regulation of signal transduction by p53 class mediator	BP	1	ANKRD1	up_ACOR_VSMC
GO:2000679	0.45	0.896	1	6	positive regulation of transcription regulatory region DNA binding	BP	1	PARK7	up_ACOR_VSMC
GO:0008344	0.45	0.883	1	25	adult locomotory behavior	BP	1	LGI4	up_AFEM_EC

GO:0035850	0.45	0.883	1	25	epithelial cell differentiation involved in	BP	1	GREM1	up_AFEM_EC
GO:0072665	0.45	0.883	1	25	protein localization to vacuole	BP	1	RAB7A	up_AFEM_EC
GO:1904591	0.45	0.883	1	25	positive regulation of protein import	BP	1	LEP	up_AFEM_EC
GO:0051247	0.45	0.892	1	502	positive regulation of protein metabolic process	BP	1	WNT7A	up_AORT_VSMC
GO:0120031	0.45	0.883	1	154	plasma membrane bounded cell projection	BP	1	ARHGEF26	up_APUL_EC
GO:0070242	0.45	0.893	1	7	thymocyte apoptotic process	BP	1	HIF1A	up_VCAV_EC
GO:0071803	0.45	0.896	1	6	positive regulation of podosome assembly	BP	1	FSCN1	up_VCAV_EC
GO:0097435	0.45	0.885	1	230	supramolecular fiber organization	BP	1	NKX2-5	up_VPOR_VSMC
GO:0080135	0.45	0.885	1	240	regulation of cellular response to stress	BP	1	EYA1	up_VFEM_VSMC
GO:0010742	0.45	0.896	1	6	macrophage derived foam cell differentiation	BP	1	SOAT1	up_VSAP_EC
GO:0040015	0.45	0.896	1	6	negative regulation of multicellular organism	BP	1	FXN	up_VSAP_EC
GO:0044788	0.45	0.896	1	6	modulation by host of viral process	BP	1	PC	up_VSAP_EC
GO:0090051	0.45	0.896	1	6	negative regulation of cell migration involved in sprouting angiogenesis	BP	1	TBXA2R	up_VSAP_EC
GO:0090077	0.45	0.896	1	6	foam cell differentiation	BP	1	SOAT1	up_VSAP_EC
GO:0007565	0.450464642	0.88338	1	23	female pregnancy	BP	1	ARHGDIB	up_ACOR_EC
GO:0007154	0.451	0.599	82	1622	cell communication	BP	1	NOTCH2,PDGFRB,SLC35F6,SMAD9,ITGB5,DCN,NDN,ANGPT1,PRNP,VASN,FBN1,ADCY6,GLIPR2,BGN,KANK2,SH3BP1,BMPR1A,EVC,RECK,IGFBP6,NUMBL,ARHGEF25,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,AKT2,DOCK10,SYDE1,CLSTN1,PLCL1,CACNB3,CSPG4,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,SEMA3C,ASPN,GNAZ,THY1,TEAD1,ARHGAP10,ATP6V0C,GLI3,PARK7,ZMAT3,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ENSCAFG00000018194,ARL2BP,IFT57,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,RAB7B,SPNS1,GLIS2,ARHGAP1,SHC1,CRCP,FBH1,GREM1,NPHP4,RAC2,FOXO3,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:0060322	0.451	0.662	13	193	head development	BP	1	HSPA5,PTPN11,AARS,HOOK3,HIF1A,UBA6,UCHL5,CTNNB1,GSK3B,EXT1,DISC1,INHBA,NRP1	down_VSAP_EC
GO:0052548	0.451	0.692	8	80	regulation of endopeptidase activity	BP	1	MBP,RECK,CST3,DAPK1,SH3RF1,SPINK2,PERP,PARK7	up_ACOR_VSMC
GO:0010001	0.451	0.713	6	54	glial cell differentiation	BP	1	SH3TC2,WASF3,ZNF365,DAG1,APP,PSEN1	up_ACOR_VSMC
GO:0009636	0.451	0.712	6	66	response to toxic substance	BP	1	TNFAIP3,PDGFB,MAPK13,TIMELESS,GCH1,RIPK1	up_VCAV_EC
GO:0032787	0.451	0.74	4	144	monocarboxylic acid metabolic process	BP	1	LEP,GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0051247	0.451	0.771	3	502	positive regulation of protein metabolic process	BP	1	ACVRL1,LYN,NEDD4	down_ACOR_EC
GO:0032946	0.451	0.772	3	29	positive regulation of mononuclear cell	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0050671	0.451	0.772	3	29	positive regulation of lymphocyte proliferation	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0043433	0.451	0.769	3	49	negative regulation of DNA-binding transcription factor activity	BP	1	PRNP,CLSTN1,GLIS2	down_VCAV_EC
GO:0061572	0.451	0.768	3	50	actin filament bundle organization	BP	1	RHOD,ENSCAFG00000014978,MYO1B	down_VCAV_EC
GO:0002791	0.451	0.766	3	104	regulation of peptide secretion	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:0022414	0.451	0.809	2	294	reproductive process	BP	1	ACSL4,SULF1	down_ACOR_EC
GO:0044248	0.451	0.816	2	691	cellular catabolic process	BP	1	ETFA,USP33	down_AFEM_EC
GO:0031099	0.451	0.809	2	30	regeneration	BP	1	THY1,RGMA	down_VCAV_EC
GO:0042073	0.451	0.815	2	16	intraciliary transport	BP	1	IFT43,ENSCAFG00000013536	up_ACOR_VSMC

GO:0002376	0.451	0.815	2	622	immune system process	BP	1	HOXA9,BPI	up_AORT_EC
GO:0048193	0.451	0.882	1	116	Golgi vesicle transport	BP	1	ACSL3	down_ACOR_EC
GO:0006283	0.451	0.893	1	7	transcription-coupled nucleotide-excision repair	BP	1	HMGN1	down_ACOR_VSMC
GO:0009154	0.451	0.893	1	7	purine ribonucleotide catabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:0010880	0.451	0.893	1	7	regulation of release of sequestered calcium ion into cytosol by	BP	1	GSTO1	down_ACOR_VSMC
GO:0014808	0.451	0.893	1	7	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	GSTO1	down_ACOR_VSMC
GO:0032682	0.451	0.893	1	7	negative regulation of chemokine production	BP	1	ARG2	down_ACOR_VSMC
GO:1903514	0.451	0.893	1	7	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	1	GSTO1	down_ACOR_VSMC
GO:0021591	0.451	0.887	1	12	ventricular system development	BP	1	NUMBL	down_VCAV_EC
GO:0034724	0.451	0.887	1	12	DNA replication-independent nucleosome	BP	1	CABIN1	down_VCAV_EC
GO:0061098	0.451	0.887	1	12	positive regulation of protein tyrosine kinase	BP	1	PRNP	down_VCAV_EC
GO:0072604	0.451	0.887	1	12	interleukin-6 secretion	BP	1	MAVS	down_VCAV_EC
GO:0060548	0.451	0.886	1	294	negative regulation of cell death	BP	1	CITED2	down_VPOR_EC
GO:0048678	0.451	0.889	1	10	response to axon injury	BP	1	DPYSL3	down_VSAP_EC
GO:0032094	0.451	0.895	1	6	response to food	BP	1	LEP	up_ACOR_VSMC
GO:0048368	0.451	0.895	1	6	lateral mesoderm development	BP	1	CITED2	up_ACOR_VSMC
GO:0060440	0.451	0.895	1	6	trachea formation	BP	1	BMP4	up_ACOR_VSMC
GO:0002098	0.451	0.891	1	8	tRNA wobble uridine modification	BP	1	TRMT9B	up_VCAV_EC
GO:0010758	0.451	0.891	1	8	regulation of macrophage chemotaxis	BP	1	MMP28	up_VCAV_EC
GO:0015937	0.451	0.891	1	8	coenzyme A biosynthetic process	BP	1	PANK3	up_VCAV_EC
GO:0040037	0.451	0.895	1	6	negative regulation of fibroblast growth factor receptor signaling	BP	1	GATA3	up_VCAV_EC
GO:0060707	0.451	0.893	1	7	trophoblast giant cell differentiation	BP	1	MDFI	up_VCAV_EC
GO:0033273	0.451	0.896	1	6	response to vitamin	BP	1	BGLAP	up_VSAP_EC
GO:0046184	0.451	0.895	1	6	aldehyde biosynthetic process	BP	1	PNPO	up_VSAP_EC
GO:2000773	0.451	0.896	1	6	negative regulation of cellular senescence	BP	1	ABL1	up_VSAP_EC
GO:0032400	0.451	0.895	1	6	melanosome localization	BP	1	RAB11B	up_VSAP_EC
GO:0032401	0.451	0.895	1	6	establishment of melanosome localization	BP	1	RAB11B	up_VSAP_EC
GO:0051875	0.451	0.895	1	6	pigment granule localization	BP	1	RAB11B	up_VSAP_EC
GO:0051905	0.451	0.895	1	6	establishment of pigment granule localization	BP	1	RAB11B	up_VSAP_EC
GO:0033627	0.451074473	0.88323	1	22	cell adhesion mediated by integrin	BP	1	FOXC2	up_ACOR_EC
GO:0019953	0.452	0.675	10	152	sexual reproduction	BP	1	CELF1,ETV6,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SPINK2,SNRPA1,KDM3A	down_VSAP_EC
GO:0110053	0.452	0.677	10	98	regulation of actin filament organization	BP	1	WNT11,ARHGEF5,SLIT2,ABL1,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,NCK1,BAG4	up_VSAP_EC
GO:0046483	0.452	0.699	9	1948	heterocycle metabolic process	BP	1	TBX15,EYA1,HOXA9,MME,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0001666	0.452	0.7	7	67	response to hypoxia	BP	1	VEGFD,ITPR1,BNIP3,EGLN1,PRKCE,EDN1,DDIT4	up_ACOR_VSMC
GO:0036293	0.452	0.7	7	67	response to decreased oxygen levels	BP	1	VEGFD,ITPR1,BNIP3,EGLN1,PRKCE,EDN1,DDIT4	up_ACOR_VSMC
GO:0072593	0.452	0.741	4	68	reactive oxygen species metabolic process	BP	1	PARK7,CYBA,GLS2,FOXO3	down_VCAV_EC
GO:0002792	0.452	0.771	3	29	negative regulation of peptide secretion	BP	1	SREBF1,ARG2,EZR	down_ACOR_VSMC
GO:1990542	0.452	0.77	3	32	mitochondrial transmembrane transport	BP	1	TIMM44,CYC1,MRPL18	down_ACOR_VSMC

GO:0009165	0.452	0.765	3	104	nucleotide biosynthetic process	BP	1	GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0051171	0.452	0.793	3	1697	regulation of nitrogen compound metabolic	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0000003	0.452	0.808	2	295	reproduction	BP	1	ACSL4,SULF1	down_ACOR_EC
GO:0051402	0.452	0.805	2	64	neuron apoptotic process	BP	1	THRB,PPARGC1A	up_AFEM_EC
GO:0031065	0.452	0.893	1	7	positive regulation of histone deacetylation	BP	1	SREBF1	down_ACOR_VSMC
GO:0032660	0.452	0.892	1	7	regulation of interleukin-17 production	BP	1	ARG2	down_ACOR_VSMC
GO:0043162	0.452	0.893	1	7	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	BP	1	NEDD4	down_ACOR_VSMC
GO:0043113	0.452	0.886	1	12	receptor clustering	BP	1	CDH2	down_VCAV_EC
GO:0090659	0.452	0.886	1	12	walking behavior	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0042558	0.452	0.887	1	11	pteridine-containing compound metabolic	BP	1	ALDH1L2	down_VSAP_EC
GO:0071392	0.452	0.895	1	6	cellular response to estradiol stimulus	BP	1	FAM210B	up_ACOR_VSMC
GO:0032890	0.452	0.895	1	6	regulation of organic acid transport	BP	1	PSEN1	up_ACOR_VSMC
GO:0070920	0.452	0.895	1	6	regulation of production of small RNA involved in gene silencing by RNA	BP	1	BMP4	up_ACOR_VSMC
GO:1903798	0.452	0.895	1	6	regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	BMP4	up_ACOR_VSMC
GO:0034333	0.452	0.882	1	25	adherens junction assembly	BP	1	GREM1	up_AFEM_EC
GO:0051149	0.452	0.882	1	25	positive regulation of muscle cell differentiation	BP	1	GREM1	up_AFEM_EC
GO:0030031	0.452	0.882	1	155	cell projection assembly	BP	1	ARHGEF26	up_APUL_EC
GO:0120039	0.452	0.882	1	158	plasma membrane bounded cell projection	BP	1	SLITRK5	up_APUL_EC
GO:2000778	0.452	0.892	1	7	positive regulation of interleukin-6 secretion	BP	1	HMGB1	up_VCAV_EC
GO:0045893	0.452	0.888	1	413	positive regulation of transcription, DNA-	BP	1	GATA5	up_VCAV_VSMC
GO:0030001	0.452	0.883	1	172	metal ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0044550	0.452	0.895	1	6	secondary metabolite biosynthetic process	BP	1	MPST	up_VSAP_EC
GO:0007179	0.452165369	0.8058	2	57	transforming growth factor beta receptor	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:0035710	0.452262729	0.88254	1	22	CD4-positive, alpha-beta T cell activation	BP	1	PTGER4	up_ACOR_EC
GO:0055024	0.452729913	0.88227	1	22	regulation of cardiac muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0009161	0.453	0.682	9	103	ribonucleoside monophosphate	BP	1	CDK1,PFAS,CYCS,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0009165	0.453	0.682	9	104	nucleotide biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,NOS2,HIF1A	up_VCAV_EC
GO:0002791	0.453	0.697	7	104	regulation of peptide secretion	BP	1	NR1H4,PTPN11,HIF1A,LYN,REST,RAB11FIP1,RHBDF2	down_VSAP_EC
GO:0043523	0.453	0.725	5	52	regulation of neuron apoptotic process	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIGMAR1,SIX4	down_ACOR_VSMC
GO:0006733	0.453	0.726	5	45	oxidoreduction coenzyme metabolic process	BP	1	NADK,COQ9,GALK1,PNP,DDIT4	up_VSAP_EC
GO:1904018	0.453	0.741	4	69	positive regulation of vasculature development	BP	1	HSPB6,MYDGF,SASH1,GREM1	down_VCAV_EC
GO:0015849	0.453	0.741	4	56	organic acid transport	BP	1	SLC7A5,SLC38A1,APOE,SLC7A11	down_VSAP_EC
GO:0046942	0.453	0.741	4	56	carboxylic acid transport	BP	1	SLC7A5,SLC38A1,APOE,SLC7A11	down_VSAP_EC
GO:0034654	0.453	0.782	3	1236	nucleobase-containing compound biosynthetic	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0048731	0.453	0.782	3	1247	system development	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0006694	0.453	0.768	3	42	steroid biosynthetic process	BP	1	NR1H4,APOE,REST	down_VSAP_EC
GO:0032368	0.453	0.771	3	26	regulation of lipid transport	BP	1	LEP,ABCA1,SCP2	up_ACOR_VSMC
GO:1901570	0.453	0.814	2	16	fatty acid derivative biosynthetic process	BP	1	EDN1,ELOVL7	up_ACOR_VSMC

GO:0033500	0.453	0.805	2	64	carbohydrate homeostasis	BP	1	LEP,CRY2	up_AFEM_EC
GO:0042593	0.453	0.805	2	64	glucose homeostasis	BP	1	LEP,CRY2	up_AFEM_EC
GO:0010605	0.453	0.816	2	745	negative regulation of macromolecule metabolic	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:1900024	0.453	0.814	2	16	regulation of substrate adhesion-dependent cell	BP	1	ABL1,FBLN1	up_VSAP_EC
GO:0034427	0.453	0.892	1	7	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	BP	1	EXOSC5	down_ACOR_VSMC
GO:0070199	0.453	0.892	1	7	establishment of protein localization to	BP	1	CCT4	down_ACOR_VSMC
GO:0033344	0.453	0.885	1	12	cholesterol efflux	BP	1	SOAT1	down_VCAV_EC
GO:0010468	0.453	0.913	1	1270	regulation of gene expression	BP	1	MOSPD1	down_VFEM_EC
GO:0009048	0.453	0.889	1	9	dosage compensation by inactivation of X	BP	1	CDYL	down_VSAP_EC
GO:0043277	0.453	0.888	1	9	apoptotic cell clearance	BP	1	ENSCAFG00000003477	down_VSAP_EC
GO:0072160	0.453	0.889	1	9	nephron tubule epithelial cell differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:1905276	0.453	0.889	1	9	regulation of epithelial tube formation	BP	1	SIX4	down_VSAP_EC
GO:0060841	0.453	0.894	1	6	venous blood vessel development	BP	1	TBX20	up_ACOR_VSMC
GO:0000288	0.453	0.882	1	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	SAMD4B	up_AFEM_EC
GO:0006641	0.453	0.882	1	25	triglyceride metabolic process	BP	1	GPAM	up_AFEM_EC
GO:0019218	0.453	0.882	1	25	regulation of steroid metabolic process	BP	1	LEP	up_AFEM_EC
GO:0050729	0.453	0.881	1	25	positive regulation of inflammatory response	BP	1	NAPEPLD	up_AFEM_EC
GO:0051289	0.453	0.882	1	25	protein homotetramerization	BP	1	ACACB	up_AFEM_EC
GO:0051240	0.453	0.89	1	489	positive regulation of multicellular organismal	BP	1	WNT7A	up_AORT_VSMC
GO:2001234	0.453	0.88	1	75	negative regulation of apoptotic signaling	BP	1	ARHGEF2	up_VPOR_EC
GO:0000479	0.453	0.894	1	6	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	RCL1	up_VSAP_EC
GO:0030903	0.453	0.894	1	6	notochord development	BP	1	WNT11	up_VSAP_EC
GO:0042249	0.453	0.895	1	6	establishment of planar polarity of embryonic	BP	1	FZD1	up_VSAP_EC
GO:0048857	0.453	0.894	1	6	neural nucleus development	BP	1	NFIB	up_VSAP_EC
GO:0016233	0.453002219	0.88211	1	22	telomere capping	BP	1	PKIB	up_ACOR_EC
GO:0007276	0.453472164	0.73839	4	130	gamete generation	BP	1	SOX9,FIGNL1,PYGO2,CCNYL1	up_ACOR_EC
GO:0046785	0.453558028	0.88158	1	23	microtubule polymerization	BP	1	TUBB4A	up_ACOR_EC
GO:0023061	0.453639466	0.76401	3	95	signal release	BP	1	NR1H4,AQP1,KCNB1	up_ACOR_EC
GO:0006518	0.454	0.624	29	290	peptide metabolic process	BP	1	PRR16,RNPEP,MRPL37,WARS2,PYM1,ZFP36L1,CTNS,EEF2,LARP6,RPL13,ANKHD1,FARS2,UBA52,RPUSD4,RPL15,EIF3G,SAMD4B,ZFP36L2,EIF3K,EIF3L,QARS,EIF3D,IDH1,TNRC6C,COA1,NCK1,MRPL4,LARS2,ENSCAFG00000006478	up_VSAP_EC
GO:0006355	0.454	0.633	24	974	regulation of transcription, DNA-templated	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC
GO:0009968	0.454	0.673	10	392	negative regulation of signal transduction	BP	1	LBH,CRY2,GREM1,GREM2,CYLD,LRRC15,RAB7A,AXIN2,ADAM17,KANK1	up_AFEM_EC
GO:0009987	0.454	0.807	8	5086	cellular process	BP	1	HOXC10,TLR2,TBX15,EYA1,HOXA9,BEND2,HOXA10,IRX5	up_AFEM_VSMC
GO:0043588	0.454	0.698	7	74	skin development	BP	1	PRKCH,FERMT1,SOX18,STMN1,FLNB,LDB2,ITGA6	up_VCAV_EC
GO:0048762	0.454	0.698	7	77	mesenchymal cell differentiation	BP	1	EDNRB,MEF2C,EDN1,MTOR,BMP2,JAG1,HIF1A	up_VCAV_EC

GO:0051091	0.454	0.708	6	87	positive regulation of DNA-binding transcription factor activity	BP	1	ARHGEF2,VEGFA,SMARCA4,MTDH,CTNNB1,DDIT3	down_VSAP_EC
GO:0045454	0.454	0.744	4	35	cell redox homeostasis	BP	1	PTGES2,DLD,TXNDC16,ENSCAFG00000006478	up_VSAP_EC
GO:0006022	0.454	0.769	3	29	aminoglycan metabolic process	BP	1	B3GNT2,XYLT1,UGDH	down_ACOR_VSMC
GO:0015748	0.454	0.813	2	16	organophosphate ester transport	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0065008	0.454	0.822	2	1056	regulation of biological quality	BP	1	HOXC10,IRX5	up_AFEM_VSMC
GO:0051253	0.454	0.807	2	359	negative regulation of RNA metabolic process	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:1901700	0.454	0.807	2	364	response to oxygen-containing compound	BP	1	AVPR1A,CYP26B1	up_VFEM_EC
GO:0006656	0.454	0.891	1	7	phosphatidylcholine biosynthetic process	BP	1	ACSL3	down_ACOR_VSMC
GO:0007017	0.454	0.884	1	273	microtubule-based process	BP	1	GPSM2	down_AFEM_EC
GO:0035561	0.454	0.885	1	12	regulation of chromatin binding	BP	1	FBH1	down_VCAV_EC
GO:0060795	0.454	0.885	1	12	cell fate commitment involved in formation of	BP	1	BMPR1A	down_VCAV_EC
GO:2000649	0.454	0.886	1	11	regulation of sodium ion transmembrane transporter activity	BP	1	YWHAH	down_VSAP_EC
GO:0030809	0.454	0.894	1	6	negative regulation of nucleotide biosynthetic	BP	1	DDIT4	up_ACOR_VSMC
GO:1900372	0.454	0.894	1	6	negative regulation of purine nucleotide	BP	1	DDIT4	up_ACOR_VSMC
GO:2001170	0.454	0.894	1	6	negative regulation of ATP biosynthetic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0019882	0.454	0.881	1	25	antigen processing and presentation	BP	1	CTSS	up_AFEM_EC
GO:0030500	0.454	0.881	1	25	regulation of bone mineralization	BP	1	GREM1	up_AFEM_EC
GO:0002532	0.454	0.881	1	25	production of molecular mediator involved in inflammatory response	BP	1	LEP	up_AFEM_EC
GO:0070227	0.454	0.881	1	25	lymphocyte apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0070613	0.454	0.881	1	25	regulation of protein processing	BP	1	GAS1	up_AFEM_EC
GO:0071347	0.454	0.881	1	25	cellular response to interleukin-1	BP	1	CCL5	up_AFEM_EC
GO:1903317	0.454	0.881	1	25	regulation of protein maturation	BP	1	GAS1	up_AFEM_EC
GO:0048858	0.454	0.88	1	159	cell projection morphogenesis	BP	1	SLITRK5	up_APUL_EC
GO:0006805	0.454	0.889	1	8	xenobiotic metabolic process	BP	1	AHR	up_VCAV_EC
GO:1901889	0.454	0.89	1	8	negative regulation of cell junction assembly	BP	1	APOD	up_VCAV_EC
GO:1902680	0.454	0.887	1	415	positive regulation of RNA biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:1903508	0.454	0.887	1	415	positive regulation of nucleic acid-templated	BP	1	GATA5	up_VCAV_VSMC
GO:0050776	0.454	0.881	1	173	regulation of immune response	BP	1	NR1H4	up_VPUL_EC
GO:0032989	0.454	0.884	1	292	cellular component morphogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0032570	0.454	0.894	1	6	response to progesterone	BP	1	NCOA2	up_VSAP_EC
GO:0033561	0.454	0.894	1	6	regulation of water loss via skin	BP	1	CLDN1	up_VSAP_EC
GO:1905048	0.454	0.894	1	6	regulation of metallopeptidase activity	BP	1	RECK	up_VSAP_EC
GO:0014068	0.454009506	0.88152	1	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	SOX9	up_ACOR_EC

GO:0006810	0.455	0.59	102	1244	transport	BP	1	HCLS1,GBP5,KIT,SELE,CXCL8,CP,OSBPL9,CALCRL,ATP8A1,LRRC8D,MX2,PDGFB,TMEM173,ATP2B1,EXOC3L2,RELN,PDE4D,IWS1,MEF2C,FERMT1,CHD7,SLC35A3,TLR4,QKI,STC1,GATA3,EDN1,RAB11A,KIF3C,APLNR,RAB27A,SLC39A8,EXOC6,CTTNBP2NL,SNCAIP,SLC49A3,IRF8,SLCO2A1,PIK3C2A,PPP3CA,YES1,SLC38A1,ARG2,HOOK3,SNAP23,LRRC8C,HHEX,RAB6A,SPNS3,CAV2,BMP2K,RALBP1,SCAMP1,RSC1A1,PDZD8,ANKRD50,ABCA1,KCNJ3,OSBPL6,ELMO1,SNX2,SLCO3A1,THOC1,SH3GLB1,AKAP12,APOD,SLC2A3,KCNJ2,EXOC5,CD200,SLC25A25,FES,HIST1H1A,EHD4,PLCG2,CTDSPL2,CREB1,PAN3,GCC2,STX11,SMG7,VPS54,HMGB1,TBC1D1,NOS2,PMAIP1,NUP133,SPTBN4,RIPK1,CHIC2,MCU,DNAJC13,ZW10,HIF1A,IPO11,ALS2,LMTK2,DOP1B,ATP2A1,RABGAP1,PEAR1,USP6NL	up_VCAV_EC
GO:0071407	0.455	0.695	7	129	cellular response to organic cyclic compound	BP	1	SMAD9,ADCY6,KANK2,NR3C1,PARK7,ZFP36L1,MAVS	down_VCAV_EC
GO:0051402	0.455	0.708	6	64	neuron apoptotic process	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIGMAR1,AIFM1,SIX4	down_ACOR_VSMC
GO:0071356	0.455	0.709	6	57	cellular response to tumor necrosis factor	BP	1	ANKRD1,F2RL1,NPNT,CCDC3,CCL5,INPP5K	up_ACOR_VSMC
GO:0050794	0.455	0.77	5	3075	regulation of cellular process	BP	1	TLR2,EYA1,HOXA9,HOXA10,IRX5	up_AFEM_VSMC
GO:0044267	0.455	0.759	4	1583	cellular protein metabolic process	BP	1	IVNS1ABP,DARS,EIF3M,USP33	down_AFEM_EC
GO:0048515	0.455	0.743	4	36	spermatid differentiation	BP	1	AFF4,SPINK2,DMC1,JAM3	up_ACOR_VSMC
GO:0009791	0.455	0.742	4	38	post-embryonic development	BP	1	TIPARP,GATA3,MTOR,ATRX	up_VCAV_EC
GO:0030154	0.455	0.776	3	1040	cell differentiation	BP	1	HOXC10,HOXA9,SGCD	up_AORT_EC
GO:0035821	0.455	0.767	3	32	modification of morphology or physiology	BP	1	LYZ,TNIP1,SMARCA4	up_VCAV_EC
GO:0072171	0.455	0.768	3	30	mesonephric tubule morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:0032368	0.455	0.808	2	26	regulation of lipid transport	BP	1	PTPN11,APOE	down_VSAP_EC
GO:0019058	0.455	0.803	2	64	viral life cycle	BP	1	LRRC15,RAB7A	up_AFEM_EC
GO:0035196	0.455	0.812	2	16	production of miRNAs involved in gene silencing	BP	1	PPP3CA,TUT7	up_VCAV_EC
GO:0072001	0.455	0.88	1	104	renal system development	BP	1	SULF1	down_ACOR_EC
GO:0001832	0.455	0.891	1	7	blastocyst growth	BP	1	GINS4	down_ACOR_VSMC
GO:0045730	0.455	0.889	1	8	respiratory burst	BP	1	RAC1	down_ACOR_VSMC
GO:0060065	0.455	0.89	1	7	uterus development	BP	1	HOXA9	down_ACOR_VSMC
GO:1901213	0.455	0.891	1	7	regulation of transcription from RNA polymerase II promoter involved in	BP	1	GREM1	down_ACOR_VSMC
GO:1901701	0.455	0.883	1	271	cellular response to oxygen-containing	BP	1	GABPA	down_AFEM_EC
GO:0097352	0.455	0.885	1	12	autophagosome maturation	BP	1	CLEC16A	down_VCAV_EC
GO:0040012	0.455	0.883	1	303	regulation of locomotion	BP	1	HDAC7	down_VPOR_EC
GO:0034063	0.455	0.888	1	9	stress granule assembly	BP	1	EIF2S1	down_VSAP_EC
GO:0061311	0.455	0.887	1	9	cell surface receptor signaling pathway involved in heart	BP	1	CTNNB1	down_VSAP_EC
GO:0043001	0.455	0.886	1	11	Golgi to plasma membrane protein	BP	1	BLZF1	down_VSAP_EC
GO:0090185	0.455	0.886	1	10	negative regulation of kidney development	BP	1	CTNNB1	down_VSAP_EC
GO:0007595	0.455	0.893	1	6	lactation	BP	1	GJA1	up_ACOR_VSMC
GO:0050716	0.455	0.893	1	6	positive regulation of interleukin-1 secretion	BP	1	NOD2	up_ACOR_VSMC
GO:0070307	0.455	0.893	1	6	lens fiber cell development	BP	1	FRS2	up_ACOR_VSMC
GO:0061077	0.455	0.88	1	25	chaperone-mediated protein folding	BP	1	UNC45B	up_AFEM_EC
GO:0023014	0.455	0.882	1	248	signal transduction by protein phosphorylation	BP	1	TAOK1	up_AORT_EC

GO:0006684	0.455	0.891	1	7	sphingomyelin metabolic process	BP	1	SPTLC2	up_VCAV_EC
GO:0032462	0.455	0.889	1	8	regulation of protein homooligomerization	BP	1	RIOK3	up_VCAV_EC
GO:0039531	0.455	0.891	1	7	regulation of viral-induced cytoplasmic pattern recognition receptor	BP	1	RIOK3	up_VCAV_EC
GO:0050878	0.455	0.879	1	75	regulation of body fluid levels	BP	1	SLC7A11	up_VPOR_EC
GO:0000165	0.455	0.882	1	236	MAPK cascade	BP	1	ANKRD6	up_VPOR_VSMC
GO:0033674	0.455	0.88	1	144	positive regulation of kinase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0051046	0.455	0.881	1	174	regulation of secretion	BP	1	NR1H4	up_VPUL_EC
GO:0022414	0.455	0.884	1	294	reproductive process	BP	1	SLIT2	up_VPUL_VSMC
GO:0006999	0.455	0.894	1	6	nuclear pore organization	BP	1	NUP98	up_VSAP_EC
GO:0034105	0.455	0.894	1	6	positive regulation of tissue remodeling	BP	1	PPARGC1B	up_VSAP_EC
GO:0039529	0.455	0.893	1	6	RIG-I signaling pathway	BP	1	NLRX1	up_VSAP_EC
GO:0099174	0.455	0.893	1	6	regulation of presynapse organization	BP	1	FZD1	up_VSAP_EC
GO:0043267	0.455	0.893	1	6	negative regulation of potassium ion transport	BP	1	KCNE3	up_VSAP_EC
GO:0045776	0.455	0.893	1	6	negative regulation of blood pressure	BP	1	RNPEP	up_VSAP_EC
GO:0043154	0.455252456	0.88059	1	23	negative regulation of cysteine-type endopeptidase activity	BP	1	IFI6	up_ACOR_EC
GO:1903522	0.455295029	0.80338	2	58	regulation of blood circulation	BP	1	GNAO1,RNLS	up_ACOR_EC
GO:0034446	0.455482612	0.88046	1	23	substrate adhesion-dependent cell spreading	BP	1	NRP1	up_ACOR_EC
GO:0051259	0.456	0.678	9	140	protein complex oligomerization	BP	1	C1QTNF6,VASP,DPYSL3,CRYAB,APOE,DDIT3,GBP5,PRMT1,TNFAIP1	down_VSAP_EC
GO:0051091	0.456	0.68	9	87	positive regulation of DNA-binding transcription factor activity	BP	1	FZD1,ARHGEF5,PPARGC1B,SAV1,PLPP3,DDR2,RBCK1,MYD88,MAVS	up_VSAP_EC
GO:1901991	0.456	0.708	6	56	negative regulation of mitotic cell cycle phase	BP	1	FAM107A,CRADD,ZFP36L1,FBXO7,ZFP36L2,TPRA1	up_VSAP_EC
GO:0031333	0.456	0.723	5	46	negative regulation of protein complex assembly	BP	1	SMAD6,TUBB4A,LMO4,CLSTN1,TBX20	up_ACOR_VSMC
GO:0009060	0.456	0.767	3	31	aerobic respiration	BP	1	SUCLG1,CYCS,PDHA1	down_ACOR_VSMC
GO:0010507	0.456	0.769	3	26	negative regulation of autophagy	BP	1	POLDIP2,HTRA2,HMOX1	up_VSAP_EC
GO:0048146	0.456	0.81	2	18	positive regulation of fibroblast proliferation	BP	1	CDK4,RNASEH2B	down_ACOR_VSMC
GO:0042632	0.456	0.807	2	27	cholesterol homeostasis	BP	1	NR1H4,APOE	down_VSAP_EC
GO:0090398	0.456	0.807	2	24	cellular senescence	BP	1	NUAK1,CDKN1A	down_VSAP_EC
GO:0055082	0.456	0.803	2	189	cellular chemical homeostasis	BP	1	C3AR1,ENSCAFG00000005494	up_VPOR_EC
GO:0071826	0.456	0.879	1	117	ribonucleoprotein complex subunit	BP	1	RPSA	down_ACOR_EC
GO:2000677	0.456	0.884	1	12	regulation of transcription regulatory region DNA	BP	1	PARK7	down_VCAV_EC
GO:0030866	0.456	0.886	1	10	cortical actin cytoskeleton organization	BP	1	TLN1	down_VSAP_EC
GO:0043368	0.456	0.887	1	9	positive T cell selection	BP	1	PTPN2	down_VSAP_EC
GO:0010566	0.456	0.893	1	6	regulation of ketone biosynthetic process	BP	1	DKKL1	up_ACOR_VSMC
GO:0002825	0.456	0.893	1	6	regulation of T-helper 1 type immune response	BP	1	IL18R1	up_ACOR_VSMC
GO:0048857	0.456	0.892	1	6	neural nucleus development	BP	1	SEC24B	up_ACOR_VSMC
GO:0050775	0.456	0.893	1	6	positive regulation of dendrite morphogenesis	BP	1	RELN	up_VCAV_EC
GO:0090200	0.456	0.886	1	10	positive regulation of release of cytochrome c	BP	1	PMAIP1	up_VCAV_EC
GO:0002684	0.456	0.882	1	239	positive regulation of immune system process	BP	1	C3AR1	up_VPOR_VSMC
GO:0000003	0.456	0.883	1	295	reproduction	BP	1	SLIT2	up_VPUL_VSMC

GO:0001990	0.456	0.893	1	6	regulation of systemic arterial blood pressure by	BP	1	F2RL1	up_VSAP_EC
GO:0010954	0.456	0.893	1	6	positive regulation of protein processing	BP	1	CCBE1	up_VSAP_EC
GO:0032890	0.456	0.892	1	6	regulation of organic acid transport	BP	1	OSR1	up_VSAP_EC
GO:0051220	0.456	0.893	1	6	cytoplasmic sequestering of protein	BP	1	KEAP1	up_VSAP_EC
GO:1901623	0.456	0.893	1	6	regulation of lymphocyte chemotaxis	BP	1	SLC8B1	up_VSAP_EC
GO:1903319	0.456	0.893	1	6	positive regulation of protein maturation	BP	1	CCBE1	up_VSAP_EC
GO:0006516	0.456	0.893	1	6	glycoprotein catabolic process	BP	1	HPSE	up_VSAP_EC
GO:0022411	0.456981835	0.73538	4	130	cellular component disassembly	BP	1	TMOD1,ACTN2,VPS16,ENSCAFG00000010493	up_ACOR_EC
GO:0005975	0.457	0.67	10	183	carbohydrate metabolic process	BP	1	CHID1,AKT2,H6PD,GLB1L,PGLS,POFUT1,ADK,B4GALT1,ENSCAFG00000017708,SLC3A2	down_VCAV_EC
GO:0006807	0.457	0.718	9	3221	nitrogen compound metabolic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0006611	0.457	0.721	5	51	protein export from nucleus	BP	1	DDX39A,HSPA9,RAN,NUP62,DDX39B	down_ACOR_VSMC
GO:0071706	0.457	0.741	4	40	tumor necrosis factor superfamily cytokine	BP	1	HMGB1,ARG2,CACTIN,ARHGEF2	down_ACOR_VSMC
GO:0007623	0.457	0.738	4	55	circadian rhythm	BP	1	BHLHE40,HTR7,MAGED1,GNAQ	down_VSAP_EC
GO:0002700	0.457	0.74	4	40	regulation of production of molecular mediator of immune response	BP	1	TLR4,GATA3,THOC1,TLR3	up_VCAV_EC
GO:0097696	0.457	0.74	4	43	STAT cascade	BP	1	HCLS1,IL7R,KIT,CNOT7	up_VCAV_EC
GO:0006413	0.457	0.764	3	42	translational initiation	BP	1	EIF4EBP1,EIF5,EIF2S1	down_VSAP_EC
GO:0099173	0.457	0.764	3	40	postsynapse organization	BP	1	APOE,NRP1,ARF4	down_VSAP_EC
GO:0043200	0.457	0.768	3	26	response to amino acid	BP	1	MTOR,PDGFD,ZEB1	up_VCAV_EC
GO:0021549	0.457	0.768	3	26	cerebellum development	BP	1	SEZ6L,ABL1,DLL1	up_VSAP_EC
GO:0070925	0.457	0.804	2	293	organelle assembly	BP	1	SPG11,RPSA	down_ACOR_EC
GO:0016999	0.457	0.805	2	30	antibiotic metabolic process	BP	1	PARK7,ACSS2	down_VCAV_EC
GO:0032879	0.457	0.813	2	767	regulation of localization	BP	1	HDAC7,RAB11B	down_VPOR_EC
GO:0030217	0.457	0.801	2	65	T cell differentiation	BP	1	LEP,CYLD	up_AFEM_EC
GO:0060711	0.457	0.808	2	21	labyrinthine layer development	BP	1	PCDH12,VASH1	up_VCAV_EC
GO:0060760	0.457	0.81	2	17	positive regulation of response to cytokine	BP	1	NLRC5,LSM14A	up_VCAV_EC
GO:0032728	0.457	0.811	2	16	positive regulation of interferon-beta	BP	1	FLOT1,MAVS	up_VSAP_EC
GO:0034134	0.457	0.89	1	7	toll-like receptor 2 signaling pathway	BP	1	IRAK1	down_ACOR_VSMC
GO:1903214	0.457	0.89	1	7	regulation of protein targeting to	BP	1	SREBF1	down_ACOR_VSMC
GO:0048066	0.457	0.883	1	12	developmental pigmentation	BP	1	GLI3	down_VCAV_EC
GO:0090140	0.457	0.885	1	10	regulation of mitochondrial fission	BP	1	BNIP3	down_VSAP_EC
GO:0000303	0.457	0.892	1	6	response to superoxide	BP	1	PARK7	up_ACOR_VSMC
GO:0000305	0.457	0.892	1	6	response to oxygen radical	BP	1	PARK7	up_ACOR_VSMC
GO:0043372	0.457	0.892	1	6	positive regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	CD83	up_ACOR_VSMC
GO:0015031	0.457	0.888	1	510	protein transport	BP	1	ARG2	up_AORT_VSMC
GO:0035066	0.457	0.89	1	7	positive regulation of histone acetylation	BP	1	GATA3	up_VCAV_EC
GO:0060261	0.457	0.888	1	8	positive regulation of transcription initiation from RNA polymerase II	BP	1	IRF8	up_VCAV_EC
GO:0010874	0.457	0.89	1	7	regulation of cholesterol efflux	BP	1	ABCA1	up_VCAV_EC
GO:0046596	0.457	0.888	1	8	regulation of viral entry into host cell	BP	1	NECTIN2	up_VCAV_EC

GO:0006936	0.457	0.878	1	74	muscle contraction	BP	1	HTR7	up_VPOR_EC
GO:0000280	0.457	0.879	1	145	nuclear division	BP	1	CYP26B1	up_VFEM_EC
GO:0002755	0.457	0.892	1	6	MyD88-dependent toll-like receptor signaling	BP	1	MYD88	up_VSAP_EC
GO:0003128	0.457	0.892	1	6	heart field specification	BP	1	AXIN2	up_VSAP_EC
GO:0031069	0.457	0.892	1	6	hair follicle morphogenesis	BP	1	FGF7	up_VSAP_EC
GO:0071542	0.457	0.892	1	6	dopaminergic neuron differentiation	BP	1	CDNF	up_VSAP_EC
GO:2000095	0.457	0.892	1	6	regulation of Wnt signaling pathway, planar cell polarity pathway	BP	1	ABL1	up_VSAP_EC
GO:0007625	0.457	0.892	1	6	grooming behavior	BP	1	CTNS	up_VSAP_EC
GO:0051851	0.457173832	0.87946	1	23	modification by host of symbiont morphology or	BP	1	AQP1	up_ACOR_EC
GO:0007417	0.457185566	0.6924	7	235	central nervous system development	BP	1	NDRG2,AQP1,SEMA6D,DIXDC1,DCLK2,NRP1,PYGO2	up_ACOR_EC
GO:0010824	0.457331982	0.87937	1	23	regulation of centrosome duplication	BP	1	CHMP4B	up_ACOR_EC
GO:0140014	0.458	0.671	10	110	mitotic nuclear division	BP	1	PDGFB,EDN1,RAB11A,MZT1,CENPC,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0002521	0.458	0.683	8	149	leukocyte differentiation	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0003205	0.458	0.695	7	67	cardiac chamber development	BP	1	FZD1,WNT11,SAV1,SHOX2,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0048519	0.458	0.719	6	1554	negative regulation of biological process	BP	1	TBX5,HOXA3,NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0015849	0.458	0.707	6	56	organic acid transport	BP	1	SLC16A12,OSR1,ABCB11,SLC25A12,SLC27A6,CTNS	up_VSAP_EC
GO:0046942	0.458	0.707	6	56	carboxylic acid transport	BP	1	SLC16A12,OSR1,ABCB11,SLC25A12,SLC27A6,CTNS	up_VSAP_EC
GO:0006928	0.458	0.72	5	557	movement of cell or subcellular component	BP	1	C3AR1,ARHGEF2,SEMA3A,CCAR1,ENSCAFG00000032731	up_VPOR_EC
GO:0097164	0.458	0.739	4	44	ammonium ion metabolic process	BP	1	SNCAIP,ODC1,SPTLC2,GCH1	up_VCAV_EC
GO:0007416	0.458	0.741	4	36	synapse assembly	BP	1	FZD1,AMIGO1,LRRN3,LRP4	up_VSAP_EC
GO:0035150	0.458	0.741	4	36	regulation of tube size	BP	1	CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0050880	0.458	0.741	4	36	regulation of blood vessel size	BP	1	CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC
GO:0048524	0.458	0.766	3	30	positive regulation of viral process	BP	1	SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0050789	0.458	0.895	2	3295	regulation of biological process	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0051591	0.458	0.81	2	16	response to cAMP	BP	1	RAPGEF1,RAPGEF2	up_VCAV_EC
GO:0051962	0.458	0.878	1	112	positive regulation of nervous system	BP	1	LYN	down_ACOR_EC
GO:0006829	0.458	0.889	1	7	zinc ion transport	BP	1	SLC30A1	down_ACOR_VSMC
GO:0034139	0.458	0.889	1	7	regulation of toll-like receptor 3 signaling	BP	1	CAV1	down_ACOR_VSMC
GO:0071577	0.458	0.889	1	7	zinc ion transmembrane transport	BP	1	SLC30A1	down_ACOR_VSMC
GO:0010669	0.458	0.885	1	10	epithelial structure maintenance	BP	1	STRAP	down_VSAP_EC
GO:0042761	0.458	0.889	1	7	very long-chain fatty acid biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0060347	0.458	0.892	1	6	heart trabecula formation	BP	1	EGLN1	up_ACOR_VSMC
GO:0042311	0.458	0.889	1	7	vasodilation	BP	1	GUCY1A1	up_VCAV_EC
GO:0050687	0.458	0.887	1	8	negative regulation of defense response to virus	BP	1	RIOK3	up_VCAV_EC
GO:0007015	0.458	0.878	1	144	actin filament organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0009100	0.458	0.878	1	139	glycoprotein metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0008610	0.458	0.879	1	177	lipid biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0032011	0.458	0.889	1	7	ARF protein signal transduction	BP	1	PSD4	up_VSAP_EC
GO:0032012	0.458	0.889	1	7	regulation of ARF protein signal transduction	BP	1	PSD4	up_VSAP_EC

GO:0070230	0.458	0.892	1	6	positive regulation of lymphocyte apoptotic	BP	1	CD274	up_VSAP_EC
GO:0050673	0.458	0.878	1	135	epithelial cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0097306	0.458674342	0.87878	1	22	cellular response to alcohol	BP	1	PTGER4	up_ACOR_EC
GO:0002456	0.458798244	0.8785	1	23	T cell mediated immunity	BP	1	FZD5	up_ACOR_EC
GO:0009185	0.458987869	0.87839	1	23	ribonucleoside diphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0006518	0.459	0.64	17	290	peptide metabolic process	BP	1	CARS,PLK3,SARS,AARS,ENSCAFG00000028814,PUM3,SESN2,MRPL1,YARS,TARS,NARS,EIF4EBP1,CNOT7,APOE,EIF5,EIF2S1,RSL24D1	down_VSAP_EC
GO:0007265	0.459	0.66	12	121	Ras protein signal transduction	BP	1	ARHGEF5,ARHGEF6,ABL1,CDC42EP5,CDC42EP2,F2RL1,MFN2,TIAM1,DLC1,FGD4,PSD4,FLOT1	up_VSAP_EC
GO:0009725	0.459	0.668	10	188	response to hormone	BP	1	ADCY6,KANK2,ENSCAFG00000014978,TIMP2,AKT2,NR3C1,PARK7,ZFP36L1,RAB31,SHC1	down_VCAV_EC
GO:0008064	0.459	0.717	5	72	regulation of actin polymerization or	BP	1	WDR1,ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0030832	0.459	0.717	5	72	regulation of actin filament length	BP	1	WDR1,ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:2000027	0.459	0.717	5	72	regulation of animal organ morphogenesis	BP	1	SULF1,HOXB7,MAGED1,CTNNB1,SIX4	down_VSAP_EC
GO:0018107	0.459	0.721	5	45	peptidyl-threonine phosphorylation	BP	1	CAMK2D,APP,PSKH1,LMTK2,INPP5K	up_ACOR_VSMC
GO:1904659	0.459	0.74	4	36	glucose transmembrane transport	BP	1	LEP,EDN1,INPP5K,SLC2A12	up_ACOR_VSMC
GO:0009893	0.459	0.744	4	995	positive regulation of metabolic process	BP	1	NR1H4,CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0007569	0.459	0.739	4	36	cell aging	BP	1	ABL1,MORC3,YPEL3,PRELP	up_VSAP_EC
GO:0031397	0.459	0.765	3	30	negative regulation of protein ubiquitination	BP	1	USP4,U2AF2,CAV1	down_ACOR_VSMC
GO:0055123	0.459	0.763	3	40	digestive system development	BP	1	HIF1A,CTNNB1,KLF5	down_VSAP_EC
GO:0007044	0.459	0.766	3	27	cell-substrate junction assembly	BP	1	FAM107A,ABL1,ACVRL1	up_VSAP_EC
GO:0051155	0.459	0.808	2	18	positive regulation of striated muscle cell	BP	1	MMP14,GREM1	down_ACOR_VSMC
GO:1903078	0.459	0.807	2	19	positive regulation of protein localization to	BP	1	ACSL3,EZR	down_ACOR_VSMC
GO:0051650	0.459	0.8	2	65	establishment of vesicle localization	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0010720	0.459	0.878	1	110	positive regulation of cell development	BP	1	LYN	down_ACOR_EC
GO:0120033	0.459	0.882	1	12	negative regulation of plasma membrane bounded cell projection	BP	1	EVI5L	down_VCAV_EC
GO:0044255	0.459	0.881	1	293	cellular lipid metabolic process	BP	1	GBGT1	down_VPOR_EC
GO:1901362	0.459	0.91	1	1293	organic cyclic compound biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0045601	0.459	0.884	1	10	regulation of endothelial cell differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:1900101	0.459	0.883	1	11	regulation of endoplasmic reticulum unfolded protein response	BP	1	PTPN2	down_VSAP_EC
GO:0031069	0.459	0.891	1	6	hair follicle morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0032400	0.459	0.891	1	6	melanosome localization	BP	1	RAB11B	up_ACOR_VSMC
GO:0032401	0.459	0.891	1	6	establishment of melanosome localization	BP	1	RAB11B	up_ACOR_VSMC
GO:0051546	0.459	0.891	1	6	keratinocyte migration	BP	1	FERMT1	up_ACOR_VSMC
GO:0051875	0.459	0.891	1	6	pigment granule localization	BP	1	RAB11B	up_ACOR_VSMC
GO:0051905	0.459	0.891	1	6	establishment of pigment granule localization	BP	1	RAB11B	up_ACOR_VSMC
GO:0060433	0.459	0.891	1	6	bronchus development	BP	1	BMP4	up_ACOR_VSMC
GO:0007156	0.459	0.878	1	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	CDH18	up_AFEM_EC
GO:0007264	0.459	0.878	1	164	small GTPase mediated signal transduction	BP	1	ARHGEF26	up_APUL_EC

GO:0001893	0.459	0.887	1	8	maternal placenta development	BP	1	PTGS2	up_VCAV_EC
GO:0033262	0.459	0.891	1	6	regulation of nuclear cell cycle DNA replication	BP	1	ATRX	up_VCAV_EC
GO:0035308	0.459	0.885	1	9	negative regulation of protein	BP	1	SWAP70	up_VCAV_EC
GO:0055003	0.459	0.889	1	7	cardiac myofibril assembly	BP	1	PROX1	up_VCAV_EC
GO:0030029	0.459	0.88	1	239	actin filament-based process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0030097	0.459	0.879	1	244	hemopoiesis	BP	1	HOXA9	up_VFEM_VSMC
GO:0007100	0.459	0.891	1	6	mitotic centrosome separation	BP	1	CEP85	up_VSAP_EC
GO:0009143	0.459	0.891	1	6	nucleoside triphosphate catabolic process	BP	1	ENTPD3	up_VSAP_EC
GO:0030809	0.459	0.891	1	6	negative regulation of nucleotide biosynthetic	BP	1	DDIT4	up_VSAP_EC
GO:0032688	0.459	0.891	1	6	negative regulation of interferon-beta	BP	1	NLRX1	up_VSAP_EC
GO:0051444	0.459	0.891	1	6	negative regulation of ubiquitin-protein	BP	1	ABL1	up_VSAP_EC
GO:1900372	0.459	0.891	1	6	negative regulation of purine nucleotide	BP	1	DDIT4	up_VSAP_EC
GO:2001170	0.459	0.891	1	6	negative regulation of ATP biosynthetic process	BP	1	DDIT4	up_VSAP_EC
GO:0030836	0.459	0.891	1	6	positive regulation of actin filament	BP	1	F2RL1	up_VSAP_EC
GO:0050805	0.459	0.891	1	6	negative regulation of synaptic transmission	BP	1	KCNB1	up_VSAP_EC
GO:0060433	0.459	0.891	1	6	bronchus development	BP	1	TGFBR2	up_VSAP_EC
GO:0048144	0.459915189	0.87784	1	23	fibroblast proliferation	BP	1	AQP1	up_ACOR_EC
GO:0048145	0.459915189	0.87784	1	23	regulation of fibroblast proliferation	BP	1	AQP1	up_ACOR_EC
GO:0032147	0.46	0.684	8	77	activation of protein kinase activity	BP	1	MAP3K14,ABL1,EMP2,MAP3K5,C1QTNF2,TRAF7,MAP2K2,TGFBR2	up_VSAP_EC
GO:0034249	0.46	0.738	4	41	negative regulation of cellular amide metabolic	BP	1	ILF3,EIF4A3,NCL,RBM14	down_ACOR_VSMC
GO:0035195	0.46	0.765	3	28	gene silencing by miRNA	BP	1	SRRT,RAN,RBM14	down_ACOR_VSMC
GO:0072665	0.46	0.767	3	25	protein localization to vacuole	BP	1	SCARB2,LAMP2,SH3BP4	up_ACOR_VSMC
GO:1901989	0.46	0.764	3	31	positive regulation of cell cycle phase transition	BP	1	RAB11A,CUL4A,TMOD3	up_VCAV_EC
GO:1903038	0.46	0.765	3	30	negative regulation of leukocyte cell-cell	BP	1	PELI1,ARG2,HMGB1	up_VCAV_EC
GO:1903708	0.46	0.799	2	65	positive regulation of hemopoiesis	BP	1	CYLD,EVI2B	up_AFEM_EC
GO:0046626	0.46	0.807	2	18	regulation of insulin receptor signaling	BP	1	BAIAP2L1,NCK1	up_VCAV_EC
GO:0072521	0.46	0.8	2	185	purine-containing compound metabolic	BP	1	AK5,FBP1	up_VPOR_EC
GO:0006188	0.46	0.888	1	7	IMP biosynthetic process	BP	1	PFAS	down_ACOR_VSMC
GO:0034244	0.46	0.888	1	7	negative regulation of transcription elongation from RNA polymerase II	BP	1	EZH2	down_ACOR_VSMC
GO:2000778	0.46	0.888	1	7	positive regulation of interleukin-6 secretion	BP	1	HMGB1	down_ACOR_VSMC
GO:0033146	0.46	0.882	1	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	KANK2	down_VCAV_EC
GO:1901031	0.46	0.882	1	12	regulation of response to reactive oxygen species	BP	1	PARK7	down_VCAV_EC
GO:1905953	0.46	0.881	1	12	negative regulation of lipid localization	BP	1	AKT2	down_VCAV_EC
GO:0015914	0.46	0.884	1	10	phospholipid transport	BP	1	APOE	down_VSAP_EC
GO:0050853	0.46	0.883	1	10	B cell receptor signaling pathway	BP	1	LYN	down_VSAP_EC
GO:1903053	0.46	0.884	1	10	regulation of extracellular matrix organization	BP	1	FSCN1	down_VSAP_EC
GO:1903671	0.46	0.883	1	10	negative regulation of sprouting angiogenesis	BP	1	STARD13	down_VSAP_EC
GO:0002755	0.46	0.891	1	6	MyD88-dependent toll-like receptor signaling	BP	1	TLR1	up_ACOR_VSMC
GO:0042755	0.46	0.891	1	6	eating behavior	BP	1	LEP	up_ACOR_VSMC

GO:0120035	0.46	0.877	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	NTRK2	up_APUL_EC
GO:0015682	0.46	0.888	1	7	ferric iron transport	BP	1	LMTK2	up_VCAV_EC
GO:0072512	0.46	0.888	1	7	trivalent inorganic cation transport	BP	1	LMTK2	up_VCAV_EC
GO:0086091	0.46	0.886	1	8	regulation of heart rate by cardiac conduction	BP	1	KCNJ2	up_VCAV_EC
GO:0090407	0.46	0.878	1	177	organophosphate biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0008210	0.46	0.891	1	6	estrogen metabolic process	BP	1	HSD17B8	up_VSAP_EC
GO:0043372	0.46	0.891	1	6	positive regulation of CD4-positive, alpha-beta T cell differentiation	BP	1	CD83	up_VSAP_EC
GO:0048368	0.46	0.891	1	6	lateral mesoderm development	BP	1	CITED2	up_VSAP_EC
GO:0071467	0.46	0.89	1	6	cellular response to pH	BP	1	RAB11B	up_VSAP_EC
GO:0072413	0.46	0.89	1	6	signal transduction involved in mitotic cell	BP	1	CRADD	up_VSAP_EC
GO:1902402	0.46	0.89	1	6	signal transduction involved in mitotic DNA	BP	1	CRADD	up_VSAP_EC
GO:1902403	0.46	0.89	1	6	signal transduction involved in mitotic DNA	BP	1	CRADD	up_VSAP_EC
GO:1903726	0.46	0.891	1	6	negative regulation of phospholipid metabolic	BP	1	PIK3IP1	up_VSAP_EC
GO:0006595	0.46	0.891	1	6	polyamine metabolic process	BP	1	AZIN2	up_VSAP_EC
GO:0032906	0.46	0.89	1	6	transforming growth factor beta2 production	BP	1	WNT11	up_VSAP_EC
GO:0032909	0.46	0.89	1	6	regulation of transforming growth factor beta2	BP	1	WNT11	up_VSAP_EC
GO:0035563	0.46	0.89	1	6	positive regulation of chromatin binding	BP	1	EBF2	up_VSAP_EC
GO:0031023	0.460043663	0.79977	2	58	microtubule organizing center organization	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0006661	0.46014572	0.8777	1	23	phosphatidylinositol biosynthetic process	BP	1	PIGS	up_ACOR_EC
GO:0007219	0.46099005	0.79899	2	59	Notch signaling pathway	BP	1	NR1H4,FOXC2	up_ACOR_EC
GO:0006259	0.461	0.614	32	354	DNA metabolic process	BP	1	PDGFB,GATA3,PSME4,FIGNL1,MTOR,UHRF2,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,ESCO1,TIMELESS,OTUD4,TOP1,ETAA1,SMG7,ASF1A,HMGB1,BLM,SMC5,RAD21,RAD17,USP37,MTA2,CUL4A,ATRX,TOPBP1,RBBP6,DCP2,TET2,GINS4	up_VCAV_EC
GO:0006950	0.461	0.622	27	1102	response to stress	BP	1	LEP,RAB20,F5,ANGPT4,CD40,CRYAB,F3,BPI,GPAM,HCK,NFE2L1,CAMK2A,CLEC16A,CYLD,TBXA2R,TFPI2,BVES,LGR6,AXIN2,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,ADAM17,KANK1,TNC,SOD1	up_AFEM_EC
GO:1903506	0.461	0.626	24	977	regulation of nucleic acid-templated transcription	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC
GO:0071407	0.461	0.654	13	129	cellular response to organic cyclic compound	BP	1	FAM107A,PPARGC1B,CDH1,ZFP36L1,CREBRF,PRMT2,OSBPL7,ZFP36L2,PQBP1,FLOT1,MAVS,LBH,DDIT4	up_VSAP_EC
GO:0045787	0.461	0.658	12	117	positive regulation of cell cycle	BP	1	CDC7,FGFR2,ATRX,CITED2,PKP4,CDKN1A,CRLF3,PRKCE,CCNT1,CCPG1,APP,EDN1	up_ACOR_VSMC
GO:0009306	0.461	0.663	11	127	protein secretion	BP	1	GBP5,FERMT1,TLR4,GATA3,ARG2,ABCA1,CD200,HMGB1,NOS2,MCU,HIF1A	up_VCAV_EC
GO:0046631	0.461	0.738	4	35	alpha-beta T cell activation	BP	1	CD83,CD274,PTPN22,IL18R1	up_ACOR_VSMC
GO:0072171	0.461	0.764	3	30	mesonephric tubule morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0006405	0.461	0.761	3	39	RNA export from nucleus	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0031060	0.461	0.804	2	23	regulation of histone methylation	BP	1	IWS1,KDM3A	down_VSAP_EC
GO:0021955	0.461	0.809	2	15	central nervous system neuron axonogenesis	BP	1	EPHB1,SPTBN4	up_VCAV_EC
GO:0010830	0.461	0.808	2	16	regulation of myotube differentiation	BP	1	SHOX2,FLOT1	up_VSAP_EC
GO:0008015	0.461	0.876	1	120	blood circulation	BP	1	ACVRL1	down_ACOR_EC

GO:0019400	0.461	0.887	1	7	alditol metabolic process	BP	1	GK5	down_ACOR_VSMC
GO:0032964	0.461	0.887	1	7	collagen biosynthetic process	BP	1	SERPINH1	down_ACOR_VSMC
GO:1901028	0.461	0.888	1	7	regulation of mitochondrial outer membrane permeabilization involved	BP	1	SLC25A5	down_ACOR_VSMC
GO:2000727	0.461	0.888	1	7	positive regulation of cardiac muscle cell	BP	1	GREM1	down_ACOR_VSMC
GO:1901379	0.461	0.881	1	12	regulation of potassium ion transmembrane	BP	1	PRNP	down_VCAV_EC
GO:0009628	0.461	0.88	1	302	response to abiotic stimulus	BP	1	RAB11B	down_VPOR_EC
GO:1901032	0.461	0.89	1	6	negative regulation of response to reactive	BP	1	PARK7	up_ACOR_VSMC
GO:1903206	0.461	0.89	1	6	negative regulation of hydrogen peroxide-	BP	1	PARK7	up_ACOR_VSMC
GO:2001039	0.461	0.89	1	6	negative regulation of cellular response to drug	BP	1	PARK7	up_ACOR_VSMC
GO:0048675	0.461	0.877	1	26	axon extension	BP	1	PLXNA4	up_AFEM_EC
GO:0000722	0.461	0.89	1	6	telomere maintenance via recombination	BP	1	SMC5	up_VCAV_EC
GO:0034377	0.461	0.888	1	7	plasma lipoprotein particle assembly	BP	1	ABCA1	up_VCAV_EC
GO:0065005	0.461	0.888	1	7	protein-lipid complex assembly	BP	1	ABCA1	up_VCAV_EC
GO:0031329	0.461	0.878	1	241	regulation of cellular catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0006655	0.461	0.89	1	6	phosphatidylglycerol biosynthetic process	BP	1	PLA2G6	up_VSAP_EC
GO:0015844	0.461	0.89	1	6	monoamine transport	BP	1	SLC6A4	up_VSAP_EC
GO:0021697	0.461	0.89	1	6	cerebellar cortex formation	BP	1	DLL1	up_VSAP_EC
GO:0046471	0.461	0.89	1	6	phosphatidylglycerol metabolic process	BP	1	PLA2G6	up_VSAP_EC
GO:0032494	0.461	0.89	1	6	response to peptidoglycan	BP	1	MYD88	up_VSAP_EC
GO:0060841	0.461	0.89	1	6	venous blood vessel development	BP	1	ACVRL1	up_VSAP_EC
GO:0071549	0.461	0.89	1	6	cellular response to dexamethasone stimulus	BP	1	DDIT4	up_VSAP_EC
GO:0045664	0.461	0.876	1	144	regulation of neuron differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0010632	0.461785358	0.75729	3	95	regulation of epithelial cell migration	BP	1	SOX9,FOXC2,NRP1	up_ACOR_EC
GO:0046849	0.461830011	0.8767	1	23	bone remodeling	BP	1	PTH1R	up_ACOR_EC
GO:0051704	0.462	0.604	41	476	multi-organism process	BP	1	IRAK1,ILF3,ACSL4,HNRNPUL1,NEDD4,SLC29A1,MTDH,NDC1,TRIP13,CTDNEP1,FBXO5,CAV1,AAAS,STMN1,CDK4,TRIM35,ARG2,NCAPH,POC1A,B4GALT1,TFRC,PPARD,HIST1H1A,EMP2,FOSL1,CACTIN,HMGB2,SMC3,DDX39B,RAD23A,SGPL1,TTK,ASPM,HOXA9,GLI1,H2AFX,EXOSC5,PPIH,CCT4,TTLL1,ANXA7	down_ACOR_VSMC
GO:0022008	0.462	0.605	41	406	neurogenesis	BP	1	SH3TC2,VEGFD,LEP,EPYC,FEZ1,ITM2C,BMP4,FGFR2,GJA1,SEC24B,WASF3,ACSL6,ZNF365,LMO4,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SMARCD3,SLITRK5,TBX20,FZD3,FRS2,RND1,DAG1,POMK,APP,PSEN1,CHD7,SIPA1L1,CLN8,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,SUN1,WASL,CRKL	up_ACOR_VSMC
GO:1901701	0.462	0.647	14	271	cellular response to oxygen-containing compound	BP	1	LRP1,PRNP,ADCY6,KANK2,COL6A1,ENSCAFG00000014978,AKT2,NR3C1,PARK7,ZFP36L1,SASH1,MPV17,RAB31,SHC1	down_VCAV_EC
GO:0008625	0.462	0.763	3	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	HMGB2,ARHGEF2,DELE1	down_ACOR_VSMC
GO:0010952	0.462	0.76	3	46	positive regulation of peptidase activity	BP	1	LYN,FAM162A,REST	down_VSAP_EC
GO:0050715	0.462	0.763	3	29	positive regulation of cytokine secretion	BP	1	FERMT1,GATA3,HMGB1	up_VCAV_EC
GO:0006355	0.462	0.77	3	974	regulation of transcription, DNA-	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0032652	0.462	0.806	2	18	regulation of interleukin-1 production	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0050732	0.462	0.806	2	18	negative regulation of peptidyl-tyrosine	BP	1	CAV1,NF2	down_ACOR_VSMC

GO:0010324	0.462	0.808	2	16	membrane invagination	BP	1	ABCA1,F2RL1	up_ACOR_VSMC
GO:0015909	0.462	0.807	2	16	long-chain fatty acid transport	BP	1	PLIN2,CFI	up_ACOR_VSMC
GO:0016310	0.462	0.806	2	641	phosphorylation	BP	1	ERC1,TAOK1	up_AORT_EC
GO:1904427	0.462	0.805	2	18	positive regulation of calcium ion	BP	1	APLNR,PLCG2	up_VCAV_EC
GO:0071495	0.462	0.801	2	365	cellular response to endogenous stimulus	BP	1	CAV1,FGF5	up_VSAP_VSMC
GO:1901700	0.462	0.801	2	364	response to oxygen-containing compound	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0048569	0.462	0.887	1	7	post-embryonic animal organ development	BP	1	HMGN1	down_ACOR_VSMC
GO:0006807	0.462	1	1	3221	nitrogen compound metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0060231	0.462	0.881	1	12	mesenchymal to epithelial transition	BP	1	GREM1	down_VCAV_EC
GO:0048820	0.462	0.883	1	9	hair follicle maturation	BP	1	CTNNB1	down_VSAP_EC
GO:0019934	0.462	0.89	1	6	cGMP-mediated signaling	BP	1	HTR2B	up_ACOR_VSMC
GO:0021871	0.462	0.889	1	6	forebrain regionalization	BP	1	BMP4	up_ACOR_VSMC
GO:0035455	0.462	0.889	1	6	response to interferon-alpha	BP	1	KLHL20	up_ACOR_VSMC
GO:0045776	0.462	0.889	1	6	negative regulation of blood pressure	BP	1	RNLS	up_ACOR_VSMC
GO:1901623	0.462	0.89	1	6	regulation of lymphocyte chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0031344	0.462	0.876	1	161	regulation of cell projection organization	BP	1	NTRK2	up_APUL_EC
GO:2001204	0.462	0.893	1	5	regulation of osteoclast development	BP	1	TJP2	up_VCAV_EC
GO:0044331	0.462	0.89	1	6	cell-cell adhesion mediated by cadherin	BP	1	MMP24	up_VCAV_EC
GO:0050798	0.462	0.885	1	8	activated T cell proliferation	BP	1	HMGB1	up_VCAV_EC
GO:0051154	0.462	0.887	1	7	negative regulation of striated muscle cell	BP	1	BMP2	up_VCAV_EC
GO:0000083	0.462	0.89	1	6	regulation of transcription involved in G1/S transition of mitotic cell	BP	1	E2F4	up_VSAP_EC
GO:0021542	0.462	0.89	1	6	dentate gyrus development	BP	1	EMX2	up_VSAP_EC
GO:0032633	0.462	0.889	1	6	interleukin-4 production	BP	1	CD83	up_VSAP_EC
GO:0034497	0.462	0.89	1	6	protein localization to phagophore assembly site	BP	1	MFN2	up_VSAP_EC
GO:0046006	0.462	0.89	1	6	regulation of activated T cell proliferation	BP	1	CD274	up_VSAP_EC
GO:0070920	0.462	0.89	1	6	regulation of production of small RNA involved in gene silencing by RNA	BP	1	ZC3H10	up_VSAP_EC
GO:1903798	0.462	0.89	1	6	regulation of production of miRNAs involved in gene silencing by miRNA	BP	1	ZC3H10	up_VSAP_EC
GO:0034143	0.462	0.89	1	6	regulation of toll-like receptor 4 signaling	BP	1	F2RL1	up_VSAP_EC
GO:0043567	0.462	0.889	1	6	regulation of insulin-like growth factor receptor	BP	1	IGFBP6	up_VSAP_EC
GO:0070262	0.462	0.889	1	6	peptidyl-serine dephosphorylation	BP	1	NCK1	up_VSAP_EC
GO:0095500	0.462	0.889	1	6	acetylcholine receptor signaling pathway	BP	1	CHRM1	up_VSAP_EC
GO:1903831	0.462	0.889	1	6	signal transduction involved in cellular response to ammonium	BP	1	CHRM1	up_VSAP_EC
GO:1905144	0.462	0.889	1	6	response to acetylcholine	BP	1	CHRM1	up_VSAP_EC
GO:1905145	0.462	0.889	1	6	cellular response to acetylcholine	BP	1	CHRM1	up_VSAP_EC
GO:0000278	0.463	0.627	21	331	mitotic cell cycle	BP	1	ASNS,PLK3,PTPN11,MZT1,PPP1R12A,TNIK,NAA10,ZPR1,EIF4EBP1,CTNNB1,KPNB1,ANLN,CDK8,PDS5B,BACH1,HTT,RBBP8,CALM1,PAK2,INHBA,CDKN1A	down_VSAP_EC
GO:0048856	0.463	0.66	13	1533	anatomical structure development	BP	1	C3AR1,BARX1,PTK7,HOOK3,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,MTDH,HOXA2,RNF6	up_VPOR_EC

GO:0048638	0.463	0.681	8	82	regulation of developmental growth	BP	1	IFRD1,MEF2C,CHD7,EDN1,RAB11A,PROX1,CREB1,SPTBN4	up_VCAV_EC
GO:0030278	0.463	0.701	6	66	regulation of ossification	BP	1	MEF2C,BMP2,BMP2K,JAG1,HIF1A,FBXO5	up_VCAV_EC
GO:0010562	0.463	0.758	3	312	positive regulation of phosphorus metabolic	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0045937	0.463	0.758	3	312	positive regulation of phosphate metabolic	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0035307	0.463	0.805	2	18	positive regulation of protein	BP	1	SLC29A1,PPP2R5D	down_ACOR_VSMC
GO:0001707	0.463	0.802	2	25	mesoderm formation	BP	1	ITGA2,INHBA	down_VSAP_EC
GO:0033143	0.463	0.802	2	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	SMARCA4,UBA5	down_VSAP_EC
GO:0055117	0.463	0.803	2	21	regulation of cardiac muscle contraction	BP	1	PDE4D,STC1	up_VCAV_EC
GO:0031272	0.463	0.884	1	8	regulation of pseudopodium assembly	BP	1	CDC42EP4	down_ACOR_VSMC
GO:0031274	0.463	0.884	1	8	positive regulation of pseudopodium assembly	BP	1	CDC42EP4	down_ACOR_VSMC
GO:0032232	0.463	0.886	1	7	negative regulation of actin filament bundle	BP	1	STMN1	down_ACOR_VSMC
GO:0051497	0.463	0.886	1	7	negative regulation of stress fiber assembly	BP	1	STMN1	down_ACOR_VSMC
GO:0045071	0.463	0.88	1	12	negative regulation of viral genome replication	BP	1	MAVS	down_VCAV_EC
GO:0060337	0.463	0.88	1	12	type I interferon signaling pathway	BP	1	MAVS	down_VCAV_EC
GO:0071357	0.463	0.88	1	12	cellular response to type I interferon	BP	1	MAVS	down_VCAV_EC
GO:0007566	0.463	0.882	1	10	embryo implantation	BP	1	PTGS2	down_VSAP_EC
GO:0021783	0.463	0.883	1	9	preganglionic parasympathetic fiber	BP	1	NRP1	down_VSAP_EC
GO:0071604	0.463	0.882	1	10	transforming growth factor beta production	BP	1	HIF1A	down_VSAP_EC
GO:0071634	0.463	0.882	1	10	regulation of transforming growth factor beta	BP	1	HIF1A	down_VSAP_EC
GO:0021756	0.463	0.889	1	6	striatum development	BP	1	SLITRK5	up_ACOR_VSMC
GO:0097186	0.463	0.889	1	6	amelogenesis	BP	1	PERP	up_ACOR_VSMC
GO:0014066	0.463	0.876	1	26	regulation of phosphatidylinositol 3-	BP	1	LEP	up_AFEM_EC
GO:0021549	0.463	0.875	1	26	cerebellum development	BP	1	DLL1	up_AFEM_EC
GO:0042475	0.463	0.875	1	26	odontogenesis of dentin-containing tooth	BP	1	CNNM4	up_AFEM_EC
GO:0097581	0.463	0.875	1	26	lamellipodium organization	BP	1	KANK1	up_AFEM_EC
GO:1903047	0.463	0.878	1	257	mitotic cell cycle process	BP	1	TAOK1	up_AORT_EC
GO:0007610	0.463	0.875	1	146	behavior	BP	1	AVPR1A	up_VFEM_EC
GO:0009628	0.463	0.878	1	302	response to abiotic stimulus	BP	1	LRRN4	up_VPUL_VSMC
GO:0035456	0.463	0.889	1	6	response to interferon-beta	BP	1	HTRA2	up_VSAP_EC
GO:0071545	0.463	0.889	1	6	inositol phosphate catabolic process	BP	1	INPP5E	up_VSAP_EC
GO:1903069	0.463	0.889	1	6	regulation of ER-associated ubiquitin-dependent protein	BP	1	UBQLN2	up_VSAP_EC
GO:0010810	0.463572231	0.79695	2	60	regulation of cell-substrate adhesion	BP	1	ARHGAP6,NRP1	up_ACOR_EC
GO:0031329	0.463659563	0.68646	7	241	regulation of cellular catabolic process	BP	1	EDEM2,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,PRKCD	up_ACOR_EC
GO:2001236	0.463812541	0.79682	2	59	regulation of extrinsic apoptotic signaling	BP	1	IFI6,NRP1	up_ACOR_EC
GO:1903322	0.463898165	0.79675	2	59	positive regulation of protein modification by small protein conjugation	BP	1	NOD2,PIAS1	up_ACOR_EC

GO:0010646	0.464	0.598	48	945	regulation of cell communication	BP	1	NOTCH2,PDGFRB,SLC35F6,DCN,PRNP,VASN,FBN1,GLIPR2,BGN,KANK2,BMPR1A,EVC,RECK,IGFBP6,ARHGEF25,AKT1S1,CHRDL1,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,ASPN,THY1,ATP6V0C,GLI3,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,NCLN,SPRED1,RAB7B,GLIS2,SHC1,FBH1,GREM1,NPHP4,FOXO3,ANKRD54,BRSK1,CDK14	down_VCAV_EC
GO:0048598	0.464	0.634	18	207	embryonic morphogenesis	BP	1	HOXB7,AMOT,MEF2C,CHD7,DLL4,GATA3,EDN1,HOXB8,HHEX,PROX1,MDFI,HOXB5,BCL10,HIF1A,ALDH1A3,LUZP1,ZEB1,CDON	up_VCAV_EC
GO:0044092	0.464	0.686	7	270	negative regulation of molecular function	BP	1	CMKLR1,CRYAB,MYO1D,CYLD,LRRC15,RECK,ACACB	up_AFEM_EC
GO:0006820	0.464	0.698	6	109	anion transport	BP	1	PRNP,FOLR2,AKT2,SCP2,SLC17A9,CLIC4	down_VCAV_EC
GO:0071222	0.464	0.716	5	46	cellular response to lipopolysaccharide	BP	1	ABCA1,SASH1,ANKRD1,PRKCE,NOD2	up_ACOR_VSMC
GO:0008283	0.464	0.714	5	545	cell proliferation	BP	1	HOOK3,HOXA3,ARHGEF2,ACVR2A,CCAR1	up_VPOR_EC
GO:0046700	0.464	0.729	4	147	heterocycle catabolic process	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:1903506	0.464	0.769	3	977	regulation of nucleic acid-templated transcription	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0000079	0.464	0.762	3	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CNPPD1,FBXO7,LATS2	up_VSAP_EC
GO:0034198	0.464	0.762	3	27	cellular response to amino acid starvation	BP	1	SESN1,MAP3K5,NPRL3	up_VSAP_EC
GO:1990928	0.464	0.762	3	27	response to amino acid starvation	BP	1	SESN1,MAP3K5,NPRL3	up_VSAP_EC
GO:0050905	0.464	0.763	3	26	neuromuscular process	BP	1	ABL1,FXN,HOXC10	up_VSAP_EC
GO:0009798	0.464	0.799	2	31	axis specification	BP	1	BMPR1A,PCSK6	down_VCAV_EC
GO:0010033	0.464	0.808	2	772	response to organic substance	BP	1	CITED2,RAB11B	down_VPOR_EC
GO:0050871	0.464	0.802	2	24	positive regulation of B cell activation	BP	1	TFRC,CDKN1A	down_VSAP_EC
GO:0032410	0.464	0.805	2	17	negative regulation of transporter activity	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:1904063	0.464	0.805	2	17	negative regulation of cation transmembrane	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:0048546	0.464	0.806	2	16	digestive tract morphogenesis	BP	1	WNT11,SHOX2	up_VSAP_EC
GO:0003013	0.464	0.874	1	121	circulatory system process	BP	1	ACVRL1	down_ACOR_EC
GO:0010259	0.464	0.886	1	7	multicellular organism aging	BP	1	RAD54L	down_ACOR_VSMC
GO:0002520	0.464	0.878	1	279	immune system development	BP	1	GABPA	down_AFEM_EC
GO:0030149	0.464	0.879	1	12	sphingolipid catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0046466	0.464	0.879	1	12	membrane lipid catabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0050434	0.464	0.881	1	10	positive regulation of viral transcription	BP	1	SMARCA4	down_VSAP_EC
GO:0030949	0.464	0.888	1	6	positive regulation of vascular endothelial growth factor receptor	BP	1	FGF18	up_ACOR_VSMC
GO:0085029	0.464	0.889	1	6	extracellular matrix assembly	BP	1	MFAP4	up_ACOR_VSMC
GO:0010629	0.464	0.884	1	502	negative regulation of gene expression	BP	1	ESR1	up_AORT_VSMC
GO:0001865	0.464	0.889	1	6	NK T cell differentiation	BP	1	BMX	up_VCAV_EC
GO:0045606	0.464	0.886	1	7	positive regulation of epidermal cell	BP	1	PRKCH	up_VCAV_EC
GO:0090022	0.464	0.882	1	9	regulation of neutrophil chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:0019318	0.464	0.873	1	75	hexose metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0002347	0.464	0.888	1	6	response to tumor cell	BP	1	CD274	up_VSAP_EC
GO:0009404	0.464	0.888	1	6	toxin metabolic process	BP	1	MPST	up_VSAP_EC
GO:0031125	0.464	0.888	1	6	rRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0034656	0.464	0.888	1	6	nucleobase-containing small molecule catabolic	BP	1	PNP	up_VSAP_EC

GO:0050926	0.464	0.888	1	6	regulation of positive chemotaxis	BP	1	F2RL1	up_VSAP_EC
GO:2001267	0.464	0.888	1	6	regulation of cysteine-type endopeptidase activity involved in	BP	1	HTRA2	up_VSAP_EC
GO:0010804	0.464	0.888	1	6	negative regulation of tumor necrosis factor-mediated signaling	BP	1	F2RL1	up_VSAP_EC
GO:0071900	0.464422723	0.72894	4	131	regulation of protein serine/threonine kinase	BP	1	PKIB,FZD5,PRKCD,CCNYL1	up_ACOR_EC
GO:2001141	0.465	0.622	24	979	regulation of RNA biosynthetic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC
GO:0009123	0.465	0.671	9	104	nucleoside monophosphate	BP	1	CDK1,PFAS,CYCS,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0006401	0.465	0.671	9	88	RNA catabolic process	BP	1	AXIN2,TENT5C,EXOSC7,PYM1,ZFP36L1,SMG9,SAMD4B,ZFP36L2,TNRC6C	up_VSAP_EC
GO:0048588	0.465	0.715	5	44	developmental cell growth	BP	1	TMEM108,NRP1,ULK2,APP,EDN1	up_ACOR_VSMC
GO:0044270	0.465	0.729	4	147	cellular nitrogen compound catabolic	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0003206	0.465	0.757	3	51	cardiac chamber morphogenesis	BP	1	NOTCH2,BMPR1A,SEMA3C	down_VCAV_EC
GO:0043491	0.465	0.757	3	50	protein kinase B signaling	BP	1	AKT2,ZFP36L1,MYDGF	down_VCAV_EC
GO:0051480	0.465	0.756	3	50	regulation of cytosolic calcium ion concentration	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:1901293	0.465	0.755	3	106	nucleoside phosphate biosynthetic process	BP	1	GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0033138	0.465	0.761	3	28	positive regulation of peptidyl-serine	BP	1	HCLS1,PRKD2,PTGS2	up_VCAV_EC
GO:0009887	0.465	0.756	3	314	animal organ morphogenesis	BP	1	HOXA3,SEMA3A,ASPN	up_VPOR_EC
GO:0045944	0.465	0.798	2	287	positive regulation of transcription by RNA polymerase II	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0002028	0.465	0.803	2	19	regulation of sodium ion transport	BP	1	NEDD4,NKAIN1	down_ACOR_VSMC
GO:0048469	0.465	0.799	2	31	cell maturation	BP	1	IRX5,FOXO3	down_VCAV_EC
GO:1900542	0.465	0.8	2	26	regulation of purine nucleotide metabolic	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:1902883	0.465	0.805	2	16	negative regulation of response to oxidative	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:1904035	0.465	0.805	2	16	regulation of epithelial cell apoptotic process	BP	1	ABL1,ZFP36L1	up_VSAP_EC
GO:0006921	0.465	0.885	1	7	cellular component disassembly involved in execution phase of	BP	1	AIFM1	down_ACOR_VSMC
GO:0009218	0.465	0.885	1	7	pyrimidine ribonucleotide metabolic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0015682	0.465	0.885	1	7	ferric iron transport	BP	1	TFRC	down_ACOR_VSMC
GO:0030262	0.465	0.885	1	7	apoptotic nuclear changes	BP	1	AIFM1	down_ACOR_VSMC
GO:0072512	0.465	0.885	1	7	trivalent inorganic cation transport	BP	1	TFRC	down_ACOR_VSMC
GO:1901838	0.465	0.882	1	9	positive regulation of transcription of nucleolar large rRNA by RNA	BP	1	SMARCA4	down_VSAP_EC
GO:1900017	0.465	0.888	1	6	positive regulation of cytokine production involved in inflammatory	BP	1	NOD2	up_ACOR_VSMC
GO:0050905	0.465	0.874	1	26	neuromuscular process	BP	1	HOXC10	up_AFEM_EC
GO:0060996	0.465	0.874	1	26	dendritic spine development	BP	1	CAMK2A	up_AFEM_EC
GO:0007398	0.465	0.888	1	6	ectoderm development	BP	1	ITGA6	up_VCAV_EC
GO:0097106	0.465	0.888	1	6	postsynaptic density organization	BP	1	RELN	up_VCAV_EC
GO:0099084	0.465	0.888	1	6	postsynaptic specialization	BP	1	RELN	up_VCAV_EC
GO:0001501	0.465	0.874	1	178	skeletal system development	BP	1	HOXA3	up_VPUL_EC
GO:0042493	0.465	0.875	1	178	response to drug	BP	1	ARHGEF2	up_VPUL_EC

GO:0036499	0.465	0.888	1	6	PERK-mediated unfolded protein response	BP	1	NCK1	up_VSAP_EC
GO:0045907	0.465	0.888	1	6	positive regulation of vasoconstriction	BP	1	TBXA2R	up_VSAP_EC
GO:0048812	0.465	0.873	1	151	neuron projection morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0051259	0.465	0.874	1	140	protein complex oligomerization	BP	1	CAV1	up_VSAP_VSMC
GO:0043933	0.465753468	0.63029	19	698	protein-containing complex subunit organization	BP	1	FMOD,TMOD1,TRPS1,KCTD12,CALY,SOX9,KCNB1,SMAD6,ACTN2,PAK3,PTGER4,PREB,FOXC2,CLSTN1,CLU,CHMP4B,VPS16,PRKCD,TUBB4A	up_ACOR_EC
GO:0050789	0.466	0.568	279	3295	regulation of biological process	BP	1	ELK3,ACSL3,FSCN1,HMGB1,RNPS1,SREBF1,USP1,IRAK1,MCM7,ANLN,ILF3,DDX39A,STXBP6,CBX5,PPRC1,USP4,FMNL3,RACGAP1,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,TFPI,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,WDR76,MED17,U2AF2,ZW10,INTS7,QSOX2,MNDA,CAPG,PSMD3,SLC29A1,MTDH,HEY1,HOXA3,PPM1G,RRBP1,TRIP13,COLGALT1,SLC25A5,PPP1R15B,SF1,PARPBP,SRRT,SDC1,ARFGAP1,CTDNEP1,RANGAP1,FBXO5,HSPA9,NAB2,SLC35C2,RAN,CFAP298,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,ENSCAFG00000030005,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,TIMELESS,THRAP3,LIMA1,TRUB2,FAM129B,TCEA1,ENSCAFG00000008236,NF2,EDC4,AURKB,PSD4,NONO,MMP14,HNRNPL,CDKN2C,TOPBP1,ABHD5,EZH2,STMN1,DEPDC1,SLC30A1,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,CLIC1,FEN1,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,HMGB3,RCC1,PCNA,DHX33,HOXA7,SMG9,BID,ARG2,ANXA5,SF3B4,UHRF1,CKS2,PDCD2,HOXC10,RNF152,NKAIN1,HOXB7,TKT,GMNN,DHCR24,POC1A,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,PRCP,PREB,TFRC,NRAS,PPARD,CDC6,NDC80,ITGB3,RAP2C,YBX3,HNRNPF,ARH	down_ACOR_VSMC
GO:1902531	0.466	0.594	52	536	regulation of intracellular signal transduction	BP	1	SEZ6L,CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,TBC1D10C,ARHGEF6,IL6R,SLIT2,ABL1,HDAC7,SESN1,MAP3K5,PDGFD,C1QTNF2,HPSE,ANKRD54,F2RL1,PDK2,MFN2,TRAF7,RBCK1,TIAM1,MYC,PIK3IP1,DLC1,FGD4,RTN4RL1,SASH1,MYD88,PTPMT1,S100A4,CASTOR1,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,FBLN1,RAF1,MAPKBP1,PSD4,QARS,ARHGAP12,FLOT1,NCK1,NPRL3,BAG4,TRADD,DDIT4	up_VSAP_EC
GO:0002376	0.466	0.609	32	622	immune system process	BP	1	GPAM,NOTCH2,LRP1,CFD,PRNP,SDC4,FBN1,BMPR1A,LMO4,TFE3,HSD3B7,CLSTN1,TRIM8,ENSCAFG00000013404,THY1,RNF216,B4GALT1,GLI3,PARK7,EEF2,ZFP36L1,BPI,CYBA,MAVS,LOXL3,RAB7B,A2M,TSC22D3,RAC2,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:1902533	0.466	0.684	7	271	positive regulation of intracellular signal	BP	1	LEP,F3,LMCD1,PLAGL2,GREM1,CLEC16A,CCL5	up_AFEM_EC
GO:0071478	0.466	0.73	4	58	cellular response to radiation	BP	1	CRYAB,EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0009116	0.466	0.733	4	39	nucleoside metabolic process	BP	1	ENPP4,PTGDR,ENSCAFG00000018611,NT5C2	up_ACOR_VSMC
GO:0001657	0.466	0.732	4	42	ureteric bud development	BP	1	HOXB7,GATA3,ARG2,BMP2	up_VCAV_EC
GO:0072163	0.466	0.732	4	42	mesonephric epithelium development	BP	1	HOXB7,GATA3,ARG2,BMP2	up_VCAV_EC
GO:0072164	0.466	0.732	4	42	mesonephric tubule development	BP	1	HOXB7,GATA3,ARG2,BMP2	up_VCAV_EC
GO:0019438	0.466	0.772	3	1258	aromatic compound biosynthetic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0048593	0.466	0.757	3	41	camera-type eye morphogenesis	BP	1	BCAR3,HIF1A,CTNNB1	down_VSAP_EC
GO:0043506	0.466	0.762	3	25	regulation of JUN kinase activity	BP	1	SASH1,EDN1,MAP3K7	up_ACOR_VSMC
GO:0040014	0.466	0.76	3	27	regulation of multicellular organism growth	BP	1	CHD7,CREB1,SPTBN4	up_VCAV_EC
GO:2001141	0.466	0.768	3	979	regulation of RNA biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0014909	0.466	0.805	2	15	smooth muscle cell migration	BP	1	SEMA6D,DOCK5	up_ACOR_VSMC
GO:0033043	0.466	0.8	2	446	regulation of organelle organization	BP	1	CCL24,ARHGEF2	up_VPUL_EC

GO:0010826	0.466	0.885	1	7	negative regulation of centrosome duplication	BP	1	RBM14	down_ACOR_VSMC
GO:0034377	0.466	0.884	1	7	plasma lipoprotein particle assembly	BP	1	ACSL3	down_ACOR_VSMC
GO:0065005	0.466	0.884	1	7	protein-lipid complex assembly	BP	1	ACSL3	down_ACOR_VSMC
GO:0090025	0.466	0.884	1	7	regulation of monocyte chemotaxis	BP	1	HMGB1	down_ACOR_VSMC
GO:0006221	0.466	0.878	1	12	pyrimidine nucleotide biosynthetic process	BP	1	GPAM	down_VCAV_EC
GO:0010524	0.466	0.878	1	12	positive regulation of calcium ion transport into	BP	1	THY1	down_VCAV_EC
GO:0045576	0.466	0.878	1	12	mast cell activation	BP	1	RAC2	down_VCAV_EC
GO:0060602	0.466	0.878	1	12	branch elongation of an epithelium	BP	1	RDH10	down_VCAV_EC
GO:0003337	0.466	0.88	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	CTNNB1	down_VSAP_EC
GO:0071425	0.466	0.88	1	10	hematopoietic stem cell proliferation	BP	1	ETV6	down_VSAP_EC
GO:0030317	0.466	0.879	1	11	flagellated sperm motility	BP	1	CCNYL1	down_VSAP_EC
GO:0097722	0.466	0.879	1	11	sperm motility	BP	1	CCNYL1	down_VSAP_EC
GO:0002088	0.466	0.874	1	26	lens development in camera-type eye	BP	1	CRYAB	up_AFEM_EC
GO:0046323	0.466	0.874	1	26	glucose import	BP	1	LEP	up_AFEM_EC
GO:0015833	0.466	0.882	1	521	peptide transport	BP	1	ARG2	up_AORT_VSMC
GO:0090066	0.466	0.873	1	162	regulation of anatomical structure size	BP	1	HTR7	up_APUL_EC
GO:0006851	0.466	0.883	1	8	mitochondrial calcium ion transmembrane transport	BP	1	MCU	up_VCAV_EC
GO:0008209	0.466	0.883	1	8	androgen metabolic process	BP	1	TIPARP	up_VCAV_EC
GO:1902175	0.466	0.884	1	7	regulation of oxidative stress-induced intrinsic apoptotic signaling	BP	1	HIF1A	up_VCAV_EC
GO:0060350	0.46635117	0.87397	1	23	endochondral bone morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0015908	0.466598757	0.87382	1	23	fatty acid transport	BP	1	CFI	up_ACOR_EC
GO:0051223	0.467	0.632	18	181	regulation of protein transport	BP	1	HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,CDH1,ABL1,IL17RC,ANXA4,F2RL1,ICE1,PIK3R1,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:0031400	0.467	0.656	11	205	negative regulation of protein modification	BP	1	KIRREL1,DCN,PRNP,BGN,AKT1S1,PRMT6,ASPN,THY1,PARK7,SPRED1,GREM1	down_VCAV_EC
GO:0010506	0.467	0.67	9	86	regulation of autophagy	BP	1	LEP,HTR2B,FEZ1,PRKAA2,TP53INP1,DAPK1,BNIP3,FEZ2,SH3BP4	up_ACOR_VSMC
GO:0016197	0.467	0.677	8	78	endosomal transport	BP	1	ACTN2,ABCA1,SGSM2,PIK3C3,RAB11B,LMTK2,VPS26A,BVES	up_ACOR_VSMC
GO:0022618	0.467	0.685	7	111	ribonucleoprotein complex assembly	BP	1	CELF1,PRPF3,DDX39B,CNOT7,STRAP,EIF2S1,RSL24D1	down_VSAP_EC
GO:0030217	0.467	0.687	7	65	T cell differentiation	BP	1	LEP,CD83,BMP4,PTPN22,CHD7,B2M,IL18R1	up_ACOR_VSMC
GO:0009205	0.467	0.696	6	98	purine ribonucleoside triphosphate metabolic	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0002449	0.467	0.712	5	53	lymphocyte mediated immunity	BP	1	HMGB1,TFRC,FAM49B,EMP2,CORO1A	down_ACOR_VSMC
GO:0000045	0.467	0.713	5	46	autophagosome assembly	BP	1	AMBRA1,MFN2,PIP4K2B,UBQLN2,NPRL3	up_VSAP_EC
GO:0046330	0.467	0.713	5	47	positive regulation of JNK cascade	BP	1	ARHGEF5,MAP3K5,F2RL1,SASH1,MYD88	up_VSAP_EC
GO:0030218	0.467	0.732	4	42	erythrocyte differentiation	BP	1	HSPA9,PRMT1,HMGB2,JMJD6	down_ACOR_VSMC
GO:0031099	0.467	0.758	3	30	regeneration	BP	1	EZH2,PPARD,GLI1	down_ACOR_VSMC
GO:0050870	0.467	0.756	3	42	positive regulation of T cell activation	BP	1	SOCS5,FAM49B,TFRC	down_VSAP_EC
GO:0062013	0.467	0.76	3	27	positive regulation of small molecule metabolic	BP	1	PPARGC1A,PRKCE,PARK7	up_ACOR_VSMC
GO:0090329	0.467	0.76	3	25	regulation of DNA-dependent DNA	BP	1	CDC7,ATRX,ZNF365	up_ACOR_VSMC
GO:0051963	0.467	0.76	3	26	regulation of synapse assembly	BP	1	FZD1,AMIGO1,LRRN3	up_VSAP_EC
GO:0032272	0.467	0.802	2	18	negative regulation of protein polymerization	BP	1	CAPG,STMN1	down_ACOR_VSMC

GO:0032963	0.467	0.802	2	18	collagen metabolic process	BP	1	MMP14,SERPINH1	down_ACOR_VSMC
GO:0044706	0.467	0.798	2	27	multi-multicellular organism process	BP	1	TMED2,PTGS2	down_VSAP_EC
GO:0042771	0.467	0.804	2	16	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	CDKN1A,DDIT4	up_ACOR_VSMC
GO:0010631	0.467	0.872	1	118	epithelial cell migration	BP	1	ACVRL1	down_ACOR_EC
GO:0090132	0.467	0.872	1	118	epithelium migration	BP	1	ACVRL1	down_ACOR_EC
GO:0045116	0.467	0.882	1	8	protein neddylation	BP	1	DCUN1D5	down_ACOR_VSMC
GO:2000737	0.467	0.884	1	7	negative regulation of stem cell differentiation	BP	1	HSPA9	down_ACOR_VSMC
GO:1902305	0.467	0.877	1	12	regulation of sodium ion transmembrane transport	BP	1	FXYD1	down_VCAV_EC
GO:1905314	0.467	0.878	1	12	semi-lunar valve development	BP	1	NOTCH2	down_VCAV_EC
GO:2000378	0.467	0.878	1	12	negative regulation of reactive oxygen species	BP	1	PARK7	down_VCAV_EC
GO:0010960	0.467	0.887	1	6	magnesium ion homeostasis	BP	1	CNNM2	up_ACOR_VSMC
GO:0019319	0.467	0.873	1	26	hexose biosynthetic process	BP	1	LEP	up_AFEM_EC
GO:0050852	0.467	0.873	1	26	T cell receptor signaling pathway	BP	1	CYLD	up_AFEM_EC
GO:1900542	0.467	0.873	1	26	regulation of purine nucleotide metabolic	BP	1	PPARGC1A	up_AFEM_EC
GO:0040011	0.467	0.882	1	505	locomotion	BP	1	WNT7A	up_AORT_VSMC
GO:1903205	0.467	0.884	1	7	regulation of hydrogen peroxide-induced cell	BP	1	RIPK1	up_VCAV_EC
GO:2001038	0.467	0.884	1	7	regulation of cellular response to drug	BP	1	RIPK1	up_VCAV_EC
GO:1900746	0.467	0.884	1	7	regulation of vascular endothelial growth factor	BP	1	JCAD	up_VCAV_EC
GO:1902547	0.467	0.884	1	7	regulation of cellular response to vascular endothelial growth factor	BP	1	JCAD	up_VCAV_EC
GO:0051254	0.467	0.879	1	431	positive regulation of RNA metabolic process	BP	1	GATA5	up_VCAV_VSMC
GO:0048762	0.467	0.872	1	77	mesenchymal cell differentiation	BP	1	SEMA3A	up_VPOR_EC
GO:0032269	0.467	0.876	1	306	negative regulation of cellular protein metabolic	BP	1	SLIT2	up_VPUL_VSMC
GO:0009100	0.467	0.873	1	139	glycoprotein metabolic process	BP	1	GALNT17	up_VSAP_VSMC
GO:0032648	0.467643156	0.87319	1	23	regulation of interferon-beta production	BP	1	MAVS	up_ACOR_EC
GO:0044249	0.468	0.572	151	1851	cellular biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,ADGRF5,ST8SIA6,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,ST6GAL1,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NOS3,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,PTGS1,ENSCAFG00000017103,ZDHHC22,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,FAM3C,GUCY1A1,ODC1,SPTLC2,ARG2,B3GNT5,TARSL2,MTOR,SAMD8,ELF4,HHAT,BMP2,HMG20A,HHEX,CHST7,CREM,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,GALNT18,PRKD2,THOC1,SH3GLB1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,MRRF,PTGS2,TOP1,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,RAD17,IMPA1,SKIL,GPBP1,USP37,PIP5K1B,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,BCAT1,ZNF146,ATRX,NR4A1,ALDH1A3,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZDHHC6,ZEB1,TET2,ARHGEF2,CDO	up_VCAV_EC
GO:1905114	0.468	0.66	10	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	PRICKLE1,SULF1,ILK,SMARCA4,NXN,CTNNB1,APOE,DDIT3,TAX1BP3,DISC1	down_VSAP_EC

GO:2001234	0.468	0.685	7	75	negative regulation of apoptotic signaling	BP	1	SLC25A5,PRELID1,NOC2L,HMGB2,TXNDC12,CTH,ARHGEF2	down_ACOR_VSMC
GO:0022411	0.468	0.683	7	130	cellular component disassembly	BP	1	GABARAP,WDR45,CLEC16A,RETREG1,DDR2,PYM1,PLEKHH2	down_VCAV_EC
GO:0051173	0.468	0.716	5	874	positive regulation of nitrogen compound	BP	1	ACVRL1,LYN,HOXA1,ACSL3,NEDD4	down_ACOR_EC
GO:0007399	0.468	0.71	5	564	nervous system development	BP	1	HOOK3,HOXA3,ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0010467	0.468	0.731	5	1787	gene expression	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:2001257	0.468	0.757	3	30	regulation of cation channel activity	BP	1	CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0018130	0.468	0.77	3	1261	heterocycle biosynthetic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0030148	0.468	0.758	3	28	sphingolipid biosynthetic process	BP	1	UGCG,ORMDL3,SMPD1	up_ACOR_VSMC
GO:0045785	0.468	0.752	3	107	positive regulation of cell adhesion	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0080090	0.468	0.781	3	1734	regulation of primary metabolic process	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0046626	0.468	0.801	2	18	regulation of insulin receptor signaling	BP	1	CDK4,NCOA5	down_ACOR_VSMC
GO:0015893	0.468	0.797	2	26	drug transport	BP	1	PTPN11,INHBA	down_VSAP_EC
GO:0050852	0.468	0.798	2	26	T cell receptor signaling pathway	BP	1	PTPN2,EIF2B1	down_VSAP_EC
GO:0051705	0.468	0.803	2	16	multi-organism behavior	BP	1	APP,CLN8	up_ACOR_VSMC
GO:1902883	0.468	0.803	2	16	negative regulation of response to oxidative	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0009636	0.468	0.793	2	66	response to toxic substance	BP	1	CRYAB,SOD1	up_AFEM_EC
GO:0050730	0.468	0.793	2	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	GREM1,ADAM17	up_AFEM_EC
GO:0006893	0.468	0.8	2	20	Golgi to plasma membrane transport	BP	1	EXOC5,CHIC2	up_VCAV_EC
GO:0046825	0.468	0.802	2	16	regulation of protein export from nucleus	BP	1	IWS1,CTDSPL2	up_VCAV_EC
GO:0007589	0.468	0.803	2	16	body fluid secretion	BP	1	CHRM1,CYBA	up_VSAP_EC
GO:1901998	0.468	0.803	2	16	toxin transport	BP	1	CD274,VPS11	up_VSAP_EC
GO:0070207	0.468	0.883	1	7	protein homotrimerization	BP	1	SIGMAR1	down_ACOR_VSMC
GO:0032269	0.468	0.876	1	306	negative regulation of cellular protein metabolic	BP	1	CST3	down_VPOR_EC
GO:0050820	0.468	0.879	1	10	positive regulation of coagulation	BP	1	SERPINE1	down_VSAP_EC
GO:0006516	0.468	0.886	1	6	glycoprotein catabolic process	BP	1	STT3B	up_ACOR_VSMC
GO:0006942	0.468	0.873	1	26	regulation of striated muscle contraction	BP	1	DMPK	up_AFEM_EC
GO:0046639	0.468	0.883	1	7	negative regulation of alpha-beta T cell	BP	1	HMGB1	up_VCAV_EC
GO:0001763	0.468	0.871	1	78	morphogenesis of a branching structure	BP	1	SEMA3A	up_VPOR_EC
GO:0048666	0.468	0.874	1	258	neuron development	BP	1	SHOX2	up_VFEM_VSMC
GO:1901137	0.468	0.874	1	232	carbohydrate derivative biosynthetic process	BP	1	FBP1	up_VFEM_VSMC
GO:0040008	0.468	0.873	1	179	regulation of growth	BP	1	TBX5	up_VPUL_EC
GO:0030168	0.468164889	0.87287	1	23	platelet activation	BP	1	PRKCD	up_ACOR_EC
GO:0032206	0.468197856	0.87285	1	23	positive regulation of telomere maintenance	BP	1	PKIB	up_ACOR_EC
GO:1901576	0.469	0.646	16	1877	organic substance biosynthetic process	BP	1	BARX1,OSTC,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0032970	0.469	0.646	13	130	regulation of actin filament-based process	BP	1	WNT11,FAM107A,ARHGEF5,SLIT2,ABL1,KCNE3,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,FRMD6,NCK1,BAG4	up_VSAP_EC
GO:0051249	0.469	0.655	11	107	regulation of lymphocyte activation	BP	1	LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,CDKN1A,PTPN22,DUSP22,NOD2,PAG1	up_ACOR_VSMC
GO:0010720	0.469	0.656	11	110	positive regulation of cell development	BP	1	HOXA11,CDON,HOXD3,ABL1,IRX3,ZEB1,SHOX2,GDPD5,CYB5D2,NCK1,MAP2K2	up_VSAP_EC
GO:0009259	0.469	0.665	9	166	ribonucleotide metabolic process	BP	1	GPAM,ADCY6,NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC

GO:0043933	0.469	0.732	4	698	protein-containing complex subunit	BP	1	IGF1R,RPSA,ACSL3,STX4	down_ACOR_EC
GO:0006413	0.469	0.73	4	42	translational initiation	BP	1	PPP1R15B,DHX33,RBM14,EIF3M	down_ACOR_VSMC
GO:0051249	0.469	0.751	3	107	regulation of lymphocyte activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0002011	0.469	0.758	3	28	morphogenesis of an epithelial sheet	BP	1	DLL4,MTOR,JAG1	up_VCAV_EC
GO:0021954	0.469	0.759	3	26	central nervous system neuron development	BP	1	EPHB1,RAPGEF2,SPTBN4	up_VCAV_EC
GO:0032088	0.469	0.759	3	26	negative regulation of NF-kappaB transcription	BP	1	ANXA4,RBCK1,PRMT2	up_VSAP_EC
GO:0046323	0.469	0.759	3	26	glucose import	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:1901222	0.469	0.795	2	32	regulation of NIK/NF-kappaB signaling	BP	1	SASH1,GREM1	down_VCAV_EC
GO:0048284	0.469	0.792	2	66	organelle fusion	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0060563	0.469	0.8	2	18	neuroepithelial cell differentiation	BP	1	BMP2,JAG1	up_VCAV_EC
GO:0042398	0.469	0.877	1	12	cellular modified amino acid biosynthetic process	BP	1	PARK7	down_VCAV_EC
GO:0007155	0.469	0.875	1	324	cell adhesion	BP	1	CITED2	down_VPOR_EC
GO:0043525	0.469	0.877	1	11	positive regulation of neuron apoptotic process	BP	1	DDIT3	down_VSAP_EC
GO:0032355	0.469	0.878	1	10	response to estradiol	BP	1	CTNNB1	down_VSAP_EC
GO:0046636	0.469	0.878	1	10	negative regulation of alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:0048103	0.469	0.878	1	10	somatic stem cell division	BP	1	ARHGEF2	down_VSAP_EC
GO:0000920	0.469	0.883	1	7	septum digestion after cytokinesis	BP	1	MITD1	up_ACOR_VSMC
GO:0044848	0.469	0.885	1	6	biological phase	BP	1	FERMT1	up_ACOR_VSMC
GO:0044851	0.469	0.885	1	6	hair cycle phase	BP	1	FERMT1	up_ACOR_VSMC
GO:0048819	0.469	0.885	1	6	regulation of hair follicle maturation	BP	1	FERMT1	up_ACOR_VSMC
GO:0044770	0.469	0.872	1	161	cell cycle phase transition	BP	1	LZTS1	up_APUL_EC
GO:0045087	0.469	0.872	1	161	innate immune response	BP	1	NR1H4	up_APUL_EC
GO:0051186	0.469	0.872	1	159	cofactor metabolic process	BP	1	ENSCAFG00000028814	up_APUL_EC
GO:0007205	0.469	0.883	1	7	protein kinase C-activating G protein-coupled receptor signaling	BP	1	EDN1	up_VCAV_EC
GO:0007417	0.469	0.874	1	235	central nervous system development	BP	1	TRPC4	up_VPOR_VSMC
GO:0009314	0.469	0.871	1	143	response to radiation	BP	1	NETO1	up_VSAP_VSMC
GO:0032990	0.469326744	0.70615	5	167	cell part morphogenesis	BP	1	BRSK1,PAK3,MAPK8IP2,LRP4,NRP1	up_ACOR_EC
GO:0043161	0.469654743	0.70581	5	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	EDEM2,PIAS1,CLU,RNF114,UBE2H	up_ACOR_EC
GO:0031110	0.469657926	0.87176	1	24	regulation of microtubule polymerization or depolymerization	BP	1	TUBB4A	up_ACOR_EC

GO:0048522	0.47	0.569	144	1484	positive regulation of cellular process	BP	1	SYNPO2L,EXPH5,ADRA1B,VEGFD,TLR1,SMAD6,ACTN2,LGR6,PLCG2,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CD83,CDC7,PCGF5,HTR2B,RASSF2,FNDC5,MBP,ZRANB1,C28H10orf71,LIPT2,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,LNPK,SYNPO2,TM7SF3,FGFR2,TP53BP1,GJA1,ATRX,MED14,TLR3,SH3RF2,WASF3,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,PKP4,ISG15,CD274,ZNF365,MARCKSL1,AR,SASH1,LMO4,TMEM108,FGF18,FAM210B,CDKN2B,PLAC8B,LIMS2,ANKRD1,F2RL1,FAM129A,MARCH5,DAPK1,BNIP3,EGLN1,AKAP6,CDKN1A,JMY,CRLF3,CLSTN1,CREBRF,NRP1,PTPN22,NPNT,UNC5B,SMARCD3,EVL,SMPD1,SLITRK5,TBX20,TBX5,CCDC3,PRKCE,CCNT1,FZD3,DKKL1,FRS2,RNF19A,CCPG1,DAG1,PARP9,CHD6,APP,PSEN1,SEMA6D,TGFBR1,CHD7,SPINK2,CCL5,DDR2,FOSL2,PERP,DUSP22,SIAH1,EDN1,AKTIP,DUSP26,NOD2,ASAP1,FAM107A,B2M,DISC1,SH3RF3,SERINC3,DCUN1D4,SCAMP5,KLF11,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,WDR48,WASL,CAT,DOCK5,ZKSCAN1,SH3BP4,ENSCAFG00000029553,PARK7,TEAD1,NGRN,IL18R1,HMBOX1,SSBP2,BVES,REB1,CRKL,PIK3C2A	up_ACOR_VSMC
GO:0007169	0.47	0.629	18	178	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	SH3TC2,VEGFD,EFNB2,ANGPT1,RASSF2,FGFR2,PTGIR,TMEM108,FGF18,NRP1,SESN3,FRS2,APP,PSEN1,SIPA1L1,ARID5B,INPP5K,PAG1	up_ACOR_VSMC
GO:1901699	0.47	0.632	17	164	cellular response to nitrogen compound	BP	1	ACTN2,ATRX,CASTOR1,ADCY6,AKAP6,UBR1,PTPN22,APLP1,SESN3,AGRN,APP,PSEN1,JUP,NOD2,GNAQ,INPP5K,SH3BP4	up_ACOR_VSMC
GO:0050794	0.47	0.712	8	3075	regulation of cellular process	BP	1	DKK2,HOXA9,LNPEP,ERC1,TAOK1,BPI,CTNNAL1,GPR155	up_AORT_EC
GO:0031349	0.47	0.693	6	90	positive regulation of defense response	BP	1	NR1H4,SERPINE1,PTGS2,PVR,LYN,GBP5	down_VSAP_EC
GO:0048015	0.47	0.71	5	48	phosphatidylinositol-mediated signaling	BP	1	PDGFD,F2RL1,ZFP36L1,PIK3R1,PIK3IP1	up_VSAP_EC
GO:0048017	0.47	0.71	5	48	inositol lipid-mediated signaling	BP	1	PDGFD,F2RL1,ZFP36L1,PIK3R1,PIK3IP1	up_VSAP_EC
GO:0051179	0.47	0.749	4	1747	localization	BP	1	HDAC7,RAB11B,ERGIC1,HSD3B7	down_VPOR_EC
GO:0070647	0.47	0.752	3	311	protein modification by small protein conjugation	BP	1	KLHL28,USP33,RNF6	up_VPOR_EC
GO:0032615	0.47	0.8	2	18	interleukin-12 production	BP	1	HMGB1,MAST2	down_ACOR_VSMC
GO:0048546	0.47	0.802	2	16	digestive tract morphogenesis	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0044085	0.47	0.81	2	1076	cellular component biogenesis	BP	1	SLITRK5,LIMK1	up_VCAV_VSMC
GO:0009617	0.47	0.87	1	133	response to bacterium	BP	1	LYN	down_ACOR_EC
GO:0043558	0.47	0.882	1	7	regulation of translational initiation in response to	BP	1	PPP1R15B	down_ACOR_VSMC
GO:0043968	0.47	0.882	1	7	histone H2A acetylation	BP	1	DMAP1	down_ACOR_VSMC
GO:0090382	0.47	0.88	1	8	phagosome maturation	BP	1	CORO1A	down_ACOR_VSMC
GO:1901881	0.47	0.883	1	7	positive regulation of protein depolymerization	BP	1	PDXP	down_ACOR_VSMC
GO:0018345	0.47	0.876	1	12	protein palmitoylation	BP	1	CLIP3	down_VCAV_EC
GO:0031440	0.47	0.875	1	13	regulation of mRNA 3'-end processing	BP	1	ZFP36L1	down_VCAV_EC
GO:0060260	0.47	0.876	1	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	CLSTN1	down_VCAV_EC
GO:0072583	0.47	0.875	1	13	clathrin-dependent endocytosis	BP	1	CLTB	down_VCAV_EC
GO:0048599	0.47	0.878	1	10	oocyte development	BP	1	CTNNB1	down_VSAP_EC
GO:0035728	0.47	0.885	1	6	response to hepatocyte growth factor	BP	1	NRP1	up_ACOR_VSMC
GO:0035729	0.47	0.885	1	6	cellular response to hepatocyte growth factor	BP	1	NRP1	up_ACOR_VSMC
GO:0060330	0.47	0.885	1	6	regulation of response to interferon-gamma	BP	1	PARP9	up_ACOR_VSMC
GO:0060334	0.47	0.885	1	6	regulation of interferon-gamma-mediated	BP	1	PARP9	up_ACOR_VSMC

GO:0044093	0.47	0.878	1	437	positive regulation of molecular function	BP	1	TLR2	up_AFEM_VSMC
GO:0042886	0.47	0.881	1	527	amide transport	BP	1	ARG2	up_AORT_VSMC
GO:0045184	0.47	0.88	1	532	establishment of protein localization	BP	1	ARG2	up_AORT_VSMC
GO:0032870	0.47	0.871	1	162	cellular response to hormone stimulus	BP	1	NR1H4	up_APUL_EC
GO:0006144	0.47	0.879	1	9	purine nucleobase metabolic process	BP	1	ACPP	up_VCAV_EC
GO:0043393	0.47	0.87	1	77	regulation of protein binding	BP	1	HOXA3	up_VPOR_EC
GO:0032787	0.47	0.871	1	144	monocarboxylic acid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0006970	0.470065639	0.87171	1	23	response to osmotic stress	BP	1	AQP1	up_ACOR_EC
GO:0060560	0.470373863	0.7918	2	58	developmental growth involved in	BP	1	SOX9,NRP1	up_ACOR_EC
GO:0048878	0.470544744	0.67123	8	283	chemical homeostasis	BP	1	NR1H4,PTH1R,AQP1,KCNB1,IFI6,SLC9A9,TMTC2,PRKACA	up_ACOR_EC
GO:0050818	0.470802758	0.87106	1	24	regulation of coagulation	BP	1	PRKCD	up_ACOR_EC
GO:0021782	0.470979988	0.87114	1	23	glial cell development	BP	1	SH3TC2	up_ACOR_EC
GO:0051641	0.471	0.581	72	858	cellular localization	BP	1	HCLS1,GBP5,KIT,PPP2R5A,TNFAIP3,MX2,AMOT,MALL,TMEM173,EXOC3L2,RELN,PDE4D,IWS1,MEF2C,FERMT1,CHD7,TSPAN15,RAB11A,KIF3C,APLNR,RAB27A,EXOC6,SNCAIP,ZDHHC22,PPP3CA,NECTIN2,HOOK3,SNAP23,TSPAN14,HHEX,RAB6A,CAV2,CEP68,PDZD8,ANKRD50,ABCA1,MZT1,EPB41,SNX2,THOC1,SH3GLB1,AKAP12,APOD,CENPC,EXOC5,FES,EHD4,RAPGEF2,PLCG2,CTDSPL2,PAN3,GCC2,CTNNA1,STX11,SMG7,VPS54,TBC1D1,NUP133,SPTBN4,RAD21,DNAJC13,ZW10,HIF1A,IPO11,ALS2,LMTK2,ATRX,DOP1B,SHROOM2,ATP2A1,RABGAP1,USP6NL	up_VCAV_EC
GO:0043066	0.471	0.613	25	253	negative regulation of apoptotic process	BP	1	SMAD6,BCL2,HTR2B,PRKAA2,BMP4,FGFR2,SH3RF2,PPARGC1A,CITED2,AR,PLAC8B,KLHL20,LIMS2,DAPK1,BNIP3,NRP1,UNC5B,SH3RF1,FZD3,PSEN1,CLN8,OXR1,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0006979	0.471	0.653	11	130	response to oxidative stress	BP	1	TNFAIP3,TLR4,PTGS1,MAPK13,APOD,GUCY1B1,PTGS2,GCH1,RIPK1,HIF1A,ALS2	up_VCAV_EC
GO:0044267	0.471	0.708	6	1583	cellular protein metabolic process	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0071840	0.471	0.733	5	2059	cellular component organization or biogenesis	BP	1	GPSM2,EIF3M,SRSF6,NDUFA10,FSCN1	down_AFEM_EC
GO:0031349	0.471	0.705	5	90	positive regulation of defense response	BP	1	PARK7,CYBA,MAVS,RAB7B,NAPEPLD	down_VCAV_EC
GO:0030838	0.471	0.729	4	37	positive regulation of actin filament	BP	1	JMY,EVL,PRKCE,WASL	up_ACOR_VSMC
GO:0042476	0.471	0.729	4	36	odontogenesis	BP	1	BMP4,FGFR2,PERP,TNFRSF11B	up_ACOR_VSMC
GO:2000117	0.471	0.756	3	27	negative regulation of cysteine-type	BP	1	CST3,SH3RF1,PARK7	up_ACOR_VSMC
GO:0002063	0.471	0.799	2	18	chondrocyte development	BP	1	POC1A,SERPINH1	down_ACOR_VSMC
GO:0048583	0.471	0.809	2	1095	regulation of response to stimulus	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0034308	0.471	0.8	2	16	primary alcohol metabolic process	BP	1	NAPEPLD,RETSAT	up_VSAP_EC
GO:0051705	0.471	0.801	2	16	multi-organism behavior	BP	1	SLC6A4,PPP3CB	up_VSAP_EC
GO:0006979	0.471	0.87	1	130	response to oxidative stress	BP	1	STX4	down_ACOR_EC
GO:0044417	0.471	0.882	1	7	translocation of molecules into host	BP	1	DDX39B	down_ACOR_VSMC
GO:0051836	0.471	0.882	1	7	translocation of molecules into other organism involved in symbiotic	BP	1	DDX39B	down_ACOR_VSMC
GO:0003254	0.471	0.875	1	12	regulation of membrane depolarization	BP	1	DCN	down_VCAV_EC
GO:0060445	0.471	0.875	1	13	branching involved in salivary gland	BP	1	SEMA3C	down_VCAV_EC
GO:0072079	0.471	0.875	1	12	nephron tubule formation	BP	1	GREM1	down_VCAV_EC
GO:0022610	0.471	0.874	1	326	biological adhesion	BP	1	CITED2	down_VPOR_EC

GO:2001026	0.471	0.877	1	10	regulation of endothelial cell chemotaxis	BP	1	VEGFA	down_VSAP_EC
GO:0045494	0.471	0.884	1	6	photoreceptor cell maintenance	BP	1	CLN8	up_ACOR_VSMC
GO:0009886	0.471	0.884	1	6	post-embryonic animal morphogenesis	BP	1	ATRX	up_ACOR_VSMC
GO:0034091	0.471	0.884	1	6	regulation of maintenance of sister chromatid	BP	1	ATRX	up_ACOR_VSMC
GO:0034182	0.471	0.884	1	6	regulation of maintenance of mitotic sister chromatid	BP	1	ATRX	up_ACOR_VSMC
GO:0003344	0.471	0.885	1	6	pericardium morphogenesis	BP	1	TBX20	up_ACOR_VSMC
GO:0099174	0.471	0.884	1	6	regulation of presynapse organization	BP	1	APP	up_ACOR_VSMC
GO:0009967	0.471	0.877	1	435	positive regulation of signal transduction	BP	1	TLR2	up_AFEM_VSMC
GO:0048534	0.471	0.873	1	262	hematopoietic or lymphoid organ	BP	1	HOXA9	up_AORT_EC
GO:0001783	0.471	0.88	1	8	B cell apoptotic process	BP	1	BCL10	up_VCAV_EC
GO:0001912	0.471	0.878	1	9	positive regulation of leukocyte mediated	BP	1	NECTIN2	up_VCAV_EC
GO:0010447	0.471	0.88	1	8	response to acidic pH	BP	1	GPR4	up_VCAV_EC
GO:0045070	0.471	0.88	1	8	positive regulation of viral genome replication	BP	1	CNOT7	up_VCAV_EC
GO:1900274	0.471	0.885	1	6	regulation of phospholipase C activity	BP	1	SELE	up_VCAV_EC
GO:0034330	0.471	0.869	1	80	cell junction organization	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0051223	0.471	0.871	1	181	regulation of protein transport	BP	1	NR1H4	up_VPUL_EC
GO:0071496	0.471507533	0.74909	3	97	cellular response to external stimulus	BP	1	SOX9,AQP1,PTGER4	up_ACOR_EC
GO:0001736	0.471793029	0.87064	1	23	establishment of planar polarity	BP	1	BRSK1	up_ACOR_EC
GO:0007164	0.471793029	0.87064	1	23	establishment of tissue polarity	BP	1	BRSK1	up_ACOR_EC
GO:0055082	0.472	0.656	10	189	cellular chemical homeostasis	BP	1	PRNP,ENSCAFG00000014978,ENSCAFG00000018277,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ORMDL3,ATOX1	down_VCAV_EC
GO:0072521	0.472	0.656	10	185	purine-containing compound metabolic	BP	1	GPAM,ADCY6,NT5C2,ATP5MC1,UQCR10,ADK,PARK7,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0001818	0.472	0.693	6	65	negative regulation of cytokine production	BP	1	HMGB1,SLC29A1,ARG2,RAC1,CACTIN,EZR	down_ACOR_VSMC
GO:0070374	0.472	0.694	6	57	positive regulation of ERK1 and ERK2 cascade	BP	1	ACKR3,C5AR2,ABL1,PDGFD,F2RL1,RAF1	up_VSAP_EC
GO:0048511	0.472	0.706	5	72	rhythmic process	BP	1	BHLHE40,HTR7,MAGED1,GNAQ,INHBA	down_VSAP_EC
GO:0045834	0.472	0.727	4	41	positive regulation of lipid metabolic process	BP	1	ACSL3,SREBF1,CTDNEP1,ABHD5	down_ACOR_VSMC
GO:0070373	0.472	0.756	3	26	negative regulation of ERK1 and ERK2 cascade	BP	1	TBC1D10C,ABL1,FBLN1	up_VSAP_EC
GO:0048194	0.472	0.798	2	18	Golgi vesicle budding	BP	1	INSIG1,PREB	down_ACOR_VSMC
GO:1904064	0.472	0.794	2	27	positive regulation of cation transmembrane	BP	1	HTT,CALM1	down_VSAP_EC
GO:0034314	0.472	0.8	2	16	Arp2/3 complex-mediated actin nucleation	BP	1	JMY,WASL	up_ACOR_VSMC
GO:0045893	0.472	0.794	2	413	positive regulation of transcription, DNA-	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0042440	0.472	0.796	2	21	pigment metabolic process	BP	1	RAPGEF2,BLVRA	up_VCAV_EC
GO:0060562	0.472	0.869	1	120	epithelial tube morphogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:0033032	0.472	0.881	1	7	regulation of myeloid cell apoptotic process	BP	1	PIK3CD	down_ACOR_VSMC
GO:0051154	0.472	0.881	1	7	negative regulation of striated muscle cell	BP	1	EZH2	down_ACOR_VSMC
GO:0001541	0.472	0.874	1	12	ovarian follicle development	BP	1	FOXO3	down_VCAV_EC
GO:0060669	0.472	0.875	1	12	embryonic placenta morphogenesis	BP	1	ZFP36L1	down_VCAV_EC
GO:0090189	0.472	0.875	1	12	regulation of branching involved in ureteric bud	BP	1	GREM1	down_VCAV_EC
GO:0043300	0.472	0.875	1	11	regulation of leukocyte degranulation	BP	1	LYN	down_VSAP_EC
GO:0032042	0.472	0.884	1	6	mitochondrial DNA metabolic process	BP	1	PPARGC1A	up_ACOR_VSMC

GO:0002673	0.472	0.884	1	6	regulation of acute inflammatory response	BP	1	PARK7	up_ACOR_VSMC
GO:0048713	0.472	0.884	1	6	regulation of oligodendrocyte	BP	1	ZNF365	up_ACOR_VSMC
GO:1990089	0.472	0.884	1	6	response to nerve growth factor	BP	1	TMEM108	up_ACOR_VSMC
GO:1990090	0.472	0.884	1	6	cellular response to nerve growth factor stimulus	BP	1	TMEM108	up_ACOR_VSMC
GO:0042592	0.472	0.879	1	522	homeostatic process	BP	1	HOXC10	up_AORT_VSMC
GO:0032990	0.472	0.87	1	167	cell part morphogenesis	BP	1	SLITRK5	up_APUL_EC
GO:0010829	0.472	0.881	1	7	negative regulation of glucose transmembrane	BP	1	RSC1A1	up_VCAV_EC
GO:0031641	0.472	0.884	1	6	regulation of myelination	BP	1	MTOR	up_VCAV_EC
GO:0032069	0.472	0.879	1	8	regulation of nuclease activity	BP	1	HMGB1	up_VCAV_EC
GO:0043558	0.472	0.881	1	7	regulation of translational initiation in response to	BP	1	NCK1	up_VCAV_EC
GO:0090148	0.472	0.881	1	7	membrane fission	BP	1	MX2	up_VCAV_EC
GO:0031503	0.472	0.869	1	79	protein-containing complex localization	BP	1	MZT1	up_VPOR_EC
GO:0080135	0.472	0.872	1	240	regulation of cellular response to stress	BP	1	ANKRD6	up_VPOR_VSMC
GO:1901617	0.472542203	0.78998	2	60	organic hydroxy compound biosynthetic	BP	1	CDH3,NR1H4	up_ACOR_EC
GO:0051702	0.472596675	0.86995	1	24	interaction with symbiont	BP	1	AQP1	up_ACOR_EC
GO:1901135	0.473	0.601	33	390	carbohydrate derivative metabolic process	BP	1	PRPSAP1,ACLY,HMGCR,RRM1,MPDU1,SLC35C2,RAN,B3GNT2,CDK1,XYLT1,PFAS,TK1,RNASEH2B,TKT,MVD,B4GALT1,ELOVL1,CYCS,UGDH,ELOVL6,CYC1,ATP5F1A,PRPS1,ENSCAFG00000013366,PDHA1,NUDT1,PGD,NUS1,GK5,CTPS1,NECAB3,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0006518	0.473	0.613	24	290	peptide metabolic process	BP	1	ILF3,EIF4A3,HNRNPD,VARS,THOP1,RRBP1,PPP1R15B,MRPS18B,TRUB2,PLK3,DHX33,FASTKD3,EIF5A,FARSA,NCL,MRPL37,GSTO1,RBM14,NOLC1,RARS,PUM3,ENSCAFG00000006478,MRPL18,EIF3M	down_ACOR_VSMC
GO:0018193	0.473	0.622	19	368	peptidyl-amino acid modification	BP	1	PDGFRB,DCN,PRNP,VKORC1,CLIP3,AKT2,PLCL1,DDOST,CSPG4,PRMT6,PARK7,MAST2,ARL2BP,LOXL3,CAMK2D,FUT8,SPRED1,CRTAP,GREM1	down_VCAV_EC
GO:1903708	0.473	0.692	6	65	positive regulation of hemopoiesis	BP	1	HMGB1,PRMT1,MMP14,PDCD2,HMGB2,TOX	down_ACOR_VSMC
GO:0009755	0.473	0.707	5	52	hormone-mediated signaling pathway	BP	1	PRCP,SMARCA4,ADIPOR2,UFSP2,KDM3A	up_VCAV_EC
GO:0009612	0.473	0.708	5	47	response to mechanical stimulus	BP	1	WNT11,MAP3K14,CRADD,DENND5A,RAF1	up_VSAP_EC
GO:0072028	0.473	0.727	4	37	nephron morphogenesis	BP	1	HOXA11,WNT11,OSR1,IRX3	up_VSAP_EC
GO:0006367	0.473	0.753	3	32	transcription initiation from RNA polymerase II	BP	1	HMGB1,THRAP3,PSMC1	down_ACOR_VSMC
GO:0090307	0.473	0.794	2	26	mitotic spindle assembly	BP	1	MZT1,KPNB1	down_VSAP_EC
GO:0007254	0.473	0.789	2	67	JNK cascade	BP	1	CYLD,CDC42EP5	up_AFEM_EC
GO:0030522	0.473	0.789	2	67	intracellular receptor signaling pathway	BP	1	LBH,CRY2	up_AFEM_EC
GO:0098586	0.473	0.797	2	19	cellular response to virus	BP	1	RIOK3,LSM14A	up_VCAV_EC
GO:0090130	0.473	0.869	1	121	tissue migration	BP	1	ACVRL1	down_ACOR_EC
GO:0046639	0.473	0.881	1	7	negative regulation of alpha-beta T cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0051657	0.473	0.881	1	7	maintenance of organelle location	BP	1	ASPM	down_ACOR_VSMC
GO:1902476	0.473	0.873	1	13	chloride transmembrane transport	BP	1	CLIC4	down_VCAV_EC
GO:0033144	0.473	0.876	1	10	negative regulation of intracellular steroid hormone receptor	BP	1	SMARCA4	down_VSAP_EC
GO:0046503	0.473	0.876	1	10	glycerolipid catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0060438	0.473	0.876	1	10	trachea development	BP	1	CTNNB1	down_VSAP_EC
GO:0070493	0.473	0.884	1	6	thrombin-activated receptor signaling	BP	1	HPGD	up_ACOR_VSMC

GO:0043254	0.473	0.869	1	164	regulation of protein complex assembly	BP	1	TUBB4A	up_APUL_EC
GO:0010659	0.473	0.881	1	7	cardiac muscle cell apoptotic process	BP	1	RGL2	up_VCAV_EC
GO:0010665	0.473	0.881	1	7	regulation of cardiac muscle cell apoptotic	BP	1	RGL2	up_VCAV_EC
GO:0031116	0.473	0.881	1	7	positive regulation of microtubule	BP	1	FES	up_VCAV_EC
GO:0044417	0.473	0.881	1	7	translocation of molecules into host	BP	1	THOC1	up_VCAV_EC
GO:0051836	0.473	0.881	1	7	translocation of molecules into other organism involved in symbiotic	BP	1	THOC1	up_VCAV_EC
GO:2000273	0.473	0.883	1	6	positive regulation of signaling receptor activity	BP	1	RELN	up_VCAV_EC
GO:0018108	0.473	0.868	1	79	peptidyl-tyrosine phosphorylation	BP	1	ARHGEF2	up_VPOR_EC
GO:0023014	0.473	0.872	1	248	signal transduction by protein phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0098609	0.473	0.87	1	181	cell-cell adhesion	BP	1	FLRT3	up_VPUL_EC
GO:0043507	0.473132333	0.86982	1	23	positive regulation of JUN kinase activity	BP	1	FZD5	up_ACOR_EC
GO:0050896	0.474	0.572	118	2346	response to stimulus	BP	1	PCOLCE,GPAM,NOTCH2,PDGFRB,SLC35F6,SMAD9,ITGB5,LRP1,DCN,CFD,NDN,ANGPT1,PRNP,MT2A,SDC4,FOLR2,VASN,FBN1,ADCY6,GLIPR2,BGN,SLC10A3,KANK2,SH3BP1,BMPR1A,VKORC1,NABP2,EVC,RECK,IGFBP6,TRPV2,COL6A1,NUMBL,CHID1,ARHGEF25,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,TIMP2,AKT2,DOCK10,TFE3,NR3C1,SYDE1,HSD3B7,PDIA4,CLSTN1,PLCL1,CSPG4,TRIM8,PRMT6,ENSCAFG00000013404,EPHX1,ANXA11,WIPF1,TMEM161A,RASSF8,GFPT2,SEMA3C,ASPN,GNAZ,THY1,FKBP5,RNF216,TEAD1,CYP1B1,ARHGAP10,ATP6V0C,B4GALT1,GLI3,PARK7,ZMAT3,MAST2,SCARA5,ZFP36L1,MYDGF,SASH1,CLEC16A,BPI,CYBA,ENSCAFG00000018194,ARL2BP,IFT57,MAVS,CDH2,LOXL3,MPV17,GSDME,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SPNS1,SEC61B,TSC22D3,GLIS2,RAB31,HM13,ARHGAP1,SHC1,CRCP,FBH1,GREM1,NPHP4,ATOX1,RAC2,NAPEPLD,FOXO3,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:1903037	0.474	0.691	6	65	regulation of leukocyte cell-cell adhesion	BP	1	HMGB1,CAV1,ARG2,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0000082	0.474	0.693	6	57	G1/S transition of mitotic cell cycle	BP	1	FAM107A,CRADD,E2F4,FBXO7,LSM10,LATS2	up_VSAP_EC
GO:0061097	0.474	0.754	3	27	regulation of protein tyrosine kinase activity	BP	1	APP,PSEN1,DUSP22	up_ACOR_VSMC
GO:0042542	0.474	0.753	3	31	response to hydrogen peroxide	BP	1	TNFAIP3,MAPK13,RIPK1	up_VCAV_EC
GO:0006606	0.474	0.789	2	67	protein import into nucleus	BP	1	LEP,CRY2	up_AFEM_EC
GO:0042063	0.474	0.789	2	67	gliogenesis	BP	1	DLL1,LGI4	up_AFEM_EC
GO:0001816	0.474	0.789	2	194	cytokine production	BP	1	C3AR1,ARHGEF2	up_VPOR_EC
GO:0030501	0.474	0.798	2	16	positive regulation of bone mineralization	BP	1	OSR2,OSR1	up_VSAP_EC
GO:0048247	0.474	0.798	2	16	lymphocyte chemotaxis	BP	1	SLC8B1,HSD3B7	up_VSAP_EC
GO:0043370	0.474	0.875	1	10	regulation of CD4-positive, alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:1901978	0.474	0.88	1	7	positive regulation of cell cycle checkpoint	BP	1	PROX1	up_VCAV_EC
GO:0032770	0.474	0.878	1	8	positive regulation of monooxygenase activity	BP	1	GCH1	up_VCAV_EC
GO:0007010	0.474	0.875	1	441	cytoskeleton organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0032496	0.474	0.867	1	77	response to lipopolysaccharide	BP	1	MTDH	up_VPOR_EC
GO:0046903	0.474	0.871	1	255	secretion	BP	1	TRPC4	up_VPOR_VSMC
GO:0019827	0.474170939	0.78876	2	59	stem cell population maintenance	BP	1	SOX9,TRIM8	up_ACOR_EC
GO:0031060	0.474710019	0.86884	1	23	regulation of histone methylation	BP	1	PYGO2	up_ACOR_EC

GO:0045595	0.47483272	0.63918	13	469	regulation of cell differentiation	BP	1	BRSK1,SOX9,CCDC3,DIXDC1,RGMA,SMAD6,PAK3,TBX5,LRP4,CLSTN1,RBM38,NRP1,EFEMP1	up_ACOR_EC
GO:0120036	0.475	0.62	19	373	plasma membrane bounded cell projection organization	BP	1	NDN,PRNP,SDC4,TRPV2,NUMBL,RHOD,TTC8,SEMA3C,THY1,TLX2,GLI3,NCDN,IFT57,UST,PRKCSH,EVI5L,RAC2,RGMA,BRSK1	down_VCAV_EC
GO:0043065	0.475	0.629	16	188	positive regulation of apoptotic process	BP	1	HMGB1,RNPS1,MNDA,PRELID1,CAV1,CASP2,MAP3K20,TRIM35,BID,PDCD2,EIF5A,B4GALT1,CYCS,MELK,AIFM1,PIK3CD	down_ACOR_VSMC
GO:0071396	0.475	0.645	12	134	cellular response to lipid	BP	1	CXCL8,TNFAIP3,TNIP1,PDE4D,MEF2C,TFPI,IRF8,YES1,ABCA1,SMARCA4,UFSP2,KDM3A	up_VCAV_EC
GO:0031331	0.475	0.688	6	110	positive regulation of cellular catabolic process	BP	1	LRP1,DCN,AKT2,ZFP36L1,CLEC16A,PACSIN3	down_VCAV_EC
GO:0002218	0.475	0.705	5	53	activation of innate immune response	BP	1	HMGB1,IRAK1,CAV1,CACTIN,RBM14	down_ACOR_VSMC
GO:0015672	0.475	0.703	5	89	monovalent inorganic cation transport	BP	1	PRNP,FXYD1,ATP5MC1,ATP6V0C,PARK7	down_VCAV_EC
GO:0021543	0.475	0.705	5	49	pallium development	BP	1	RELN,PROX1,ENSCAFG00000010224,HIF1A,CDON	up_VCAV_EC
GO:0031325	0.475	0.729	4	914	positive regulation of cellular metabolic process	BP	1	NR1H4,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0016999	0.475	0.752	3	30	antibiotic metabolic process	BP	1	ACLY,SUCLG1,PDHA1	down_ACOR_VSMC
GO:0021675	0.475	0.753	3	29	nerve development	BP	1	HOXA3,NAV2,SIX4	down_ACOR_VSMC
GO:0010833	0.475	0.752	3	30	telomere maintenance via telomere lengthening	BP	1	HMBOX1,SMG7,DCP2	up_VCAV_EC
GO:0042303	0.475	0.752	3	30	molting cycle	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:0042633	0.475	0.752	3	30	hair cycle	BP	1	FERMT1,SOX18,LDB2	up_VCAV_EC
GO:0031324	0.475	0.755	3	735	negative regulation of cellular metabolic process	BP	1	NR1H4,PTGER2,FLRT3	up_VPUL_EC
GO:0015918	0.475	0.753	3	27	sterol transport	BP	1	LIPC,LCAT,SOAT1	up_VSAP_EC
GO:0030301	0.475	0.753	3	27	cholesterol transport	BP	1	LIPC,LCAT,SOAT1	up_VSAP_EC
GO:0030032	0.475	0.795	2	19	lamellipodium assembly	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:0044088	0.475	0.797	2	17	regulation of vacuole organization	BP	1	FEZ1,FEZ2	up_ACOR_VSMC
GO:0006950	0.475	0.806	2	1102	response to stress	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:1902680	0.475	0.792	2	415	positive regulation of RNA biosynthetic process	BP	1	NPNT,HOXA1	up_APUL_EC
GO:1903508	0.475	0.792	2	415	positive regulation of nucleic acid-templated	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0006766	0.475	0.797	2	16	vitamin metabolic process	BP	1	CLYBL,PNPO	up_VSAP_EC
GO:0007338	0.475	0.797	2	16	single fertilization	BP	1	HOXA11,HOXA9	up_VSAP_EC
GO:0009066	0.475	0.797	2	16	aspartate family amino acid metabolic process	BP	1	GOT1,ASS1	up_VSAP_EC
GO:0032717	0.475	0.88	1	7	negative regulation of interleukin-8 production	BP	1	CACTIN	down_ACOR_VSMC
GO:0032814	0.475	0.88	1	7	regulation of natural killer cell activation	BP	1	TOX	down_ACOR_VSMC
GO:0050789	0.475	1	1	3295	regulation of biological process	BP	1	GATA5	down_AFEM_VSMC
GO:0006778	0.475	0.873	1	12	porphyrin-containing compound metabolic	BP	1	UROS	down_VCAV_EC
GO:0042168	0.475	0.873	1	12	heme metabolic process	BP	1	UROS	down_VCAV_EC
GO:0071470	0.475	0.872	1	13	cellular response to osmotic stress	BP	1	ZFP36L1	down_VCAV_EC
GO:0070525	0.475	0.879	1	7	tRNA threonylcarbamoyladenosine metabolic process	BP	1	OSGEPL1	up_ACOR_VSMC
GO:0042249	0.475	0.882	1	6	establishment of planar polarity of embryonic	BP	1	SEC24B	up_ACOR_VSMC
GO:0007044	0.475	0.868	1	27	cell-substrate junction assembly	BP	1	GREM1	up_AFEM_EC
GO:0007605	0.475	0.868	1	27	sensory perception of sound	BP	1	THRB	up_AFEM_EC
GO:0040014	0.475	0.868	1	27	regulation of multicellular organism growth	BP	1	GPAM	up_AFEM_EC
GO:0007017	0.475	0.87	1	273	microtubule-based process	BP	1	TAOK1	up_AORT_EC
GO:0051239	0.475	0.886	1	859	regulation of multicellular organismal process	BP	1	TBX5	up_APUL_VSMC

GO:0006482	0.475	0.886	1	5	protein demethylation	BP	1	KDM3A	up_VCAV_EC
GO:0008214	0.475	0.886	1	5	protein dealkylation	BP	1	KDM3A	up_VCAV_EC
GO:0016577	0.475	0.886	1	5	histone demethylation	BP	1	KDM3A	up_VCAV_EC
GO:0070076	0.475	0.886	1	5	histone lysine demethylation	BP	1	KDM3A	up_VCAV_EC
GO:1902916	0.475	0.877	1	8	positive regulation of protein polyubiquitination	BP	1	UBE2D1	up_VCAV_EC
GO:2000404	0.475	0.88	1	7	regulation of T cell migration	BP	1	APOD	up_VCAV_EC
GO:0009967	0.475	0.875	1	435	positive regulation of signal transduction	BP	1	GATA5	up_VCAV_VSMC
GO:0043066	0.476	0.614	22	253	negative regulation of apoptotic process	BP	1	SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,FAM129B,AURKB,GREM1,PLK3,ARG2,DHCR24,NOC2L,NUP62,HMGB2,ENSCAFG00000005299,CORO1A,TXNDC12,CTH,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0090066	0.476	0.628	16	162	regulation of anatomical structure size	BP	1	PRR16,SLIT2,SLC6A4,ABL1,CHRM1,CDC42EP5,PLXNA4,CDC42EP2,F2RL1,TBXA2R,AGTR1,DPYSL2,E2F4,TTL,NCK1,BAG4	up_VSAP_EC
GO:0030900	0.476	0.655	10	101	forebrain development	BP	1	EMX2,CDON,SLIT2,PLXNA4,RTN4RL1,GDPD5,MCPH1,KDM2B,NFIB,HTRA2	up_VSAP_EC
GO:0044242	0.476	0.691	6	57	cellular lipid catabolic process	BP	1	PLCG2,LEP,ACAD11,SMPD1,NEU3,ENSCAFG00000029553	up_ACOR_VSMC
GO:0006470	0.476	0.704	5	54	protein dephosphorylation	BP	1	SLC29A1,PPM1G,PPP1R15B,PPP2R5D,YWHAB	down_ACOR_VSMC
GO:0043393	0.476	0.702	5	77	regulation of protein binding	BP	1	TRIB3,PLCL1,APOE,GSK3B,DISC1	down_VSAP_EC
GO:0031399	0.476	0.703	5	559	regulation of protein modification process	BP	1	ARHGEF2,ASPN,ACVR2A,PUM3,ENSCAFG00000032731	up_VPOR_EC
GO:0009967	0.476	0.722	4	435	positive regulation of signal transduction	BP	1	ENSCAFG00000002015,ACVR2A,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:0031057	0.476	0.795	2	18	negative regulation of histone modification	BP	1	BRCA1,NOC2L	down_ACOR_VSMC
GO:2000059	0.476	0.794	2	19	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC
GO:0031050	0.476	0.796	2	17	dsRNA processing	BP	1	PPP3CA,TUT7	up_VCAV_EC
GO:0070918	0.476	0.796	2	17	production of small RNA involved in gene silencing	BP	1	PPP3CA,TUT7	up_VCAV_EC
GO:0031664	0.476	0.879	1	7	regulation of lipopolysaccharide-mediated signaling	BP	1	CACTIN	down_ACOR_VSMC
GO:0060317	0.476	0.873	1	11	cardiac epithelial to mesenchymal transition	BP	1	TGFBR1	down_VSAP_EC
GO:0010559	0.476	0.882	1	6	regulation of glycoprotein biosynthetic process	BP	1	ITM2C	up_ACOR_VSMC
GO:0033599	0.476	0.881	1	6	regulation of mammary gland epithelial cell proliferation	BP	1	RREB1	up_ACOR_VSMC
GO:0051043	0.476	0.879	1	7	regulation of membrane protein ectodomain proteolysis	BP	1	PTPN3	up_ACOR_VSMC
GO:1903018	0.476	0.882	1	6	regulation of glycoprotein metabolic process	BP	1	ITM2C	up_ACOR_VSMC
GO:0022037	0.476	0.868	1	27	metencephalon development	BP	1	DLL1	up_AFEM_EC
GO:0000902	0.476	0.869	1	266	cell morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0001568	0.476	0.869	1	252	blood vessel development	BP	1	EYA1	up_VFEM_VSMC
GO:0031098	0.477	0.648	11	109	stress-activated protein kinase signaling cascade	BP	1	MAP3K14,ARHGEF5,MAP3K5,CDC42EP5,F2RL1,ZFP36L1,MYC,SASH1,MYD88,QARS,MAP2K2	up_VSAP_EC
GO:1901293	0.477	0.66	9	106	nucleoside phosphate biosynthetic process	BP	1	NPR1,PANK3,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,GUCY1B1,NOS2,HIF1A	up_VCAV_EC
GO:0032102	0.477	0.678	7	67	negative regulation of response to external stimulus	BP	1	C5AR2,SLIT2,KLKB1,RTN4RL1,NLRX1,TKFC,MAPKBP1	up_VSAP_EC
GO:0060255	0.477	0.723	5	1782	regulation of macromolecule metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0051865	0.477	0.75	3	31	protein autoubiquitination	BP	1	UBE2T,UHRF1,BRCA1	down_ACOR_VSMC
GO:0034404	0.477	0.747	3	50	nucleobase-containing small molecule metabolic process	BP	1	ENTPD3,ADK,ACAT1	down_VCAV_EC
GO:0007260	0.477	0.793	2	19	tyrosine phosphorylation of STAT protein	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0051279	0.477	0.794	2	19	regulation of release of sequestered calcium ion into cytosol	BP	1	GSTO1,CORO1A	down_ACOR_VSMC

GO:0019080	0.477	0.791	2	26	viral gene expression	BP	1	SMARCA4,REST	down_VSAP_EC
GO:0051098	0.477	0.866	1	129	regulation of binding	BP	1	HOXA3	down_ACOR_EC
GO:0010862	0.477	0.871	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	BMPR1A	down_VCAV_EC
GO:1902110	0.477	0.872	1	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	SLC35F6	down_VCAV_EC
GO:1902686	0.477	0.872	1	12	mitochondrial outer membrane permeabilization involved	BP	1	SLC35F6	down_VCAV_EC
GO:0008045	0.477	0.875	1	9	motor neuron axon guidance	BP	1	NRP1	down_VSAP_EC
GO:0071158	0.477	0.873	1	10	positive regulation of cell cycle arrest	BP	1	CDKN1A	down_VSAP_EC
GO:0090181	0.477	0.874	1	10	regulation of cholesterol metabolic process	BP	1	APOE	down_VSAP_EC
GO:0015918	0.477	0.867	1	27	sterol transport	BP	1	LEP	up_AFEM_EC
GO:0030301	0.477	0.867	1	27	cholesterol transport	BP	1	LEP	up_AFEM_EC
GO:0039694	0.477	0.875	1	9	viral RNA genome replication	BP	1	CXCL8	up_VCAV_EC
GO:0006954	0.477	0.866	1	147	inflammatory response	BP	1	CYP26B1	up_VFEM_EC
GO:0035313	0.477	0.878	1	7	wound healing, spreading of epidermal cells	BP	1	ACVRL1	up_VSAP_EC
GO:0045669	0.477986764	0.86659	1	24	positive regulation of osteoblast differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0009893	0.478	0.571	85	995	positive regulation of metabolic process	BP	1	ACSL3,HMGB1,SREBF1,IRAK1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,NEDD4,U2AF2,SLC29A1,MTDH,CTDNEP1,PRELID1,RFC2,INSIG1,CAV1,CDK1,RFC5,RFC3,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,AURKB,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,SMARCC1,PLK3,PCNA,DHX33,SF3B4,CKS2,PDCD2,RNF152,BRCA1,FASTKD3,EIF5A,E2F8,TFRC,PPARD,RAP2C,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,EZR,CLSPN,ELOVL6,RBM14,RAD23A,CDC20,PSMC1,AIFM1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,JMJD6,NUS1,CCT4,ENSCAFG00000017103,AMER1,DCUN1D5,PIK3CD	down_ACOR_VSMC
GO:0031401	0.478	0.594	35	358	positive regulation of protein modification process	BP	1	FZD1,CDON,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,IL6R,FGF7,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,PLPP3,CAMKK2,TNKS1BP1,F2RL1,DDR2,TRAF7,SASH1,FBXO4,MYD88,LRP4,PHF1,CDK9,RAF1,ACVRL1,FLOT1,MAVS,MAP2K2,TGFBR2,BAG4	up_VSAP_EC
GO:0006812	0.478	0.612	22	222	cation transport	BP	1	AMIGO1,SLC8B1,TPCN2,NIPAL3,SLC6A4,ABL1,KCNE3,OSR1,CCS,KLHL24,RAB11B,SLC25A28,CRACR2B,SCARA5,NIPAL1,STEAP3,KCNB1,FTL,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0060322	0.478	0.65	10	193	head development	BP	1	SMAD9,BMPR1A,NUMBL,NAGLU,ENSCAFG00000018277,CRISPLD2,PEX5,GLI3,CDH2,FOXO3	down_VCAV_EC
GO:0051092	0.478	0.703	5	47	positive regulation of NF-kappaB transcription	BP	1	TLR3,AR,APP,NOD2,IL18R1	up_ACOR_VSMC
GO:0001657	0.478	0.722	4	42	ureteric bud development	BP	1	GREM1,ARG2,HOXB7,SIX4	down_ACOR_VSMC
GO:0072163	0.478	0.722	4	42	mesonephric epithelium development	BP	1	GREM1,ARG2,HOXB7,SIX4	down_ACOR_VSMC
GO:0072164	0.478	0.722	4	42	mesonephric tubule development	BP	1	GREM1,ARG2,HOXB7,SIX4	down_ACOR_VSMC
GO:0021537	0.478	0.718	4	73	telencephalon development	BP	1	NUMBL,PEX5,GLI3,CDH2	down_VCAV_EC
GO:0034502	0.478	0.75	3	30	protein localization to chromosome	BP	1	RAD21,ZW10,ATRX	up_VCAV_EC
GO:0042472	0.478	0.751	3	27	inner ear morphogenesis	BP	1	INSIG2,LRIG3,ZEB1	up_VSAP_EC
GO:1904064	0.478	0.751	3	27	positive regulation of cation transmembrane	BP	1	AMIGO1,ABL1,FXYD1	up_VSAP_EC
GO:0032728	0.478	0.795	2	16	positive regulation of interferon-beta	BP	1	TLR3,PTPN22	up_ACOR_VSMC

GO:0019222	0.478	0.923	1	1934	regulation of metabolic process	BP	1	CST3	down_AORT_EC
GO:0072077	0.478	0.87	1	13	renal vesicle morphogenesis	BP	1	GREM1	down_VCAV_EC
GO:0072273	0.478	0.87	1	13	metanephric nephron morphogenesis	BP	1	GREM1	down_VCAV_EC
GO:0000186	0.478	0.873	1	10	activation of MAPKK activity	BP	1	TNIK	down_VSAP_EC
GO:0007212	0.478	0.872	1	11	dopamine receptor signaling pathway	BP	1	GNAQ	down_VSAP_EC
GO:0038179	0.478	0.873	1	10	neurotrophin signaling pathway	BP	1	PTPN11	down_VSAP_EC
GO:0051654	0.478	0.88	1	6	establishment of mitochondrion	BP	1	RHOT1	up_ACOR_VSMC
GO:0006446	0.478	0.866	1	27	regulation of translational initiation	BP	1	CTIF	up_AFEM_EC
GO:1904064	0.478	0.866	1	27	positive regulation of cation transmembrane	BP	1	FXYD1	up_AFEM_EC
GO:0033157	0.478	0.865	1	82	regulation of intracellular protein transport	BP	1	GCC2	up_VPOR_EC
GO:0051345	0.478	0.866	1	151	positive regulation of hydrolase activity	BP	1	TIAM1	up_VFEM_EC
GO:0051248	0.478	0.87	1	316	negative regulation of protein metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0055008	0.478261051	0.86641	1	24	cardiac muscle tissue morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0061053	0.478391501	0.86633	1	24	somite development	BP	1	FOXC2	up_ACOR_EC
GO:0048598	0.478538238	0.68379	6	207	embryonic morphogenesis	BP	1	SOX9,FZD5,FOXC2,TBX5,LRP4,EFEMP1	up_ACOR_EC
GO:1901362	0.478806773	0.59638	35	1293	organic cyclic compound biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0050794	0.479	0.66	14	3075	regulation of cellular process	BP	1	HOXA11,HOXA10,HOXA9,PITX1,EMX2,NETO1,SALL1,IRX5,MAB21L1,PRR16,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0006464	0.479	0.657	10	1162	cellular protein modification process	BP	1	OSTC,OGA,ARHGEF2,ASPN,ACVR2A,KLHL28,PUM3,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0036211	0.479	0.657	10	1162	protein modification process	BP	1	OSTC,OGA,ARHGEF2,ASPN,ACVR2A,KLHL28,PUM3,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0019439	0.479	0.664	8	150	aromatic compound catabolic process	BP	1	MAOA,SAMD4B,EPHX1,ENTPD3,ZFP36L1,PYM1,FBH1,ACAT1	down_VCAV_EC
GO:0061013	0.479	0.787	2	32	regulation of mRNA catabolic process	BP	1	SAMD4B,ZFP36L1	down_VCAV_EC
GO:0055092	0.479	0.789	2	28	sterol homeostasis	BP	1	NR1H4,APOE	down_VSAP_EC
GO:2000116	0.479	0.784	2	67	regulation of cysteine-type endopeptidase	BP	1	CRYAB,F3	up_AFEM_EC
GO:0048583	0.479	0.804	2	1095	regulation of response to stimulus	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0044255	0.479	0.868	1	293	cellular lipid metabolic process	BP	1	ETFA	down_AFEM_EC
GO:0007215	0.479	0.87	1	13	glutamate receptor signaling pathway	BP	1	PRNP	down_VCAV_EC
GO:0008535	0.479	0.871	1	12	respiratory chain complex IV assembly	BP	1	COA1	down_VCAV_EC
GO:0051248	0.479	0.869	1	316	negative regulation of protein metabolic process	BP	1	CST3	down_VPOR_EC
GO:0014037	0.479	0.872	1	10	Schwann cell differentiation	BP	1	ILK	down_VSAP_EC
GO:0071803	0.479	0.88	1	6	positive regulation of podosome assembly	BP	1	ASAP1	up_ACOR_VSMC
GO:0030203	0.479	0.866	1	27	glycosaminoglycan metabolic process	BP	1	XYLT1	up_AFEM_EC
GO:0046364	0.479	0.865	1	27	monosaccharide biosynthetic process	BP	1	LEP	up_AFEM_EC
GO:0061097	0.479	0.865	1	27	regulation of protein tyrosine kinase activity	BP	1	ADAM17	up_AFEM_EC
GO:0034214	0.479	0.877	1	7	protein hexamerization	BP	1	LRRC8C	up_VCAV_EC
GO:0036445	0.479	0.88	1	6	neuronal stem cell division	BP	1	ARHGEF2	up_VCAV_EC
GO:0055057	0.479	0.88	1	6	neuroblast division	BP	1	ARHGEF2	up_VCAV_EC
GO:0008154	0.479	0.864	1	81	actin polymerization or depolymerization	BP	1	TWF1	up_VPOR_EC

GO:0010959	0.479	0.864	1	79	regulation of metal ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0032886	0.479	0.864	1	81	regulation of microtubule-based process	BP	1	ARHGEF2	up_VPOR_EC
GO:0097191	0.479	0.864	1	79	extrinsic apoptotic signaling pathway	BP	1	ARHGEF2	up_VPOR_EC
GO:2001233	0.479	0.865	1	149	regulation of apoptotic signaling pathway	BP	1	EYA1	up_VFEM_EC
GO:0043066	0.479	0.867	1	253	negative regulation of apoptotic process	BP	1	EYA1	up_VFEM_VSMC
GO:0055086	0.479	0.867	1	237	nucleobase-containing small molecule metabolic	BP	1	FBP1	up_VFEM_VSMC
GO:0090087	0.479	0.866	1	185	regulation of peptide transport	BP	1	NR1H4	up_VPUL_EC
GO:0106027	0.479855739	0.86541	1	24	neuron projection organization	BP	1	PAK3	up_ACOR_EC
GO:0001775	0.48	0.61	22	219	cell activation	BP	1	TLR1,PLCG2,LEP,CD83,BMP4,TP53BP1,PDE5A,CD274,LMO4,F2RL1,CDKN1A,PTPN22,PRKCE,APP,PSEN1,TGFBR1,CHD7,DUSP22,NOD2,B2M,IL18R1,PAG1	up_ACOR_VSMC
GO:0051493	0.48	0.617	19	188	regulation of cytoskeleton organization	BP	1	SYNPO2L,FGF13,ARHGAP28,ACTN2,MID1,PRKAA2,SYNPO2,TUBB4A,F2RL1,JMY,NRP1,EVL,PRKCE,SSH3,EDN1,FAM107A,JAM3,INPP5K,WASL	up_ACOR_VSMC
GO:0051259	0.48	0.631	14	140	protein complex oligomerization	BP	1	ACACB,C1QTNF2,CLDN1,HSD17B8,SCARA5,SBF2,CLYBL,KCNB1,PCBD1,KCNC4,HTRA2,FLOT1,HMOX1,JCHAIN	up_VSAP_EC
GO:0010631	0.48	0.64	12	118	epithelial cell migration	BP	1	FERMT1,BMP4,SASH1,FGF18,NRP1,EVL,PRKCE,SYNJ2BP,JUP,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0090132	0.48	0.64	12	118	epithelium migration	BP	1	FERMT1,BMP4,SASH1,FGF18,NRP1,EVL,PRKCE,SYNJ2BP,JUP,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0045321	0.48	0.649	10	191	leukocyte activation	BP	1	GPAM,PRNP,SDC4,THY1,GLI3,ZFP36L1,BPI,LOXL3,RAC2,ZBTB16	down_VCAV_EC
GO:0006644	0.48	0.65	10	118	phospholipid metabolic process	BP	1	TEK,ADGRF5,PDGFB,SERINC5,SPTLC2,SAMD8,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0019216	0.48	0.657	9	101	regulation of lipid metabolic process	BP	1	ACSL3,SREBF1,SF1,CTDNEP1,INSIG1,CAV1,ABHD5,CDK4,BRCA1	down_ACOR_VSMC
GO:0052547	0.48	0.665	8	82	regulation of peptidase activity	BP	1	MBP,RECK,CST3,DAPK1,SH3RF1,SPINK2,PERP,PARK7	up_ACOR_VSMC
GO:0045785	0.48	0.672	7	107	positive regulation of cell adhesion	BP	1	VEGFA,SOCS5,FAM49B,ENSCAFG00000002015,TFRC,GSK3B,NRP1	down_VSAP_EC
GO:1901136	0.48	0.721	4	38	carbohydrate derivative catabolic process	BP	1	PDE5A,ENPP4,STT3B,NEU3	up_ACOR_VSMC
GO:0009892	0.48	0.723	4	835	negative regulation of metabolic process	BP	1	HOXC10,MAP2K6,HOXA7,SIX1	up_VFEM_EC
GO:0030838	0.48	0.721	4	37	positive regulation of actin filament	BP	1	CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:0043523	0.48	0.744	3	52	regulation of neuron apoptotic process	BP	1	PRNP,PARK7,FOXO3	down_VCAV_EC
GO:0031098	0.48	0.742	3	109	stress-activated protein kinase signaling cascade	BP	1	LEP,CYLD,CDC42EP5	up_AFEM_EC
GO:0022037	0.48	0.749	3	27	metencephalon development	BP	1	SEZ6L,ABL1,DLL1	up_VSAP_EC
GO:0043271	0.48	0.788	2	28	negative regulation of ion transport	BP	1	REM1,CALM1	down_VSAP_EC
GO:0050905	0.48	0.788	2	26	neuromuscular process	BP	1	AARS,UBA5	down_VSAP_EC
GO:0006623	0.48	0.794	2	16	protein targeting to vacuole	BP	1	SCARB2,LAMP2	up_ACOR_VSMC
GO:0042246	0.48	0.792	2	17	tissue regeneration	BP	1	LGR6,GJA1	up_ACOR_VSMC
GO:0006875	0.48	0.864	1	129	cellular metal ion homeostasis	BP	1	LYN	down_ACOR_EC
GO:0009896	0.48	0.864	1	127	positive regulation of catabolic process	BP	1	NEDD4	down_ACOR_EC
GO:0060074	0.48	0.877	1	7	synapse maturation	BP	1	CDC20	down_ACOR_VSMC
GO:0071801	0.48	0.877	1	7	regulation of podosome assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0086091	0.48	0.874	1	8	regulation of heart rate by cardiac conduction	BP	1	CAV1	down_ACOR_VSMC
GO:0048048	0.48	0.869	1	13	embryonic eye morphogenesis	BP	1	FBN1	down_VCAV_EC
GO:0001676	0.48	0.872	1	10	long-chain fatty acid metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0001702	0.48	0.871	1	10	gastrulation with mouth forming second	BP	1	CTNNB1	down_VSAP_EC
GO:0060561	0.48	0.871	1	11	apoptotic process involved in	BP	1	CRYAB	down_VSAP_EC

GO:0035336	0.48	0.876	1	7	long-chain fatty-acyl-CoA metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:1901658	0.48	0.876	1	7	glycosyl compound catabolic process	BP	1	ENPP4	up_ACOR_VSMC
GO:0034763	0.48	0.865	1	27	negative regulation of transmembrane transport	BP	1	LEP	up_AFEM_EC
GO:0044706	0.48	0.865	1	27	multi-multicellular organism process	BP	1	RECK	up_AFEM_EC
GO:0062013	0.48	0.865	1	27	positive regulation of small molecule metabolic	BP	1	PPARGC1A	up_AFEM_EC
GO:2000117	0.48	0.865	1	27	negative regulation of cysteine-type	BP	1	CRYAB	up_AFEM_EC
GO:1903530	0.48	0.865	1	165	regulation of secretion by cell	BP	1	NR1H4	up_APUL_EC
GO:0046131	0.48	0.874	1	8	pyrimidine ribonucleoside metabolic process	BP	1	CDA	up_VCAV_EC
GO:0033043	0.48	0.871	1	446	regulation of organelle organization	BP	1	LIMK1	up_VCAV_VSMC
GO:0050767	0.48	0.865	1	184	regulation of neurogenesis	BP	1	ARHGEF2	up_VPUL_EC
GO:0006720	0.480816922	0.86461	1	25	isoprenoid metabolic process	BP	1	RARRES2	up_ACOR_EC
GO:0042981	0.481	0.587	40	471	regulation of apoptotic process	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,DHCR24,NOC2L,EIF5A,B4GALT1,CYCS,NUP62,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:1901362	0.481	0.65	11	1293	organic cyclic compound biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0051604	0.481	0.65	10	102	protein maturation	BP	1	PRDX4,LIPT2,PSEN2,ERO1B,SCG5,PSEN1,PCSK6,PERP,NCSTN,LMF1	up_ACOR_VSMC
GO:0042113	0.481	0.685	6	64	B cell activation	BP	1	MNDA,TXLNA,MMP14,HMGB3,TFRC,CTPS1	down_ACOR_VSMC
GO:0043409	0.481	0.699	5	54	negative regulation of MAPK cascade	BP	1	HMGCR,CAV1,NF2,NUP62,EZR	down_ACOR_VSMC
GO:0021987	0.481	0.721	4	37	cerebral cortex development	BP	1	RELN,ENSCAFG00000010224,HIF1A,CDON	up_VCAV_EC
GO:0048523	0.481	0.732	4	1399	negative regulation of cellular process	BP	1	EYA1,HOXA9,FBP1,SHOX2	up_VFEM_VSMC
GO:0006417	0.481	0.741	3	109	regulation of translation	BP	1	PRR16,CTIF,SAMD4B	up_AFEM_EC
GO:1903901	0.481	0.791	2	19	negative regulation of viral life cycle	BP	1	ILF3,TRIM35	down_ACOR_VSMC
GO:0043392	0.481	0.793	2	16	negative regulation of DNA binding	BP	1	CLSTN1,PSEN1	up_ACOR_VSMC
GO:0007435	0.481	0.791	2	18	salivary gland morphogenesis	BP	1	NTN4,BTBD7	up_VCAV_EC
GO:0098739	0.481	0.79	2	20	import across plasma membrane	BP	1	SLC39A8,KCNJ3	up_VCAV_EC
GO:0032968	0.481	0.876	1	7	positive regulation of transcription elongation from RNA polymerase II	BP	1	SUPT16H	down_ACOR_VSMC
GO:0006120	0.481	0.869	1	12	mitochondrial electron transport, NADH to	BP	1	PARK7	down_VCAV_EC
GO:0060325	0.481	0.868	1	13	face morphogenesis	BP	1	CRISPLD2	down_VCAV_EC
GO:1901890	0.481	0.869	1	13	positive regulation of cell junction assembly	BP	1	THY1	down_VCAV_EC
GO:0021696	0.481	0.871	1	10	cerebellar cortex morphogenesis	BP	1	PTPN11	down_VSAP_EC
GO:0043279	0.481	0.871	1	10	response to alkaloid	BP	1	HOMER1	down_VSAP_EC
GO:0006978	0.481	0.876	1	7	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	BP	1	CDKN1A	up_ACOR_VSMC
GO:0019226	0.481	0.879	1	6	transmission of nerve impulse	BP	1	JAM3	up_ACOR_VSMC
GO:0021604	0.481	0.879	1	6	cranial nerve structural organization	BP	1	NRP1	up_ACOR_VSMC
GO:0021612	0.481	0.879	1	6	facial nerve structural organization	BP	1	NRP1	up_ACOR_VSMC
GO:0032682	0.481	0.876	1	7	negative regulation of chemokine production	BP	1	F2RL1	up_ACOR_VSMC

GO:0042772	0.481	0.876	1	7	DNA damage response, signal transduction resulting in transcription	BP	1	CDKN1A	up_ACOR_VSMC
GO:0051180	0.481	0.876	1	7	vitamin transport	BP	1	TCN2	up_ACOR_VSMC
GO:0072574	0.481	0.879	1	6	hepatocyte proliferation	BP	1	LIMS2	up_ACOR_VSMC
GO:0072575	0.481	0.879	1	6	epithelial cell proliferation involved in liver	BP	1	LIMS2	up_ACOR_VSMC
GO:0072576	0.481	0.879	1	6	liver morphogenesis	BP	1	LIMS2	up_ACOR_VSMC
GO:0006081	0.481	0.865	1	27	cellular aldehyde metabolic process	BP	1	ALDH3B1	up_AFEM_EC
GO:0046907	0.481	0.874	1	536	intracellular transport	BP	1	WNT7A	up_AORT_VSMC
GO:0034315	0.481	0.874	1	8	regulation of Arp2/3 complex-mediated actin	BP	1	NCKAP1	up_VCAV_EC
GO:0060716	0.481	0.872	1	9	labyrinthine layer blood vessel development	BP	1	VASH1	up_VCAV_EC
GO:0086001	0.481	0.873	1	9	cardiac muscle cell action potential	BP	1	KCNJ2	up_VCAV_EC
GO:0098754	0.481	0.872	1	9	detoxification	BP	1	GCH1	up_VCAV_EC
GO:0032787	0.481	0.864	1	144	monocarboxylic acid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0120039	0.481	0.864	1	158	plasma membrane bounded cell projection	BP	1	SHOX2	up_VSAP_VSMC
GO:0090150	0.48110404	0.78299	2	64	establishment of protein localization to membrane	BP	1	KCNB1,CHMP4B	up_ACOR_EC
GO:0032608	0.481684875	0.86425	1	24	interferon-beta production	BP	1	MAVS	up_ACOR_EC
GO:0032481	0.48181952	0.86416	1	24	positive regulation of type I interferon production	BP	1	MAVS	up_ACOR_EC
GO:0050789	0.482	0.675	12	3295	regulation of biological process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,RGS1,STK32B,WIF1,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0090407	0.482	0.642	11	177	organophosphate biosynthetic process	BP	1	NR1H4,PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ALDOC,PAPSS1,AK5,SH3GLB1,CMPK1	down_VSAP_EC
GO:0051234	0.482	0.649	11	1283	establishment of localization	BP	1	HOOK3,XPOT,HOXA3,ENSCAFG00000002015,SLC7A11,ENSCAFG00000005494,GOLT1B,GCC2,SLC25A16,SRP54,TMEM87B	up_VPOR_EC
GO:0051248	0.482	0.661	8	316	negative regulation of protein metabolic process	BP	1	GAS1,CRYAB,GREM1,CLEC16A,CYLD,LRRC15,RECK,SAMD4B	up_AFEM_EC
GO:0019222	0.482	0.681	8	1934	regulation of metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,LZTS1,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0098742	0.482	0.7	5	44	cell-cell adhesion via plasma-membrane	BP	1	GATA5,MBP,CDH18,CELSR2,ATP2C1	up_ACOR_VSMC
GO:0090316	0.482	0.7	5	48	positive regulation of intracellular protein	BP	1	CDH1,ICE1,PIK3R1,KCNB1,MAVS	up_VSAP_EC
GO:0010038	0.482	0.716	4	62	response to metal ion	BP	1	HIF1A,BNIP3,CALM1,HOMER1	down_VSAP_EC
GO:1903039	0.482	0.743	3	43	positive regulation of leukocyte cell-cell	BP	1	SOCS5,FAM49B,TFRC	down_VSAP_EC
GO:0042110	0.482	0.74	3	109	T cell activation	BP	1	LEP,GPAM,CYLD	up_AFEM_EC
GO:0030182	0.482	0.742	3	327	neuron differentiation	BP	1	ARHGEF2,SEMA3A,RNF6	up_VPOR_EC
GO:0050793	0.482	0.793	2	731	regulation of developmental process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0007548	0.482	0.782	2	68	sex differentiation	BP	1	HOXA9,IRX5	up_AFEM_EC
GO:0048566	0.482	0.868	1	13	embryonic digestive tract development	BP	1	GLI3	down_VCAV_EC
GO:2000179	0.482	0.867	1	14	positive regulation of neural precursor cell	BP	1	GLI3	down_VCAV_EC
GO:0060677	0.482	0.878	1	6	ureteric bud elongation	BP	1	BMP4	up_ACOR_VSMC
GO:2001244	0.482	0.864	1	27	positive regulation of intrinsic apoptotic	BP	1	PLAGL2	up_AFEM_EC
GO:0006469	0.482	0.862	1	78	negative regulation of protein kinase activity	BP	1	ASPN	up_VPOR_EC
GO:0016042	0.482	0.862	1	80	lipid catabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0018212	0.482	0.862	1	81	peptidyl-tyrosine modification	BP	1	ARHGEF2	up_VPOR_EC
GO:0120031	0.482	0.863	1	154	plasma membrane bounded cell projection	BP	1	CDC42EP5	up_VFEM_EC
GO:0070201	0.482	0.864	1	187	regulation of establishment of protein	BP	1	NR1H4	up_VPUL_EC
GO:0006952	0.482	0.867	1	319	defense response	BP	1	IL22RA1	up_VPUL_VSMC

GO:0072657	0.482	0.863	1	144	protein localization to membrane	BP	1	CAV1	up_VSAP_VSMC
GO:0019882	0.482076485	0.86381	1	25	antigen processing and presentation	BP	1	TAPBP	up_ACOR_EC
GO:0060491	0.48208225	0.78232	2	62	regulation of cell projection assembly	BP	1	NRP1,PRKCD	up_ACOR_EC
GO:0120032	0.48208225	0.78232	2	62	regulation of plasma membrane bounded cell	BP	1	NRP1,PRKCD	up_ACOR_EC
GO:0045844	0.482721521	0.86359	1	24	positive regulation of striated muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0048636	0.482721521	0.86359	1	24	positive regulation of muscle organ	BP	1	TBX5	up_ACOR_EC
GO:0031324	0.483	0.616	18	735	negative regulation of cellular metabolic process	BP	1	LEP,CRY2,GAS1,HOXA7,CRYAB,LMCD1,THRB,MYO1D,GREM1,TENT5C,CLEC16A,CYLD,LRRC15,RECK,NR3C1,AXIN2,ACACB,SAMD4B	up_AFEM_EC
GO:0010628	0.483	0.632	13	527	positive regulation of gene expression	BP	1	HOXA9,LBH,PRR16,DLL1,MLLT11,THRB,GREM1,NFE2L1,TENT5C,MYBL1,AXIN2,PPARGC1A,TNC	up_AFEM_EC
GO:0051253	0.483	0.653	9	359	negative regulation of RNA metabolic process	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,TENT5C,NR3C1,AXIN2	up_AFEM_EC
GO:0043170	0.483	0.712	7	2980	macromolecule metabolic process	BP	1	IVNS1ABP,DARS,EIF3M,SRSF6,USP33,GABPA,TSEN15	down_AFEM_EC
GO:0072593	0.483	0.672	7	68	reactive oxygen species metabolic process	BP	1	SESN1,F2RL1,CYBA,ZNF205,ASS1,TGFBR2,DDIT4	up_VSAP_EC
GO:1901215	0.483	0.684	6	57	negative regulation of neuron death	BP	1	PPARGC1A,NRP1,UNC5B,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0008064	0.483	0.714	4	72	regulation of actin polymerization or	BP	1	KIRREL1,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0030832	0.483	0.714	4	72	regulation of actin filament length	BP	1	KIRREL1,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0030833	0.483	0.715	4	59	regulation of actin filament polymerization	BP	1	ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0099504	0.483	0.743	3	42	synaptic vesicle cycle	BP	1	CANX,CTNNB1,GSK3B	down_VSAP_EC
GO:0097581	0.483	0.747	3	26	lamellipodium organization	BP	1	WASF3,SSH3,RREB1	up_ACOR_VSMC
GO:0097193	0.483	0.739	3	109	intrinsic apoptotic signaling pathway	BP	1	MLLT11,PLAGL2,CYLD	up_AFEM_EC
GO:0060428	0.483	0.79	2	17	lung epithelium development	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0021602	0.483	0.792	2	16	cranial nerve morphogenesis	BP	1	CITED2,NRP1	up_ACOR_VSMC
GO:0010634	0.483	0.782	2	68	positive regulation of epithelial cell migration	BP	1	ANGPT4,ADAM17	up_AFEM_EC
GO:0071375	0.483	0.781	2	68	cellular response to peptide hormone stimulus	BP	1	CAMK2A,KANK1	up_AFEM_EC
GO:0018200	0.483	0.872	1	8	peptidyl-glutamic acid modification	BP	1	TTLL1	down_ACOR_VSMC
GO:0001974	0.483	0.867	1	13	blood vessel remodeling	BP	1	SEMA3C	down_VCAV_EC
GO:0060119	0.483	0.87	1	10	inner ear receptor cell development	BP	1	SDC4	down_VSAP_EC
GO:0033160	0.483	0.878	1	6	positive regulation of protein import into	BP	1	PSEN1	up_ACOR_VSMC
GO:0060272	0.483	0.875	1	7	embryonic skeletal joint morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0061550	0.483	0.878	1	6	cranial ganglion development	BP	1	NRP1	up_ACOR_VSMC
GO:0031664	0.483	0.875	1	7	regulation of lipopolysaccharide-	BP	1	TNFAIP3	up_VCAV_EC
GO:0009152	0.483	0.862	1	80	purine ribonucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0051782	0.483	0.875	1	7	negative regulation of cell division	BP	1	MYC	up_VSAP_EC
GO:0048858	0.483	0.862	1	159	cell projection morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0008585	0.483003865	0.86341	1	24	female gonad development	BP	1	LHX9	up_ACOR_EC
GO:0046545	0.483003865	0.86341	1	24	development of primary female sexual	BP	1	LHX9	up_ACOR_EC
GO:0015698	0.483157802	0.86331	1	24	inorganic anion transport	BP	1	CLIC3	up_ACOR_EC
GO:0098727	0.483320491	0.78145	2	60	maintenance of cell number	BP	1	SOX9,TRIM8	up_ACOR_EC
GO:0051289	0.483741729	0.86274	1	25	protein homotetramerization	BP	1	ACTN2	up_ACOR_EC
GO:0006605	0.484	0.647	10	99	protein targeting	BP	1	PEX7,PEX2,MFN2,HPS4,FBXO7,KCNB1,LONP2,PEX6,BAG4,NCOA4	up_VSAP_EC

GO:0016331	0.484	0.682	6	66	morphogenesis of embryonic epithelium	BP	1	GATA3,HHEX,BCL10,HIF1A,ALDH1A3,LUZP1	up_VCAV_EC
GO:0006475	0.484	0.697	5	54	internal protein amino acid acetylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:0035556	0.484	0.72	4	845	intracellular signal transduction	BP	1	MAP2K6,TIAM1,CDC42EP5,ADCY3	up_VFEM_EC
GO:0060759	0.484	0.718	4	37	regulation of response to cytokine stimulus	BP	1	SLIT2,F2RL1,CREBRF,MAVS	up_VSAP_EC
GO:2000779	0.484	0.746	3	25	regulation of double-strand break repair	BP	1	TP53BP1,ZNF365,PARP9	up_ACOR_VSMC
GO:0031338	0.484	0.746	3	28	regulation of vesicle fusion	BP	1	TBC1D1,RABGAP1,USP6NL	up_VCAV_EC
GO:0002709	0.484	0.788	2	19	regulation of T cell mediated immunity	BP	1	HMGB1,FAM49B	down_ACOR_VSMC
GO:0046580	0.484	0.789	2	18	negative regulation of Ras protein signal	BP	1	STMN1,NUP62	down_ACOR_VSMC
GO:0070265	0.484	0.788	2	19	necrotic cell death	BP	1	CAV1,ARHGEF2	down_ACOR_VSMC
GO:0000244	0.484	0.874	1	7	spliceosomal tri-snRNP complex assembly	BP	1	USP4	down_ACOR_VSMC
GO:0033617	0.484	0.872	1	8	mitochondrial respiratory chain complex IV	BP	1	FASTKD3	down_ACOR_VSMC
GO:0001961	0.484	0.867	1	13	positive regulation of cytokine-mediated	BP	1	MAVS	down_VCAV_EC
GO:0051353	0.484	0.866	1	13	positive regulation of oxidoreductase activity	BP	1	PARK7	down_VCAV_EC
GO:0099024	0.484	0.867	1	13	plasma membrane invagination	BP	1	SNX18	down_VCAV_EC
GO:0045892	0.484	0.866	1	328	negative regulation of transcription, DNA-	BP	1	HDAC7	down_VPOR_EC
GO:0001522	0.484	0.868	1	11	pseudouridine synthesis	BP	1	MRPL1	down_VSAP_EC
GO:0060765	0.484	0.869	1	10	regulation of androgen receptor signaling	BP	1	SMARCA4	down_VSAP_EC
GO:0030031	0.484	0.862	1	155	cell projection assembly	BP	1	CDC42EP5	up_VFEM_EC
GO:0001933	0.484	0.862	1	146	negative regulation of protein phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0050871	0.484042421	0.86274	1	24	positive regulation of B cell activation	BP	1	NOD2	up_ACOR_EC
GO:0002532	0.484383967	0.86233	1	25	production of molecular mediator involved in inflammatory response	BP	1	NOD2	up_ACOR_EC
GO:0002376	0.484424801	0.61714	17	622	immune system process	BP	1	C7,NR1H4,SOX9,FZD5,NOD2,IL33,SMAD6,MMP28,TRIM8,PTGER4,MAVS,IFIT2,CLSTN1,TAPBP,RARRES2,AGBL5,PRKCD	up_ACOR_EC
GO:0007163	0.484428353	0.78056	2	60	establishment or maintenance of cell	BP	1	BRSK1,AQP1	up_ACOR_EC
GO:2001242	0.484456391	0.78042	2	62	regulation of intrinsic apoptotic signaling	BP	1	FIGNL1,CLU	up_ACOR_EC
GO:0071345	0.484659803	0.67813	6	210	cellular response to cytokine stimulus	BP	1	NR1H4,CCDC3,MAVS,LRRC15,IFIT2,LRRC4	up_ACOR_EC
GO:0050794	0.485	0.55	260	3075	regulation of cellular process	BP	1	ELK3,ACSL3,FSCN1,HMGB1,RNPS1,SREBF1,USP1,IRAK1,MCM7,ANLN,ILF3,STXBP6,CBX5,PPRC1,USP4,FMNL3,RACGAP1,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,WDR76,MED17,U2AF2,ZW10,INTS7,QSOX2,MNDA,CAPG,SLC29A1,MTDH,HEY1,HOXA3,PPM1G,RRBP1,TRIP13,COLGALT1,SLC25A5,PPP1R15B,PARPBP,SRRT,SDC1,ARFGAP1,CTDNEP1,RANGAP1,FBXO5,HSPA9,NAB2,SLC35C2,CFAP298,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,ENSCAFG00000030005,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,TIMELESS,THRAP3,LIMA1,TRUB2,FAM129B,TCEA1,ENSCAFG00000008236,NF2,AURKB,PSD4,NONO,MMP14,HNRNPL,CDKN2C,TOPBP1,ABHD5,EZH2,STMN1,DEPDC1,SLC30A1,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,CLIC1,FEN1,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,HMGB3,RCC1,PCNA,DHX33,HOXA7,BID,ARG2,SF3B4,UHRF1,CKS2,PDCD2,RNF152,GMNN,DHCR24,POC1A,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,PRCP,PREB,TFRC,NRAS,PPARD,CDC6,NDC80,ITGB3,RAP2C,YBX3,HNRNPF,ARHGDIA,YWHAB,HIST1H1A,CYCS,FAM49B,NCL,RAC1,NUP62,EMP2,DTL,GNB2,PDXP,P	down_ACOR_VSMC
GO:0097193	0.485	0.641	11	109	intrinsic apoptotic signaling pathway	BP	1	ACKR3,PLEKHF1,MAP3K5,PDK2,PIK3R1,HIC1,PTPMT1,HTRA2,NCK1,KRCC1,DDIT4	up_VSAP_EC

GO:0051403	0.485	0.652	9	89	stress-activated MAPK cascade	BP	1	ARHGEF5,MAP3K5,CDC42EP5,F2RL1,ZFP36L1,MYC,SASH1,MYD88,QARS	up_VSAP_EC
GO:0002793	0.485	0.696	5	54	positive regulation of peptide secretion	BP	1	FERMT1,GATA3,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0050714	0.485	0.696	5	54	positive regulation of protein secretion	BP	1	FERMT1,GATA3,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0006354	0.485	0.743	3	30	DNA-templated transcription, elongation	BP	1	EZH2,DDX39B,SUPT16H	down_ACOR_VSMC
GO:0006446	0.485	0.745	3	27	regulation of translational initiation	BP	1	ANKHD1,EIF3K,NCK1	up_VSAP_EC
GO:0032479	0.485	0.783	2	33	regulation of type I interferon production	BP	1	RNF216,MAVS	down_VCAV_EC
GO:0032210	0.485	0.787	2	20	regulation of telomere maintenance via	BP	1	HMBOX1,DCP2	up_VCAV_EC
GO:0050688	0.485	0.787	2	20	regulation of defense response to virus	BP	1	TMEM173,RIOK3	up_VCAV_EC
GO:1904356	0.485	0.787	2	20	regulation of telomere maintenance via telomere lengthening	BP	1	HMBOX1,DCP2	up_VCAV_EC
GO:0048608	0.485	0.861	1	129	reproductive structure development	BP	1	SULF1	down_ACOR_EC
GO:0044238	0.485	1	1	3383	primary metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0060571	0.485	0.866	1	13	morphogenesis of an epithelial fold	BP	1	RDH10	down_VCAV_EC
GO:0072202	0.485	0.866	1	13	cell differentiation involved in metanephros	BP	1	GREM1	down_VCAV_EC
GO:1902679	0.485	0.865	1	329	negative regulation of RNA biosynthetic process	BP	1	HDAC7	down_VPOR_EC
GO:1903507	0.485	0.865	1	329	negative regulation of nucleic acid-templated	BP	1	HDAC7	down_VPOR_EC
GO:0021884	0.485	0.869	1	10	forebrain neuron development	BP	1	NRP1	down_VSAP_EC
GO:0097028	0.485	0.867	1	11	dendritic cell differentiation	BP	1	LYN	down_VSAP_EC
GO:0050892	0.485	0.876	1	6	intestinal absorption	BP	1	LEP	up_ACOR_VSMC
GO:1902533	0.485	0.864	1	271	positive regulation of intracellular signal	BP	1	TAOK1	up_AORT_EC
GO:0046112	0.485	0.872	1	8	nucleobase biosynthetic process	BP	1	MTOR	up_VCAV_EC
GO:0055082	0.485	0.862	1	189	cellular chemical homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0006337	0.485	0.874	1	7	nucleosome disassembly	BP	1	SMARCD2	up_VSAP_EC
GO:0032986	0.485	0.874	1	7	protein-DNA complex disassembly	BP	1	SMARCD2	up_VSAP_EC
GO:0002286	0.485007566	0.86212	1	24	T cell activation involved in immune response	BP	1	PTGER4	up_ACOR_EC
GO:0090398	0.485281386	0.86195	1	24	cellular senescence	BP	1	PRKCD	up_ACOR_EC
GO:1902750	0.485382214	0.86188	1	24	negative regulation of cell cycle G2/M phase	BP	1	BRSK1	up_ACOR_EC
GO:0009132	0.485440397	0.86165	1	25	nucleoside diphosphate metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0035107	0.485612003	0.77961	2	60	appendage morphogenesis	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0035108	0.485612003	0.77961	2	60	limb morphogenesis	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0044248	0.486	0.568	67	691	cellular catabolic process	BP	1	PLCG2,LEP,HTR2B,ENOSF1,ZRANB1,FEZ1,ENSCAFG00000002977,SKP2,PRKAA2,PNRC1,SH3RF2,PDE5A,TP53INP1,MAOA,ISG15,ZNRF3,CTSS,PTPN3,FMO4,KLHL20,ACAD11,ENPP4,GABARAPL1,DAPK1,CTSB,BNIP3,DCP1B,UBR1,ULK2,OS9,STT3B,SMPD1,UBE2H,MOXD1,PYGM,RNF24,SARDH,RNF19A,PSEN1,PIK3C3,LAMP2,CLN8,SIAH1,ALDOC,CTSF,ENTPD3,ATG16L2,PCYOX1,DDIT4,DISC1,RNF181,NEU3,USP20,HERPUD1,GAA,FEZ2,FAF2,CNOT4,WFS1,CTIF,CAT,DZIP3,SH3BP4,ERAP1,ENSCAFG00000029553,PARK7,ZFYVE1	up_ACOR_VSMC
GO:0045087	0.486	0.619	16	161	innate immune response	BP	1	TLR1,LEP,COCH,MX1,TLR3,ISG15,F2RL1,DAPK1,C1S,PTPN22,EVL,PRKCE,PARP9,CCL5,NOD2,SERINC3	up_ACOR_VSMC
GO:0001525	0.486	0.622	15	173	angiogenesis	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,NCL,EMP2,JMJD6,NUS1	down_ACOR_VSMC
GO:0120035	0.486	0.626	14	160	regulation of plasma membrane bounded cell projection organization	BP	1	IFRD1,PODXL,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,MTOR,NCKAP1,NCK1,FES,RAPGEF2,FSCN1	up_VCAV_EC

GO:0044703	0.486	0.649	9	172	multi-organism reproductive process	BP	1	ADAMTS2,RECK,SYDE1,MEA1,B4GALT1,ENSCAFG00000017708,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0031667	0.486	0.651	9	102	response to nutrient levels	BP	1	P2RX7,SELL,ATF3,RALB,MTOR,SLC25A25,BCL10,PMAIP1,P2RX2	up_VCAV_EC
GO:0006979	0.486	0.666	7	130	response to oxidative stress	BP	1	PRNP,TMEM161A,PARK7,MPV17,FUT8,ATOX1,FOXO3	down_VCAV_EC
GO:0048489	0.486	0.716	4	38	synaptic vesicle transport	BP	1	FBXL20,STX11,PSEN1,PREPL	up_ACOR_VSMC
GO:0097480	0.486	0.716	4	38	establishment of synaptic vesicle localization	BP	1	FBXL20,STX11,PSEN1,PREPL	up_ACOR_VSMC
GO:0043271	0.486	0.743	3	28	negative regulation of ion transport	BP	1	ACTN2,KCNE3,INPP5K	up_ACOR_VSMC
GO:0010605	0.486	0.746	3	745	negative regulation of macromolecule metabolic	BP	1	NR1H4,PTGER2,FLRT3	up_VPUL_EC
GO:0006984	0.486	0.786	2	19	ER-nucleus signaling pathway	BP	1	PPP1R15B,INSIG1	down_ACOR_VSMC
GO:0007528	0.486	0.788	2	17	neuromuscular junction development	BP	1	ALS2,P2RX2	up_VCAV_EC
GO:1901566	0.486	0.788	2	598	organonitrogen compound biosynthetic	BP	1	GATM,FBP1	up_VFEM_VSMC
GO:0043297	0.486	0.788	2	17	apical junction assembly	BP	1	WNT11,CLDN1	up_VSAP_EC
GO:0001655	0.486	0.86	1	116	urogenital system development	BP	1	SULF1	down_ACOR_EC
GO:0098801	0.486	0.871	1	8	regulation of renal system process	BP	1	EMP2	down_ACOR_VSMC
GO:0008631	0.486	0.865	1	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	PARK7	down_VCAV_EC
GO:0031113	0.486	0.866	1	13	regulation of microtubule polymerization	BP	1	CLIP3	down_VCAV_EC
GO:0007267	0.486	0.864	1	332	cell-cell signaling	BP	1	RAB11B	down_VPOR_EC
GO:0002507	0.486	0.873	1	7	tolerance induction	BP	1	CD274	up_ACOR_VSMC
GO:1900274	0.486	0.876	1	6	regulation of phospholipase C activity	BP	1	HTR2B	up_ACOR_VSMC
GO:0051093	0.486	0.863	1	273	negative regulation of developmental process	BP	1	HOXA9	up_AORT_EC
GO:0021800	0.486	0.876	1	6	cerebral cortex tangential migration	BP	1	RELN	up_VCAV_EC
GO:0050679	0.486636648	0.77867	2	62	positive regulation of epithelial cell proliferation	BP	1	CDH3,SOX9	up_ACOR_EC
GO:0008150	0.487	0.775	12	5646	biological_process	BP	1	HOXA3,TBX5,GATA5,HOXA2,TMEM176A,TMEM176B,IL22RA1,ARSI,LRRN4,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0043065	0.487	0.642	10	188	positive regulation of apoptotic process	BP	1	PRNP,CLIP3,B4GALT1,PARK7,ADAMTSL4,IFT57,GSDME,FBH1,FOXO3,ZBTB16	down_VCAV_EC
GO:0007005	0.487	0.642	10	175	mitochondrion organization	BP	1	ENSCAFG00000007260,SESN2,HIF1A,BNIP3,FAM162A,GSK3B,CDC37,SH3GLB1,HTT,SLC25A46	down_VSAP_EC
GO:0019827	0.487	0.68	6	59	stem cell population maintenance	BP	1	DLL1,SAV1,KDM2B,ZFP36L2,RAF1,LBH	up_VSAP_EC
GO:1902850	0.487	0.694	5	52	microtubule cytoskeleton organization involved in	BP	1	PLK2,RAB11A,MZT1,STMN1,ZW10	up_VCAV_EC
GO:1905037	0.487	0.695	5	47	autophagosome organization	BP	1	AMBRA1,MFN2,PIP4K2B,UBQLN2,NPRL3	up_VSAP_EC
GO:0060759	0.487	0.715	4	37	regulation of response to cytokine stimulus	BP	1	F2RL1,CREBRF,CCDC3,PARP9	up_ACOR_VSMC
GO:0001738	0.487	0.743	3	27	morphogenesis of a polarized epithelium	BP	1	FZD1,WNT11,ABL1	up_VSAP_EC
GO:0030510	0.487	0.743	3	27	regulation of BMP signaling pathway	BP	1	FZD1,ABL1,ACVRL1	up_VSAP_EC
GO:0001885	0.487	0.786	2	19	endothelial cell development	BP	1	RAP2C,EZR	down_ACOR_VSMC
GO:1904029	0.487	0.782	2	28	regulation of cyclin-dependent protein kinase	BP	1	CCNYL1,CDKN1A	down_VSAP_EC
GO:0010769	0.487	0.778	2	69	regulation of cell morphogenesis involved	BP	1	PLXNA4,KANK1	up_AFEM_EC
GO:0030150	0.487	0.869	1	9	protein import into mitochondrial matrix	BP	1	TIMM44	down_ACOR_VSMC
GO:0006835	0.487	0.865	1	13	dicarboxylic acid transport	BP	1	FOLR2	down_VCAV_EC
GO:0022602	0.487	0.865	1	13	ovulation cycle process	BP	1	FOXO3	down_VCAV_EC
GO:0050772	0.487	0.865	1	13	positive regulation of axonogenesis	BP	1	TRPV2	down_VCAV_EC
GO:0060972	0.487	0.865	1	13	left/right pattern formation	BP	1	IFT57	down_VCAV_EC

GO:0061512	0.487	0.868	1	10	protein localization to cilium	BP	1	ARF4	down_VSAP_EC
GO:0031061	0.487	0.868	1	10	negative regulation of histone methylation	BP	1	KDM3A	down_VSAP_EC
GO:1902305	0.487	0.865	1	12	regulation of sodium ion transmembrane transport	BP	1	YWHAH	down_VSAP_EC
GO:0048012	0.487	0.873	1	7	hepatocyte growth factor receptor signaling	BP	1	NRP1	up_ACOR_VSMC
GO:0001934	0.487	0.863	1	274	positive regulation of protein phosphorylation	BP	1	TAOK1	up_AORT_EC
GO:0007167	0.487	0.863	1	274	enzyme linked receptor protein signaling pathway	BP	1	LNPEP	up_AORT_EC
GO:0035337	0.487	0.869	1	9	fatty-acyl-CoA metabolic process	BP	1	ELOVL7	up_VCAV_EC
GO:0015711	0.487	0.859	1	81	organic anion transport	BP	1	SLC7A11	up_VPOR_EC
GO:0048534	0.487	0.862	1	262	hematopoietic or lymphoid organ	BP	1	HOXA9	up_VFEM_VSMC
GO:0002460	0.487325509	0.77817	2	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	FZD5,PRKCD	up_ACOR_EC
GO:0044093	0.487582725	0.63119	12	437	positive regulation of molecular function	BP	1	CDH3,PLCL1,PKIB,FZD5,NOD2,DYNC1I1,ACTN2,PAK3,MAVS,CLU,PRKCD,PYGO2	up_ACOR_EC
GO:0071396	0.487628282	0.70844	4	134	cellular response to lipid	BP	1	NR1H4,AQP1,NOD2,PTGER4	up_ACOR_EC
GO:0043065	0.488	0.611	18	188	positive regulation of apoptotic process	BP	1	RASSF2,NACC2,ITM2C,BMP4,LATS2,TP53INP1,CD274,ANKRD1,DAPK1,BNIP3,JMY,DKKL1,PSEN1,SPINK2,SIAH1,SERINC3,KLF11,PARK7	up_ACOR_VSMC
GO:0001655	0.488	0.632	12	116	urogenital system development	BP	1	SMAD6,BMP4,TBX18,FGFR2,CLSTN1,NRP1,NPNT,FRS2,NID1,ARID5B,SERPINB5,WFS1	up_ACOR_VSMC
GO:0021953	0.488	0.694	5	49	central nervous system neuron differentiation	BP	1	SLIT2,PLXNA4,HOXC10,GDPD5,NFIB	up_VSAP_EC
GO:0007626	0.488	0.737	3	53	locomotory behavior	BP	1	NAGLU,PARK7,ENSCAFG00000017708	down_VCAV_EC
GO:0014074	0.488	0.743	3	26	response to purine-containing compound	BP	1	AKAP6,P2RX7,INPP5K	up_ACOR_VSMC
GO:0046683	0.488	0.742	3	26	response to organophosphorus	BP	1	AKAP6,P2RX7,INPP5K	up_ACOR_VSMC
GO:0060255	0.488	0.765	3	1782	regulation of macromolecule metabolic	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0036473	0.488	0.742	3	27	cell death in response to oxidative stress	BP	1	FZD1,MAP3K5,FBXO7	up_VSAP_EC
GO:0001824	0.488	0.781	2	27	blastocyst development	BP	1	ZPR1,RBBP8	down_VSAP_EC
GO:0048332	0.488	0.782	2	26	mesoderm morphogenesis	BP	1	ITGA2,INHBA	down_VSAP_EC
GO:0001914	0.488	0.87	1	8	regulation of T cell mediated cytotoxicity	BP	1	FAM49B	down_ACOR_VSMC
GO:0022603	0.488	0.863	1	301	regulation of anatomical structure morphogenesis	BP	1	SRSF6	down_AFEM_EC
GO:0021532	0.488	0.864	1	13	neural tube patterning	BP	1	GLI3	down_VCAV_EC
GO:0045910	0.488	0.863	1	14	negative regulation of DNA recombination	BP	1	FBH1	down_VCAV_EC
GO:0000469	0.488	0.865	1	12	cleavage involved in rRNA processing	BP	1	MRPL1	down_VSAP_EC
GO:0060441	0.488	0.866	1	11	epithelial tube branching involved in lung	BP	1	CTNNB1	down_VSAP_EC
GO:2000273	0.488	0.875	1	6	positive regulation of signaling receptor activity	BP	1	PARK7	up_ACOR_VSMC
GO:0002011	0.488	0.86	1	28	morphogenesis of an epithelial sheet	BP	1	ADAM17	up_AFEM_EC
GO:0061005	0.488	0.86	1	28	cell differentiation involved in kidney	BP	1	GREM1	up_AFEM_EC
GO:0043086	0.488	0.86	1	170	negative regulation of catalytic activity	BP	1	PCSK1N	up_APUL_EC
GO:0002089	0.488	0.87	1	8	lens morphogenesis in camera-type eye	BP	1	PROX1	up_VCAV_EC
GO:0032446	0.488	0.862	1	255	protein modification by small protein conjugation	BP	1	EYA1	up_VFEM_VSMC
GO:0006954	0.488	0.859	1	147	inflammatory response	BP	1	TLR2	up_VSAP_VSMC
GO:2001233	0.488	0.859	1	149	regulation of apoptotic signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0050776	0.488210778	0.689	5	173	regulation of immune response	BP	1	C7,NR1H4,FZD5,NOD2,MAVS	up_ACOR_EC

GO:0072384	0.488219519	0.86005	1	24	organelle transport along microtubule	BP	1	DYNC1I1	up_ACOR_EC
GO:0006351	0.48822992	0.5929	29	1069	transcription, DNA-templated	BP	1	NR1H4,GATA4,TRPS1,TBX18,SOX9,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0002690	0.488730866	0.85934	1	26	positive regulation of leukocyte chemotaxis	BP	1	RARRES2	up_ACOR_EC
GO:0031323	0.489	0.63	15	1788	regulation of cellular metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ABHD5,PUM3,EIF5,CCAR1,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0001503	0.489	0.636	11	109	ossification	BP	1	SMAD6,RASSF2,BMP4,FGFR2,GJA1,ISG15,FGF18,CLSTN1,NPNT,DDR2,SLC8A1	up_ACOR_VSMC
GO:0009126	0.489	0.675	6	100	purine nucleoside monophosphate metabolic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0009167	0.489	0.675	6	100	purine ribonucleoside monophosphate metabolic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0009199	0.489	0.675	6	100	ribonucleoside triphosphate metabolic	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0051050	0.489	0.675	6	235	positive regulation of transport	BP	1	LEP,DLL1,GREM1,CAMK2A,FXYD1,RAB7A	up_AFEM_EC
GO:0050792	0.489	0.692	5	55	regulation of viral process	BP	1	ILF3,TRIM35,SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0008277	0.489	0.74	3	31	regulation of G protein-coupled receptor signaling	BP	1	STMN1,YWHAB,PRMT5	down_ACOR_VSMC
GO:0010466	0.489	0.74	3	32	negative regulation of peptidase activity	BP	1	BIRC5,DHCR24,ENSCAFG00000005299	down_ACOR_VSMC
GO:0010951	0.489	0.74	3	32	negative regulation of endopeptidase activity	BP	1	BIRC5,DHCR24,ENSCAFG00000005299	down_ACOR_VSMC
GO:0045017	0.489	0.736	3	52	glycerolipid biosynthetic process	BP	1	GPAM,LCAT,PIGS	down_VCAV_EC
GO:0097006	0.489	0.784	2	19	regulation of plasma lipoprotein particle levels	BP	1	ACSL3,LIPC	down_ACOR_VSMC
GO:0043487	0.489	0.779	2	33	regulation of RNA stability	BP	1	SAMD4B,ZFP36L1	down_VCAV_EC
GO:2001243	0.489	0.779	2	33	negative regulation of intrinsic apoptotic	BP	1	TMEM161A,PARK7	down_VCAV_EC
GO:0048167	0.489	0.781	2	28	regulation of synaptic plasticity	BP	1	APOE,LRRTM2	down_VSAP_EC
GO:0050886	0.489	0.786	2	17	endocrine process	BP	1	F2RL1,EDN1	up_ACOR_VSMC
GO:1902743	0.489	0.786	2	16	regulation of lamellipodium	BP	1	SSH3,RREB1	up_ACOR_VSMC
GO:0051170	0.489	0.776	2	69	import into nucleus	BP	1	LEP,CRY2	up_AFEM_EC
GO:0061387	0.489	0.785	2	18	regulation of extent of cell growth	BP	1	IFRD1,RAB11A	up_VCAV_EC
GO:0033687	0.489	0.864	1	13	osteoblast proliferation	BP	1	GREM1	down_VCAV_EC
GO:0051187	0.489	0.863	1	13	cofactor catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0048523	0.489	0.896	1	1399	negative regulation of cellular process	BP	1	MOSPD1	down_VFEM_EC
GO:1905146	0.489	0.874	1	6	lysosomal protein catabolic process	BP	1	LAMP2	up_ACOR_VSMC
GO:0042127	0.489	0.866	1	452	regulation of cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:1902531	0.489	0.869	1	536	regulation of intracellular signal transduction	BP	1	ESR1	up_AORT_VSMC
GO:0003176	0.489	0.868	1	9	aortic valve development	BP	1	GATA3	up_VCAV_EC
GO:0030220	0.489	0.871	1	7	platelet formation	BP	1	MEF2C	up_VCAV_EC
GO:0071539	0.489	0.869	1	8	protein localization to centrosome	BP	1	HOOK3	up_VCAV_EC
GO:1905508	0.489	0.869	1	8	protein localization to microtubule organizing	BP	1	HOOK3	up_VCAV_EC
GO:0072182	0.489	0.871	1	7	regulation of nephron tubule epithelial cell	BP	1	OSR1	up_VSAP_EC
GO:0071621	0.489834383	0.85846	1	27	granulocyte chemotaxis	BP	1	RARRES2	up_ACOR_EC
GO:0000819	0.49	0.655	8	87	sister chromatid segregation	BP	1	RAB11A,CENPC,ESCO1,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0043588	0.49	0.689	5	74	skin development	BP	1	ERRFI1,CASP3,FLNB,CTNNB1,INHBA	down_VSAP_EC

GO:0042475	0.49	0.741	3	26	odontogenesis of dentin-containing tooth	BP	1	BMP4,PERP,TNFRSF11B	up_ACOR_VSMC
GO:0043085	0.49	0.735	3	323	positive regulation of catalytic activity	BP	1	ENSCAFG00000002015,ABHD5,ENSCAFG00000032731	up_VPOR_EC
GO:0035195	0.49	0.74	3	28	gene silencing by miRNA	BP	1	ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0044257	0.49	0.779	2	327	cellular protein catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0030279	0.49	0.784	2	19	negative regulation of ossification	BP	1	GREM1,TWIST2	down_ACOR_VSMC
GO:0120163	0.49	0.785	2	17	negative regulation of cold-induced	BP	1	PLCL1,IL18R1	up_ACOR_VSMC
GO:0051648	0.49	0.775	2	69	vesicle localization	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0032011	0.49	0.871	1	7	ARF protein signal transduction	BP	1	PSD4	down_ACOR_VSMC
GO:0032012	0.49	0.871	1	7	regulation of ARF protein signal transduction	BP	1	PSD4	down_ACOR_VSMC
GO:0006505	0.49	0.863	1	13	GPI anchor metabolic process	BP	1	PIGS	down_VCAV_EC
GO:0006506	0.49	0.863	1	13	GPI anchor biosynthetic process	BP	1	PIGS	down_VCAV_EC
GO:0032720	0.49	0.863	1	13	negative regulation of tumor necrosis factor	BP	1	BPI	down_VCAV_EC
GO:1902186	0.49	0.863	1	13	regulation of viral release from host cell	BP	1	TRIM8	down_VCAV_EC
GO:0016043	0.49	0.918	1	1973	cellular component organization	BP	1	JUP	down_VFEM_VSMC
GO:1904036	0.49	0.866	1	10	negative regulation of epithelial cell apoptotic	BP	1	SERPINE1	down_VSAP_EC
GO:0016339	0.49	0.874	1	6	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion	BP	1	ATP2C1	up_ACOR_VSMC
GO:0032964	0.49	0.87	1	7	collagen biosynthetic process	BP	1	BMP4	up_ACOR_VSMC
GO:0072337	0.49	0.871	1	7	modified amino acid transport	BP	1	SLC25A20	up_ACOR_VSMC
GO:0008589	0.49	0.858	1	28	regulation of smoothened signaling pathway	BP	1	GAS1	up_AFEM_EC
GO:0045621	0.49	0.858	1	28	positive regulation of lymphocyte	BP	1	CYLD	up_AFEM_EC
GO:0120034	0.49	0.859	1	28	positive regulation of plasma membrane bounded cell projection	BP	1	CDC42EP5	up_AFEM_EC
GO:0090312	0.49	0.868	1	8	positive regulation of protein deacetylation	BP	1	PRKD2	up_VCAV_EC
GO:0043069	0.49	0.86	1	262	negative regulation of programmed cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0044260	0.490526057	0.57077	69	2593	cellular macromolecule metabolic process	BP	1	NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,CALY,SOX9,PKNOX2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,LRRC4,CLU,SFMBT2,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,HM13,PRKCD,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0051493	0.491	0.628	12	188	regulation of cytoskeleton organization	BP	1	ARHGEF2,FSCN1,WDR1,ACTR3,CTNNB1,TWF1,PLEKHG2,GSK3B,NEXN,CAPG,NRP1,MID1	down_VSAP_EC
GO:1905330	0.491	0.691	5	48	regulation of morphogenesis of an	BP	1	FZD1,WNT11,FGF7,ABL1,NTN4	up_VSAP_EC
GO:0042542	0.491	0.738	3	31	response to hydrogen peroxide	BP	1	PPP1R15B,EZH2,SIGMAR1	down_ACOR_VSMC
GO:0031323	0.491	0.763	3	1788	regulation of cellular metabolic process	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0051893	0.491	0.782	2	20	regulation of focal adhesion assembly	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0090109	0.491	0.782	2	20	regulation of cell-substrate junction	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0038066	0.491	0.783	2	19	p38MAPK cascade	BP	1	MAP3K3,BMP2	up_VCAV_EC
GO:2000113	0.491	0.778	2	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	HOXA7,SIX1	up_VFEM_EC

GO:0032689	0.491	0.868	1	8	negative regulation of interferon-gamma	BP	1	HMGB1	down_ACOR_VSMC
GO:0045737	0.491	0.868	1	8	positive regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CKS2	down_ACOR_VSMC
GO:0050798	0.491	0.868	1	8	activated T cell proliferation	BP	1	HMGB1	down_ACOR_VSMC
GO:0046470	0.491	0.862	1	13	phosphatidylcholine metabolic process	BP	1	LCAT	down_VCAV_EC
GO:0070988	0.491	0.862	1	14	demethylation	BP	1	HR	down_VCAV_EC
GO:0006656	0.491	0.87	1	7	phosphatidylcholine biosynthetic process	BP	1	LCAT	up_ACOR_VSMC
GO:0021801	0.491	0.873	1	6	cerebral cortex radial glia guided migration	BP	1	SUN1	up_ACOR_VSMC
GO:0022030	0.491	0.873	1	6	telencephalon glial cell migration	BP	1	SUN1	up_ACOR_VSMC
GO:0032660	0.491	0.87	1	7	regulation of interleukin-17 production	BP	1	NOD2	up_ACOR_VSMC
GO:0060872	0.491	0.873	1	6	semicircular canal development	BP	1	CHD7	up_ACOR_VSMC
GO:0010827	0.491	0.857	1	28	regulation of glucose transmembrane transport	BP	1	LEP	up_AFEM_EC
GO:0035050	0.491	0.858	1	28	embryonic heart tube development	BP	1	DLL1	up_AFEM_EC
GO:0050868	0.491	0.858	1	28	negative regulation of T cell activation	BP	1	CYLD	up_AFEM_EC
GO:0051928	0.491	0.858	1	28	positive regulation of calcium ion transport	BP	1	CAMK2A	up_AFEM_EC
GO:0030001	0.491	0.858	1	172	metal ion transport	BP	1	HOXA3	up_APUL_EC
GO:0002726	0.491	0.868	1	8	positive regulation of T cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:0001944	0.491	0.86	1	263	vasculature development	BP	1	EYA1	up_VFEM_VSMC
GO:0007155	0.491	0.862	1	324	cell adhesion	BP	1	GATA5	up_VPUL_VSMC
GO:2000105	0.491	0.87	1	7	positive regulation of DNA-dependent DNA	BP	1	CIZ1	up_VSAP_EC
GO:0019218	0.491017036	0.85803	1	25	regulation of steroid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0018130	0.491070499	0.58521	34	1261	heterocycle biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0016054	0.491526734	0.77477	2	61	organic acid catabolic process	BP	1	THNSL2,SARDH	up_ACOR_EC
GO:0046395	0.491526734	0.77477	2	61	carboxylic acid catabolic process	BP	1	THNSL2,SARDH	up_ACOR_EC
GO:0044260	0.492	0.543	218	2593	cellular macromolecule metabolic process	BP	1	ELK3,HMGB1,MCM6,RNPS1,SREBF1,MCM4,POLE3,USP1,IRAK1,MCM7,RPA1,ILF3,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,HNRNPD,SREBF2,MCM3,SMC1A,HINFP,VARS,UBE2S,NEDD4,RRM1,MED17,U2AF2,PSMD3,POLA1,PSMD7,SLC29A1,MTDH,HEY1,METAP2,PPM1G,RRBP1,TOP3A,TRIP13,PPP1R15B,PARPBP,POLA2,MPDU1,SRRT,GINS4,RAD54L,POLE,NAB2,SLC35C2,MRPS18B,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,XYLT1,FANCD2,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,EDC4,AURKB,NONO,TK1,CDKN2C,TOPBP1,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,FBL,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,PCNA,DHX33,HOXA7,SMG9,TONSL,MCM10,UHRF1,CKS2,PDCD2,RNF152,DIS3,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,FARSA,TFRC,PPARD,CDC6,POLH,NEIL3,RAP2C,YBX3,UBE2J2,YWHAB,CYCS,NCL,RAC1,NUP62,MRPL37,EMP2,DTL,FOSL1,SUV39H1,HASPIN,THUMPD2,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,RBBP8,EZR,CLSPN,SMC6,UBE2K,RBM14,RBM17,RAD23	down_ACOR_VSMC

GO:0048666	0.492	0.592	26	258	neuron development	BP	1	LEP,EPYC,FEZ1,ITM2C,FGFR2,SEC24B,ZNF365,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,FZD3,RND1,DAG1,APP,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,WASL	up_ACOR_VSMC
GO:0031331	0.492	0.634	11	110	positive regulation of cellular catabolic process	BP	1	PLEKHF1,MFN2,ZFP36L1,FBXO7,RNF166,PIP4K2B,OSBPL7,ZFP36L2,UBQLN2,TNRC6C,HMOX1	up_VSAP_EC
GO:0009205	0.492	0.639	10	98	purine ribonucleoside triphosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0040013	0.492	0.64	10	100	negative regulation of locomotion	BP	1	HOXA7,WNT11,C5AR2,SLIT2,CDH1,FUZ,RECK,TBXA2R,FBLN1,ACVRL1	up_VSAP_EC
GO:0009101	0.492	0.645	9	113	glycoprotein biosynthetic process	BP	1	ST8SIA6,TNIP1,ST6GAL1,B3GNT5,CHST7,ST3GAL6,GALNT18,MFNG,TET2	up_VCAV_EC
GO:0007159	0.492	0.654	8	79	leukocyte cell-cell adhesion	BP	1	LEP,CD83,BMP4,PDE5A,CD274,PTPN22,DUSP22,PAG1	up_ACOR_VSMC
GO:0007052	0.492	0.71	4	42	mitotic spindle organization	BP	1	PLK2,RAB11A,MZT1,STMN1	up_VCAV_EC
GO:0014066	0.492	0.739	3	26	regulation of phosphatidylinositol 3-	BP	1	LEP,F2RL1,UNC5B	up_ACOR_VSMC
GO:0051209	0.492	0.739	3	28	release of sequestered calcium ion into cytosol	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0051283	0.492	0.739	3	28	negative regulation of sequestering of calcium	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:1905954	0.492	0.782	2	19	positive regulation of lipid localization	BP	1	SREBF2,PRELID1	down_ACOR_VSMC
GO:1902806	0.492	0.777	2	33	regulation of cell cycle G1/S phase transition	BP	1	KANK2,LSM10	down_VCAV_EC
GO:0007631	0.492	0.783	2	17	feeding behavior	BP	1	LEP,APP	up_ACOR_VSMC
GO:0061025	0.492	0.774	2	69	membrane fusion	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0016477	0.492	0.779	2	426	cell migration	BP	1	TBX5,NTRK2	up_APUL_EC
GO:0001954	0.492	0.783	2	17	positive regulation of cell-matrix adhesion	BP	1	ABL1,EMP2	up_VSAP_EC
GO:0033173	0.492	0.784	2	17	calcineurin-NFAT signaling cascade	BP	1	TBC1D10C,PPP3CB	up_VSAP_EC
GO:0097720	0.492	0.784	2	17	calcineurin-mediated signaling	BP	1	TBC1D10C,PPP3CB	up_VSAP_EC
GO:0061458	0.492	0.856	1	131	reproductive system development	BP	1	SULF1	down_ACOR_EC
GO:0043627	0.492	0.867	1	8	response to estrogen	BP	1	CAV1	down_ACOR_VSMC
GO:0050829	0.492	0.867	1	8	defense response to Gram-negative bacterium	BP	1	HMGB2	down_ACOR_VSMC
GO:0051603	0.492	0.861	1	305	proteolysis involved in cellular protein catabolic	BP	1	USP33	down_AFEM_EC
GO:0048339	0.492	0.861	1	13	paraxial mesoderm development	BP	1	BMPR1A	down_VCAV_EC
GO:2000648	0.492	0.861	1	14	positive regulation of stem cell proliferation	BP	1	GLI3	down_VCAV_EC
GO:0034067	0.492	0.863	1	11	protein localization to Golgi apparatus	BP	1	GBP5	down_VSAP_EC
GO:0043403	0.492	0.863	1	11	skeletal muscle tissue regeneration	BP	1	IFRD1	down_VSAP_EC
GO:0050830	0.492	0.862	1	12	defense response to Gram-positive bacterium	BP	1	ADAM17	down_VSAP_EC
GO:0006089	0.492	0.87	1	7	lactate metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0031641	0.492	0.872	1	6	regulation of myelination	BP	1	WASF3	up_ACOR_VSMC
GO:0003222	0.492	0.873	1	6	ventricular trabecula myocardium	BP	1	CHD7	up_ACOR_VSMC
GO:0006140	0.492	0.857	1	28	regulation of nucleotide metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0048167	0.492	0.857	1	28	regulation of synaptic plasticity	BP	1	CAMK2A	up_AFEM_EC
GO:2000573	0.492	0.857	1	28	positive regulation of DNA biosynthetic process	BP	1	GREM1	up_AFEM_EC
GO:0010647	0.492	0.864	1	460	positive regulation of cell communication	BP	1	TLR2	up_AFEM_VSMC
GO:0002520	0.492	0.859	1	279	immune system development	BP	1	HOXA9	up_AORT_EC
GO:1901566	0.492	0.867	1	598	organonitrogen compound biosynthetic	BP	1	ARG2	up_AORT_VSMC
GO:0071875	0.492	0.873	1	6	adrenergic receptor signaling pathway	BP	1	RAPGEF2	up_VCAV_EC

GO:0071880	0.492	0.873	1	6	adenylate cyclase-activating adrenergic receptor signaling	BP	1	RAPGEF2	up_VCAV_EC
GO:0045923	0.492	0.867	1	8	positive regulation of fatty acid metabolic process	BP	1	PTGS2	up_VCAV_EC
GO:0007033	0.492	0.856	1	82	vacuole organization	BP	1	HOOK3	up_VPOR_EC
GO:1901653	0.492	0.856	1	84	cellular response to peptide	BP	1	ARHGEF2	up_VPOR_EC
GO:0120035	0.492	0.856	1	160	regulation of plasma membrane bounded cell projection organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0006953	0.492	0.869	1	7	acute-phase response	BP	1	SAA1	up_VSAP_EC
GO:0006366	0.492237629	0.61234	16	583	transcription by RNA polymerase II	BP	1	NR1H4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,NOD2,RGMA,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,GMEB2	up_ACOR_EC
GO:2001244	0.49242552	0.85676	1	27	positive regulation of intrinsic apoptotic	BP	1	CLU	up_ACOR_EC
GO:0023051	0.493	0.57	48	954	regulation of signaling	BP	1	NOTCH2,PDGFRB,SLC35F6,DCN,PRNP,VASN,FBN1,GLIPR2,BGN,KANK2,BMPR1A,EVC,RECK,IGFBP6,ARHGEF25,AKT1S1,CHRDL1,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,ASPN,THY1,ATP6V0C,GLI3,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,NCLN,SPRED1,RAB7B,GLIS2,SHC1,FBH1,GREM1,NPHP4,FOXO3,ANKRD54,BRSK1,CDK14	down_VCAV_EC
GO:0043068	0.493	0.611	16	190	positive regulation of programmed cell death	BP	1	HMGB1,RNPS1,MNDA,PRELID1,CAV1,CASP2,MAP3K20,TRIM35,BID,PDCD2,EIF5A,B4GALT1,CYCS,MELK,AIFM1,PIK3CD	down_ACOR_VSMC
GO:0006417	0.493	0.661	7	109	regulation of translation	BP	1	AARS,PUM3,SESN2,EIF4EBP1,CNOT7,EIF5,EIF2S1	down_VSAP_EC
GO:1903322	0.493	0.675	6	59	positive regulation of protein modification by small protein conjugation	BP	1	SKP2,PTPN22,NOD2,FAM107A,DCUN1D4,WFS1	up_ACOR_VSMC
GO:0032496	0.493	0.687	5	77	response to lipopolysaccharide	BP	1	NR1H4,SERPINE1,MTDH,ADAM17,LYN	down_VSAP_EC
GO:0005977	0.493	0.738	3	26	glycogen metabolic process	BP	1	PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0006073	0.493	0.738	3	26	cellular glucan metabolic process	BP	1	PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0044042	0.493	0.738	3	26	glucan metabolic process	BP	1	PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0061005	0.493	0.737	3	28	cell differentiation involved in kidney	BP	1	OSR1,KLF15,GLIS2	up_VSAP_EC
GO:0003014	0.493	0.778	2	27	renal system process	BP	1	SULF1,MYO1E	down_VSAP_EC
GO:0043647	0.493	0.782	2	17	inositol phosphate metabolic process	BP	1	INPP5E,PPIP5K1	up_VSAP_EC
GO:0055081	0.493	0.783	2	17	anion homeostasis	BP	1	HNF4A,GOT1	up_VSAP_EC
GO:0060760	0.493	0.783	2	17	positive regulation of response to cytokine	BP	1	CREBRF,MAVS	up_VSAP_EC
GO:1903825	0.493	0.783	2	17	organic acid transmembrane transport	BP	1	OSR1,SLC25A12	up_VSAP_EC
GO:1905039	0.493	0.783	2	17	carboxylic acid transmembrane transport	BP	1	OSR1,SLC25A12	up_VSAP_EC
GO:0022604	0.493	0.855	1	122	regulation of cell morphogenesis	BP	1	PDPN	down_ACOR_EC
GO:0031468	0.493	0.866	1	8	nuclear envelope reassembly	BP	1	REEP4	down_ACOR_VSMC
GO:0071071	0.493	0.867	1	8	regulation of phospholipid biosynthetic process	BP	1	ACSL3	down_ACOR_VSMC
GO:0032269	0.493	0.86	1	306	negative regulation of cellular protein metabolic	BP	1	IVNS1ABP	down_AFEM_EC
GO:0006811	0.493	0.86	1	330	ion transport	BP	1	RAB11B	down_VPOR_EC
GO:0042789	0.493	0.864	1	10	mRNA transcription by RNA polymerase II	BP	1	DDIT3	down_VSAP_EC
GO:0009593	0.493	0.863	1	11	detection of chemical stimulus	BP	1	CALM1	down_VSAP_EC
GO:0045576	0.493	0.862	1	12	mast cell activation	BP	1	LYN	down_VSAP_EC
GO:0045736	0.493	0.863	1	11	negative regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CDKN1A	down_VSAP_EC
GO:1904030	0.493	0.863	1	11	negative regulation of cyclin-dependent protein	BP	1	CDKN1A	down_VSAP_EC

GO:0021800	0.493	0.872	1	6	cerebral cortex tangential migration	BP	1	NRP1	up_ACOR_VSMC
GO:0045652	0.493	0.869	1	7	regulation of megakaryocyte	BP	1	CNOT4	up_ACOR_VSMC
GO:1900221	0.493	0.872	1	6	regulation of amyloid-beta clearance	BP	1	LRPAP1	up_ACOR_VSMC
GO:1904706	0.493	0.869	1	7	negative regulation of vascular smooth muscle	BP	1	CDKN1A	up_ACOR_VSMC
GO:0140029	0.493	0.856	1	28	exocytic process	BP	1	CAMK2A	up_AFEM_EC
GO:0045944	0.493	0.859	1	287	positive regulation of transcription by RNA polymerase II	BP	1	HOXA9	up_AORT_EC
GO:0003044	0.493	0.867	1	8	regulation of systemic arterial blood pressure mediated by a chemical	BP	1	EDN1	up_VCAV_EC
GO:0072182	0.493	0.869	1	7	regulation of nephron tubule epithelial cell	BP	1	GATA3	up_VCAV_EC
GO:0006811	0.493	0.86	1	330	ion transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0022610	0.493	0.86	1	326	biological adhesion	BP	1	GATA5	up_VPUL_VSMC
GO:0030182	0.493	0.86	1	327	neuron differentiation	BP	1	SLIT2	up_VPUL_VSMC
GO:0031646	0.493	0.869	1	7	positive regulation of neurological system	BP	1	WASF3	up_VSAP_EC
GO:0072170	0.493	0.869	1	7	metanephric tubule development	BP	1	OSR1	up_VSAP_EC
GO:0072207	0.493	0.869	1	7	metanephric epithelium development	BP	1	OSR1	up_VSAP_EC
GO:0072234	0.493	0.869	1	7	metanephric nephron tubule development	BP	1	OSR1	up_VSAP_EC
GO:0072243	0.493	0.869	1	7	metanephric nephron epithelium development	BP	1	OSR1	up_VSAP_EC
GO:0097327	0.49327334	0.85655	1	25	response to antineoplastic agent	BP	1	AQP1	up_ACOR_EC
GO:0000079	0.493809578	0.85601	1	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CCNYL1	up_ACOR_EC
GO:0001525	0.494	0.608	17	173	angiogenesis	BP	1	VEGFD,LEP,ANGPT1,BMP4,FGFR2,TLR3,SASH1,FGF18,EGLN1,NRP1,TBX20,SYNJ2BP,JUP,EDN1,JAM3,ERAP1,PIK3C2A	up_ACOR_VSMC
GO:0071345	0.494	0.63	11	210	cellular response to cytokine stimulus	BP	1	PCOLCE,DCN,BGN,NUMBL,GFPT2,ASPN,ZFP36L1,MAVS,GSDME,RAB7B,FOXO3	down_VCAV_EC
GO:0061448	0.494	0.651	8	89	connective tissue development	BP	1	HOXA3,GREM1,CDK4,POC1A,PPARD,HOXC4,SERPINH1,AMER1	down_ACOR_VSMC
GO:0072659	0.494	0.661	7	82	protein localization to plasma membrane	BP	1	PPP2R5A,TSPAN15,RAB11A,ZDHHC22,TSPAN14,EXOC5,RAPGEF2	up_VCAV_EC
GO:0006605	0.494	0.67	6	99	protein targeting	BP	1	TRAM1,SRP54,MYO1C,SSR1,SRPRA,SRP72	down_VSAP_EC
GO:0043583	0.494	0.674	6	59	ear development	BP	1	OSR2,INSIG2,LRIG3,DLL1,OSR1,ZEB1	up_VSAP_EC
GO:0071897	0.494	0.688	5	54	DNA biosynthetic process	BP	1	PDGFB,HMBOX1,PRKD2,SMG7,DCP2	up_VCAV_EC
GO:0060349	0.494	0.708	4	38	bone morphogenesis	BP	1	BMP4,FGFR2,CITED2,FGF18	up_ACOR_VSMC
GO:0051224	0.494	0.707	4	47	negative regulation of protein transport	BP	1	FERMT1,ARG2,APOD,CD200	up_VCAV_EC
GO:1904950	0.494	0.707	4	47	negative regulation of establishment of protein localization	BP	1	FERMT1,ARG2,APOD,CD200	up_VCAV_EC
GO:0070665	0.494	0.735	3	31	positive regulation of leukocyte proliferation	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0042733	0.494	0.737	3	27	embryonic digit morphogenesis	BP	1	BMP4,LNPK,GJA1	up_ACOR_VSMC
GO:1903321	0.494	0.735	3	33	negative regulation of protein modification by small protein conjugation	BP	1	TNFAIP3,HMG20A,IVNS1ABP	up_VCAV_EC
GO:0006893	0.494	0.78	2	20	Golgi to plasma membrane transport	BP	1	ACSL3,STXBP6	down_ACOR_VSMC
GO:0030534	0.494	0.775	2	33	adult behavior	BP	1	PARK7,ENSCAFG00000017708	down_VCAV_EC
GO:0031663	0.494	0.782	2	17	lipopolysaccharide-mediated signaling	BP	1	SASH1,PRKCE	up_ACOR_VSMC
GO:1900015	0.494	0.782	2	17	regulation of cytokine production involved in inflammatory response	BP	1	LEP,NOD2	up_ACOR_VSMC
GO:0002082	0.494	0.866	1	8	regulation of oxidative phosphorylation	BP	1	CDK1	down_ACOR_VSMC

GO:0031571	0.494	0.866	1	8	mitotic G1 DNA damage checkpoint	BP	1	CASP2	down_ACOR_VSMC
GO:0043248	0.494	0.866	1	8	proteasome assembly	BP	1	PSMD13	down_ACOR_VSMC
GO:0044783	0.494	0.866	1	8	G1 DNA damage checkpoint	BP	1	CASP2	down_ACOR_VSMC
GO:0044819	0.494	0.866	1	8	mitotic G1/S transition checkpoint	BP	1	CASP2	down_ACOR_VSMC
GO:0046131	0.494	0.866	1	8	pyrimidine ribonucleoside metabolic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0015985	0.494	0.86	1	13	energy coupled proton transport, down	BP	1	ATP5MC1	down_VCAV_EC
GO:0015986	0.494	0.86	1	13	ATP synthesis coupled proton transport	BP	1	ATP5MC1	down_VCAV_EC
GO:0045843	0.494	0.86	1	13	negative regulation of striated muscle tissue	BP	1	TSC22D3	down_VCAV_EC
GO:1904353	0.494	0.86	1	13	regulation of telomere capping	BP	1	NABP2	down_VCAV_EC
GO:0051241	0.494	0.86	1	336	negative regulation of multicellular organismal	BP	1	HDAC7	down_VPOR_EC
GO:0023056	0.494	0.863	1	462	positive regulation of signaling	BP	1	TLR2	up_AFEM_VSMC
GO:0001525	0.494	0.856	1	173	angiogenesis	BP	1	HOXA3	up_APUL_EC
GO:0030334	0.494	0.858	1	267	regulation of cell migration	BP	1	C3AR1	up_VPOR_VSMC
GO:0031441	0.494	0.868	1	7	negative regulation of mRNA 3'-end processing	BP	1	CDK9	up_VSAP_EC
GO:0060074	0.494	0.868	1	7	synapse maturation	BP	1	SEZ6L	up_VSAP_EC
GO:1900364	0.494	0.868	1	7	negative regulation of mRNA polyadenylation	BP	1	CDK9	up_VSAP_EC
GO:0048701	0.494049977	0.85604	1	25	embryonic cranial skeleton morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0097659	0.494736909	0.58653	29	1072	nucleic acid-templated transcription	BP	1	NR1H4,GATA4,TRPS1,TBX18,SOX9,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:2000112	0.495	0.589	27	1119	regulation of cellular macromolecule biosynthetic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0030030	0.495	0.601	19	377	cell projection organization	BP	1	NDN,PRNP,SDC4,TRPV2,NUMBL,RHOD,TTC8,SEMA3C,THY1,TLX2,GLI3,NCDN,IFT57,UST,PRKCSH,EVI5L,RAC2,RGMA,BRSK1	down_VCAV_EC
GO:0031344	0.495	0.616	14	161	regulation of cell projection organization	BP	1	IFRD1,PODXL,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,MTOR,NCKAP1,NCK1,FES,RAPGEF2,FSCN1	up_VCAV_EC
GO:0034645	0.495	0.629	13	1546	cellular macromolecule biosynthetic process	BP	1	BARX1,OSTC,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:0090068	0.495	0.652	8	78	positive regulation of cell cycle process	BP	1	CDC7,ATRX,PKP4,CDKN1A,CRLF3,PRKCE,APP,EDN1	up_ACOR_VSMC
GO:0048705	0.495	0.65	8	95	skeletal system morphogenesis	BP	1	HOXB7,MEF2C,TIPARP,STC1,HOXB8,MDFI,HOXB5,ZEB1	up_VCAV_EC
GO:0097191	0.495	0.652	8	79	extrinsic apoptotic signaling pathway	BP	1	PIK3R1,RBCK1,RAF1,STX4,HTRA2,HMOX1,TRADD,DEDD2	up_VSAP_EC
GO:0060041	0.495	0.732	3	41	retina development in camera-type eye	BP	1	SMARCA4,HIF1A,NRP1	down_VSAP_EC
GO:0009408	0.495	0.736	3	27	response to heat	BP	1	SCARA5,HTRA2,HMOX1	up_VSAP_EC
GO:0002027	0.495	0.779	2	20	regulation of heart rate	BP	1	SREBF1,CAV1	down_ACOR_VSMC
GO:0042475	0.495	0.776	2	26	odontogenesis of dentin-containing tooth	BP	1	SERPINE1,CTNNB1	down_VSAP_EC
GO:0048729	0.495	0.772	2	209	tissue morphogenesis	BP	1	PTK7,SEMA3A	up_VPOR_EC
GO:0032970	0.495	0.854	1	130	regulation of actin filament-based process	BP	1	PDPN	down_ACOR_EC
GO:0006098	0.495	0.865	1	8	pentose-phosphate shunt	BP	1	PGD	down_ACOR_VSMC
GO:0008209	0.495	0.865	1	8	androgen metabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0032369	0.495	0.865	1	8	negative regulation of lipid transport	BP	1	SREBF2	down_ACOR_VSMC
GO:0051156	0.495	0.865	1	8	glucose 6-phosphate metabolic process	BP	1	PGD	down_ACOR_VSMC

GO:0032370	0.495	0.86	1	13	positive regulation of lipid transport	BP	1	SCP2	down_VCAV_EC
GO:0042531	0.495	0.859	1	13	positive regulation of tyrosine phosphorylation	BP	1	ARL2BP	down_VCAV_EC
GO:0048663	0.495	0.859	1	13	neuron fate commitment	BP	1	GLI3	down_VCAV_EC
GO:0032881	0.495	0.861	1	11	regulation of polysaccharide metabolic	BP	1	ENPP1	down_VSAP_EC
GO:0032885	0.495	0.861	1	11	regulation of polysaccharide	BP	1	ENPP1	down_VSAP_EC
GO:0010605	0.495	0.871	1	745	negative regulation of macromolecule metabolic	BP	1	GATA5	down_VSAP_VSMC
GO:0001556	0.495	0.868	1	7	oocyte maturation	BP	1	DMC1	up_ACOR_VSMC
GO:0009301	0.495	0.87	1	6	snRNA transcription	BP	1	ELL2	up_ACOR_VSMC
GO:0009950	0.495	0.871	1	6	dorsal/ventral axis specification	BP	1	SMAD6	up_ACOR_VSMC
GO:1903427	0.495	0.867	1	7	negative regulation of reactive oxygen species biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0000209	0.495	0.853	1	83	protein polyubiquitination	BP	1	RNF6	up_VPOR_EC
GO:0006816	0.495	0.853	1	84	calcium ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0009260	0.495	0.853	1	83	ribonucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0046390	0.495	0.853	1	83	ribose phosphate biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0048666	0.495	0.858	1	258	neuron development	BP	1	CHL1	up_VPOR_VSMC
GO:0031344	0.495	0.855	1	161	regulation of cell projection organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0035850	0.495035819	0.85538	1	25	epithelial cell differentiation involved in	BP	1	FOXC2	up_ACOR_EC
GO:0001707	0.495403981	0.85514	1	25	mesoderm formation	BP	1	FOXC2	up_ACOR_EC
GO:0034612	0.495406783	0.77148	2	63	response to tumor necrosis factor	BP	1	NR1H4,CCDC3	up_ACOR_EC
GO:1901576	0.496	0.543	152	1877	organic substance biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,ADGRF5,ST8SIA6,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,ST6GAL1,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GK5,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,PTGS1,ENSCAFG00000017103,ZDHHC22,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,FAM3C,GUCY1A1,ODC1,SPTLC2,ARG2,B3GNT5,TARSL2,MTOR,SAMD8,ELF4,HHAT,BMP2,HMG20A,HHEX,CHST7,CREM,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,GALNT18,PRKD2,THOC1,SH3GLB1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,MRRF,PTGS2,TOP1,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,LBR,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,RAD17,IMPA1,SKIL,GPBP1,USP37,PIP5K1B,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,BCAT1,ZNF146,ATRX,NR4A1,ALDH1A3,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZDHHC6,ZEB1,TET2,ARHGEF2,	up_VCAV_EC
GO:0048666	0.496	0.592	23	258	neuron development	BP	1	EPHB1,EDNRB,IFRD1,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,NTN4,PPP3CA,PREX2,GDPD5,ENSCAFG00000010224,STMN1,PAK2,APOD,NCK1,FES,RAPGEF2,CREB1,SPTBN4,SKIL,ALS2	up_VCAV_EC
GO:0060485	0.496	0.65	8	93	mesenchyme development	BP	1	EDNRB,MEF2C,EDN1,MTOR,BMP2,JAG1,NUP133,HIF1A	up_VCAV_EC
GO:0015711	0.496	0.659	7	81	organic anion transport	BP	1	ATP8A1,LRRC8D,SLC35A3,SLC38A1,ABCA1,SLCO3A1,NOS2	up_VCAV_EC
GO:0032944	0.496	0.687	5	48	regulation of mononuclear cell	BP	1	CD274,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0050670	0.496	0.687	5	48	regulation of lymphocyte proliferation	BP	1	CD274,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0042592	0.496	0.733	3	522	homeostatic process	BP	1	LYN,HOXA3,STX4	down_ACOR_EC

GO:0006140	0.496	0.735	3	28	regulation of nucleotide metabolic process	BP	1	PPARGC1A,DDIT4,PARK7	up_ACOR_VSMC
GO:0006140	0.496	0.775	2	28	regulation of nucleotide metabolic process	BP	1	PGAM1,HIF1A	down_VSAP_EC
GO:0007166	0.496	0.78	2	686	cell surface receptor signaling pathway	BP	1	DKK2,LNPEP	up_AORT_EC
GO:0051254	0.496	0.775	2	431	positive regulation of RNA metabolic process	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0001510	0.496	0.777	2	22	RNA methylation	BP	1	WTAP,ZC3H13	up_VCAV_EC
GO:0071674	0.496	0.777	2	23	mononuclear cell migration	BP	1	PDGFB,HMGB1	up_VCAV_EC
GO:0001756	0.496	0.78	2	17	somitogenesis	BP	1	AXIN2,DLL1	up_VSAP_EC
GO:0022411	0.496	0.854	1	130	cellular component disassembly	BP	1	PDPN	down_ACOR_EC
GO:0071407	0.496	0.854	1	129	cellular response to organic cyclic compound	BP	1	NEDD4	down_ACOR_EC
GO:0046112	0.496	0.865	1	8	nucleobase biosynthetic process	BP	1	PRPS1	down_ACOR_VSMC
GO:2000514	0.496	0.859	1	13	regulation of CD4-positive, alpha-beta T cell	BP	1	LOXL3	down_VCAV_EC
GO:0001523	0.496	0.86	1	12	retinoid metabolic process	BP	1	RDH11	down_VSAP_EC
GO:0006911	0.496	0.86	1	11	phagocytosis, engulfment	BP	1	MYH9	down_VSAP_EC
GO:0048486	0.496	0.862	1	10	parasympathetic nervous system development	BP	1	NRP1	down_VSAP_EC
GO:0036445	0.496	0.87	1	6	neuronal stem cell division	BP	1	FGFR2	up_ACOR_VSMC
GO:0055057	0.496	0.87	1	6	neuroblast division	BP	1	FGFR2	up_ACOR_VSMC
GO:0072710	0.496	0.87	1	6	response to hydroxyurea	BP	1	ATRX	up_ACOR_VSMC
GO:0097329	0.496	0.87	1	6	response to antimetabolite	BP	1	ATRX	up_ACOR_VSMC
GO:0032101	0.496	0.854	1	173	regulation of response to external stimulus	BP	1	NR1H4	up_APUL_EC
GO:0051188	0.496	0.853	1	81	cofactor biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:1901699	0.496	0.854	1	164	cellular response to nitrogen compound	BP	1	CAV1	up_VSAP_VSMC
GO:0032774	0.496931414	0.58437	29	1073	RNA biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,SOX9,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0006325	0.497	0.595	21	234	chromatin organization	BP	1	IWS1,CHD7,GATA3,PSME4,NASP,UHRF2,ARID4B,BAZ1A,PRKD2,SMARCA4,NSD1,HIST1H1A,TOP1,ASF1A,NUP133,KDM5A,KDM3A,ATRX,HIST2H2AC,HP1BP3,TET2	up_VCAV_EC
GO:0006412	0.497	0.597	20	245	translation	BP	1	ILF3,EIF4A3,HNRNPD,VARS,RRBP1,PPP1R15B,MRPS18B,TRUB2,DHX33,FASTKD3,EIF5A,FARSA,NCL,MRPL37,RBM14,NOLC1,RARS,PUM3,MRPL18,EIF3M	down_ACOR_VSMC
GO:0048519	0.497	0.628	13	1554	negative regulation of biological process	BP	1	BARX1,CXHXorf57,HOOK3,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,FBP1,MTDH,ABHD5,TWF1,RNF6	up_VPOR_EC
GO:0045860	0.497	0.619	13	132	positive regulation of protein kinase activity	BP	1	MAP3K14,ARHGEF5,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CAMKK2,DDR2,TRAF7,SASH1,MAP2K2,TGFBR2	up_VSAP_EC
GO:2001020	0.497	0.649	8	88	regulation of response to DNA damage stimulus	BP	1	FIGNL1,THOC1,TIMELESS,ETAA1,HMGB1,PMAIP1,SKIL,CUL4A	up_VCAV_EC
GO:0031668	0.497	0.659	7	79	cellular response to extracellular stimulus	BP	1	SREBF1,SREBF2,RNF152,PDXP,FOSL1,MIOS,NUDT1	down_ACOR_VSMC
GO:0030522	0.497	0.659	7	67	intracellular receptor signaling pathway	BP	1	LBH,SKP2,MED14,AR,PTPN22,NOD2,PARK7	up_ACOR_VSMC
GO:0002253	0.497	0.668	6	92	activation of immune response	BP	1	NR1H4,PTPN2,EIF2B1,SKAP2,LYN,A2M	down_VSAP_EC
GO:0009892	0.497	0.708	4	835	negative regulation of metabolic process	BP	1	PITX1,HOXC10,CAV1,SHOX2	up_VSAP_VSMC
GO:0046824	0.497	0.734	3	30	positive regulation of nucleocytoplasmic	BP	1	NEDD4,RAN,DMAP1	down_ACOR_VSMC
GO:0098656	0.497	0.731	3	42	anion transmembrane transport	BP	1	LRRC8A,SLC38A1,CLCN3	down_VSAP_EC
GO:0071621	0.497	0.734	3	27	granulocyte chemotaxis	BP	1	C5AR2,SLIT2,IL17RC	up_VSAP_EC
GO:0014031	0.497	0.774	2	27	mesenchymal cell development	BP	1	HIF1A,NRP1	down_VSAP_EC

GO:0014032	0.497	0.774	2	27	neural crest cell development	BP	1	HIF1A,NRP1	down_VSAP_EC
GO:0080134	0.497	0.773	2	386	regulation of response to stress	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0001701	0.497	0.853	1	134	in utero embryonic development	BP	1	ACVRL1	down_ACOR_EC
GO:0006760	0.497	0.864	1	8	folic acid-containing compound metabolic	BP	1	GGH	down_ACOR_VSMC
GO:0031112	0.497	0.864	1	8	positive regulation of microtubule polymerization or	BP	1	RAC1	down_ACOR_VSMC
GO:0046174	0.497	0.864	1	8	polyol catabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:0046718	0.497	0.858	1	13	viral entry into host cell	BP	1	TRIM8	down_VCAV_EC
GO:0050885	0.497	0.857	1	14	neuromuscular process controlling balance	BP	1	ENSCAFG00000017708	down_VCAV_EC
GO:0060429	0.497	0.858	1	341	epithelium development	BP	1	CITED2	down_VPOR_EC
GO:0006376	0.497	0.86	1	11	mRNA splice site selection	BP	1	CELF1	down_VSAP_EC
GO:0009994	0.497	0.86	1	11	oocyte differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0009154	0.497	0.867	1	7	purine ribonucleotide catabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:0042119	0.497	0.866	1	7	neutrophil activation	BP	1	F2RL1	up_ACOR_VSMC
GO:0003272	0.497	0.866	1	7	endocardial cushion formation	BP	1	TBX20	up_ACOR_VSMC
GO:0071875	0.497	0.869	1	6	adrenergic receptor signaling pathway	BP	1	ADRA1B	up_ACOR_VSMC
GO:0071880	0.497	0.869	1	6	adenylate cyclase-activating adrenergic receptor signaling	BP	1	ADRA1B	up_ACOR_VSMC
GO:0050776	0.497	0.854	1	173	regulation of immune response	BP	1	NR1H4	up_APUL_EC
GO:0045933	0.497	0.864	1	8	positive regulation of muscle contraction	BP	1	ATP2A1	up_VCAV_EC
GO:2001028	0.497	0.864	1	8	positive regulation of endothelial cell	BP	1	PRKD2	up_VCAV_EC
GO:0072358	0.497	0.856	1	268	cardiovascular system development	BP	1	EYA1	up_VFEM_VSMC
GO:0060322	0.497	0.854	1	193	head development	BP	1	FLRT3	up_VPUL_EC
GO:0060638	0.497	0.866	1	7	mesenchymal-epithelial cell signaling	BP	1	FGF7	up_VSAP_EC
GO:0071801	0.497	0.866	1	7	regulation of podosome assembly	BP	1	ARHGEF5	up_VSAP_EC
GO:0090322	0.497	0.866	1	7	regulation of superoxide metabolic process	BP	1	F2RL1	up_VSAP_EC
GO:1901863	0.497104085	0.85401	1	25	positive regulation of muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0055114	0.498	0.61	15	157	oxidation-reduction process	BP	1	LEP,PPARGC1A,FRRS1,FMO4,TMX3,ACAD11,BNIP3,SUMF1,PYGM,GAA,INPP5K,SLC25A12,NDUFA4L2,PARK7,FMO3	up_ACOR_VSMC
GO:0006412	0.498	0.613	14	245	translation	BP	1	CARS,SARS,AARS,PUM3,SESN2,MRPL1,YARS,TARS,NARS,EIF4EBP1,CNOT7,EIF5,EIF2S1,RSL24D1	down_VSAP_EC
GO:0060627	0.498	0.632	10	165	regulation of vesicle-mediated transport	BP	1	VEGFA,SERPINE1,MSN,YIPF5,APOE,LYN,GSK3B,SDC4,REST,LRRTM2	down_VSAP_EC
GO:0062012	0.498	0.634	10	100	regulation of small molecule metabolic	BP	1	INSIG2,ACACB,C1QTNF2,LMF1,PDK2,CLYBL,PASK,LONP2,NCOA2,DDIT4	up_VSAP_EC
GO:0060255	0.498	0.662	8	1782	regulation of macromolecule metabolic	BP	1	EYA1,HOXA9,MAP2K6,HOXA10,HOXA7,SIX1,YBX3,CYP26B1	up_VFEM_EC
GO:0035303	0.498	0.669	6	65	regulation of dephosphorylation	BP	1	PPP2R5A,MEF2C,BMP2,PPP1R2,SWAP70,FKBP15	up_VCAV_EC
GO:0034767	0.498	0.732	3	31	positive regulation of ion transmembrane transport	BP	1	RELN,APLNR,PLCG2	up_VCAV_EC
GO:1902106	0.498	0.732	3	31	negative regulation of leukocyte differentiation	BP	1	HMGB1,CUL4A,TJP2	up_VCAV_EC
GO:0014013	0.498	0.777	2	19	regulation of gliogenesis	BP	1	NF2,EZH2	down_ACOR_VSMC
GO:0038061	0.498	0.772	2	34	NIK/NF-kappaB signaling	BP	1	SASH1,GREM1	down_VCAV_EC
GO:0002377	0.498	0.774	2	26	immunoglobulin production	BP	1	TFRC,BTK	down_VSAP_EC
GO:0006814	0.498	0.774	2	28	sodium ion transport	BP	1	NKAIN1,YWHAH	down_VSAP_EC
GO:0008543	0.498	0.773	2	27	fibroblast growth factor receptor signaling	BP	1	SULF1,CTNNB1	down_VSAP_EC

GO:0051963	0.498	0.774	2	26	regulation of synapse assembly	BP	1	LRRTM2,SIX4	down_VSAP_EC
GO:0042058	0.498	0.779	2	17	regulation of epidermal growth factor receptor	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:1905954	0.498	0.777	2	19	positive regulation of lipid localization	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0048598	0.498	0.77	2	207	embryonic morphogenesis	BP	1	HOXA3,ACVR2A	up_VPOR_EC
GO:0010558	0.498	0.773	2	392	negative regulation of macromolecule biosynthetic process	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0002753	0.498	0.779	2	17	cytoplasmic pattern recognition receptor	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0009261	0.498	0.863	1	8	ribonucleotide catabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:0036314	0.498	0.864	1	8	response to sterol	BP	1	INSIG1	down_ACOR_VSMC
GO:0043928	0.498	0.864	1	8	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	BP	1	EXOSC5	down_ACOR_VSMC
GO:0090279	0.498	0.863	1	8	regulation of calcium ion import	BP	1	SLC30A1	down_ACOR_VSMC
GO:0090314	0.498	0.859	1	11	positive regulation of protein targeting to membrane	BP	1	MYO1C	down_VSAP_EC
GO:1904294	0.498	0.866	1	7	positive regulation of ERAD pathway	BP	1	HERPUD1	up_ACOR_VSMC
GO:0021675	0.498	0.853	1	29	nerve development	BP	1	PLXNA4	up_AFEM_EC
GO:0055080	0.498	0.853	1	176	cation homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0090036	0.498	0.866	1	7	regulation of protein kinase C signaling	BP	1	AKAP12	up_VCAV_EC
GO:1905521	0.498	0.862	1	9	regulation of macrophage migration	BP	1	MMP28	up_VCAV_EC
GO:0009615	0.498	0.851	1	83	response to virus	BP	1	OAS3	up_VPOR_EC
GO:0007267	0.498	0.857	1	332	cell-cell signaling	BP	1	TBX5	up_VPUL_VSMC
GO:0060026	0.498	0.866	1	7	convergent extension	BP	1	WNT11	up_VSAP_EC
GO:0008038	0.498	0.866	1	7	neuron recognition	BP	1	AMIGO1	up_VSAP_EC
GO:0032368	0.498259851	0.85305	1	26	regulation of lipid transport	BP	1	PRKCD	up_ACOR_EC
GO:0048519	0.499	0.553	78	1554	negative regulation of biological process	BP	1	CST3,GPAM,NOTCH2,SLC35F6,KIRREL1,DCN,NAB2,NDN,PRNP,MT2A,SDC4,VASN,FBN1,BGN,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,CHID1,AKT1S1,CHRDL1,TIMP2,AKT2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PLCL1,TRIM8,PRMT6,TMEM161A,CXXC5,ASPN,POLDIP2,LRPAP1,THY1,ARHGAP10,TLX2,CC2D1A,B4GALT1,GLI3,PARK7,ZFP36L1,MYDGF,CLEC16A,BPI,CYBA,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,SPRED1,RAB7B,A2M,TSC22D3,GLIS2,TWIST2,ARHGAP1,PRKCSH,SHC1,PYM1,FBH1,GREM1,PLEKHH2,NPHP4,EVI5L,FOXO3,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA,BRSK1	down_VCAV_EC
GO:0009790	0.499	0.576	33	335	embryo development	BP	1	SMAD6,AFF3,HTR2B,MBP,RECK,SHROOM3,BMP4,LNPK,FGFR2,GJA1,SEC24B,LATS2,CITED2,SPINT1,LMO4,EGLN1,ENSCAFG00000006238,NRP1,SPINT2,TBX20,TBX5,FZD3,FRS2,DAG1,LAMA3,PSEN1,PCSK6,CHD7,C10H2orf49,EDN1,INPP5K,WDR48,TEAD1	up_ACOR_VSMC
GO:0042110	0.499	0.655	7	109	T cell activation	BP	1	SOCS5,FAM49B,MSN,PTPN2,CTNNB1,TFRC,SDC4	down_VSAP_EC
GO:0021700	0.499	0.668	6	65	developmental maturation	BP	1	TRIP13,FBXO5,XYLT1,GREM1,ARCN1,CDC20	down_ACOR_VSMC
GO:2001236	0.499	0.669	6	59	regulation of extrinsic apoptotic signaling	BP	1	RBCK1,RAF1,STX4,HTRA2,HMOX1,DEDD2	up_VSAP_EC
GO:0071478	0.499	0.683	5	58	cellular response to radiation	BP	1	GATA3,FIGNL1,MAPK13,USP28,BLM	up_VCAV_EC
GO:0030038	0.499	0.732	3	31	contractile actin filament bundle assembly	BP	1	NF2,STMN1,RAC1	down_ACOR_VSMC
GO:0043149	0.499	0.732	3	31	stress fiber assembly	BP	1	NF2,STMN1,RAC1	down_ACOR_VSMC
GO:0014706	0.499	0.725	3	112	striated muscle tissue development	BP	1	DLL1,GREM1,BVES	up_AFEM_EC

GO:0043473	0.499	0.732	3	28	pigmentation	BP	1	RAB11B,HPS4,VANGL1	up_VSAP_EC
GO:1905952	0.499	0.771	2	33	regulation of lipid localization	BP	1	AKT2,SCP2	down_VCAV_EC
GO:0006278	0.499	0.773	2	26	RNA-dependent DNA biosynthetic process	BP	1	SMG7,CTNNB1	down_VSAP_EC
GO:0007004	0.499	0.773	2	26	telomere maintenance via telomerase	BP	1	SMG7,CTNNB1	down_VSAP_EC
GO:0050810	0.499	0.778	2	17	regulation of steroid biosynthetic process	BP	1	LEP,DKKL1	up_ACOR_VSMC
GO:0009135	0.499	0.775	2	22	purine nucleoside diphosphate metabolic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0009179	0.499	0.775	2	22	purine ribonucleoside diphosphate metabolic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0010171	0.499	0.777	2	18	body morphogenesis	BP	1	TIPARP,CDON	up_VCAV_EC
GO:0046031	0.499	0.775	2	22	ADP metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:1990266	0.499	0.774	2	24	neutrophil migration	BP	1	CXCL8,PDE4D	up_VCAV_EC
GO:0030858	0.499	0.778	2	17	positive regulation of epithelial cell	BP	1	BTG1,ACVRL1	up_VSAP_EC
GO:0042176	0.499	0.852	1	140	regulation of protein catabolic process	BP	1	NEDD4	down_ACOR_EC
GO:0032331	0.499	0.863	1	8	negative regulation of chondrocyte	BP	1	GREM1	down_ACOR_VSMC
GO:0032620	0.499	0.863	1	8	interleukin-17 production	BP	1	ARG2	down_ACOR_VSMC
GO:0061037	0.499	0.863	1	8	negative regulation of cartilage development	BP	1	GREM1	down_ACOR_VSMC
GO:0090312	0.499	0.863	1	8	positive regulation of protein deacetylation	BP	1	SREBF1	down_ACOR_VSMC
GO:0060421	0.499	0.856	1	14	positive regulation of heart growth	BP	1	BMPR1A	down_VCAV_EC
GO:0097734	0.499	0.857	1	13	extracellular exosome biogenesis	BP	1	SDC4	down_VCAV_EC
GO:1990182	0.499	0.857	1	13	exosomal secretion	BP	1	SDC4	down_VCAV_EC
GO:0048286	0.499	0.859	1	11	lung alveolus development	BP	1	ERRFI1	down_VSAP_EC
GO:0007062	0.499	0.852	1	29	sister chromatid cohesion	BP	1	AXIN2	up_AFEM_EC
GO:0051046	0.499	0.852	1	174	regulation of secretion	BP	1	NR1H4	up_APUL_EC
GO:0043516	0.499	0.86	1	10	regulation of DNA damage response, signal transduction by p53 class	BP	1	PMAIP1	up_VCAV_EC
GO:2000758	0.499	0.863	1	8	positive regulation of peptidyl-lysine acetylation	BP	1	GATA3	up_VCAV_EC
GO:0032373	0.499	0.863	1	8	positive regulation of sterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0032376	0.499	0.863	1	8	positive regulation of cholesterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0032870	0.499	0.852	1	162	cellular response to hormone stimulus	BP	1	AVPR1A	up_VFEM_EC
GO:0033523	0.499	0.865	1	7	histone H2B ubiquitination	BP	1	CDK9	up_VSAP_EC
GO:0043558	0.499	0.865	1	7	regulation of translational initiation in response to	BP	1	NCK1	up_VSAP_EC
GO:0043506	0.49939851	0.85247	1	25	regulation of JUN kinase activity	BP	1	FZD5	up_ACOR_EC
GO:0008344	0.499969219	0.85209	1	25	adult locomotory behavior	BP	1	TMOD1	up_ACOR_EC
GO:0032446	0.5	0.585	25	255	protein modification by small protein conjugation	BP	1	FAM107A,ABL1,KLHL36,DTX2,DDB2,CISH,KLHL24,KLHDC8B,TRAF7,RBCK1,KBTBD12,RNF24,SASH1,FBXO4,RMND5A,FBXW5,FBXO7,ASB8,RNF166,CDK9,KDM2B,RNF216,CDC26,ZER1,KEAP1	up_VSAP_EC
GO:0050790	0.5	0.615	13	532	regulation of catalytic activity	BP	1	LEP,CRYAB,F3,MYO1D,GREM1,RASGEF1B,LRRC15,RECK,DCUN1D3,BVES,ACACB,CCL5,ADAM17	up_AFEM_EC
GO:0030111	0.5	0.626	11	108	regulation of Wnt signaling pathway	BP	1	LGR6,ZRANB1,RECK,MLLT3,FERMT1,FGFR2,LATS2,ZNRF3,CLSTN1,PSEN1,DISC1	up_ACOR_VSMC
GO:0002791	0.5	0.637	9	104	regulation of peptide secretion	BP	1	FERMT1,CHD7,TLR4,GATA3,ARG2,CD200,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0070997	0.5	0.68	5	93	neuron death	BP	1	PRNP,AKT2,PARK7,FOXO3,THRB	down_VCAV_EC
GO:0002218	0.5	0.726	3	53	activation of innate immune response	BP	1	CYBA,MAVS,RAB7B	down_VCAV_EC

GO:0007173	0.5	0.732	3	27	epidermal growth factor receptor signaling	BP	1	RASSF2,APP,PSEN1	up_ACOR_VSMC
GO:0009056	0.5	0.779	2	755	catabolic process	BP	1	ETFA,USP33	down_AFEM_EC
GO:0030042	0.5	0.777	2	17	actin filament depolymerization	BP	1	ACTN2,F2RL1	up_ACOR_VSMC
GO:0030834	0.5	0.777	2	17	regulation of actin filament depolymerization	BP	1	ACTN2,F2RL1	up_ACOR_VSMC
GO:0038034	0.5	0.774	2	21	signal transduction in absence of ligand	BP	1	CTNNA1,RIPK1	up_VCAV_EC
GO:0097192	0.5	0.774	2	21	extrinsic apoptotic signaling pathway in	BP	1	CTNNA1,RIPK1	up_VCAV_EC
GO:0009968	0.5	0.771	2	392	negative regulation of signal transduction	BP	1	EYA1,CYP26B1	up_VFEM_EC
GO:0051049	0.5	0.773	2	479	regulation of transport	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:1900015	0.5	0.777	2	17	regulation of cytokine production involved in inflammatory response	BP	1	IL17RC,MYD88	up_VSAP_EC
GO:0051259	0.5	0.851	1	140	protein complex oligomerization	BP	1	IGF1R	down_ACOR_EC
GO:0035970	0.5	0.862	1	8	peptidyl-threonine dephosphorylation	BP	1	PPM1G	down_ACOR_VSMC
GO:0010676	0.5	0.856	1	13	positive regulation of cellular carbohydrate	BP	1	AKT2	down_VCAV_EC
GO:0061217	0.5	0.856	1	13	regulation of mesonephros	BP	1	GREM1	down_VCAV_EC
GO:0060351	0.5	0.858	1	11	cartilage development involved in endochondral bone morphogenesis	BP	1	SERPINH1	down_VSAP_EC
GO:0001710	0.5	0.865	1	7	mesodermal cell fate commitment	BP	1	BMP4	up_ACOR_VSMC
GO:0034367	0.5	0.864	1	7	protein-containing complex remodeling	BP	1	LCAT	up_ACOR_VSMC
GO:0034368	0.5	0.864	1	7	protein-lipid complex remodeling	BP	1	LCAT	up_ACOR_VSMC
GO:0034369	0.5	0.864	1	7	plasma lipoprotein particle remodeling	BP	1	LCAT	up_ACOR_VSMC
GO:0048846	0.5	0.867	1	6	axon extension involved in axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:1902284	0.5	0.867	1	6	neuron projection extension involved in neuron projection	BP	1	NRP1	up_ACOR_VSMC
GO:1904738	0.5	0.868	1	6	vascular associated smooth muscle cell	BP	1	DOCK5	up_ACOR_VSMC
GO:1904752	0.5	0.868	1	6	regulation of vascular associated smooth muscle	BP	1	DOCK5	up_ACOR_VSMC
GO:0051657	0.5	0.865	1	7	maintenance of organelle location	BP	1	ATP2A1	up_VCAV_EC
GO:0060333	0.5	0.862	1	8	interferon-gamma-mediated signaling	BP	1	NLRC5	up_VCAV_EC
GO:0010506	0.5	0.85	1	86	regulation of autophagy	BP	1	MTDH	up_VPOR_EC
GO:0090307	0.500346663	0.85165	1	26	mitotic spindle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0048514	0.500471015	0.66337	6	214	blood vessel morphogenesis	BP	1	AQP1,ENSCAFG00000004331,FZD5,ESM1,FOXC2,NRP1	up_ACOR_EC
GO:0050790	0.501	0.564	45	532	regulation of catalytic activity	BP	1	HMGB1,IRAK1,HMGCR,HNRNPD,UBE2S,SLC29A1,PRELID1,RFC2,BIRC5,CAV1,RFC5,RFC3,NF2,AURKB,CDKN2C,ABHD5,EZH2,GREM1,MAP3K20,RFC4,NEK2,PCNA,CKS2,PDCD2,DHCR24,RAP2C,YWHAB,CYCS,NUP62,EMP2,IQGAP1,IQGAP2,HMGB2,ENSCAFG00000005299,CLSPN,CDC20,AIFM1,TRAPPC6A,KNL1,DELE1,CCNB3,NUS1,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC
GO:0044087	0.501	0.578	29	339	regulation of cellular component biogenesis	BP	1	FSCN1,HMGB1,ANLN,STXBP6,SMC1A,CAPG,SDC1,INSIG1,CAV1,NF2,STMN1,GREM1,DHX33,PREB,RAC1,NUP62,FOSL1,PLK4,IQGAP2,CDC42EP4,SMC3,STAG1,EZR,RBM14,CORO1A,ARPC1B,PSMC1,SIX4,TPBG	down_ACOR_VSMC
GO:0019693	0.501	0.601	17	172	ribose phosphate metabolic process	BP	1	ACSM3,ACACB,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0022411	0.501	0.615	13	130	cellular component disassembly	BP	1	FGF13,DNAJC6,ACTN2,MID1,CTSS,F2RL1,GABARAPL1,BNIP3,SMARCD3,LAMP2,DDR2,DDIT4,KIF9	up_ACOR_VSMC
GO:0043068	0.501	0.629	10	190	positive regulation of programmed cell death	BP	1	PRNP,CLIP3,B4GALT1,PARK7,ADAMTSL4,IFT57,GSDME,FBH1,FOXO3,ZBTB16	down_VCAV_EC

GO:0048705	0.501	0.664	6	95	skeletal system morphogenesis	BP	1	SULF1,SERPINH1,CHSY1,HOXB7,CTNNB1,SIX4	down_VSAP_EC
GO:0034613	0.501	0.681	5	576	cellular protein localization	BP	1	MZT1,HOOK3,XPOT,GCC2,SRP54	up_VPOR_EC
GO:0032271	0.501	0.698	4	73	regulation of protein polymerization	BP	1	KIRREL1,CLIP3,ENSCAFG00000014978,ACTR3B	down_VCAV_EC
GO:1903076	0.501	0.729	3	32	regulation of protein localization to plasma	BP	1	ACSL3,MMP14,EZR	down_ACOR_VSMC
GO:0032091	0.501	0.728	3	34	negative regulation of protein binding	BP	1	PDGFB,RALB,STMN1	up_VCAV_EC
GO:0032637	0.501	0.771	2	26	interleukin-8 production	BP	1	SERPINE1,DDIT3	down_VSAP_EC
GO:0051591	0.501	0.777	2	16	response to cAMP	BP	1	AKAP6,INPP5K	up_ACOR_VSMC
GO:1901019	0.501	0.774	2	20	regulation of calcium ion transmembrane transporter activity	BP	1	PDE4D,PLCG2	up_VCAV_EC
GO:0002763	0.501	0.777	2	17	positive regulation of myeloid leukocyte	BP	1	PPARGC1B,ZFP36L1	up_VSAP_EC
GO:0051965	0.501	0.776	2	17	positive regulation of synapse assembly	BP	1	AMIGO1,LRRN3	up_VSAP_EC
GO:0090342	0.501	0.776	2	17	regulation of cell aging	BP	1	ABL1,YPEL3	up_VSAP_EC
GO:0031347	0.501	0.851	1	144	regulation of defense response	BP	1	LYN	down_ACOR_EC
GO:0045662	0.501	0.862	1	8	negative regulation of myoblast differentiation	BP	1	PPARD	down_ACOR_VSMC
GO:0006805	0.501	0.862	1	8	xenobiotic metabolic process	BP	1	GSTO1	down_ACOR_VSMC
GO:0044237	0.501	1	1	3491	cellular metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0045123	0.501	0.858	1	11	cellular extravasation	BP	1	CX3CL1	down_VSAP_EC
GO:0007175	0.501	0.864	1	7	negative regulation of epidermal growth factor-activated receptor activity	BP	1	PSEN1	up_ACOR_VSMC
GO:0030277	0.501	0.864	1	7	maintenance of gastrointestinal	BP	1	NOD2	up_ACOR_VSMC
GO:0031629	0.501	0.862	1	8	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	STX11	up_ACOR_VSMC
GO:0099500	0.501	0.862	1	8	vesicle fusion to plasma membrane	BP	1	STX11	up_ACOR_VSMC
GO:2000272	0.501	0.864	1	7	negative regulation of signaling receptor activity	BP	1	PSEN1	up_ACOR_VSMC
GO:0048585	0.501	0.858	1	475	negative regulation of response to stimulus	BP	1	EYA1	up_AFEM_VSMC
GO:1902533	0.501	0.853	1	271	positive regulation of intracellular signal	BP	1	ANKRD6	up_VPOR_VSMC
GO:0002043	0.501	0.864	1	7	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	HMOX1	up_VSAP_EC
GO:0016075	0.501	0.864	1	7	rRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0035904	0.501164043	0.85129	1	25	aorta development	BP	1	SMAD6	up_ACOR_EC
GO:0051303	0.501893076	0.85061	1	26	establishment of chromosome localization	BP	1	CHMP4B	up_ACOR_EC
GO:0009058	0.502	0.615	16	1910	biosynthetic process	BP	1	BARX1,OSTC,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0010608	0.502	0.642	8	154	posttranscriptional regulation of gene	BP	1	LARP6,SAMD4B,EIF3K,EEF2,ZFP36L1,PYM1,FOXO3,EIF4EBP1	down_VCAV_EC
GO:0043434	0.502	0.644	8	80	response to peptide hormone	BP	1	GOT1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0072330	0.502	0.665	6	68	monocarboxylic acid biosynthetic process	BP	1	SCD,INSIG1,BRCA1,ELOVL1,ELOVL6,LIPC	down_ACOR_VSMC
GO:0045446	0.502	0.729	3	32	endothelial cell differentiation	BP	1	RAP2C,HOXB5,EZR	down_ACOR_VSMC
GO:0006955	0.502	0.724	3	327	immune response	BP	1	ARHGEF2,OAS3,ENSCAFG00000032731	up_VPOR_EC
GO:0007267	0.502	0.724	3	332	cell-cell signaling	BP	1	BARX1,HTR7,SV2C	up_VPOR_EC
GO:0033138	0.502	0.73	3	28	positive regulation of peptidyl-serine	BP	1	TNKS1BP1,RAF1,BAG4	up_VSAP_EC
GO:0065007	0.502	0.874	2	3499	biological regulation	BP	1	PLCL1,MOSPD1	down_VFEM_EC
GO:0044281	0.502	0.774	2	622	small molecule metabolic process	BP	1	GATM,FBP1	up_VFEM_VSMC

GO:0032516	0.502	0.861	1	8	positive regulation of phosphoprotein phosphatase activity	BP	1	SLC29A1	down_ACOR_VSMC
GO:0070296	0.502	0.861	1	8	sarcoplasmic reticulum calcium ion transport	BP	1	GSTO1	down_ACOR_VSMC
GO:1902188	0.502	0.861	1	8	positive regulation of viral release from host cell	BP	1	SMC3	down_ACOR_VSMC
GO:1901564	0.502	0.913	1	2053	organonitrogen compound metabolic	BP	1	CST3	down_AORT_EC
GO:0001941	0.502	0.854	1	14	postsynaptic membrane organization	BP	1	CDH2	down_VCAV_EC
GO:0045880	0.502	0.854	1	14	positive regulation of smoothened signaling	BP	1	EVC	down_VCAV_EC
GO:0071622	0.502	0.855	1	13	regulation of granulocyte chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0009648	0.502	0.857	1	11	photoperiodism	BP	1	BHLHE40	down_VSAP_EC
GO:0043153	0.502	0.857	1	11	entrainment of circadian clock by photoperiod	BP	1	BHLHE40	down_VSAP_EC
GO:1903793	0.502	0.857	1	11	positive regulation of anion transport	BP	1	APOE	down_VSAP_EC
GO:0032731	0.502	0.863	1	7	positive regulation of interleukin-1 beta	BP	1	NOD2	up_ACOR_VSMC
GO:0060675	0.502	0.85	1	29	ureteric bud morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:1900076	0.502	0.85	1	29	regulation of cellular response to insulin	BP	1	KANK1	up_AFEM_EC
GO:1901888	0.502	0.85	1	29	regulation of cell junction assembly	BP	1	GREM1	up_AFEM_EC
GO:0007169	0.502	0.851	1	178	transmembrane receptor protein tyrosine kinase	BP	1	NR1H4	up_APUL_EC
GO:0040008	0.502	0.851	1	179	regulation of growth	BP	1	TBX5	up_APUL_EC
GO:0060999	0.502	0.863	1	7	positive regulation of dendritic spine	BP	1	RELN	up_VCAV_EC
GO:0051093	0.502	0.852	1	273	negative regulation of developmental process	BP	1	HOXA9	up_VFEM_VSMC
GO:0044283	0.502	0.851	1	201	small molecule biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0048668	0.502	0.863	1	7	collateral sprouting	BP	1	ABL1	up_VSAP_EC
GO:2000251	0.502	0.863	1	7	positive regulation of actin cytoskeleton	BP	1	ABL1	up_VSAP_EC
GO:0032870	0.502	0.85	1	162	cellular response to hormone stimulus	BP	1	CAV1	up_VSAP_VSMC
GO:2000779	0.502164886	0.85061	1	25	regulation of double-strand break repair	BP	1	FIGNL1	up_ACOR_EC
GO:0001775	0.503	0.594	19	219	cell activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,TXLNA,MMP14,HMGB3,ARG2,TFRC,ITGB3,FAM49B,TOX,CORO1A,ELF4,PRMT5,HOXA9,JMJD6,CTPS1,PIK3CD	down_ACOR_VSMC
GO:0046486	0.503	0.635	9	102	glycerolipid metabolic process	BP	1	ACSL3,SREBF1,CTDNEP1,INSIG1,CAV1,ABHD5,VAC14,LIPC,GK5	down_ACOR_VSMC
GO:1902115	0.503	0.644	8	77	regulation of organelle assembly	BP	1	FEZ1,PRKAA2,EVI5L,ATXN2,EDN1,ASAP1,KIF9,FEZ2	up_ACOR_VSMC
GO:0001503	0.503	0.651	7	109	ossification	BP	1	ILK,FHL2,CHSY1,HIF1A,CTNNB1,REST,EXT1	down_VSAP_EC
GO:0006486	0.503	0.652	7	91	protein glycosylation	BP	1	ST8SIA6,ST6GAL1,B3GNT5,ST3GAL6,GALNT18,MFNG,TET2	up_VCAV_EC
GO:0043413	0.503	0.652	7	91	macromolecule glycosylation	BP	1	ST8SIA6,ST6GAL1,B3GNT5,ST3GAL6,GALNT18,MFNG,TET2	up_VCAV_EC
GO:1901605	0.503	0.664	6	67	alpha-amino acid metabolic process	BP	1	BCAT1,PFAS,ARG2,AADAT,CTH,CTPS1	down_ACOR_VSMC
GO:1901342	0.503	0.662	6	114	regulation of vasculature development	BP	1	HSPB6,DCN,MYDGF,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0009913	0.503	0.681	5	47	epidermal cell differentiation	BP	1	EXPH5,BMP4,SEC24B,LATS2,FOSL2	up_ACOR_VSMC
GO:0016441	0.503	0.728	3	30	posttranscriptional gene silencing	BP	1	SRRT,RAN,RBM14	down_ACOR_VSMC
GO:0035194	0.503	0.728	3	30	posttranscriptional gene silencing by RNA	BP	1	SRRT,RAN,RBM14	down_ACOR_VSMC
GO:0120162	0.503	0.727	3	31	positive regulation of cold-induced thermogenesis	BP	1	CAV1,ADIPOR2,ELOVL6	down_ACOR_VSMC
GO:0009119	0.503	0.768	2	32	ribonucleoside metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:0016064	0.503	0.77	2	26	immunoglobulin mediated immune	BP	1	TFRC,BTK	down_VSAP_EC
GO:0019724	0.503	0.77	2	26	B cell mediated immunity	BP	1	TFRC,BTK	down_VSAP_EC

GO:0140056	0.503	0.769	2	28	organelle localization by membrane tethering	BP	1	EXOC5,ESYT3	down_VSAP_EC
GO:0017144	0.503	0.765	2	199	drug metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0000266	0.503	0.775	2	17	mitochondrial fission	BP	1	DDHD1,MTFR1L	up_VSAP_EC
GO:0031663	0.503	0.775	2	17	lipopolysaccharide-mediated signaling	BP	1	SASH1,MYD88	up_VSAP_EC
GO:0032770	0.503	0.861	1	8	positive regulation of monooxygenase activity	BP	1	NUS1	down_ACOR_VSMC
GO:0033028	0.503	0.86	1	8	myeloid cell apoptotic process	BP	1	PIK3CD	down_ACOR_VSMC
GO:0030835	0.503	0.856	1	11	negative regulation of actin filament	BP	1	CAPG	down_VSAP_EC
GO:0048488	0.503	0.857	1	10	synaptic vesicle endocytosis	BP	1	CANX	down_VSAP_EC
GO:0060343	0.503	0.856	1	11	trabecula formation	BP	1	FHL2	down_VSAP_EC
GO:0060674	0.503	0.855	1	12	placenta blood vessel development	BP	1	TMED2	down_VSAP_EC
GO:0140238	0.503	0.857	1	10	presynaptic endocytosis	BP	1	CANX	down_VSAP_EC
GO:0033539	0.503	0.862	1	7	fatty acid beta-oxidation using acyl-CoA	BP	1	ACAD11	up_ACOR_VSMC
GO:0048011	0.503	0.863	1	7	neurotrophin TRK receptor signaling	BP	1	TMEM108	up_ACOR_VSMC
GO:1904293	0.503	0.862	1	7	negative regulation of ERAD pathway	BP	1	OS9	up_ACOR_VSMC
GO:0043255	0.503	0.849	1	29	regulation of carbohydrate biosynthetic	BP	1	LEP	up_AFEM_EC
GO:0002792	0.503	0.849	1	29	negative regulation of peptide secretion	BP	1	LEP	up_AFEM_EC
GO:0071479	0.503	0.849	1	29	cellular response to ionizing radiation	BP	1	CRYAB	up_AFEM_EC
GO:0098773	0.503	0.85	1	29	skin epidermis development	BP	1	DLL1	up_AFEM_EC
GO:2000045	0.503	0.849	1	29	regulation of G1/S transition of mitotic cell	BP	1	DCUN1D3	up_AFEM_EC
GO:2000106	0.503	0.849	1	29	regulation of leukocyte apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0071705	0.503	0.86	1	582	nitrogen compound transport	BP	1	ARG2	up_AORT_VSMC
GO:0090407	0.503	0.849	1	177	organophosphate biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0048668	0.503	0.862	1	7	collateral sprouting	BP	1	IFRD1	up_VCAV_EC
GO:0062009	0.503	0.86	1	8	secondary palate development	BP	1	CHD7	up_VCAV_EC
GO:2000737	0.503	0.863	1	7	negative regulation of stem cell differentiation	BP	1	JAG1	up_VCAV_EC
GO:0030336	0.503	0.848	1	86	negative regulation of cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0051093	0.503	0.852	1	273	negative regulation of developmental process	BP	1	NKX2-5	up_VPOR_VSMC
GO:1903214	0.503	0.863	1	7	regulation of protein targeting to	BP	1	BAG4	up_VSAP_EC
GO:0043114	0.503	0.863	1	7	regulation of vascular permeability	BP	1	SLIT2	up_VSAP_EC
GO:0030163	0.503338127	0.62633	10	365	protein catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,AZIN2,HM13	up_ACOR_EC
GO:1901568	0.503468916	0.84954	1	26	fatty acid derivative metabolic process	BP	1	PTGDS	up_ACOR_EC
GO:0044257	0.503483696	0.63261	9	327	cellular protein catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,HM13	up_ACOR_EC
GO:0015893	0.503528896	0.8495	1	26	drug transport	BP	1	AQP1	up_ACOR_EC
GO:0042632	0.503633099	0.84925	1	27	cholesterol homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0010469	0.503761291	0.84934	1	26	regulation of signaling receptor activity	BP	1	MAPK8IP2	up_ACOR_EC
GO:0098655	0.504	0.616	12	142	cation transmembrane transport	BP	1	NNT,NEDD4,CAV1,SLC30A1,GSTO1,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0051098	0.504	0.64	8	129	regulation of binding	BP	1	TRIB3,PLCL1,CTNNB1,APOE,DDIT3,GSK3B,CALM1,DISC1	down_VSAP_EC
GO:0098727	0.504	0.664	6	60	maintenance of cell number	BP	1	DLL1,SAV1,KDM2B,ZFP36L2,RAF1,LBH	up_VSAP_EC
GO:0031338	0.504	0.728	3	28	regulation of vesicle fusion	BP	1	TBC1D10C,TBC1D2B,VPS11	up_VSAP_EC

GO:1903051	0.504	0.768	2	29	negative regulation of proteolysis involved in cellular protein catabolic	BP	1	UCHL5,USP14	down_VSAP_EC
GO:1901264	0.504	0.773	2	18	carbohydrate derivative transport	BP	1	SLC17A5,PRKCE	up_ACOR_VSMC
GO:0002064	0.504	0.764	2	71	epithelial cell development	BP	1	DLL1,FOSL2	up_AFEM_EC
GO:0051248	0.504	0.852	1	316	negative regulation of protein metabolic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0030901	0.504	0.853	1	14	midbrain development	BP	1	SMAD9	down_VCAV_EC
GO:0035909	0.504	0.853	1	14	aorta morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0001709	0.504	0.856	1	11	cell fate determination	BP	1	CTNNB1	down_VSAP_EC
GO:0006022	0.504	0.849	1	29	aminoglycan metabolic process	BP	1	XYLT1	up_AFEM_EC
GO:0045833	0.504	0.849	1	29	negative regulation of lipid metabolic process	BP	1	ACACB	up_AFEM_EC
GO:0060688	0.504	0.849	1	29	regulation of morphogenesis of a	BP	1	GREM1	up_AFEM_EC
GO:0042327	0.504	0.851	1	289	positive regulation of phosphorylation	BP	1	TAOK1	up_AORT_EC
GO:0048878	0.504	0.851	1	283	chemical homeostasis	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0008610	0.504	0.849	1	177	lipid biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0030155	0.504	0.849	1	180	regulation of cell adhesion	BP	1	NPNT	up_APUL_EC
GO:0008207	0.504	0.86	1	8	C21-steroid hormone metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0032988	0.504	0.86	1	8	ribonucleoprotein complex disassembly	BP	1	MRRF	up_VCAV_EC
GO:0071709	0.504	0.86	1	8	membrane assembly	BP	1	CAV2	up_VCAV_EC
GO:0031330	0.504	0.847	1	85	negative regulation of cellular catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0000226	0.504	0.85	1	197	microtubule cytoskeleton organization	BP	1	ARHGEF2	up_VPUL_EC
GO:0030162	0.504	0.849	1	202	regulation of proteolysis	BP	1	PTGER2	up_VPUL_EC
GO:0044087	0.504	0.853	1	339	regulation of cellular component biogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0043486	0.504	0.862	1	7	histone exchange	BP	1	CENPP	up_VSAP_EC
GO:0032990	0.504	0.849	1	167	cell part morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0002708	0.504805101	0.84863	1	26	positive regulation of lymphocyte mediated	BP	1	FZD5	up_ACOR_EC
GO:0044265	0.505	0.567	36	423	cellular macromolecule catabolic process	BP	1	RNPS1,USP1,USP4,EIF4A3,EDC3,HNRNPD,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,THRAP3,EDC4,FEN1,SMARCC1,RNASEH2B,PLK3,SMG9,DIS3,FASTKD3,UBE2J2,DTL,EZR,UBE2K,RAD23A,CDC20,BAP1,PSMC1,AIFM1,ENSCAFG00000015189,RNASEH2C,EXOSC5,UBE2C,AMER1	down_ACOR_VSMC
GO:0018394	0.505	0.677	5	55	peptidyl-lysine acetylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:0110020	0.505	0.726	3	31	regulation of actomyosin structure organization	BP	1	NF2,STMN1,RAC1	down_ACOR_VSMC
GO:1902106	0.505	0.726	3	31	negative regulation of leukocyte differentiation	BP	1	HMGB1,HMGB3,HOXA7	down_ACOR_VSMC
GO:0001659	0.505	0.722	3	54	temperature homeostasis	BP	1	TRPV2,PLCL1,NAPEPLD	down_VCAV_EC
GO:0048704	0.505	0.723	3	46	embryonic skeletal system morphogenesis	BP	1	HOXB7,CTNNB1,SIX4	down_VSAP_EC
GO:0008543	0.505	0.728	3	27	fibroblast growth factor receptor signaling	BP	1	FGFR2,FGF18,FRS2	up_ACOR_VSMC
GO:0007043	0.505	0.727	3	28	cell-cell junction assembly	BP	1	WNT11,HDAC7,CLDN1	up_VSAP_EC
GO:0048483	0.505	0.772	2	19	autonomic nervous system development	BP	1	NAV2,PHACTR4	down_ACOR_VSMC
GO:0003151	0.505	0.766	2	34	outflow tract morphogenesis	BP	1	BMPR1A,SEMA3C	down_VCAV_EC
GO:1990138	0.505	0.766	2	35	neuron projection extension	BP	1	NDN,TRPV2	down_VCAV_EC
GO:0009892	0.505	0.776	2	835	negative regulation of metabolic process	BP	1	CST3,HDAC7	down_VPOR_EC
GO:0030593	0.505	0.771	2	19	neutrophil chemotaxis	BP	1	CCL5,JAM3	up_ACOR_VSMC

GO:0002066	0.505	0.773	2	17	columnar/cuboidal epithelial cell	BP	1	BMP4,SEC24B	up_ACOR_VSMC
GO:0010563	0.505	0.764	2	203	negative regulation of phosphorus metabolic	BP	1	ASPN,FBP1	up_VPOR_EC
GO:0045936	0.505	0.764	2	203	negative regulation of phosphate metabolic	BP	1	ASPN,FBP1	up_VPOR_EC
GO:0009887	0.505	0.852	1	314	animal organ morphogenesis	BP	1	SRSF6	down_AFEM_EC
GO:0065007	0.505	1	1	3499	biological regulation	BP	1	GATA5	down_AFEM_VSMC
GO:0032722	0.505	0.852	1	14	positive regulation of chemokine production	BP	1	MAVS	down_VCAV_EC
GO:0035794	0.505	0.853	1	13	positive regulation of mitochondrial membrane permeability	BP	1	SLC35F6	down_VCAV_EC
GO:0050764	0.505	0.853	1	13	regulation of phagocytosis	BP	1	CYBA	down_VCAV_EC
GO:1905710	0.505	0.853	1	13	positive regulation of membrane permeability	BP	1	SLC35F6	down_VCAV_EC
GO:0072395	0.505	0.855	1	11	signal transduction involved in cell cycle	BP	1	CDKN1A	down_VSAP_EC
GO:0072401	0.505	0.855	1	11	signal transduction involved in DNA integrity	BP	1	CDKN1A	down_VSAP_EC
GO:0072422	0.505	0.855	1	11	signal transduction involved in DNA damage	BP	1	CDKN1A	down_VSAP_EC
GO:0001829	0.505	0.861	1	7	trophectodermal cell differentiation	BP	1	CITED2	up_ACOR_VSMC
GO:0010880	0.505	0.861	1	7	regulation of release of sequestered calcium ion into cytosol by	BP	1	CHD7	up_ACOR_VSMC
GO:0014808	0.505	0.861	1	7	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	CHD7	up_ACOR_VSMC
GO:1903514	0.505	0.861	1	7	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	1	CHD7	up_ACOR_VSMC
GO:0070167	0.505	0.848	1	29	regulation of biomineral tissue development	BP	1	GREM1	up_AFEM_EC
GO:0070555	0.505	0.848	1	29	response to interleukin-1	BP	1	CCL5	up_AFEM_EC
GO:1903051	0.505	0.848	1	29	negative regulation of proteolysis involved in cellular protein catabolic	BP	1	CLEC16A	up_AFEM_EC
GO:0042981	0.505	0.856	1	471	regulation of apoptotic process	BP	1	EYA1	up_AFEM_VSMC
GO:0098609	0.505	0.849	1	181	cell-cell adhesion	BP	1	NPNT	up_APUL_EC
GO:2000114	0.505	0.865	1	6	regulation of establishment of cell	BP	1	GATA3	up_VCAV_EC
GO:0033233	0.505	0.857	1	9	regulation of protein sumoylation	BP	1	HMG20A	up_VCAV_EC
GO:0060479	0.505	0.859	1	8	lung cell differentiation	BP	1	CREB1	up_VCAV_EC
GO:1902894	0.505	0.859	1	8	negative regulation of pri-miRNA transcription by RNA polymerase II	BP	1	PDGFB	up_VCAV_EC
GO:0048872	0.505	0.846	1	85	homeostasis of number of cells	BP	1	ACVR2A	up_VPOR_EC
GO:0019637	0.505	0.852	1	342	organophosphate metabolic process	BP	1	PHEX	up_VPUL_VSMC
GO:0032814	0.505	0.862	1	7	regulation of natural killer cell activation	BP	1	TOX	up_VSAP_EC
GO:0071025	0.505	0.861	1	7	RNA surveillance	BP	1	EXOSC7	up_VSAP_EC
GO:0071027	0.505	0.861	1	7	nuclear RNA surveillance	BP	1	EXOSC7	up_VSAP_EC
GO:0071028	0.505	0.861	1	7	nuclear mRNA surveillance	BP	1	EXOSC7	up_VSAP_EC
GO:0046649	0.505	0.848	1	162	lymphocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:0006090	0.505593899	0.84809	1	26	pyruvate metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0019080	0.505598001	0.84809	1	26	viral gene expression	BP	1	TRIM8	up_ACOR_EC
GO:0060996	0.505622668	0.84807	1	26	dendritic spine development	BP	1	PAK3	up_ACOR_EC
GO:0097190	0.505827665	0.6583	6	217	apoptotic signaling pathway	BP	1	IFI6,MAPK8IP2,FIGNL1,CLU,NRP1,PRKCD	up_ACOR_EC

GO:0010605	0.506	0.594	18	745	negative regulation of macromolecule metabolic process	BP	1	LEP,CRY2,GAS1,HOXA7,CRYAB,LMCD1,THRB,GREM1,TENT5C,CLEC16A,CYLD,LRRC15,RECK,NR3C1,AXIN2,ACACB,CTIF,SAMD4B	up_AFEM_EC
GO:0044267	0.506	0.652	8	1583	cellular protein metabolic process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,RPSA,ASPN,NEDD4	down_ACOR_EC
GO:0006869	0.506	0.641	8	81	lipid transport	BP	1	LIPC,ABCB11,APOL5,SLC27A6,ABCA9,LCAT,OSBPL7,SOAT1	up_VSAP_EC
GO:0046578	0.506	0.65	7	77	regulation of Ras protein signal transduction	BP	1	ENSCAFG00000030005,PSD4,STMN1,NUP62,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0034599	0.506	0.65	7	81	cellular response to oxidative stress	BP	1	TNFAIP3,TLR4,MAPK13,GUCY1B1,GCH1,RIPK1,HIF1A	up_VCAV_EC
GO:0048762	0.506	0.675	5	77	mesenchymal cell differentiation	BP	1	TGFBR1,HIF1A,STRAP,GSK3B,NRP1	down_VSAP_EC
GO:0070727	0.506	0.676	5	579	cellular macromolecule localization	BP	1	MZT1,HOOK3,XPOT,GCC2,SRP54	up_VPOR_EC
GO:0006476	0.506	0.725	3	31	protein deacetylation	BP	1	SREBF1,RBM14,TADA2A	down_ACOR_VSMC
GO:0010633	0.506	0.727	3	28	negative regulation of epithelial cell migration	BP	1	EVL,SYNJ2BP,JUP	up_ACOR_VSMC
GO:0043244	0.506	0.766	2	34	regulation of protein complex disassembly	BP	1	CLEC16A,PLEKHH2	down_VCAV_EC
GO:0021954	0.506	0.767	2	26	central nervous system neuron development	BP	1	CDH11,NRP1	down_VSAP_EC
GO:0046825	0.506	0.773	2	16	regulation of protein export from nucleus	BP	1	PARK7,PTPN14	up_ACOR_VSMC
GO:0002573	0.506	0.763	2	71	myeloid leukocyte differentiation	BP	1	HOXA7,EVI2B	up_AFEM_EC
GO:0007010	0.506	0.767	2	441	cytoskeleton organization	BP	1	TUBB4A,PDLIM3	up_APUL_EC
GO:0055017	0.506	0.771	2	19	cardiac muscle tissue growth	BP	1	MEF2C,EDN1	up_VCAV_EC
GO:0032410	0.506	0.772	2	17	negative regulation of transporter activity	BP	1	KCNE3,OSR1	up_VSAP_EC
GO:0009719	0.506	0.766	2	395	response to endogenous stimulus	BP	1	CAV1,FGF5	up_VSAP_VSMC
GO:0007026	0.506	0.858	1	8	negative regulation of microtubule	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0035886	0.506	0.858	1	8	vascular smooth muscle cell differentiation	BP	1	CTH	down_ACOR_VSMC
GO:0051693	0.506	0.858	1	8	actin filament capping	BP	1	CAPG	down_ACOR_VSMC
GO:1900087	0.506	0.858	1	8	positive regulation of G1/S transition of mitotic	BP	1	MTBP	down_ACOR_VSMC
GO:0043266	0.506	0.851	1	14	regulation of potassium ion transport	BP	1	PRNP	down_VCAV_EC
GO:0072087	0.506	0.852	1	14	renal vesicle development	BP	1	GREM1	down_VCAV_EC
GO:0008347	0.506	0.854	1	11	glial cell migration	BP	1	CTNNB1	down_VSAP_EC
GO:0007097	0.506	0.861	1	7	nuclear migration	BP	1	SUN1	up_ACOR_VSMC
GO:0033238	0.506	0.861	1	7	regulation of cellular amine metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0051647	0.506	0.861	1	7	nucleus localization	BP	1	SUN1	up_ACOR_VSMC
GO:0051049	0.506	0.855	1	479	regulation of transport	BP	1	TLR2	up_AFEM_VSMC
GO:0098771	0.506	0.848	1	180	inorganic ion homeostasis	BP	1	HOXA3	up_APUL_EC
GO:0061014	0.506	0.858	1	8	positive regulation of mRNA catabolic process	BP	1	CNOT7	up_VCAV_EC
GO:1990126	0.506	0.858	1	8	retrograde transport, endosome to plasma	BP	1	ANKRD50	up_VCAV_EC
GO:0070372	0.506	0.846	1	85	regulation of ERK1 and ERK2 cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:2001020	0.506	0.846	1	88	regulation of response to DNA damage stimulus	BP	1	CXHXorf57	up_VPOR_EC
GO:0008285	0.506	0.848	1	201	negative regulation of cell proliferation	BP	1	TBX5	up_VPUL_EC
GO:0001516	0.506	0.861	1	7	prostaglandin biosynthetic process	BP	1	PTGES	up_VSAP_EC
GO:0031664	0.506	0.861	1	7	regulation of lipopolysaccharide-	BP	1	SASH1	up_VSAP_EC
GO:0032594	0.506	0.861	1	7	protein transport within lipid bilayer	BP	1	RILPL2	up_VSAP_EC
GO:0048557	0.506	0.861	1	7	embryonic digestive tract morphogenesis	BP	1	SHOX2	up_VSAP_EC
GO:0090335	0.506	0.861	1	7	regulation of brown fat cell differentiation	BP	1	NAPEPLD	up_VSAP_EC

GO:0046457	0.506	0.861	1	7	prostanoid biosynthetic process	BP	1	PTGES	up_VSAP_EC
GO:0062013	0.506128944	0.84754	1	27	positive regulation of small molecule metabolic	BP	1	NR1H4	up_ACOR_EC
GO:0044706	0.50650218	0.84729	1	27	multi-multicellular organism process	BP	1	ARHGDIB	up_ACOR_EC
GO:0009100	0.506632995	0.69111	4	139	glycoprotein metabolic process	BP	1	GALNT5,PORCN,EDEM2,B3GNT7	up_ACOR_EC
GO:0010507	0.506715897	0.84732	1	26	negative regulation of autophagy	BP	1	CHMP4B	up_ACOR_EC
GO:0071310	0.507	0.55	61	634	cellular response to organic substance	BP	1	FZD1,FAM107A,PTGFR,PPARGC1B,SLIT2,CDH1,SLC6A4,FGF7,ABL1,GOT1,CHRM1,DLL1,EPN2,OSR1,PDGFD,KLF15,CDC42EP2,RARG,CCBE1,STAT5A,STAT6,F2RL1,RAB11B,PDK2,ZFP36L1,PIK3R1,GAS1,ZEB1,SULF2,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,STK16,CASTOR1,KCNB1,CDK9,PRMT2,OSBPL7,ZFP36L2,HPGD,RAF1,NCOA2,STX4,PQBP1,ACVRL1,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,TGFBR2,CITED2,BAG4,LBH,KEAP1,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC
GO:0022607	0.507	0.551	58	969	cellular component assembly	BP	1	VEGFA,CELF1,NR1H4,C1QTNF6,ACTN1,VASP,SEC24D,PTPN11,EXOC5,FSCN1,MZT1,DPYSL3,FBLIM1,ANKRA2,SRP54,WDR1,MYO1C,MSN,RPGR,DYNLL1,TUBB,TNIK,PRPF3,DDX39B,BRD2,CNOT7,ACTR3,CTNNB1,KPNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,PLOD3,KLF5,STRAP,DDIT3,TWF1,PLEKHG2,TLN1,PLS3,GSK3B,GBP5,SH3GLB1,SDC4,HTT,EIF2S1,PRMT1,DISC1,CLTC,LRRTM2,CAPG,SIX4,RSL24D1,NRP1,TNFAIP1,SEC13,MYBPC2	down_VSAP_EC
GO:0031324	0.507	0.564	37	735	negative regulation of cellular metabolic process	BP	1	CST3,KIRREL1,DCN,NAB2,PRNP,BGN,KANK2,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,ASPN,POLDIP2,LRPAP1,THY1,CC2D1A,GLI3,PARK7,ZFP36L1,CLEC16A,LOXL3,ORMDL3,SPRED1,A2M,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0034622	0.507	0.567	33	421	cellular protein-containing complex assembly	BP	1	HCLS1,GBP5,MX2,BAIAP2L1,TLR4,SMAD1,SNAP91,TMOD1,NASP,MTOR,SNAP23,SCAF11,CNOT6,NCKAP1,MZT1,IQGAP2,STMN1,CENPC,NCK1,FES,HIST1H1A,SENP6,PAN3,PRPF39,CNOT7,ASF1A,HMGB1,ARPC5L,LSM14A,ATRX,HP1BP3,TMOD3,FBXO5	up_VCAV_EC
GO:0010467	0.507	0.654	8	1787	gene expression	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,CYP26B1	up_VFEM_EC
GO:0048869	0.507	0.733	3	1119	cellular developmental process	BP	1	HOXC10,HOXA9,SGCD	up_AORT_EC
GO:0002702	0.507	0.725	3	28	positive regulation of production of molecular mediator of immune	BP	1	STAT6,F2RL1,STX4	up_VSAP_EC
GO:1904063	0.507	0.772	2	17	negative regulation of cation transmembrane	BP	1	KCNE3,OSR1	up_VSAP_EC
GO:0006954	0.507	0.846	1	147	inflammatory response	BP	1	LYN	down_ACOR_EC
GO:0071225	0.507	0.858	1	8	cellular response to muramyl dipeptide	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0071704	0.507	1	1	3535	organic substance metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0060043	0.507	0.851	1	14	regulation of cardiac muscle cell proliferation	BP	1	BMPR1A	down_VCAV_EC
GO:0071364	0.507	0.851	1	14	cellular response to epidermal growth factor	BP	1	ZFP36L1	down_VCAV_EC
GO:0071398	0.507	0.851	1	14	cellular response to fatty acid	BP	1	ADCY6	down_VCAV_EC
GO:0071840	0.507	0.911	1	2059	cellular component organization or biogenesis	BP	1	JUP	down_VFEM_VSMC
GO:0051567	0.507	0.855	1	10	histone H3-K9 methylation	BP	1	KDM3A	down_VSAP_EC
GO:0031272	0.507	0.858	1	8	regulation of pseudopodium assembly	BP	1	F2RL1	up_ACOR_VSMC
GO:0031274	0.507	0.858	1	8	positive regulation of pseudopodium assembly	BP	1	F2RL1	up_ACOR_VSMC
GO:0048557	0.507	0.86	1	7	embryonic digestive tract morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:1902018	0.507	0.86	1	7	negative regulation of cilium assembly	BP	1	EVI5L	up_ACOR_VSMC
GO:0070242	0.507	0.86	1	7	thymocyte apoptotic process	BP	1	BMP4	up_ACOR_VSMC

GO:0050767	0.507	0.847	1	184	regulation of neurogenesis	BP	1	NTRK2	up_APUL_EC
GO:0051223	0.507	0.847	1	181	regulation of protein transport	BP	1	NR1H4	up_APUL_EC
GO:0031646	0.507	0.86	1	7	positive regulation of neurological system	BP	1	RELN	up_VCAV_EC
GO:0035988	0.507	0.856	1	9	chondrocyte proliferation	BP	1	STC1	up_VCAV_EC
GO:0036230	0.507	0.856	1	9	granulocyte activation	BP	1	CXCL8	up_VCAV_EC
GO:0001934	0.507	0.849	1	274	positive regulation of protein phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0030335	0.507	0.847	1	165	positive regulation of cell migration	BP	1	TIAM1	up_VFEM_EC
GO:0048285	0.507	0.847	1	166	organelle fission	BP	1	CYP26B1	up_VFEM_EC
GO:0010563	0.507	0.848	1	203	negative regulation of phosphorus metabolic	BP	1	FLRT3	up_VPUL_EC
GO:0045936	0.507	0.848	1	203	negative regulation of phosphate metabolic	BP	1	FLRT3	up_VPUL_EC
GO:0000478	0.507	0.86	1	7	endonucleolytic cleavage involved in rRNA	BP	1	RCL1	up_VSAP_EC
GO:0051402	0.507641007	0.76128	2	64	neuron apoptotic process	BP	1	USP53,NRP1	up_ACOR_EC
GO:0045893	0.508	0.56	41	413	positive regulation of transcription, DNA-templated	BP	1	SMAD6,LBH,GATA5,GATA4,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0010942	0.508	0.589	19	200	positive regulation of cell death	BP	1	RASSF2,NACC2,ITM2C,BMP4,LATS2,TP53INP1,CD274,ANKRD1,DAPK1,BNIP3,CDKN1A,JMY,DKKL1,PSEN1,SPINK2,SIAH1,SERINC3,KLF11,PARK7	up_ACOR_VSMC
GO:0033674	0.508	0.604	14	144	positive regulation of kinase activity	BP	1	MAP3K14,ARHGEF5,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CAMKK2,AMBRA1,DDR2,TRAF7,SASH1,MAP2K2,TGFBR2	up_VSAP_EC
GO:0098655	0.508	0.605	14	142	cation transmembrane transport	BP	1	AMIGO1,SLC8B1,ABL1,KCNE3,OSR1,KLHL24,SLC25A28,SCARA5,STEAP3,KCNB1,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0001816	0.508	0.611	12	194	cytokine production	BP	1	ARHGEF2,SULF1,NR1H4,SERPINE1,SOCS5,FAM49B,HIF1A,ADAM17,LYN,DDIT3,GBP5,BTK	down_VSAP_EC
GO:0007159	0.508	0.648	7	79	leukocyte cell-cell adhesion	BP	1	HMGB1,CAV1,ARG2,TFRC,FAM49B,EZR,CORO1A	down_ACOR_VSMC
GO:0051051	0.508	0.657	6	112	negative regulation of transport	BP	1	SLC35F6,AKT2,LRPAP1,PARK7,ARHGAP1,PACSIN3	down_VCAV_EC
GO:0016192	0.508	0.692	4	452	vesicle-mediated transport	BP	1	HOOK3,GOLT1B,GCC2,TMEM87B	up_VPOR_EC
GO:0009790	0.508	0.719	3	335	embryo development	BP	1	HOXA3,SEMA3A,ACVR2A	up_VPOR_EC
GO:0046426	0.508	0.768	2	20	negative regulation of JAK-STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:1904893	0.508	0.768	2	20	negative regulation of STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0002753	0.508	0.77	2	17	cytoplasmic pattern recognition receptor	BP	1	PTPN22,NOD2	up_ACOR_VSMC
GO:0033866	0.508	0.767	2	22	nucleoside bisphosphate biosynthetic process	BP	1	PANK3,ELOVL7	up_VCAV_EC
GO:0034030	0.508	0.767	2	22	ribonucleoside bisphosphate biosynthetic	BP	1	PANK3,ELOVL7	up_VCAV_EC
GO:0034033	0.508	0.767	2	22	purine nucleoside bisphosphate biosynthetic	BP	1	PANK3,ELOVL7	up_VCAV_EC
GO:0051172	0.508	0.769	2	663	negative regulation of nitrogen compound	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:0010823	0.508	0.771	2	17	negative regulation of mitochondrion	BP	1	HTRA2,BAG4	up_VSAP_EC
GO:0032703	0.508	0.857	1	8	negative regulation of interleukin-2 production	BP	1	EZR	down_ACOR_VSMC
GO:0043029	0.508	0.857	1	8	T cell homeostasis	BP	1	CORO1A	down_ACOR_VSMC
GO:0060261	0.508	0.857	1	8	positive regulation of transcription initiation from RNA polymerase II	BP	1	PSMC1	down_ACOR_VSMC
GO:0060323	0.508	0.85	1	14	head morphogenesis	BP	1	CRISPLD2	down_VCAV_EC
GO:2000243	0.508	0.851	1	14	positive regulation of reproductive process	BP	1	SYDE1	down_VCAV_EC

GO:0010874	0.508	0.86	1	7	regulation of cholesterol efflux	BP	1	ABCA1	up_ACOR_VSMC
GO:0042554	0.508	0.86	1	7	superoxide anion generation	BP	1	F2RL1	up_ACOR_VSMC
GO:0045116	0.508	0.857	1	8	protein neddylation	BP	1	DCUN1D4	up_ACOR_VSMC
GO:0090136	0.508	0.86	1	7	epithelial cell-cell adhesion	BP	1	BVES	up_ACOR_VSMC
GO:0006213	0.508	0.855	1	9	pyrimidine nucleoside metabolic process	BP	1	CDA	up_VCAV_EC
GO:0045616	0.508	0.855	1	9	regulation of keratinocyte differentiation	BP	1	PRKCH	up_VCAV_EC
GO:0090103	0.508	0.857	1	8	cochlea morphogenesis	BP	1	ZEB1	up_VCAV_EC
GO:0006164	0.508	0.845	1	86	purine nucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0033673	0.508	0.845	1	84	negative regulation of kinase activity	BP	1	ASPN	up_VPOR_EC
GO:0002237	0.508	0.845	1	85	response to molecule of bacterial origin	BP	1	MTDH	up_VPOR_EC
GO:0072337	0.508	0.859	1	7	modified amino acid transport	BP	1	CTNS	up_VSAP_EC
GO:1904064	0.508198399	0.84612	1	27	positive regulation of cation transmembrane	BP	1	ACTN2	up_ACOR_EC
GO:0032088	0.508716349	0.84594	1	26	negative regulation of NF-kappaB transcription	BP	1	NR1H4	up_ACOR_EC
GO:0051234	0.508752945	0.56778	34	1283	establishment of localization	BP	1	SH3TC2,CA4,CDH3,NR1H4,CLIC3,BRSK1,CALY,AQP1,ENSCAFG00000004331,KCNB1,EDEM2,FZD5,NOD2,DYNC1I1,PLS1,ACTN2,CFI,PTGER4,PREB,SLC25A42,MAPK8IP2,MAVS,SLC9A9,CHMP4B,RARRES2,VPS16,ABCB9,NRP1,AZIN2,HM13,PRKCD,PM20D1,ENSCAFG00000010493,ATP7B	up_ACOR_EC
GO:0010941	0.509	0.552	50	524	regulation of cell death	BP	1	SMAD6,PLCG2,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,TM7SF3,FGFR2,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,EGLN1,CDKN1A,JMY,NRP1,LRPAP1,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,PSEN1,SPINK2,CCL5,CLN8,SIAH1,OXR1,NOD2,SERINC3,TNFRSF11B,KLF11,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0080134	0.509	0.577	24	386	regulation of response to stress	BP	1	ARHGEF2,P4HB,NR1H4,SERPINE1,SOCS5,HYOU1,NUAK1,SESN2,PTGS2,HIF1A,TNIK,PTPN2,PVR,DDX39B,CNOT7,CTNNB1,APOE,LYN,CDC37,GBP5,A2M,SH3RF3,USP14,MID1	down_VSAP_EC
GO:0050776	0.509	0.593	17	173	regulation of immune response	BP	1	CD274,ABL1,TRAFD1,STAT6,F2RL1,RBCK1,MYD88,CFD,NLRX1,TKFC,CYBA,STX4,PQBP1,UNC93B1,FLOT1,PPP3CB,MAVS	up_VSAP_EC
GO:0098662	0.509	0.616	11	131	inorganic cation transmembrane transport	BP	1	NNT,NEDD4,CAV1,SLC30A1,GSTO1,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,ATP5F1D	down_ACOR_VSMC
GO:0043900	0.509	0.629	9	104	regulation of multi-organism process	BP	1	ILF3,CAV1,TRIM35,ARG2,B4GALT1,CACTIN,SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0008154	0.509	0.638	8	81	actin polymerization or depolymerization	BP	1	FAM107A,SLIT2,CDC42EP5,CDC42EP2,F2RL1,WIPF1,NCK1,BAG4	up_VSAP_EC
GO:0006950	0.509	0.681	5	1102	response to stress	BP	1	EYA1,MAP2K6,CYP26B1,CDC42EP5,MTSS1	up_VFEM_EC
GO:0006886	0.509	0.718	3	332	intracellular protein transport	BP	1	XPOT,GCC2,SRP54	up_VPOR_EC
GO:0008589	0.509	0.724	3	28	regulation of smoothened signaling pathway	BP	1	GLIS2,GAS1,SHOX2	up_VSAP_EC
GO:0042773	0.509	0.763	2	32	ATP synthesis coupled electron transport	BP	1	UQCR10,PARK7	down_VCAV_EC
GO:0051094	0.509	0.763	2	388	positive regulation of developmental process	BP	1	HOXA11,SHOX2	up_VSAP_VSMC
GO:0005978	0.509	0.85	1	14	glycogen biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0009250	0.509	0.85	1	14	glucan biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0022617	0.509	0.852	1	11	extracellular matrix disassembly	BP	1	FSCN1	down_VSAP_EC
GO:0050650	0.509	0.852	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	CHSY1	down_VSAP_EC
GO:0070206	0.509	0.852	1	11	protein trimerization	BP	1	C1QTNF6	down_VSAP_EC
GO:2000516	0.509	0.858	1	7	positive regulation of CD4-positive, alpha-beta T cell activation	BP	1	CD83	up_ACOR_VSMC

GO:0034613	0.509	0.857	1	576	cellular protein localization	BP	1	ESR1	up_AORT_VSMC
GO:0071801	0.509	0.859	1	7	regulation of podosome assembly	BP	1	FSCN1	up_VCAV_EC
GO:0032270	0.509	0.853	1	479	positive regulation of cellular protein metabolic	BP	1	C6	up_VCAV_VSMC
GO:0051049	0.509	0.853	1	479	regulation of transport	BP	1	CA2	up_VCAV_VSMC
GO:0005996	0.509	0.844	1	85	monosaccharide metabolic process	BP	1	FBP1	up_VPOR_EC
GO:2000145	0.509	0.848	1	279	regulation of cell motility	BP	1	C3AR1	up_VPOR_VSMC
GO:0002520	0.509	0.848	1	279	immune system development	BP	1	HOXA9	up_VFEM_VSMC
GO:0001829	0.509	0.859	1	7	trophectodermal cell differentiation	BP	1	CITED2	up_VSAP_EC
GO:0001832	0.509	0.859	1	7	blastocyst growth	BP	1	TAF8	up_VSAP_EC
GO:0051299	0.509	0.859	1	7	centrosome separation	BP	1	CEP85	up_VSAP_EC
GO:0061307	0.509	0.859	1	7	cardiac neural crest cell differentiation involved in heart development	BP	1	CITED2	up_VSAP_EC
GO:0061308	0.509	0.859	1	7	cardiac neural crest cell development involved in heart development	BP	1	CITED2	up_VSAP_EC
GO:0034763	0.509443489	0.84526	1	27	negative regulation of transmembrane transport	BP	1	ACTN2	up_ACOR_EC
GO:0065009	0.51	0.561	37	735	regulation of molecular function	BP	1	CST3,PDGFRB,SNX18,LRP1,DCN,PRNP,BGN,LARP6,LMO4,RECK,FXYD1,ENSCAFG00000014978,AKT1S1,TIMP2,AKT2,SYDE1,CLSTN1,PLCL1,CACNB3,CSPG4,ASPN,LRPAP1,THY1,PARK7,SASH1,IFT57,MAVS,SPRED1,RAB7B,MAPRE3,GLIS2,ARHGAP1,DDR2,SHC1,FBH1,GREM1,EVI5L	down_VCAV_EC
GO:0009967	0.51	0.58	22	435	positive regulation of signal transduction	BP	1	NOTCH2,PDGFRB,DCN,GLIPR2,BMPR1A,EVC,CSPG4,ATP6V0C,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,SPRED1,SHC1,FBH1,GREM1	down_VCAV_EC
GO:1904951	0.51	0.644	7	108	positive regulation of establishment of protein localization	BP	1	NR1H4,PLK3,MYO1C,HIF1A,ZPR1,GSK3B,SH3GLB1	down_VSAP_EC
GO:0070304	0.51	0.691	4	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	TNIK,LYN,SH3RF3,MID1	down_VSAP_EC
GO:0046425	0.51	0.694	4	39	regulation of JAK-STAT cascade	BP	1	LEP,CRLF3,PARP9,LRRC4	up_ACOR_VSMC
GO:0050709	0.51	0.722	3	28	negative regulation of protein secretion	BP	1	F2RL1,PTPN22,PFKL	up_ACOR_VSMC
GO:0065008	0.51	0.729	3	1056	regulation of biological quality	BP	1	HOXC10,GATM,NETO1	up_VFEM_VSMC
GO:0048675	0.51	0.764	2	26	axon extension	BP	1	IFRD1,NRP1	down_VSAP_EC
GO:0009967	0.51	0.764	2	435	positive regulation of signal transduction	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0032785	0.51	0.856	1	8	negative regulation of DNA-templated transcription, elongation	BP	1	EZH2	down_ACOR_VSMC
GO:0000132	0.51	0.851	1	11	establishment of mitotic spindle orientation	BP	1	HTT	down_VSAP_EC
GO:0051294	0.51	0.851	1	11	establishment of spindle orientation	BP	1	HTT	down_VSAP_EC
GO:0006692	0.51	0.852	1	11	prostanoid metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0006693	0.51	0.852	1	11	prostaglandin metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0045922	0.51	0.85	1	12	negative regulation of fatty acid metabolic	BP	1	TRIB3	down_VSAP_EC
GO:0002043	0.51	0.858	1	7	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0055003	0.51	0.858	1	7	cardiac myofibril assembly	BP	1	NEBL	up_ACOR_VSMC
GO:0051240	0.51	0.853	1	489	positive regulation of multicellular organismal	BP	1	TLR2	up_AFEM_VSMC
GO:0044281	0.51	0.856	1	622	small molecule metabolic process	BP	1	ARG2	up_AORT_VSMC
GO:0031343	0.51	0.852	1	10	positive regulation of cell killing	BP	1	NECTIN2	up_VCAV_EC

GO:0009894	0.51	0.847	1	277	regulation of catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0007218	0.51	0.858	1	7	neuropeptide signaling pathway	BP	1	GPR1	up_VSAP_EC
GO:0044346	0.51	0.858	1	7	fibroblast apoptotic process	BP	1	BTG1	up_VSAP_EC
GO:0048730	0.51	0.858	1	7	epidermis morphogenesis	BP	1	FGF7	up_VSAP_EC
GO:0060707	0.51	0.858	1	7	trophoblast giant cell differentiation	BP	1	GJB5	up_VSAP_EC
GO:2000269	0.51	0.858	1	7	regulation of fibroblast apoptotic process	BP	1	BTG1	up_VSAP_EC
GO:0006897	0.51	0.844	1	158	endocytosis	BP	1	CAV1	up_VSAP_VSMC
GO:0045892	0.510015252	0.62631	9	328	negative regulation of transcription, DNA-	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:0016064	0.510208589	0.84491	1	26	immunoglobulin mediated immune	BP	1	PRKCD	up_ACOR_EC
GO:0019724	0.510208589	0.84491	1	26	B cell mediated immunity	BP	1	PRKCD	up_ACOR_EC
GO:0048332	0.510320365	0.84483	1	26	mesoderm morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0032446	0.510657482	0.64243	7	255	protein modification by small protein conjugation	BP	1	NOD2,KLHL25,PIAS1,KLHDC8B,SH3RF3,RNF114,UBE2H	up_ACOR_EC
GO:0070887	0.511	0.558	39	775	cellular response to chemical stimulus	BP	1	PCOLCE,PDGFRB,SMAD9,LRP1,DCN,NDN,PRNP,MT2A,VASN,FBN1,ADCY6,BGN,KANK2,COL6A1,NUMBL,ENSCAFG00000014978,AKT1S1,CHRDL1,AKT2,NR3C1,HSD3B7,TMEM161A,GFPT2,ASPN,CYP1B1,PARK7,ZFP36L1,SASH1,MAVS,MPV17,GSDME,FUT8,RAB7B,RAB31,SHC1,GREM1,RAC2,FOXO3,RGMA	down_VCAV_EC
GO:0031175	0.511	0.584	20	224	neuron projection development	BP	1	EPHB1,IFRD1,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,PREX2,GDPD5,ENSCAFG00000010224,STMN1,PAK2,APOD,NCK1,FES,RAPGEF2,CREB1,SPTBN4,ALS2	up_VCAV_EC
GO:0044403	0.511	0.621	10	116	symbiont process	BP	1	ILF3,NEDD4,SLC29A1,CAV1,TRIM35,TFRC,SMC3,DDX39B,RAD23A,PPIH	down_ACOR_VSMC
GO:0010876	0.511	0.628	9	92	lipid localization	BP	1	LIPC,ACACB,ABCB11,APOL5,SLC27A6,ABCA9,LCAT,OSBPL7,SOAT1	up_VSAP_EC
GO:0051346	0.511	0.67	5	78	negative regulation of hydrolase activity	BP	1	PTGS2,CRYAB,ARFGEF3,PAK2,SPINK2	down_VSAP_EC
GO:0001823	0.511	0.692	4	45	mesonephros development	BP	1	HOXB7,GATA3,ARG2,BMP2	up_VCAV_EC
GO:0031328	0.511	0.72	3	512	positive regulation of cellular biosynthetic	BP	1	ACVRL1,HOXA1,ACSL3	down_ACOR_EC
GO:0006814	0.511	0.722	3	28	sodium ion transport	BP	1	OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:1903391	0.511	0.766	2	21	regulation of adherens junction organization	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0002275	0.511	0.767	2	18	myeloid cell activation involved in immune	BP	1	F2RL1,PRKCE	up_ACOR_VSMC
GO:0021766	0.511	0.766	2	20	hippocampus development	BP	1	RELN,PROX1	up_VCAV_EC
GO:0000184	0.511	0.767	2	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	PYM1,SMG9	up_VSAP_EC
GO:0008089	0.511	0.848	1	14	anterograde axonal transport	BP	1	MGARP	down_VCAV_EC
GO:0060191	0.511	0.848	1	14	regulation of lipase activity	BP	1	PDGFRB	down_VCAV_EC
GO:0016070	0.511	0.884	1	1479	RNA metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0006684	0.511	0.857	1	7	sphingomyelin metabolic process	BP	1	SMPD1	up_ACOR_VSMC
GO:0033630	0.511	0.858	1	7	positive regulation of cell adhesion mediated by	BP	1	FERMT1	up_ACOR_VSMC
GO:0006112	0.511	0.844	1	30	energy reserve metabolic process	BP	1	LEP	up_AFEM_EC
GO:0043067	0.511	0.852	1	479	regulation of programmed cell death	BP	1	EYA1	up_AFEM_VSMC
GO:0022414	0.511	0.847	1	294	reproductive process	BP	1	HOXA9	up_AORT_EC
GO:0055085	0.511	0.846	1	284	transmembrane transport	BP	1	GPR155	up_AORT_EC
GO:0070727	0.511	0.855	1	579	cellular macromolecule localization	BP	1	ESR1	up_AORT_VSMC
GO:0046831	0.511	0.861	1	6	regulation of RNA export from nucleus	BP	1	IWS1	up_VCAV_EC
GO:0019752	0.511	0.847	1	283	carboxylic acid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC

GO:1901701	0.511	0.847	1	271	cellular response to oxygen-containing	BP	1	CYP26B1	up_VPOR_VSMC
GO:0009150	0.511	0.844	1	161	purine ribonucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0031400	0.511	0.845	1	205	negative regulation of protein modification	BP	1	FLRT3	up_VPUL_EC
GO:0034427	0.511	0.857	1	7	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	BP	1	EXOSC7	up_VSAP_EC
GO:0060306	0.511	0.857	1	7	regulation of membrane repolarization	BP	1	KCNE3	up_VSAP_EC
GO:0086009	0.511	0.857	1	7	membrane repolarization	BP	1	KCNE3	up_VSAP_EC
GO:0090136	0.511	0.858	1	7	epithelial cell-cell adhesion	BP	1	SERPINB8	up_VSAP_EC
GO:1904707	0.511	0.858	1	7	positive regulation of vascular smooth muscle	BP	1	MFN2	up_VSAP_EC
GO:0055089	0.511	0.857	1	7	fatty acid homeostasis	BP	1	GOT1	up_VSAP_EC
GO:0030324	0.511473092	0.75805	2	64	lung development	BP	1	ADAMTSL2,TBX5	up_ACOR_EC
GO:0045445	0.511571737	0.84378	1	27	myoblast differentiation	BP	1	SOX9	up_ACOR_EC
GO:0006508	0.51183523	0.60345	13	483	proteolysis	BP	1	PCSK1N,EDEM2,IFI6,KLHL25,CST3,PIAS1,USP53,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,HM13	up_ACOR_EC
GO:0071495	0.512	0.561	35	365	cellular response to endogenous stimulus	BP	1	FZD1,FAM107A,PTGFR,PPARGC1B,SLIT2,CDH1,FGF7,ABL1,GOT1,CHRM1,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,SULF2,CREBRF,LRP4,STK16,CASTOR1,PRMT2,ZFP36L2,HPGD,NCOA2,ACVRL1,NCK1,BGLAP,TGFBR2,CITED2,BAG4,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0008150	0.512	0.693	20	5646	biological_process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,RGS1,IL18BP,MRC1,HOXA2,MYBPC2,STK32B,ENSCAFG00000028814,NR4A2,WIF1,CCL24,HTR7,PTGER2,FLRT3,ARHGEF2,NEO1,MXRA5	up_VPUL_EC
GO:0090407	0.512	0.59	17	177	organophosphate biosynthetic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,CHPT1,PPARGC1A,PIGN,PIGS,ADCY6,PPIP5K1,PIGG,CRLS1,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0002694	0.512	0.614	11	126	regulation of leukocyte activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,MMP14,HMGB3,ARG2,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0006520	0.512	0.619	10	114	cellular amino acid metabolic process	BP	1	ENSCAFG00000016095,BCAT1,VARS,PFAS,ARG2,FARSA,AADAT,RARS,CTH,CTPS1	down_ACOR_VSMC
GO:0009144	0.512	0.653	6	103	purine nucleoside triphosphate metabolic	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0010827	0.512	0.721	3	28	regulation of glucose transmembrane transport	BP	1	LEP,EDN1,INPP5K	up_ACOR_VSMC
GO:0048538	0.512	0.765	2	20	thymus development	BP	1	HOXA3,SIX4	down_ACOR_VSMC
GO:0006672	0.512	0.761	2	33	ceramide metabolic process	BP	1	ORMDL3,ENSCAFG00000017708	down_VCAV_EC
GO:0048661	0.512	0.767	2	17	positive regulation of smooth muscle cell	BP	1	BMP4,EDN1	up_ACOR_VSMC
GO:0051496	0.512	0.767	2	17	positive regulation of stress fiber assembly	BP	1	NRP1,EVL	up_ACOR_VSMC
GO:0008064	0.512	0.757	2	72	regulation of actin polymerization or	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0030832	0.512	0.757	2	72	regulation of actin filament length	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0031669	0.512	0.757	2	72	cellular response to nutrient levels	BP	1	CLEC16A,POSTN	up_AFEM_EC
GO:0048511	0.512	0.757	2	72	rhythmic process	BP	1	CRY2,PPARGC1A	up_AFEM_EC
GO:0006464	0.512	0.778	2	1162	cellular protein modification process	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0036211	0.512	0.778	2	1162	protein modification process	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0008306	0.512	0.764	2	21	associative learning	BP	1	RELN,HIF1A	up_VCAV_EC
GO:0060333	0.512	0.854	1	8	interferon-gamma-mediated signaling	BP	1	SLC29A1	down_ACOR_VSMC
GO:0071539	0.512	0.855	1	8	protein localization to centrosome	BP	1	NUP62	down_ACOR_VSMC
GO:1903010	0.512	0.855	1	8	regulation of bone development	BP	1	GREM1	down_ACOR_VSMC
GO:1905508	0.512	0.855	1	8	protein localization to microtubule organizing	BP	1	NUP62	down_ACOR_VSMC
GO:0010922	0.512	0.847	1	14	positive regulation of phosphatase activity	BP	1	PDGFRB	down_VCAV_EC

GO:0010955	0.512	0.847	1	14	negative regulation of protein processing	BP	1	A2M	down_VCAV_EC
GO:1903318	0.512	0.847	1	14	negative regulation of protein maturation	BP	1	A2M	down_VCAV_EC
GO:0048522	0.512	0.884	1	1484	positive regulation of cellular process	BP	1	MOSPD1	down_VFEM_EC
GO:0007549	0.512	0.85	1	11	dosage compensation	BP	1	CDYL	down_VSAP_EC
GO:0035115	0.512	0.849	1	12	embryonic forelimb morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0042092	0.512	0.85	1	11	type 2 immune response	BP	1	SOCS5	down_VSAP_EC
GO:0046620	0.512	0.843	1	30	regulation of organ growth	BP	1	ACACB	up_AFEM_EC
GO:0046824	0.512	0.843	1	30	positive regulation of nucleocytoplasmic	BP	1	LEP	up_AFEM_EC
GO:0050954	0.512	0.843	1	30	sensory perception of mechanical stimulus	BP	1	THRB	up_AFEM_EC
GO:0000003	0.512	0.846	1	295	reproduction	BP	1	HOXA9	up_AORT_EC
GO:0006928	0.512	0.855	1	557	movement of cell or subcellular component	BP	1	WNT7A	up_AORT_VSMC
GO:0030855	0.512	0.844	1	183	epithelial cell differentiation	BP	1	ARHGEF26	up_APUL_EC
GO:0032989	0.512	0.846	1	292	cellular component morphogenesis	BP	1	SHOX2	up_VFEM_VSMC
GO:0002820	0.512	0.857	1	7	negative regulation of adaptive immune	BP	1	PPP3CB	up_VSAP_EC
GO:0002823	0.512	0.857	1	7	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	PPP3CB	up_VSAP_EC
GO:0002374	0.512	0.857	1	7	cytokine secretion involved in immune	BP	1	F2RL1	up_VSAP_EC
GO:0051154	0.512	0.857	1	7	negative regulation of striated muscle cell	BP	1	DLL1	up_VSAP_EC
GO:0032660	0.512	0.857	1	7	regulation of interleukin-17 production	BP	1	MYD88	up_VSAP_EC
GO:1901881	0.512	0.857	1	7	positive regulation of protein depolymerization	BP	1	F2RL1	up_VSAP_EC
GO:0006511	0.512023701	0.64114	7	253	ubiquitin-dependent protein catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,TP53INP2,RNF114,UBE2H	up_ACOR_EC
GO:0006886	0.512499572	0.62389	9	332	intracellular protein transport	BP	1	SH3TC2,KCNB1,EDEM2,PREB,MAVS,CHMP4B,VPS16,HM13,PRKCD	up_ACOR_EC
GO:0014074	0.51253334	0.84329	1	26	response to purine-containing compound	BP	1	AQP1	up_ACOR_EC
GO:0046683	0.512767871	0.84313	1	26	response to organophosphorus	BP	1	AQP1	up_ACOR_EC
GO:0031324	0.513	0.54	71	735	negative regulation of cellular metabolic process	BP	1	SMAD6,LEP,HTR2B,RASSF2,RECK,FEZ1,NACC2,PRKAA2,ITM2C,BMP4,FGFR2,TP53BP1,EIF4A2,ATRX,TRPS1,SH3RF2,LATS2,ATXN2,ISG15,PTPN3,NDRG2,CDKN2B,CST3,ZNF174,ANKRD1,F2RL1,FAM129A,DAPK1,BNIP3,CDKN1A,ENSCAFG00000006238,CLSTN1,PTPN22,LRPAP1,OS9,ORMDL3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,MARF1,DKKL1,DAG1,PPP1R26,PARP9,PSEN1,SYNJ2BP,MXI1,SPINK2,NR3C1,WWC2,DUSP22,EDN1,OXR1,DUSP26,CBX7,LRRC4,DDIT4,KLF11,FEZ2,INPP5K,WFS1,ENSCAFG00000029553,ID3,PARK7,GPATCH2,ZFYVE1,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0051172	0.513	0.592	16	663	negative regulation of nitrogen compound metabolic process	BP	1	LEP,CRY2,GAS1,HOXA7,CRYAB,LMCD1,THRB,GREM1,TENT5C,CLEC16A,CYLD,LRRC15,RECK,NR3C1,AXIN2,SAMD4B	up_AFEM_EC
GO:0043043	0.513	0.598	14	247	peptide biosynthetic process	BP	1	CARS,SARS,AARS,PUM3,SESN2,MRPL1,YARS,TARS,NARS,EIF4EBP1,CNOT7,EIF5,EIF2S1,RSL24D1	down_VSAP_EC
GO:0009059	0.513	0.612	13	1563	macromolecule biosynthetic process	BP	1	BARX1,OSTC,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,RSL24D1,RPL10L,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:1990778	0.513	0.626	9	91	protein localization to cell periphery	BP	1	PLEKHF1,CDH1,EMP2,RILPL2,PIK3R1,TSPAN5,STX4,FLOT1,BAG4	up_VSAP_EC
GO:0018108	0.513	0.643	7	79	peptidyl-tyrosine phosphorylation	BP	1	CAV1,NF2,GREM1,RAP2C,TTK,MELK,ARHGEF2	down_ACOR_VSMC
GO:0031329	0.513	0.652	6	241	regulation of cellular catabolic process	BP	1	LEP,TENT5C,CLEC16A,AXIN2,ACACB,SAMD4B	up_AFEM_EC
GO:0043901	0.513	0.69	4	44	negative regulation of multi-organism process	BP	1	ILF3,TRIM35,ARG2,CACTIN	down_ACOR_VSMC

GO:0030041	0.513	0.688	4	62	actin filament polymerization	BP	1	ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0060560	0.513	0.688	4	58	developmental growth involved in	BP	1	IFRD1,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:2001056	0.513	0.691	4	38	positive regulation of cysteine-type	BP	1	CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0008584	0.513	0.691	4	39	male gonad development	BP	1	HOXA11,HOXA9,PATZ1,CITED2	up_VSAP_EC
GO:0046546	0.513	0.691	4	39	development of primary male sexual	BP	1	HOXA11,HOXA9,PATZ1,CITED2	up_VSAP_EC
GO:0006811	0.513	0.715	3	330	ion transport	BP	1	HOXA3,SLC7A11,ENSCAFG00000005494	up_VPOR_EC
GO:0071310	0.513	0.72	3	634	cellular response to organic substance	BP	1	MME,AVPR1A,CYP26B1	up_VFEM_EC
GO:1903573	0.513	0.764	2	20	negative regulation of response to endoplasmic	BP	1	PPP1R15B,TXNDC12	down_ACOR_VSMC
GO:0019079	0.513	0.76	2	29	viral genome replication	BP	1	CNOT7,RAD23A	down_VSAP_EC
GO:0007099	0.513	0.765	2	19	centriole replication	BP	1	PLK2,SASS6	up_VCAV_EC
GO:0098534	0.513	0.765	2	19	centriole assembly	BP	1	PLK2,SASS6	up_VCAV_EC
GO:0032480	0.513	0.854	1	8	negative regulation of type I interferon	BP	1	CACTIN	down_ACOR_VSMC
GO:1902894	0.513	0.854	1	8	negative regulation of pri-miRNA transcription by RNA polymerase II	BP	1	PPARD	down_ACOR_VSMC
GO:1904262	0.513	0.854	1	8	negative regulation of TORC1 signaling	BP	1	RNF152	down_ACOR_VSMC
GO:0010799	0.513	0.847	1	14	regulation of peptidyl-threonine	BP	1	SPRED1	down_VCAV_EC
GO:0042698	0.513	0.847	1	14	ovulation cycle	BP	1	FOXO3	down_VCAV_EC
GO:0043666	0.513	0.847	1	14	regulation of phosphoprotein	BP	1	PDGFRB	down_VCAV_EC
GO:0010517	0.513	0.849	1	11	regulation of phospholipase activity	BP	1	ARF4	down_VSAP_EC
GO:0033344	0.513	0.848	1	12	cholesterol efflux	BP	1	APOE	down_VSAP_EC
GO:0001963	0.513	0.856	1	7	synaptic transmission, dopaminergic	BP	1	PARK7	up_ACOR_VSMC
GO:0006517	0.513	0.856	1	7	protein deglycosylation	BP	1	PARK7	up_ACOR_VSMC
GO:0030497	0.513	0.854	1	8	fatty acid elongation	BP	1	ELOVL7	up_ACOR_VSMC
GO:0043951	0.513	0.856	1	7	negative regulation of cAMP-mediated signaling	BP	1	APLP1	up_ACOR_VSMC
GO:0090148	0.513	0.856	1	7	membrane fission	BP	1	MX1	up_ACOR_VSMC
GO:1902175	0.513	0.856	1	7	regulation of oxidative stress-induced intrinsic apoptotic signaling	BP	1	PARK7	up_ACOR_VSMC
GO:0010923	0.513	0.842	1	30	negative regulation of phosphatase activity	BP	1	MYO1D	up_AFEM_EC
GO:0042552	0.513	0.842	1	30	myelination	BP	1	LGI4	up_AFEM_EC
GO:0048589	0.513	0.843	1	188	developmental growth	BP	1	TBX5	up_APUL_EC
GO:0006508	0.513	0.851	1	483	proteolysis	BP	1	C6	up_VCAV_VSMC
GO:0006364	0.513	0.841	1	87	rRNA processing	BP	1	RRP15	up_VPOR_EC
GO:0001710	0.513	0.856	1	7	mesodermal cell fate commitment	BP	1	HOXA11	up_VSAP_EC
GO:0033539	0.513	0.856	1	7	fatty acid beta-oxidation using acyl-CoA	BP	1	GCDH	up_VSAP_EC
GO:0048011	0.513	0.856	1	7	neurotrophin TRK receptor signaling	BP	1	RAF1	up_VSAP_EC
GO:0086002	0.513	0.856	1	7	cardiac muscle cell action potential involved in	BP	1	KCNE3	up_VSAP_EC
GO:0098901	0.513	0.856	1	7	regulation of cardiac muscle cell action	BP	1	KCNE3	up_VSAP_EC
GO:2000116	0.513224063	0.7564	2	67	regulation of cysteine-type endopeptidase	BP	1	IFI6,CST3	up_ACOR_EC
GO:0048675	0.513392043	0.84269	1	26	axon extension	BP	1	NRP1	up_ACOR_EC
GO:1902679	0.513820754	0.62263	9	329	negative regulation of RNA biosynthetic process	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1, FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:1903507	0.513820754	0.62263	9	329	negative regulation of nucleic acid-templated	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1, FOXC2,CLSTN1,RIOX2	up_ACOR_EC

GO:0006278	0.513872133	0.84236	1	26	RNA-dependent DNA biosynthetic process	BP	1	PKIB	up_ACOR_EC
GO:0007004	0.513872133	0.84236	1	26	telomere maintenance via telomerase	BP	1	PKIB	up_ACOR_EC
GO:0006446	0.513905836	0.84215	1	27	regulation of translational initiation	BP	1	KLHL25	up_ACOR_EC
GO:0070727	0.514	0.565	29	579	cellular macromolecule localization	BP	1	LRP1,PRNP,TLN2,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,TRIM8,CLTB,SSR3,WDR45,PEX5,GLI3,PARK7,ZFP36L1,ARL2BP,MAVS,CDH2,TOM1,SEC61B,GLIS2,RAB31,HM13,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0043043	0.514	0.58	20	247	peptide biosynthetic process	BP	1	ILF3,EIF4A3,HNRNPD,VARS,RRBP1,PPP1R15B,MRPS18B,TRUB2,DHX33,FASTKD3,EIF5A,FARSA,NCL,MRPL37,RBM14,NOLC1,RARS,PUM3,MRPL18,EIF3M	down_ACOR_VSMC
GO:0002009	0.514	0.588	17	177	morphogenesis of an epithelium	BP	1	HOXA11,FZD1,WNT11,SLIT2,FGF7,ABL1,DLL1,OSR1,FUZ,RARG,IRX3,NTN4,KDM2B,ARHGAP12,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0033365	0.514	0.597	14	276	protein localization to organelle	BP	1	NABP2,ENSCAFG00000014978,SNUPN,TRIM8,SSR3,PEX5,GLI3,PARK7,ARL2BP,MAVS,SEC61B,GLIS2,LONP2,SEC61A1	down_VCAV_EC
GO:0090130	0.514	0.607	12	121	tissue migration	BP	1	FERMT1,BMP4,SASH1,FGF18,NRP1,EVL,PRKCE,SYNJ2BP,JUP,DOCK5,RREB1,PIK3C2A	up_ACOR_VSMC
GO:0044260	0.514	0.673	7	2593	cellular macromolecule metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0002757	0.514	0.667	5	78	immune response-activating signal	BP	1	NR1H4,PTPN2,EIF2B1,SKAP2,LYN	down_VSAP_EC
GO:0120039	0.514	0.684	4	158	plasma membrane bounded cell projection	BP	1	PLXNA4,CAMK2A,LRRN2,KANK1	up_AFEM_EC
GO:0043170	0.514	0.779	3	2980	macromolecule metabolic process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0010463	0.514	0.72	3	28	mesenchymal cell proliferation	BP	1	BMP4,FGFR2,CLSTN1	up_ACOR_VSMC
GO:0021954	0.514	0.72	3	26	central nervous system neuron development	BP	1	LEP,FGFR2,NRP1	up_ACOR_VSMC
GO:0030879	0.514	0.759	2	34	mammary gland development	BP	1	B4GALT1,GLI3	down_VCAV_EC
GO:0048709	0.514	0.766	2	17	oligodendrocyte differentiation	BP	1	WASF3,ZNF365	up_ACOR_VSMC
GO:0071560	0.514	0.755	2	72	cellular response to transforming growth	BP	1	NR3C1,ADAM17	up_AFEM_EC
GO:2000027	0.514	0.756	2	72	regulation of animal organ morphogenesis	BP	1	THRB,GREM1	up_AFEM_EC
GO:2000756	0.514	0.763	2	20	regulation of peptidyl-lysine acetylation	BP	1	IWS1,GATA3	up_VCAV_EC
GO:0002026	0.514	0.853	1	8	regulation of the force of heart contraction	BP	1	CAV1	down_ACOR_VSMC
GO:2000781	0.514	0.853	1	8	positive regulation of double-strand break	BP	1	TIMELESS	down_ACOR_VSMC
GO:0030204	0.514	0.846	1	14	chondroitin sulfate metabolic process	BP	1	DCN	down_VCAV_EC
GO:0045606	0.514	0.855	1	7	positive regulation of epidermal cell	BP	1	BMP4	up_ACOR_VSMC
GO:0048730	0.514	0.855	1	7	epidermis morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0051154	0.514	0.855	1	7	negative regulation of striated muscle cell	BP	1	FRS2	up_ACOR_VSMC
GO:0072171	0.514	0.841	1	30	mesonephric tubule morphogenesis	BP	1	GREM1	up_AFEM_EC
GO:1903038	0.514	0.841	1	30	negative regulation of leukocyte cell-cell	BP	1	CYLD	up_AFEM_EC
GO:0090087	0.514	0.842	1	185	regulation of peptide transport	BP	1	NR1H4	up_APUL_EC
GO:0060575	0.514	0.851	1	9	intestinal epithelial cell differentiation	BP	1	HIF1A	up_VCAV_EC
GO:1900117	0.514	0.854	1	8	regulation of execution phase of apoptosis	BP	1	PAK2	up_VCAV_EC
GO:0045935	0.514	0.85	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA5	up_VCAV_VSMC
GO:0040007	0.514	0.845	1	276	growth	BP	1	NKX2-5	up_VPOR_VSMC
GO:0003272	0.514	0.855	1	7	endocardial cushion formation	BP	1	TGFBR2	up_VSAP_EC
GO:0045987	0.514	0.855	1	7	positive regulation of smooth muscle	BP	1	TBXA2R	up_VSAP_EC
GO:0071243	0.514	0.855	1	7	cellular response to arsenic-containing	BP	1	HMOX1	up_VSAP_EC
GO:0071548	0.514	0.855	1	7	response to dexamethasone	BP	1	DDIT4	up_VSAP_EC

GO:0003014	0.514981128	0.84139	1	27	renal system process	BP	1	AQP1	up_ACOR_EC
GO:0051716	0.515	0.523	169	2001	cellular response to stimulus	BP	1	HMGB1,SREBF1,FLNB,USP1,IRAK1,MCM7,RPA1,DDX39A,CBX5,RACGAP1,HMGA1,HMGCR,TFPI,SREBF2,SMC1A,HINFP,NEDD4,WDR76,INTS7,MNDA,POLA1,SLC29A1,MTDH,HEY1,RRBP1,TRIP13,SLC25A5,PPP1R15B,PARPBP,GINS4,SDC1,CTDNEP1,RAD54L,RANGAP1,POLE,SLC35C2,B3GNT2,PRELID1,HM13,UBE2T,RFC2,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,FANCD2,TIMELESS,THRAP3,ENSCAFG00000008236,NF2,AURKB,PSD4,MMP14,TOPBP1,EZH2,STMN1,DEPDC1,PPP2R5D,GREM1,MAP3K20,RFC4,ADIPOR2,FEN1,CDK4,SMARCC1,MND1,RNASEH2B,PLK3,PCNA,DHX33,TONSL,ARG2,MCM10,RNF152,BRCA1,NOC2L,PRCP,TFRC,NRAS,PPARD,POLH,ITGB3,NEIL3,RAP2C,UBE2J2,ARHGDIA,YWHAB,NCL,RAC1,NUP62,EMP2,DTL,GNB2,PDXP,FOSL1,IQGAP1,SUV39H1,HASPIN,RSL1D1,IQGAP2,CACTIN,HMGB2,GSTO1,DMAP1,CDC42EP4,CDK2,FGF5,SMARCB1,DDX39B,ENSCAFG00000030087,CCNA2,SNX15,ENSCAFG00000005299,RBBP8,EZR,CLSPN,SMC6,RBM14,MIOS,RBM17,RAD23A,CORO1A,SGPL1,BEND6,PHACTR4,SIGMAR1,ASPM,MAST2,MELK,SMARCAL1,PRKD3,ENSCAFG00000010224,TXNDC12,RADIL,REM1,PRMT5,ITGA2,	down_ACOR_VSMC
GO:1903506	0.515	0.532	95	977	regulation of nucleic acid-templated transcription	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0009141	0.515	0.611	11	110	nucleoside triphosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,ENTPD3,CTNS,NDUFS2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0051251	0.515	0.642	7	69	positive regulation of lymphocyte activation	BP	1	LEP,CD83,TP53BP1,CD274,CDKN1A,PTPN22,NOD2	up_ACOR_VSMC
GO:0009895	0.515	0.665	5	94	negative regulation of catabolic process	BP	1	TIMP2,PSMF1,POLDIP2,PARK7,CLEC16A	down_VCAV_EC
GO:0030308	0.515	0.669	5	49	negative regulation of cell growth	BP	1	WNT11,HNF4A,SLIT2,SMARCA2,ACVRL1	up_VSAP_EC
GO:0050727	0.515	0.685	4	74	regulation of inflammatory response	BP	1	CHID1,PARK7,A2M,NAPEPLD	down_VCAV_EC
GO:0046488	0.515	0.688	4	44	phosphatidylinositol metabolic process	BP	1	PDGFB,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0051173	0.515	0.692	4	874	positive regulation of nitrogen compound	BP	1	EYA1,HOXA9,MAP2K6,SIX1	up_VFEM_EC
GO:0000956	0.515	0.713	3	55	nuclear-transcribed mRNA catabolic process	BP	1	SAMD4B,ZFP36L1,PYM1	down_VCAV_EC
GO:1903051	0.515	0.718	3	29	negative regulation of proteolysis involved in cellular protein catabolic	BP	1	OS9,PSEN1,PARK7	up_ACOR_VSMC
GO:0016052	0.515	0.716	3	34	carbohydrate catabolic process	BP	1	GALE,ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0035195	0.515	0.719	3	28	gene silencing by miRNA	BP	1	MOV10,PPP3CA,TUT7	up_VCAV_EC
GO:0051252	0.515	0.726	3	1051	regulation of RNA metabolic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0051153	0.515	0.718	3	28	regulation of striated muscle cell differentiation	BP	1	DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:1904029	0.515	0.718	3	28	regulation of cyclin-dependent protein kinase	BP	1	CNPPD1,FBXO7,LATS2	up_VSAP_EC
GO:1901019	0.515	0.763	2	20	regulation of calcium ion transmembrane transporter activity	BP	1	GSTO1,REM1	down_ACOR_VSMC

GO:0009653	0.515	0.767	2	773	anatomical structure morphogenesis	BP	1	SRSF6,FSCN1	down_AFEM_EC
GO:2001233	0.515	0.84	1	149	regulation of apoptotic signaling pathway	BP	1	STX4	down_ACOR_EC
GO:0086001	0.515	0.851	1	9	cardiac muscle cell action potential	BP	1	CAV1	down_ACOR_VSMC
GO:1900117	0.515	0.853	1	8	regulation of execution phase of apoptosis	BP	1	AIFM1	down_ACOR_VSMC
GO:2000042	0.515	0.853	1	8	negative regulation of double-strand break repair via homologous	BP	1	PARPBP	down_ACOR_VSMC
GO:1904705	0.515	0.846	1	14	regulation of vascular smooth muscle cell	BP	1	BMPR1A	down_VCAV_EC
GO:1990874	0.515	0.846	1	14	vascular smooth muscle cell proliferation	BP	1	BMPR1A	down_VCAV_EC
GO:0007165	0.515	0.882	1	1496	signal transduction	BP	1	PLCL1	down_VFEM_EC
GO:0006638	0.515	0.841	1	30	neutral lipid metabolic process	BP	1	GPAM	up_AFEM_EC
GO:0006639	0.515	0.841	1	30	acylglycerol metabolic process	BP	1	GPAM	up_AFEM_EC
GO:0015718	0.515	0.841	1	30	monocarboxylic acid transport	BP	1	LEP	up_AFEM_EC
GO:0042133	0.515	0.841	1	30	neurotransmitter metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0021522	0.515	0.853	1	8	spinal cord motor neuron differentiation	BP	1	GDPD5	up_VCAV_EC
GO:0010557	0.515	0.849	1	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0044255	0.515	0.844	1	293	cellular lipid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0018410	0.515	0.855	1	7	C-terminal protein amino acid modification	BP	1	TTL	up_VSAP_EC
GO:0031145	0.515	0.855	1	7	anaphase-promoting complex-dependent	BP	1	CDC26	up_VSAP_EC
GO:0070584	0.515	0.855	1	7	mitochondrion morphogenesis	BP	1	POLDIP2	up_VSAP_EC
GO:0072172	0.515	0.855	1	7	mesonephric tubule formation	BP	1	OSR1	up_VSAP_EC
GO:0010712	0.515	0.855	1	7	regulation of collagen metabolic process	BP	1	LARP6	up_VSAP_EC
GO:0042119	0.515	0.855	1	7	neutrophil activation	BP	1	F2RL1	up_VSAP_EC
GO:0043162	0.515	0.855	1	7	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	BP	1	VPS36	up_VSAP_EC
GO:1904294	0.515	0.855	1	7	positive regulation of ERAD pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0050000	0.515720243	0.84087	1	27	chromosome localization	BP	1	CHMP4B	up_ACOR_EC
GO:0009410	0.515821939	0.8408	1	27	response to xenobiotic stimulus	BP	1	AQP1	up_ACOR_EC
GO:0030510	0.515951432	0.84071	1	27	regulation of BMP signaling pathway	BP	1	SMAD6	up_ACOR_EC
GO:0017144	0.516	0.591	15	199	drug metabolic process	BP	1	CD34,ST6GAL1,TLR4,NOS3,SNCAIP,PIPOX,ADSS,ACPP,BMP2,ENSCAFG00000024323,SLC25A25,GCH1,NOS2,HIF1A,KDM3A	up_VCAV_EC
GO:0032940	0.516	0.595	14	231	secretion by cell	BP	1	NR1H4,PTPN11,EXOC5,SEL1L,HIF1A,LYN,GSK3B,GBP5,SDC4,REST,SCAMP1,RAB11FIP1,INHBA,RHBDF2	down_VSAP_EC
GO:0022409	0.516	0.667	5	56	positive regulation of cell-cell adhesion	BP	1	HMGB1,CAV1,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0019058	0.516	0.685	4	64	viral life cycle	BP	1	P4HB,CNOT7,APOE,RAD23A	down_VSAP_EC
GO:0030003	0.516	0.683	4	157	cellular cation homeostasis	BP	1	RAB20,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0046824	0.516	0.717	3	30	positive regulation of nucleocytoplasmic	BP	1	HCLS1,TMEM173,CTDSPL2	up_VCAV_EC
GO:0010633	0.516	0.717	3	28	negative regulation of epithelial cell migration	BP	1	SLIT2,TBXA2R,ACVRL1	up_VSAP_EC
GO:0035050	0.516	0.717	3	28	embryonic heart tube development	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:0051897	0.516	0.762	2	20	positive regulation of protein kinase B signaling	BP	1	SLC29A1,MTDH	down_ACOR_VSMC
GO:0002224	0.516	0.757	2	34	toll-like receptor signaling pathway	BP	1	CYBA,RAB7B	down_VCAV_EC
GO:0006687	0.516	0.763	2	18	glycosphingolipid metabolic process	BP	1	UGCG,NEU3	up_ACOR_VSMC

GO:0009892	0.516	0.767	2	835	negative regulation of metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0021522	0.516	0.852	1	8	spinal cord motor neuron differentiation	BP	1	HOXC10	down_ACOR_VSMC
GO:0090022	0.516	0.85	1	9	regulation of neutrophil chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:0046834	0.516	0.845	1	14	lipid phosphorylation	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0048635	0.516	0.845	1	14	negative regulation of muscle organ	BP	1	TSC22D3	down_VCAV_EC
GO:0072528	0.516	0.845	1	14	pyrimidine-containing compound biosynthetic	BP	1	GPAM	down_VCAV_EC
GO:0050856	0.516	0.846	1	12	regulation of T cell receptor signaling	BP	1	PTPN2	down_VSAP_EC
GO:0060231	0.516	0.847	1	12	mesenchymal to epithelial transition	BP	1	CTNNB1	down_VSAP_EC
GO:0033146	0.516	0.846	1	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	UBA5	down_VSAP_EC
GO:0071384	0.516	0.846	1	12	cellular response to corticosteroid stimulus	BP	1	REST	down_VSAP_EC
GO:0071385	0.516	0.846	1	12	cellular response to glucocorticoid stimulus	BP	1	REST	down_VSAP_EC
GO:1903205	0.516	0.854	1	7	regulation of hydrogen peroxide-induced cell	BP	1	PARK7	up_ACOR_VSMC
GO:2001038	0.516	0.854	1	7	regulation of cellular response to drug	BP	1	PARK7	up_ACOR_VSMC
GO:0048524	0.516	0.84	1	30	positive regulation of viral process	BP	1	RAB7A	up_AFEM_EC
GO:0003281	0.516	0.841	1	30	ventricular septum development	BP	1	LUZP1	up_AFEM_EC
GO:0010658	0.516	0.852	1	8	striated muscle cell apoptotic process	BP	1	RGL2	up_VCAV_EC
GO:0010662	0.516	0.852	1	8	regulation of striated muscle cell apoptotic	BP	1	RGL2	up_VCAV_EC
GO:2000147	0.516	0.84	1	169	positive regulation of cell motility	BP	1	TIAM1	up_VFEM_EC
GO:0051043	0.516	0.854	1	7	regulation of membrane protein ectodomain	BP	1	TIMP2	up_VSAP_EC
GO:0051238	0.516	0.854	1	7	sequestering of metal ion	BP	1	FTL	up_VSAP_EC
GO:0003181	0.516	0.854	1	7	atrioventricular valve morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:1901658	0.516	0.854	1	7	glycosyl compound catabolic process	BP	1	PNP	up_VSAP_EC
GO:0006656	0.516	0.854	1	7	phosphatidylcholine biosynthetic process	BP	1	LCAT	up_VSAP_EC
GO:0032509	0.516	0.854	1	7	endosome transport via multivesicular body sorting pathway	BP	1	VPS36	up_VSAP_EC
GO:0030335	0.516	0.84	1	165	positive regulation of cell migration	BP	1	CAV1	up_VSAP_VSMC
GO:0045682	0.516587785	0.84026	1	27	regulation of epidermis development	BP	1	CDH3	up_ACOR_EC
GO:0009408	0.516679468	0.8402	1	27	response to heat	BP	1	PRKACA	up_ACOR_EC
GO:0006366	0.517	0.542	57	583	transcription by RNA polymerase II	BP	1	SMAD6,LEP,GATA5,PCGF5,NACC2,BMP4,FGFR2,TP53BP1,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,AR,LMO4,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,TBX20,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,MXI1,CHD7,NR3C1,WWC2,DUSP22,EDN1,GTF2A1L,DUSP26,CBX7,NOD2,ENSCAFG00000018360,KLF11,RPRD1B,WFS1,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0030099	0.517	0.599	13	133	myeloid cell differentiation	BP	1	RASSF2,BMP4,CITED2,ISG15,FAM210B,P4HTM,CDKN2B,F2RL1,CLSTN1,APP,PSEN1,B2M,CNOT4	up_ACOR_VSMC
GO:0018212	0.517	0.63	8	81	peptidyl-tyrosine modification	BP	1	ENPP2,IL6R,FGF7,ABL1,PDGFD,PLPP3,LRP4,TTL	up_VSAP_EC
GO:0007098	0.517	0.666	5	56	centrosome cycle	BP	1	PLK2,CEP68,FES,HAUS3,SASS6	up_VCAV_EC
GO:0051208	0.517	0.716	3	29	sequestering of calcium ion	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0051282	0.517	0.716	3	29	regulation of sequestering of calcium ion	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0071482	0.517	0.756	2	34	cellular response to light stimulus	BP	1	AKT2,TMEM161A	down_VCAV_EC

GO:0030224	0.517	0.762	2	18	monocyte differentiation	BP	1	BMP4,CLSTN1	up_ACOR_VSMC
GO:0060760	0.517	0.763	2	17	positive regulation of response to cytokine	BP	1	CREBRF,PARP9	up_ACOR_VSMC
GO:1903131	0.517	0.762	2	18	mononuclear cell differentiation	BP	1	BMP4,CLSTN1	up_ACOR_VSMC
GO:0007431	0.517	0.761	2	19	salivary gland development	BP	1	NTN4,BTBD7	up_VCAV_EC
GO:0030279	0.517	0.762	2	19	negative regulation of ossification	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0045943	0.517	0.763	2	17	positive regulation of transcription by RNA	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0006308	0.517	0.851	1	8	DNA catabolic process	BP	1	AIFM1	down_ACOR_VSMC
GO:0035308	0.517	0.849	1	9	negative regulation of protein	BP	1	YWHAB	down_ACOR_VSMC
GO:0044257	0.517	0.844	1	327	cellular protein catabolic process	BP	1	USP33	down_AFEM_EC
GO:0034142	0.517	0.844	1	14	toll-like receptor 4 signaling pathway	BP	1	RAB7B	down_VCAV_EC
GO:1903556	0.517	0.844	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	BPI	down_VCAV_EC
GO:0051253	0.517	0.844	1	359	negative regulation of RNA metabolic process	BP	1	HDAC7	down_VPOR_EC
GO:1901700	0.517	0.844	1	364	response to oxygen-containing compound	BP	1	RAB11B	down_VPOR_EC
GO:0044271	0.517	0.881	1	1501	cellular nitrogen compound biosynthetic	BP	1	MOSPD1	down_VFEM_EC
GO:0002833	0.517	0.846	1	12	positive regulation of response to biotic	BP	1	PVR	down_VSAP_EC
GO:0045830	0.517	0.847	1	11	positive regulation of isotype switching	BP	1	TFRC	down_VSAP_EC
GO:0002823	0.517	0.854	1	7	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	DUSP22	up_ACOR_VSMC
GO:0002820	0.517	0.854	1	7	negative regulation of adaptive immune	BP	1	DUSP22	up_ACOR_VSMC
GO:0051493	0.517	0.84	1	188	regulation of cytoskeleton organization	BP	1	TUBB4A	up_APUL_EC
GO:0006310	0.517	0.838	1	93	DNA recombination	BP	1	CXHXorf57	up_VPOR_EC
GO:0044262	0.517	0.838	1	89	cellular carbohydrate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0060627	0.517	0.84	1	165	regulation of vesicle-mediated transport	BP	1	TRIM9	up_VFEM_EC
GO:0010638	0.517	0.84	1	207	positive regulation of organelle organization	BP	1	CCL24	up_VPUL_EC
GO:0006122	0.517	0.853	1	7	mitochondrial electron transport, ubiquinol to	BP	1	ENSCAFG00000004260	up_VSAP_EC
GO:0019321	0.517	0.854	1	7	pentose metabolic process	BP	1	DHDH	up_VSAP_EC
GO:0032964	0.517	0.853	1	7	collagen biosynthetic process	BP	1	LARP6	up_VSAP_EC
GO:0042761	0.517	0.853	1	7	very long-chain fatty acid biosynthetic process	BP	1	HACD4	up_VSAP_EC
GO:1901028	0.517	0.854	1	7	regulation of mitochondrial outer membrane permeabilization involved	BP	1	ZNF205	up_VSAP_EC
GO:0032682	0.517	0.853	1	7	negative regulation of chemokine production	BP	1	F2RL1	up_VSAP_EC
GO:0055092	0.517494788	0.83945	1	28	sterol homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:0032943	0.518	0.651	6	60	mononuclear cell proliferation	BP	1	LEP,BMP4,PDE5A,CD274,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0046651	0.518	0.651	6	60	lymphocyte proliferation	BP	1	LEP,BMP4,PDE5A,CD274,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0051216	0.518	0.65	6	70	cartilage development	BP	1	MEF2C,STC1,EDN1,BMP2,HIF1A,ZEB1	up_VCAV_EC
GO:0043536	0.518	0.714	3	32	positive regulation of blood vessel endothelial	BP	1	HMGB1,NUS1,AMOTL1	down_ACOR_VSMC
GO:0050796	0.518	0.714	3	33	regulation of insulin secretion	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0060429	0.518	0.71	3	341	epithelium development	BP	1	BARX1,PTK7,SEMA3A	up_VPOR_EC

GO:1904377	0.518	0.759	2	21	positive regulation of protein localization to cell	BP	1	ACSL3,EZR	down_ACOR_VSMC
GO:0035637	0.518	0.76	2	21	multicellular organismal signaling	BP	1	KCNJ2,SPTBN4	up_VCAV_EC
GO:1901135	0.518	0.756	2	390	carbohydrate derivative metabolic process	BP	1	ADCY3,CHST7	up_VFEM_EC
GO:0045655	0.518	0.849	1	9	regulation of monocyte differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:0061430	0.518	0.851	1	8	bone trabecula morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:1901862	0.518	0.843	1	14	negative regulation of muscle tissue	BP	1	TSC22D3	down_VCAV_EC
GO:0071495	0.518	0.843	1	365	cellular response to endogenous stimulus	BP	1	CITED2	down_VPOR_EC
GO:0010862	0.518	0.845	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	INHBA	down_VSAP_EC
GO:0033993	0.518	0.839	1	186	response to lipid	BP	1	NR1H4	up_APUL_EC
GO:0051782	0.518	0.853	1	7	negative regulation of cell division	BP	1	BLM	up_VCAV_EC
GO:1904467	0.518	0.851	1	8	regulation of tumor necrosis factor secretion	BP	1	ARG2	up_VCAV_EC
GO:2000105	0.518	0.853	1	7	positive regulation of DNA-dependent DNA	BP	1	ATRX	up_VCAV_EC
GO:0061448	0.518	0.837	1	89	connective tissue development	BP	1	HOXA3	up_VPOR_EC
GO:0044089	0.518	0.839	1	170	positive regulation of cellular component	BP	1	CDC42EP5	up_VFEM_EC
GO:0051272	0.518	0.839	1	170	positive regulation of cellular component	BP	1	TIAM1	up_VFEM_EC
GO:0045765	0.518009793	0.70817	3	105	regulation of angiogenesis	BP	1	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0009165	0.518194889	0.70803	3	104	nucleotide biosynthetic process	BP	1	NMNAT2,GUCY1B1,ALDOC	up_ACOR_EC
GO:0003002	0.519	0.613	10	118	regionalization	BP	1	HOXA3,GREM1,HOXA7,HOXC10,HOXB7,HOXC6,HOXB5,HOXC4,HOXA9,GLI1	down_ACOR_VSMC
GO:0009199	0.519	0.614	10	100	ribonucleoside triphosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0051099	0.519	0.639	7	70	positive regulation of binding	BP	1	ABL1,EBF2,TIAM1,LARP6,CDK9,EIF3D,FLOT1	up_VSAP_EC
GO:0009161	0.519	0.647	6	103	ribonucleoside monophosphate	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0048858	0.519	0.679	4	159	cell projection morphogenesis	BP	1	PLXNA4,CAMK2A,LRRN2,KANK1	up_AFEM_EC
GO:0090288	0.519	0.685	4	44	negative regulation of cellular response to growth factor stimulus	BP	1	GATA3,HHEX,CTDSPL2,SKIL	up_VCAV_EC
GO:0022408	0.519	0.711	3	44	negative regulation of cell-cell adhesion	BP	1	SOCS5,PTPN2,SDC4	down_VSAP_EC
GO:0046620	0.519	0.714	3	30	regulation of organ growth	BP	1	MEF2C,EDN1,PROX1	up_VCAV_EC
GO:0140056	0.519	0.715	3	28	organelle localization by membrane tethering	BP	1	SCFD2,STX4,VPS11	up_VSAP_EC
GO:0032606	0.519	0.754	2	35	type I interferon production	BP	1	RNF216,MAVS	down_VCAV_EC
GO:0051239	0.519	0.765	2	859	regulation of multicellular organismal process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0051641	0.519	0.765	2	858	cellular localization	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:0070231	0.519	0.76	2	18	T cell apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0001708	0.519	0.759	2	20	cell fate specification	BP	1	SOX18,CDON	up_VCAV_EC
GO:0045934	0.519	0.755	2	407	negative regulation of nucleobase-containing compound metabolic	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0007422	0.519	0.76	2	18	peripheral nervous system development	BP	1	PLXNA4,CITED2	up_VSAP_EC
GO:0032366	0.519	0.85	1	8	intracellular sterol transport	BP	1	NUS1	down_ACOR_VSMC
GO:0032367	0.519	0.85	1	8	intracellular cholesterol transport	BP	1	NUS1	down_ACOR_VSMC
GO:0035459	0.519	0.85	1	8	cargo loading into vesicle	BP	1	INSIG1	down_ACOR_VSMC
GO:0090110	0.519	0.85	1	8	cargo loading into COPII-coated vesicle	BP	1	INSIG1	down_ACOR_VSMC
GO:1904467	0.519	0.85	1	8	regulation of tumor necrosis factor secretion	BP	1	ARG2	down_ACOR_VSMC

GO:0045892	0.519	0.842	1	328	negative regulation of transcription, DNA-	BP	1	GABPA	down_AFEM_EC
GO:0008156	0.519	0.842	1	15	negative regulation of DNA replication	BP	1	FBH1	down_VCAV_EC
GO:0031076	0.519	0.843	1	14	embryonic camera-type eye development	BP	1	RDH10	down_VCAV_EC
GO:2000826	0.519	0.843	1	14	regulation of heart morphogenesis	BP	1	SEMA3C	down_VCAV_EC
GO:0060026	0.519	0.852	1	7	convergent extension	BP	1	ENSCAFG00000006238	up_ACOR_VSMC
GO:0060439	0.519	0.853	1	7	trachea morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:2000251	0.519	0.852	1	7	positive regulation of actin cytoskeleton	BP	1	NRP1	up_ACOR_VSMC
GO:0070201	0.519	0.838	1	187	regulation of establishment of protein	BP	1	NR1H4	up_APUL_EC
GO:0010575	0.519	0.85	1	8	positive regulation of vascular endothelial growth factor production	BP	1	HIF1A	up_VCAV_EC
GO:0010907	0.519	0.846	1	10	positive regulation of glucose metabolic process	BP	1	PMAIP1	up_VCAV_EC
GO:0021544	0.519	0.85	1	8	subpallium development	BP	1	ALDH1A3	up_VCAV_EC
GO:0036344	0.519	0.85	1	8	platelet morphogenesis	BP	1	MEF2C	up_VCAV_EC
GO:0045103	0.519	0.85	1	8	intermediate filament-based process	BP	1	VPS54	up_VCAV_EC
GO:0045104	0.519	0.85	1	8	intermediate filament cytoskeleton organization	BP	1	VPS54	up_VCAV_EC
GO:0030148	0.519178892	0.83825	1	28	sphingolipid biosynthetic process	BP	1	PRKCD	up_ACOR_EC
GO:0060415	0.519353998	0.8383	1	27	muscle tissue morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0043271	0.519516458	0.83801	1	28	negative regulation of ion transport	BP	1	ACTN2	up_ACOR_EC
GO:1904029	0.519714681	0.83787	1	28	regulation of cyclin-dependent protein kinase	BP	1	CCNYL1	up_ACOR_EC
GO:0030323	0.519888802	0.75081	2	65	respiratory tube development	BP	1	ADAMTSL2,TBX5	up_ACOR_EC
GO:1902680	0.52	0.548	41	415	positive regulation of RNA biosynthetic process	BP	1	SMAD6,LBH,GATA5,GATA4,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2	up_ACOR_VSMC
GO:1903508	0.52	0.548	41	415	positive regulation of nucleic acid-templated transcription	BP	1	SMAD6,LBH,GATA5,GATA4,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0009892	0.52	0.576	20	835	negative regulation of metabolic process	BP	1	HOXC10,LEP,CRY2,GAS1,HOXA7,CRYAB,LMCD1,THRB,MYO1D,GREM1,TENT5C,CLEC16A,CYLD,LRRC15,RECK,NR3C1,AXIN2,ACACB,CTIF,SAMD4B	up_AFEM_EC
GO:0009725	0.52	0.585	16	188	response to hormone	BP	1	HCLS1,KIT,PRCP,PPARG,BAIAP2L1,MEF2C,TFPI,MTOR,ENSCAFG00000010596,SMARCA4,NCK1,CREB1,ADIPOR2,UFSP2,KDM3A,NR4A1	up_VCAV_EC
GO:0044419	0.52	0.611	10	117	interspecies interaction between organisms	BP	1	ILF3,NEDD4,SLC29A1,CAV1,TRIM35,TFRC,SMC3,DDX39B,RAD23A,PPIH	down_ACOR_VSMC
GO:0008152	0.52	0.664	10	3714	metabolic process	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0051716	0.52	0.645	8	2001	cellular response to stimulus	BP	1	NR1H4,MAPK10,PLCL1,ARHGEF26,ZDHHC16,NPNT,NTRK2,PDE1A	up_APUL_EC
GO:0040029	0.52	0.637	7	74	regulation of gene expression, epigenetic	BP	1	MOV10,PPP3CA,CDYL,TUT7,UHRF2,ARID4B,HIST2H2AC	up_VCAV_EC
GO:0006464	0.52	0.656	6	1162	cellular protein modification process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,ASPN	down_ACOR_EC
GO:0036211	0.52	0.656	6	1162	protein modification process	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,ASPN	down_ACOR_EC
GO:0016482	0.52	0.681	4	63	cytosolic transport	BP	1	HOOK3,TMEM87B,MSN,RAB6A	down_VSAP_EC
GO:0030509	0.52	0.683	4	47	BMP signaling pathway	BP	1	SMAD1,BMP2,CTDSPL2,SKIL	up_VCAV_EC
GO:0006351	0.52	0.692	4	1069	transcription, DNA-templated	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC

GO:0044085	0.52	0.691	4	1076	cellular component biogenesis	BP	1	NR1H4,MYBPC2,CCL24,FLRT3	up_VPUL_EC
GO:0009891	0.52	0.712	3	521	positive regulation of biosynthetic process	BP	1	ACVRL1,HOXA1,ACSL3	down_ACOR_EC
GO:0000018	0.52	0.713	3	31	regulation of DNA recombination	BP	1	PARPBP,RAD51,TFRC	down_ACOR_VSMC
GO:0007160	0.52	0.708	3	56	cell-matrix adhesion	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0033002	0.52	0.708	3	55	muscle cell proliferation	BP	1	PDGFRB,BMPR1A,CLSTN1	down_VCAV_EC
GO:0022037	0.52	0.715	3	27	metencephalon development	BP	1	SEC24B,ZNF365,ATRN	up_ACOR_VSMC
GO:0046916	0.52	0.711	3	35	cellular transition metal ion homeostasis	BP	1	CP,SLC39A8,HIF1A	up_VCAV_EC
GO:0010770	0.52	0.713	3	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	ABL1,SHOX2,MAP2K2	up_VSAP_EC
GO:0010827	0.52	0.714	3	28	regulation of glucose transmembrane transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0002376	0.52	0.713	3	622	immune system process	BP	1	HOXA9,TLR2,CAV1	up_VSAP_VSMC
GO:0006096	0.52	0.76	2	18	glycolytic process	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:0006165	0.52	0.76	2	18	nucleoside diphosphate phosphorylation	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:0006757	0.52	0.76	2	18	ATP generation from ADP	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:0042866	0.52	0.76	2	18	pyruvate biosynthetic process	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:0001947	0.52	0.757	2	21	heart looping	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0061371	0.52	0.757	2	21	determination of heart left/right asymmetry	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0060420	0.52	0.759	2	18	regulation of heart growth	BP	1	ACACB,SAV1	up_VSAP_EC
GO:1902679	0.52	0.841	1	329	negative regulation of RNA biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:1903507	0.52	0.841	1	329	negative regulation of nucleic acid-templated	BP	1	GABPA	down_AFEM_EC
GO:0006220	0.52	0.842	1	14	pyrimidine nucleotide metabolic process	BP	1	GPAM	down_VCAV_EC
GO:0008206	0.52	0.845	1	11	bile acid metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0051560	0.52	0.843	1	12	mitochondrial calcium ion homeostasis	BP	1	DISC1	down_VSAP_EC
GO:0007588	0.52	0.852	1	7	excretion	BP	1	EDN1	up_ACOR_VSMC
GO:0001516	0.52	0.852	1	7	prostaglandin biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0034214	0.52	0.852	1	7	protein hexamerization	BP	1	LRRC8C	up_ACOR_VSMC
GO:0046457	0.52	0.852	1	7	prostanoid biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0071599	0.52	0.847	1	9	otic vesicle development	BP	1	GATA3	up_VCAV_EC
GO:1903204	0.52	0.847	1	9	negative regulation of oxidative stress-induced	BP	1	HIF1A	up_VCAV_EC
GO:1903959	0.52	0.849	1	8	regulation of anion transmembrane transport	BP	1	RIPK1	up_VCAV_EC
GO:0010876	0.52	0.836	1	92	lipid localization	BP	1	ABHD5	up_VPOR_EC
GO:1903530	0.52	0.837	1	165	regulation of secretion by cell	BP	1	TLR2	up_VSAP_VSMC
GO:0070925	0.520392561	0.62387	8	293	organelle assembly	BP	1	MYOZ2,TMOD1,ATG16L2,PLS1,ACTN2,CHMP4B,TP53INP2,ENSCAFG00000010493	up_ACOR_EC
GO:2001235	0.52059324	0.75	2	69	positive regulation of apoptotic signaling	BP	1	CLU,PRKCD	up_ACOR_EC
GO:0042060	0.520786647	0.7057	3	103	wound healing	BP	1	AQP1,FOXC2,PRKCD	up_ACOR_EC
GO:0120034	0.520879627	0.83703	1	28	positive regulation of plasma membrane bounded cell projection	BP	1	NRP1	up_ACOR_EC
GO:0042113	0.520977367	0.74994	2	64	B cell activation	BP	1	NOD2,PRKCD	up_ACOR_EC

GO:0008219	0.521	0.536	59	611	cell death	BP	1	FZD1,THRB,WNT11,CD274,ACKR3,MAP3K14,AXIN2,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,EMP2,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,DFFB,PDK2,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,HIC1,PTPMT1,NPAS2,FBXO7,WISP2,ENSCAFG00000011993,PRMT2,KDM2B,RAF1,ZNF205,XKR8,STX4,QARS,EMP3,ARHGAP10,HTRA2,NCK1,KRCC1,HMOX1,MAP2K2,TGFBR2,CITED2,CASP12,TRADD,DEDD2,DDIT4,LATS2	up_VSAP_EC
GO:0009890	0.521	0.57	21	420	negative regulation of biosynthetic process	BP	1	NAB2,KANK2,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,PARK7,ZFP36L1,LOXL3,ORMDL3,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0006163	0.521	0.582	17	174	purine nucleotide metabolic process	BP	1	ACSM3,ACACB,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0051171	0.521	0.601	14	1697	regulation of nitrogen compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,PUM3,EIF5,CCAR1,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0061351	0.521	0.664	5	50	neural precursor cell proliferation	BP	1	EMX2,CDON,LIMS2,DAGLB,KDM2B	up_VSAP_EC
GO:0072078	0.521	0.711	3	33	nephron tubule morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:0050851	0.521	0.752	2	34	antigen receptor-mediated signaling	BP	1	PRNP,THY1	down_VCAV_EC
GO:0032271	0.521	0.75	2	73	regulation of protein polymerization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0010648	0.521	0.754	2	407	negative regulation of cell communication	BP	1	EYA1,CYP26B1	up_VFEM_EC
GO:0098754	0.521	0.846	1	9	detoxification	BP	1	GSTO1	down_ACOR_VSMC
GO:2001014	0.521	0.848	1	8	regulation of skeletal muscle cell differentiation	BP	1	SIX4	down_ACOR_VSMC
GO:0031572	0.521	0.841	1	15	G2 DNA damage checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:2001023	0.521	0.842	1	14	regulation of response to drug	BP	1	PARK7	down_VCAV_EC
GO:0001541	0.521	0.843	1	12	ovarian follicle development	BP	1	INHBA	down_VSAP_EC
GO:0060914	0.521	0.844	1	11	heart formation	BP	1	CTNNB1	down_VSAP_EC
GO:0031664	0.521	0.851	1	7	regulation of lipopolysaccharide-mediated signaling	BP	1	SASH1	up_ACOR_VSMC
GO:0009725	0.521	0.837	1	188	response to hormone	BP	1	NR1H4	up_APUL_EC
GO:0018198	0.521	0.845	1	10	peptidyl-cysteine modification	BP	1	NOS2	up_VCAV_EC
GO:0031112	0.521	0.848	1	8	positive regulation of microtubule polymerization or depolymerization	BP	1	FES	up_VCAV_EC
GO:0003171	0.521	0.845	1	10	atrioventricular valve development	BP	1	BMP2	up_VCAV_EC
GO:0009636	0.521107755	0.74971	2	66	response to toxic substance	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:0040008	0.521202782	0.65817	5	179	regulation of growth	BP	1	PLS1,ESM1,FOXC2,TBX5,NRP1	up_ACOR_EC
GO:0070936	0.521329031	0.83671	1	28	protein K48-linked ubiquitination	BP	1	UBE2H	up_ACOR_EC
GO:0001501	0.522	0.586	15	178	skeletal system development	BP	1	HOXB7,KIT,FLI1,MEF2C,CHD7,TIPARP,STC1,EDN1,HOXB8,BMP2,MDFI,HOXB5,HIF1A,ZEB1,TJP2	up_VCAV_EC
GO:0048732	0.522	0.643	6	116	gland development	BP	1	BMPR1A,LMO4,SEMA3C,B4GALT1,GLI3,PRKCSH	down_VCAV_EC
GO:0032943	0.522	0.647	6	60	mononuclear cell proliferation	BP	1	CD274,ABL1,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0046651	0.522	0.647	6	60	lymphocyte proliferation	BP	1	CD274,ABL1,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0007623	0.522	0.662	5	55	circadian rhythm	BP	1	SREBF1,HNRNPD,TIMELESS,THRAP3,EZH2	down_ACOR_VSMC
GO:0010647	0.522	0.68	4	460	positive regulation of cell communication	BP	1	ENSCAFG00000002015,ACVR2A,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:0097659	0.522	0.689	4	1072	nucleic acid-templated transcription	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0007006	0.522	0.709	3	35	mitochondrial membrane organization	BP	1	SLC25A5,CHCHD3,SAMM50	down_ACOR_VSMC

GO:0002262	0.522	0.707	3	54	myeloid cell homeostasis	BP	1	ZFP36L1,FOXO3,ANKRD54	down_VCAV_EC
GO:0007275	0.522	0.725	3	1370	multicellular organism development	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0007612	0.522	0.71	3	33	learning	BP	1	ATP8A1,RELN,HIF1A	up_VCAV_EC
GO:0009311	0.522	0.756	2	21	oligosaccharide metabolic process	BP	1	MPDU1,B4GALT1	down_ACOR_VSMC
GO:0061614	0.522	0.756	2	20	pri-miRNA transcription by RNA polymerase II	BP	1	PPARD,FOSL1	down_ACOR_VSMC
GO:0032007	0.522	0.753	2	27	negative regulation of TOR signaling	BP	1	SESN2,HIF1A	down_VSAP_EC
GO:0016485	0.522	0.749	2	73	protein processing	BP	1	GAS1,F3	up_AFEM_EC
GO:0009117	0.522	0.749	2	208	nucleotide metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0043367	0.522	0.758	2	18	CD4-positive, alpha-beta T cell differentiation	BP	1	STAT6,CD83	up_VSAP_EC
GO:0035024	0.522	0.848	1	8	negative regulation of Rho protein signal	BP	1	STMN1	down_ACOR_VSMC
GO:0003230	0.522	0.841	1	14	cardiac atrium development	BP	1	NOTCH2	down_VCAV_EC
GO:0003209	0.522	0.841	1	14	cardiac atrium morphogenesis	BP	1	NOTCH2	down_VCAV_EC
GO:1903035	0.522	0.84	1	14	negative regulation of response to wounding	BP	1	RGMA	down_VCAV_EC
GO:0042790	0.522	0.843	1	11	nucleolar large rRNA transcription by RNA	BP	1	SMARCA4	down_VSAP_EC
GO:1901836	0.522	0.843	1	11	regulation of transcription of nucleolar large rRNA by RNA polymerase I	BP	1	SMARCA4	down_VSAP_EC
GO:0060603	0.522	0.85	1	7	mammary gland duct morphogenesis	BP	1	FGFR2	up_ACOR_VSMC
GO:0034086	0.522	0.85	1	7	maintenance of sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0034088	0.522	0.85	1	7	maintenance of mitotic sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0002021	0.522	0.846	1	9	response to dietary excess	BP	1	SLC25A25	up_VCAV_EC
GO:0006337	0.522	0.85	1	7	nucleosome disassembly	BP	1	SMARCA4	up_VCAV_EC
GO:0032986	0.522	0.85	1	7	protein-DNA complex disassembly	BP	1	SMARCA4	up_VCAV_EC
GO:0031589	0.522	0.835	1	93	cell-substrate adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0009259	0.522	0.836	1	166	ribonucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0030155	0.522217437	0.65719	5	180	regulation of cell adhesion	BP	1	ARHGAP6,DUSP26,FOXC2,NRP1,PRKCD	up_ACOR_EC
GO:0042733	0.522280759	0.8362	1	27	embryonic digit morphogenesis	BP	1	LRP4	up_ACOR_EC
GO:0001738	0.522436819	0.83609	1	27	morphogenesis of a polarized epithelium	BP	1	BRSK1	up_ACOR_EC
GO:2001141	0.523	0.523	95	979	regulation of RNA biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0048870	0.523	0.543	43	451	cell motility	BP	1	EMX2,HOXA7,PEX7,TWIST2,WNT11,FAM107A,ARHGEF5,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,IL17RC,FUZ,PDGFD,HSD3B7,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,LIMD1,FBLN1,ZNF580,STX4,ZFAND5,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,SAA1,BAG4	up_VSAP_EC

GO:0051674	0.523	0.543	43	451	localization of cell	BP	1	EMX2,HOXA7,PEX7,TWIST2,WNT11,FAM107A,ARHGEF5,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,IL17RC,FUZ,PDGFD,HSD3B7,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,LIMD1,FBLN1,ZNF580,STX4,ZFAND5,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,SAA1,BAG4	up_VSAP_EC
GO:0002263	0.523	0.634	7	68	cell activation involved in immune response	BP	1	PLCG2,TP53BP1,F2RL1,PRKCE,APP,PSEN1,IL18R1	up_ACOR_VSMC
GO:0010038	0.523	0.646	6	62	response to metal ion	BP	1	TNNT2,PRKAA2,BNIP3,B2M,SLC25A12,PARK7	up_ACOR_VSMC
GO:0034101	0.523	0.68	4	45	erythrocyte homeostasis	BP	1	HSPA9,PRMT1,HMGB2,JMJD6	down_ACOR_VSMC
GO:0032774	0.523	0.689	4	1073	RNA biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0035264	0.523	0.706	3	56	multicellular organism growth	BP	1	GPAM,PEX5,ZFP36L1	down_VCAV_EC
GO:0048732	0.523	0.704	3	116	gland development	BP	1	HOXA9,LBH,TNC	up_AFEM_EC
GO:0043271	0.523	0.711	3	28	negative regulation of ion transport	BP	1	GABRE,KCNE3,OSR1	up_VSAP_EC
GO:0140029	0.523	0.711	3	28	exocytic process	BP	1	SCFD2,STX4,VPS11	up_VSAP_EC
GO:1901224	0.523	0.756	2	20	positive regulation of NIK/NF-kappaB signaling	BP	1	IRAK1,GREM1	down_ACOR_VSMC
GO:1901292	0.523	0.751	2	34	nucleoside phosphate catabolic process	BP	1	ENTPD3,ACAT1	down_VCAV_EC
GO:0001942	0.523	0.753	2	28	hair follicle development	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0022404	0.523	0.753	2	28	molting cycle process	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0022405	0.523	0.753	2	28	hair cycle process	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0050732	0.523	0.758	2	18	negative regulation of peptidyl-tyrosine	BP	1	PSEN1,DUSP22	up_ACOR_VSMC
GO:0002204	0.523	0.758	2	18	somatic recombination of immunoglobulin genes involved in immune	BP	1	THOC1,SWAP70	up_VCAV_EC
GO:0002208	0.523	0.758	2	18	somatic diversification of immunoglobulins involved in immune response	BP	1	THOC1,SWAP70	up_VCAV_EC
GO:0045190	0.523	0.758	2	18	isotype switching	BP	1	THOC1,SWAP70	up_VCAV_EC
GO:0023057	0.523	0.751	2	409	negative regulation of signaling	BP	1	EYA1,CYP26B1	up_VFEM_EC
GO:0016055	0.523	0.835	1	134	Wnt signaling pathway	BP	1	SULF1	down_ACOR_EC
GO:0198738	0.523	0.835	1	134	cell-cell signaling by wnt	BP	1	SULF1	down_ACOR_EC
GO:0000278	0.523	0.84	1	331	mitotic cell cycle	BP	1	GPSM2	down_AFEM_EC
GO:0046622	0.523	0.839	1	15	positive regulation of organ growth	BP	1	BMPR1A	down_VCAV_EC
GO:0061098	0.523	0.841	1	12	positive regulation of protein tyrosine kinase	BP	1	ADAM17	down_VSAP_EC
GO:0010591	0.523	0.842	1	12	regulation of lamellipodium assembly	BP	1	FSCN1	down_VSAP_EC
GO:0071825	0.523	0.842	1	12	protein-lipid complex subunit organization	BP	1	APOE	down_VSAP_EC
GO:0071827	0.523	0.842	1	12	plasma lipoprotein particle organization	BP	1	APOE	down_VSAP_EC
GO:0002320	0.523	0.849	1	7	lymphoid progenitor cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0035640	0.523	0.85	1	7	exploration behavior	BP	1	PRKCE	up_ACOR_VSMC
GO:0055082	0.523	0.836	1	189	cellular chemical homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0071363	0.523	0.836	1	188	cellular response to growth factor stimulus	BP	1	NPNT	up_APUL_EC
GO:0003012	0.523	0.834	1	90	muscle system process	BP	1	HTR7	up_VPOR_EC
GO:0007605	0.523097308	0.83562	1	27	sensory perception of sound	BP	1	USP53	up_ACOR_EC
GO:0007156	0.523179311	0.83575	1	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	CDH3	up_ACOR_EC
GO:0006814	0.52350793	0.83514	1	28	sodium ion transport	BP	1	SLC9A9	up_ACOR_EC

GO:0030163	0.524	0.549	35	365	protein catabolic process	BP	1	ZRANB1,FBXL20,SKP2,SH3RF2,ISG15,ZNRF3,CTSS,PTPN3,KLHL20,CTSB,BNIP3,EGLN1,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,LYPLAL1,PSEN1,LAMP2,CLN8,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,AZIN2,DZIP3,PARK7	up_ACOR_VSMC
GO:0009617	0.524	0.593	13	133	response to bacterium	BP	1	PTGFR,ABL1,F2RL1,PLA2G6,TBXA2R,SASH1,MYD88,CFD,MAPKBP1,CYBA,CA5B,MAVS,JCHAIN	up_VSAP_EC
GO:0034504	0.524	0.603	11	111	protein localization to nucleus	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PARP9,PSEN1,JUP,SUN1,RPAIN,PARK7	up_ACOR_VSMC
GO:0051495	0.524	0.623	8	82	positive regulation of cytoskeleton organization	BP	1	WNT11,ARHGEF5,ABL1,CDC42EP5,CDC42EP2,F2RL1,NCK1,BAG4	up_VSAP_EC
GO:0010594	0.524	0.633	7	71	regulation of endothelial cell migration	BP	1	BMP4,SASH1,FGF18,NRP1,SYNJ2BP,JUP,PIK3C2A	up_ACOR_VSMC
GO:0008285	0.524	0.655	5	201	negative regulation of cell proliferation	BP	1	DLL1,GREM1,OVOL1,AXIN2,FAP	up_AFEM_EC
GO:0051480	0.524	0.66	5	50	regulation of cytosolic calcium ion concentration	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:0048583	0.524	0.666	5	1095	regulation of response to stimulus	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0019538	0.524	0.7	4	1713	protein metabolic process	BP	1	IVNS1ABP,DARS,EIF3M,USP33	down_AFEM_EC
GO:0051896	0.524	0.681	4	39	regulation of protein kinase B signaling	BP	1	LEP,SESN3,DAG1,INPP5K	up_ACOR_VSMC
GO:0006418	0.524	0.709	3	31	tRNA aminoacylation for protein translation	BP	1	VARS,FARSA,RARS	down_ACOR_VSMC
GO:0051128	0.524	0.759	2	790	regulation of cellular component organization	BP	1	GPSM2,FSCN1	down_AFEM_EC
GO:0002534	0.524	0.756	2	18	cytokine production involved in inflammatory	BP	1	LEP,NOD2	up_ACOR_VSMC
GO:0048870	0.524	0.752	2	451	cell motility	BP	1	TBX5,NTRK2	up_APUL_EC
GO:0051674	0.524	0.752	2	451	localization of cell	BP	1	TBX5,NTRK2	up_APUL_EC
GO:0061180	0.524	0.755	2	20	mammary gland epithelium development	BP	1	GATA3,HIF1A	up_VCAV_EC
GO:0002228	0.524	0.844	1	9	natural killer cell mediated immunity	BP	1	CORO1A	down_ACOR_VSMC
GO:0003299	0.524	0.847	1	8	muscle hypertrophy in response to stress	BP	1	EZH2	down_ACOR_VSMC
GO:0014887	0.524	0.847	1	8	cardiac muscle adaptation	BP	1	EZH2	down_ACOR_VSMC
GO:0014898	0.524	0.847	1	8	cardiac muscle hypertrophy in response	BP	1	EZH2	down_ACOR_VSMC
GO:0042267	0.524	0.844	1	9	natural killer cell mediated cytotoxicity	BP	1	CORO1A	down_ACOR_VSMC
GO:2000144	0.524	0.841	1	12	positive regulation of DNA-templated transcription,	BP	1	CTNNB1	down_VSAP_EC
GO:0042088	0.524	0.841	1	12	T-helper 1 type immune response	BP	1	SOCS5	down_VSAP_EC
GO:0072577	0.524	0.842	1	11	endothelial cell apoptotic process	BP	1	SERPINE1	down_VSAP_EC
GO:2000351	0.524	0.842	1	11	regulation of endothelial cell apoptotic process	BP	1	SERPINE1	down_VSAP_EC
GO:0006953	0.524	0.849	1	7	acute-phase response	BP	1	ENSCAFG00000029553	up_ACOR_VSMC
GO:0032717	0.524	0.849	1	7	negative regulation of interleukin-8 production	BP	1	PTPN22	up_ACOR_VSMC
GO:0050766	0.524	0.846	1	8	positive regulation of phagocytosis	BP	1	F2RL1	up_ACOR_VSMC
GO:0002230	0.524	0.844	1	9	positive regulation of defense response to virus	BP	1	TMEM173	up_VCAV_EC
GO:0045920	0.524	0.845	1	9	negative regulation of exocytosis	BP	1	RSC1A1	up_VCAV_EC
GO:0010629	0.524	0.843	1	502	negative regulation of gene expression	BP	1	GATA5	up_VCAV_VSMC
GO:0006874	0.524	0.833	1	91	cellular calcium ion homeostasis	BP	1	C3AR1	up_VPOR_EC
GO:0070925	0.524	0.837	1	293	organelle assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0043408	0.524	0.835	1	211	regulation of MAPK cascade	BP	1	CCL24	up_VPUL_EC
GO:0007173	0.524614964	0.83452	1	27	epidermal growth factor receptor signaling	BP	1	SOX9	up_ACOR_EC
GO:0042472	0.524748154	0.83442	1	27	inner ear morphogenesis	BP	1	SOX9	up_ACOR_EC

GO:0030036	0.525	0.572	19	223	actin cytoskeleton organization	BP	1	FSCN1,FLNB,FMNL3,CAPG,LIMA1,NF2,STMN1,GAS2L3,RAC1,EMP2,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,PHACTR4,ARPC1B,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0006954	0.525	0.587	14	147	inflammatory response	BP	1	TLR1,LEP,HRH1,TLR3,CLSTN1,PTGDR,APP,PSEN1,CCL5,NOD2,JAM3,TNFRSF11B,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0002696	0.525	0.632	7	80	positive regulation of leukocyte activation	BP	1	HMGB1,CAV1,MMP14,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0035556	0.525	0.634	7	845	intracellular signal transduction	BP	1	ARHGEF2,ENSCAFG00000002015,ASPN,FBP1,MTDH,STK17B,ENSCAFG00000032731	up_VPOR_EC
GO:0000724	0.525	0.645	6	57	double-strand break repair via homologous	BP	1	CDC7,TP53BP1,ZNF365,DMC1,WDR48,FAN1	up_ACOR_VSMC
GO:0043583	0.525	0.644	6	59	ear development	BP	1	BMP4,FGFR2,SEC24B,FZD3,CHD7,EDN1	up_ACOR_VSMC
GO:0090316	0.525	0.66	5	48	positive regulation of intracellular protein	BP	1	LEP,TCAF1,PTPN22,PSEN1,JUP	up_ACOR_VSMC
GO:0043433	0.525	0.66	5	49	negative regulation of DNA-binding transcription factor activity	BP	1	ANXA4,GLIS2,RBCK1,PRMT2,KEAP1	up_VSAP_EC
GO:0008593	0.525	0.708	3	33	regulation of Notch signaling pathway	BP	1	SLC35C2,MMP14,BEND6	down_ACOR_VSMC
GO:1903321	0.525	0.707	3	33	negative regulation of protein modification by small protein conjugation	BP	1	USP4,U2AF2,CAV1	down_ACOR_VSMC
GO:0009966	0.525	0.76	2	868	regulation of signal transduction	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0008589	0.525	0.751	2	28	regulation of smoothened signaling pathway	BP	1	PRKACB,CHSY1	down_VSAP_EC
GO:0071479	0.525	0.75	2	29	cellular response to ionizing radiation	BP	1	CRYAB,CDKN1A	down_VSAP_EC
GO:0072655	0.525	0.749	2	33	establishment of protein localization to	BP	1	DDIT3,SH3GLB1	down_VSAP_EC
GO:1901224	0.525	0.754	2	20	positive regulation of NIK/NF-kappaB signaling	BP	1	TLR3,ENSCAFG00000002015	up_VCAV_EC
GO:0051155	0.525	0.756	2	18	positive regulation of striated muscle cell	BP	1	SHOX2,FLOT1	up_VSAP_EC
GO:1903432	0.525	0.756	2	18	regulation of TORC1 signaling	BP	1	SESN1,CASTOR1	up_VSAP_EC
GO:0006821	0.525	0.756	2	18	chloride transport	BP	1	GABRE,CLCN2	up_VSAP_EC
GO:0061318	0.525	0.846	1	8	renal filtration cell differentiation	BP	1	IQGAP1	down_ACOR_VSMC
GO:0072010	0.525	0.846	1	8	glomerular epithelium development	BP	1	IQGAP1	down_ACOR_VSMC
GO:0072112	0.525	0.846	1	8	glomerular visceral epithelial cell	BP	1	IQGAP1	down_ACOR_VSMC
GO:0072311	0.525	0.846	1	8	glomerular epithelial cell differentiation	BP	1	IQGAP1	down_ACOR_VSMC
GO:0018126	0.525	0.838	1	14	protein hydroxylation	BP	1	CRTAP	down_VCAV_EC
GO:0044818	0.525	0.838	1	15	mitotic G2/M transition checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:0055010	0.525	0.838	1	15	ventricular cardiac muscle tissue morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0009299	0.525	0.841	1	11	mRNA transcription	BP	1	DDIT3	down_VSAP_EC
GO:0002686	0.525	0.84	1	12	negative regulation of leukocyte migration	BP	1	MMP28	down_VSAP_EC
GO:0016101	0.525	0.84	1	13	diterpenoid metabolic process	BP	1	RDH11	down_VSAP_EC
GO:0021772	0.525	0.841	1	11	olfactory bulb development	BP	1	EXT1	down_VSAP_EC
GO:0021988	0.525	0.841	1	11	olfactory lobe development	BP	1	EXT1	down_VSAP_EC
GO:0032768	0.525	0.84	1	12	regulation of monooxygenase activity	BP	1	APOE	down_VSAP_EC
GO:0032814	0.525	0.848	1	7	regulation of natural killer cell activation	BP	1	LEP	up_ACOR_VSMC
GO:0007272	0.525	0.834	1	31	ensheathment of neurons	BP	1	LGI4	up_AFEM_EC
GO:0008366	0.525	0.834	1	31	axon ensheathment	BP	1	LGI4	up_AFEM_EC
GO:0034767	0.525	0.834	1	31	positive regulation of ion transmembrane transport	BP	1	FXYD1	up_AFEM_EC
GO:0065003	0.525	0.846	1	616	protein-containing complex assembly	BP	1	ESR1	up_AORT_VSMC
GO:0007520	0.525	0.846	1	8	myoblast fusion	BP	1	CDON	up_VCAV_EC

GO:0034260	0.525	0.848	1	7	negative regulation of GTPase activity	BP	1	AMOT	up_VCAV_EC
GO:0042326	0.525	0.834	1	163	negative regulation of phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:2000147	0.525	0.834	1	169	positive regulation of cell motility	BP	1	CAV1	up_VSAP_VSMC
GO:0045165	0.525741438	0.74576	2	65	cell fate commitment	BP	1	SOX9,FOXC2	up_ACOR_EC
GO:0019222	0.526	0.543	46	1934	regulation of metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXC10,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,MYO1D,MFAP4,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ACACB,PPARGC1A,CCL5,CTIF,FAP,ADAM17,SAMD4B,TNC	up_AFEM_EC
GO:0070201	0.526	0.574	18	187	regulation of establishment of protein localization	BP	1	HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,CDH1,ABL1,IL17RC,ANXA4,F2RL1,ICE1,PIK3R1,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:1901214	0.526	0.622	8	81	regulation of neuron death	BP	1	PPARGC1A,EGLN1,NRP1,UNC5B,CCL5,OXR1,WFS1,PARK7	up_ACOR_VSMC
GO:0006733	0.526	0.677	4	45	oxidoreduction coenzyme metabolic process	BP	1	NNT,PDHA1,PGD,PDSS1	down_ACOR_VSMC
GO:0050794	0.526	0.738	4	3075	regulation of cellular process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0023056	0.526	0.676	4	462	positive regulation of signaling	BP	1	ENSCAFG00000002015,ACVR2A,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:1902600	0.526	0.707	3	31	proton transmembrane transport	BP	1	ATP6V0E1,NDUFA4L2,PARK7	up_ACOR_VSMC
GO:0044403	0.526	0.701	3	116	symbiont process	BP	1	LRRC15,RAB7A,NAPEPLD	up_AFEM_EC
GO:0006351	0.526	0.717	3	1069	transcription, DNA-templated	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0071310	0.526	0.707	3	634	cellular response to organic substance	BP	1	TLR2,CAV1,FGF5	up_VSAP_VSMC
GO:1901566	0.526	0.707	3	598	organonitrogen compound biosynthetic	BP	1	GATM,GALNT17,PRR16	up_VSAP_VSMC
GO:0051055	0.526	0.753	2	21	negative regulation of lipid biosynthetic process	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:2000106	0.526	0.749	2	29	regulation of leukocyte apoptotic process	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0009185	0.526	0.751	2	23	ribonucleoside diphosphate metabolic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0031327	0.526	0.749	2	412	negative regulation of cellular biosynthetic	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0072523	0.526	0.838	1	14	purine-containing compound catabolic	BP	1	ACAT1	down_VCAV_EC
GO:1900744	0.526	0.837	1	15	regulation of p38MAPK cascade	BP	1	SASH1	down_VCAV_EC
GO:2000737	0.526	0.848	1	7	negative regulation of stem cell differentiation	BP	1	LBH	up_ACOR_VSMC
GO:2001044	0.526	0.845	1	8	regulation of integrin-mediated signaling	BP	1	LIMS2	up_ACOR_VSMC
GO:0009798	0.526	0.833	1	31	axis specification	BP	1	DLL1	up_AFEM_EC
GO:0030307	0.526	0.833	1	31	positive regulation of cell growth	BP	1	ADAM17	up_AFEM_EC
GO:0042306	0.526	0.833	1	31	regulation of protein import into nucleus	BP	1	LEP	up_AFEM_EC
GO:0042542	0.526	0.833	1	31	response to hydrogen peroxide	BP	1	CRYAB	up_AFEM_EC
GO:0044458	0.526	0.843	1	9	motile cilium assembly	BP	1	SPATA6	up_VCAV_EC
GO:0006839	0.526	0.832	1	86	mitochondrial transport	BP	1	SLC25A16	up_VPOR_EC
GO:0000904	0.526	0.833	1	181	cell morphogenesis involved in differentiation	BP	1	RADIL	up_VFEM_EC
GO:0045932	0.526	0.845	1	8	negative regulation of muscle contraction	BP	1	KCNE3	up_VSAP_EC
GO:0065003	0.527	0.544	36	616	protein-containing complex assembly	BP	1	VEGFA,CELF1,C1QTNF6,VASP,SEC24D,PTPN11,FSCN1,MZT1,DPYSL3,FBLIM1,ANKRA2,SRP54,MSN,PRPF3,DDX39B,BRD2,CNOT7,ACTR3,CTNNB1,CRYAB,APOE,STRAP,DDIT3,TWF1,PLEKHG2,TLN1,GSK3B,GBP5,EIF2S1,PRMT1,CLTC,CAPG,RSL24D1,TNFAIP1,SEC13,MYBPC2	down_VSAP_EC
GO:0002252	0.527	0.578	16	166	immune effector process	BP	1	MAP3K14,ABL1,EMP2,DLL1,STAT6,F2RL1,MYD88,CFD,NLRX1,TKFC,RNF216,STX4,PQBP1,PPP3CB,MAVS,DDIT4	up_VSAP_EC

GO:0006807	0.527	0.712	5	3221	nitrogen compound metabolic process	BP	1	CYP1A1,LIMK1,GATA5,C6,ENSCAFG00000028814	up_VCAV_VSMC
GO:0002695	0.527	0.676	4	44	negative regulation of leukocyte activation	BP	1	HMGB1,MNDA,HMGB3,ARG2	down_ACOR_VSMC
GO:0048565	0.527	0.678	4	38	digestive tract development	BP	1	GATA5,GATA4,BMP4,FGFR2	up_ACOR_VSMC
GO:0032231	0.527	0.706	3	32	regulation of actin filament bundle assembly	BP	1	NF2,STMN1,RAC1	down_ACOR_VSMC
GO:0051128	0.527	0.709	3	790	regulation of cellular component organization	BP	1	CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0007156	0.527	0.75	2	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	PVR,CDH11	down_VSAP_EC
GO:0031175	0.527	0.745	2	224	neuron projection development	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0071360	0.527	0.842	1	9	cellular response to exogenous dsRNA	BP	1	CAV1	down_ACOR_VSMC
GO:0101023	0.527	0.845	1	8	vascular endothelial cell proliferation	BP	1	HMGB1	down_ACOR_VSMC
GO:1905562	0.527	0.845	1	8	regulation of vascular endothelial cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0003338	0.527	0.837	1	15	metanephros morphogenesis	BP	1	GREM1	down_VCAV_EC
GO:0015696	0.527	0.837	1	14	ammonium transport	BP	1	PARK7	down_VCAV_EC
GO:0030516	0.527	0.836	1	15	regulation of axon extension	BP	1	TRPV2	down_VCAV_EC
GO:0090184	0.527	0.837	1	14	positive regulation of kidney development	BP	1	GREM1	down_VCAV_EC
GO:0001662	0.527	0.847	1	7	behavioral fear response	BP	1	FBXL20	up_ACOR_VSMC
GO:0001914	0.527	0.845	1	8	regulation of T cell mediated cytotoxicity	BP	1	B2M	up_ACOR_VSMC
GO:0002209	0.527	0.847	1	7	behavioral defense response	BP	1	FBXL20	up_ACOR_VSMC
GO:0042596	0.527	0.847	1	7	fear response	BP	1	FBXL20	up_ACOR_VSMC
GO:2000178	0.527	0.847	1	7	negative regulation of neural precursor cell	BP	1	LIMS2	up_ACOR_VSMC
GO:0031623	0.527	0.832	1	31	receptor internalization	BP	1	GREM1	up_AFEM_EC
GO:0051817	0.527	0.832	1	31	modification of morphology or physiology of other organism	BP	1	NAPEPLD	up_AFEM_EC
GO:0071804	0.527	0.832	1	31	cellular potassium ion transport	BP	1	KCNC4	up_AFEM_EC
GO:0071805	0.527	0.832	1	31	potassium ion transmembrane transport	BP	1	KCNC4	up_AFEM_EC
GO:0006518	0.527	0.836	1	290	peptide metabolic process	BP	1	LNPEP	up_AORT_EC
GO:0045321	0.527	0.833	1	191	leukocyte activation	BP	1	BPI	up_APUL_EC
GO:0050999	0.527	0.842	1	9	regulation of nitric-oxide synthase activity	BP	1	GCH1	up_VCAV_EC
GO:1900087	0.527	0.845	1	8	positive regulation of G1/S transition of mitotic	BP	1	CUL4A	up_VCAV_EC
GO:0051247	0.527	0.841	1	502	positive regulation of protein metabolic process	BP	1	C6	up_VCAV_VSMC
GO:0006302	0.527	0.831	1	97	double-strand break repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0042327	0.527	0.835	1	289	positive regulation of phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0014070	0.527	0.832	1	172	response to organic cyclic compound	BP	1	CAV1	up_VSAP_VSMC
GO:0051272	0.527	0.832	1	170	positive regulation of cellular component	BP	1	CAV1	up_VSAP_VSMC
GO:0042592	0.528	0.537	44	522	homeostatic process	BP	1	HMGB1,RPA1,HNRNPD,SREBF2,RALY,UBE2S,QSOX2,SLC29A1,HOXA3,HSPA9,BIRC5,INSIG1,PRMT1,CAV1,RAD51,AURKB,EZH2,STMN1,SLC30A1,NEK2,ADIPOR2,HOXC10,PRCP,TFRC,HMGB2,GSTO1,ENSCAFG00000005299,SMC6,ELOVL6,CORO1A,BAP1,PRDX1,ENSCAFG00000006478,TXNDC12,NCOA5,TINF2,JMJD6,LIPC,UBE2C,NUS1,CCT4,THADA,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0009617	0.528	0.617	8	133	response to bacterium	BP	1	NR1H4,SERPINE1,MTDH,ADAM17,LYN,BNIP3,GBP5,DEFB124	down_VSAP_EC
GO:0034599	0.528	0.619	8	81	cellular response to oxidative stress	BP	1	PRKAA2,PPARGC1A,TP53INP1,DAPK1,FUT8,CHD6,OXR1,PARK7	up_ACOR_VSMC

GO:0050789	0.528	0.678	7	3295	regulation of biological process	BP	1	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0032147	0.528	0.654	5	77	activation of protein kinase activity	BP	1	VEGFA,PTPN11,TNIK,PAK2,MADD	down_VSAP_EC
GO:0032436	0.528	0.677	4	40	positive regulation of proteasomal ubiquitin-dependent protein	BP	1	SH3RF2,RNF19A,PSEN1,HERPUD1	up_ACOR_VSMC
GO:0033135	0.528	0.677	4	40	regulation of peptidyl-serine phosphorylation	BP	1	TNKS1BP1,RAF1,NCK1,BAG4	up_VSAP_EC
GO:0032774	0.528	0.715	3	1073	RNA biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0097659	0.528	0.715	3	1072	nucleic acid-templated transcription	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0006029	0.528	0.706	3	29	proteoglycan metabolic process	BP	1	HPSE,SULF2,CHST7	up_VSAP_EC
GO:0051130	0.528	0.746	2	342	positive regulation of cellular component	BP	1	LYN,PDPN	down_ACOR_EC
GO:0007586	0.528	0.752	2	20	digestion	BP	1	LIMA1,EZR	down_ACOR_VSMC
GO:0022600	0.528	0.752	2	20	digestive system process	BP	1	LIMA1,EZR	down_ACOR_VSMC
GO:0009150	0.528	0.831	1	161	purine ribonucleotide metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0071800	0.528	0.844	1	8	podosome assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:1902742	0.528	0.837	1	14	apoptotic process involved in development	BP	1	B4GALT1	down_VCAV_EC
GO:0034645	0.528	0.874	1	1546	cellular macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0007157	0.528	0.838	1	12	heterophilic cell-cell adhesion via plasma membrane cell adhesion	BP	1	PVR	down_VSAP_EC
GO:0031954	0.528	0.844	1	8	positive regulation of protein	BP	1	RASSF2	up_ACOR_VSMC
GO:0051865	0.528	0.832	1	31	protein autoubiquitination	BP	1	RNF181	up_AFEM_EC
GO:0003177	0.528	0.844	1	8	pulmonary valve development	BP	1	JAG1	up_VCAV_EC
GO:0031639	0.528	0.842	1	9	plasminogen activation	BP	1	KLKB1	up_VCAV_EC
GO:0045980	0.528	0.84	1	10	negative regulation of nucleotide metabolic	BP	1	CDA	up_VCAV_EC
GO:0070861	0.528	0.842	1	9	regulation of protein exit from endoplasmic	BP	1	GCC2	up_VCAV_EC
GO:0071225	0.528	0.844	1	8	cellular response to muramyl dipeptide	BP	1	ARHGEF2	up_VCAV_EC
GO:2000146	0.528	0.83	1	92	negative regulation of cell motility	BP	1	SEMA3A	up_VPOR_EC
GO:0001525	0.528	0.831	1	173	angiogenesis	BP	1	HOXA7	up_VFEM_EC
GO:0060627	0.528	0.831	1	165	regulation of vesicle-mediated transport	BP	1	CAV1	up_VSAP_VSMC
GO:0007162	0.52803533	0.7437	2	66	negative regulation of cell adhesion	BP	1	ARHGAP6,PRKCD	up_ACOR_EC
GO:0097190	0.529	0.564	21	217	apoptotic signaling pathway	BP	1	ACKR3,PLEKHF1,CRADD,MAP3K5,PDK2,TRAF7,PIK3R1,RBCK1,HIC1,PTPMT1,RAF1,ZNF205,STX4,QARS,HTRA2,NCK1,KRCC1,HMOX1,TRADD,DEDD2,DDIT4	up_VSAP_EC
GO:0032990	0.529	0.58	15	167	cell part morphogenesis	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,PPP3CA,NECTIN2,PREX2,ENSCAFG00000010224,STMN1,SNX2,RAPGEF2,CREB1,SPTBN4,ALS2	up_VCAV_EC
GO:0007264	0.529	0.584	14	164	small GTPase mediated signal transduction	BP	1	ENSCAFG00000030005,PSD4,STMN1,RAP2C,ARHGDIA,RAC1,NUP62,CDC42EP4,CDK2,CCNA2,PHACTR4,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0051090	0.529	0.587	13	134	regulation of DNA-binding transcription factor activity	BP	1	FZD1,ARHGEF5,PPARGC1B,SAV1,ANXA4,PLP3,GLIS2,DDR2,RBCK1,MYD88,PRMT2,MAVS,KEAP1	up_VSAP_EC
GO:0043900	0.529	0.603	10	104	regulation of multi-organism process	BP	1	PRDX4,MX1,PDE5A,ISG15,SASH1,F2RL1,PTPN22,PARP9,SPINK2,INPP5K	up_ACOR_VSMC
GO:0009123	0.529	0.637	6	104	nucleoside monophosphate	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDOC,AK5	down_VSAP_EC
GO:0009952	0.529	0.672	4	66	anterior/posterior pattern specification	BP	1	TMED2,HOXB7,CTNNB1,DDIT3	down_VSAP_EC
GO:0120035	0.529	0.67	4	160	regulation of plasma membrane bounded cell projection organization	BP	1	PLXNA4,CYLD,CDC42EP5,KANK1	up_AFEM_EC
GO:0050921	0.529	0.677	4	39	positive regulation of chemotaxis	BP	1	SLIT2,F2RL1,ZNF580,STX4	up_VSAP_EC

GO:0032091	0.529	0.704	3	34	negative regulation of protein binding	BP	1	CAV1,AURKB,STMN1	down_ACOR_VSMC
GO:0072078	0.529	0.704	3	33	nephron tubule morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0010770	0.529	0.747	2	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	ENSCAFG00000002015,NRP1	down_VSAP_EC
GO:0009581	0.529	0.752	2	18	detection of external stimulus	BP	1	JUP,GNAQ	up_ACOR_VSMC
GO:0009582	0.529	0.752	2	18	detection of abiotic stimulus	BP	1	JUP,GNAQ	up_ACOR_VSMC
GO:0006270	0.529	0.752	2	19	DNA replication initiation	BP	1	TOPBP1,GINS4	up_VCAV_EC
GO:0046626	0.529	0.752	2	18	regulation of insulin receptor signaling	BP	1	PIK3R1,NCK1	up_VSAP_EC
GO:0002092	0.529	0.841	1	9	positive regulation of receptor internalization	BP	1	GREM1	down_ACOR_VSMC
GO:0061548	0.529	0.843	1	8	ganglion development	BP	1	SIX4	down_ACOR_VSMC
GO:0009790	0.529	0.835	1	335	embryo development	BP	1	GABPA	down_AFEM_EC
GO:0008299	0.529	0.836	1	14	isoprenoid biosynthetic process	BP	1	RDH10	down_VCAV_EC
GO:0070542	0.529	0.835	1	15	response to fatty acid	BP	1	ADCY6	down_VCAV_EC
GO:0006221	0.529	0.838	1	12	pyrimidine nucleotide biosynthetic process	BP	1	CMPK1	down_VSAP_EC
GO:0040018	0.529	0.838	1	11	positive regulation of multicellular organism	BP	1	CELF1	down_VSAP_EC
GO:0015031	0.529	0.84	1	510	protein transport	BP	1	TLR2	up_AFEM_VSMC
GO:2000781	0.529	0.843	1	8	positive regulation of double-strand break	BP	1	TIMELESS	up_VCAV_EC
GO:0014912	0.529	0.843	1	8	negative regulation of smooth muscle cell	BP	1	MEF2C	up_VCAV_EC
GO:0072522	0.529	0.829	1	91	purine-containing compound biosynthetic	BP	1	FBP1	up_VPOR_EC
GO:0043161	0.529	0.831	1	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:0044089	0.529	0.831	1	170	positive regulation of cellular component	BP	1	CAV1	up_VSAP_VSMC
GO:0030217	0.529927017	0.7421	2	65	T cell differentiation	BP	1	FZD5,PTGER4	up_ACOR_EC
GO:0044260	0.53	0.512	155	2593	cellular macromolecule metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,MEIS2,SGK1,ERO1A,HSP90B1,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,CBX5,SARS,WSB1,BCAR3,NUAK1,PTPN11,AARS,ENSCAFG00000032470,TRIB3,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CHSY1,MSN,SEL1L,HIF1A,FOXP4,USP12,MRPL1,IWS1,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YARS,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,GTF2H1,ARMCX3,CUL2,HTT,REST,RBBP8,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,NR4A2,EXT1,SPOP,CALM1,GLO1,DISC1,RAD23A,CDYL,PAK2,LRRTM2,A2M,INHBA,LRRFIP2,CAMK2D,NR4A1,ENSCAFG00000018360,HIF1AN,BTK,MSRB3,SIX4,CDKN1A,TMTC3,RSL24D1,NRP1,SPINK2,SH3RF3,USP14,ARF4,YWHAH,TNFAIP1,MADD,RPN1,KDM3A,MID1	down_VSAP_EC
GO:0043067	0.53	0.539	40	479	regulation of programmed cell death	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,DHCR24,NOC2L,EIF5A,B4GALT1,CYCS,NUP62,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0031032	0.53	0.64	6	61	actomyosin structure organization	BP	1	WNT11,ARHGEF5,ABL1,PIK3R1,FRMD6,BAG4	up_VSAP_EC

GO:0043112	0.53	0.653	5	57	receptor metabolic process	BP	1	NEDD4,CAV1,GREM1,TFRC,EZR	down_ACOR_VSMC
GO:0032412	0.53	0.674	4	46	regulation of ion transmembrane	BP	1	NEDD4,CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0071453	0.53	0.673	4	46	cellular response to oxygen levels	BP	1	CAV1,PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:1904892	0.53	0.675	4	40	regulation of STAT cascade	BP	1	LEP,CRLF3,PARP9,LRRC4	up_ACOR_VSMC
GO:0008150	0.53	1	3	5646	biological_process	BP	1	PLCL1,MOSPD1,USP12	down_VFEM_EC
GO:0032946	0.53	0.746	2	29	positive regulation of mononuclear cell	BP	1	TFRC,CDKN1A	down_VSAP_EC
GO:0050671	0.53	0.746	2	29	positive regulation of lymphocyte proliferation	BP	1	TFRC,CDKN1A	down_VSAP_EC
GO:0060393	0.53	0.75	2	19	regulation of pathway-restricted SMAD protein	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:0050727	0.53	0.742	2	74	regulation of inflammatory response	BP	1	LEP,NAPEPLD	up_AFEM_EC
GO:0019359	0.53	0.748	2	23	nicotinamide nucleotide biosynthetic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0019363	0.53	0.748	2	23	pyridine nucleotide biosynthetic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0006753	0.53	0.742	2	211	nucleoside phosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0002098	0.53	0.842	1	8	tRNA wobble uridine modification	BP	1	TRMT9B	up_ACOR_VSMC
GO:0031328	0.53	0.839	1	512	positive regulation of cellular biosynthetic	BP	1	GATA5	up_VCAV_VSMC
GO:0022414	0.53	0.834	1	294	reproductive process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0051270	0.53	0.833	1	296	regulation of cellular component movement	BP	1	C3AR1	up_VPOR_VSMC
GO:0060284	0.53	0.831	1	212	regulation of cell development	BP	1	ARHGEF2	up_VPUL_EC
GO:2000573	0.530453883	0.83008	1	28	positive regulation of DNA biosynthetic process	BP	1	PKIB	up_ACOR_EC
GO:0120031	0.531	0.585	13	154	plasma membrane bounded cell projection assembly	BP	1	FSCN1,ANLN,CFAP298,CAV1,POC1A,RAC1,EMP2,CDC42EP4,EZR,ENSCAFG00000010224,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0035690	0.531	0.616	8	91	cellular response to drug	BP	1	RAD51,TIMELESS,EZH2,CDK4,TFRC,PDXP,SIGMAR1,ARHGEF2	down_ACOR_VSMC
GO:0031214	0.531	0.673	4	45	biomineral tissue development	BP	1	HOXA3,FBXO5,GREM1,SLC20A1	down_ACOR_VSMC
GO:0006873	0.531	0.669	4	160	cellular ion homeostasis	BP	1	RAB20,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0007165	0.531	0.688	4	1496	signal transduction	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0001938	0.531	0.701	3	34	positive regulation of endothelial cell	BP	1	HMGB1,NRAS,HMGB2	down_ACOR_VSMC
GO:0032946	0.531	0.704	3	29	positive regulation of mononuclear cell	BP	1	LEP,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0050671	0.531	0.704	3	29	positive regulation of lymphocyte proliferation	BP	1	LEP,CDKN1A,PTPN22	up_ACOR_VSMC
GO:2000045	0.531	0.703	3	29	regulation of G1/S transition of mitotic cell	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC
GO:0051301	0.531	0.696	3	117	cell division	BP	1	LBH,DLL1,ANXA11	up_AFEM_EC
GO:0043467	0.531	0.744	2	35	regulation of generation of precursor metabolites	BP	1	AKT2,PARK7	down_VCAV_EC
GO:0051101	0.531	0.743	2	35	regulation of DNA binding	BP	1	CLSTN1,PARK7	down_VCAV_EC
GO:0010569	0.531	0.751	2	17	regulation of double-strand break repair via homologous	BP	1	TP53BP1,ZNF365	up_ACOR_VSMC
GO:0035307	0.531	0.75	2	18	positive regulation of protein	BP	1	SMPD1,DUSP26	up_ACOR_VSMC
GO:0001912	0.531	0.839	1	9	positive regulation of leukocyte mediated	BP	1	FAM49B	down_ACOR_VSMC
GO:0006749	0.531	0.834	1	14	glutathione metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0055021	0.531	0.833	1	15	regulation of cardiac muscle tissue growth	BP	1	BMPR1A	down_VCAV_EC
GO:1902108	0.531	0.834	1	14	regulation of mitochondrial membrane permeability involved in	BP	1	SLC35F6	down_VCAV_EC
GO:0021591	0.531	0.836	1	12	ventricular system development	BP	1	UCHL5	down_VSAP_EC
GO:0050829	0.531	0.842	1	8	defense response to Gram-negative bacterium	BP	1	F2RL1	up_ACOR_VSMC

GO:0072498	0.531	0.841	1	8	embryonic skeletal joint development	BP	1	BMP4	up_ACOR_VSMC
GO:0000226	0.531	0.83	1	197	microtubule cytoskeleton organization	BP	1	TUBB4A	up_APUL_EC
GO:0070848	0.531	0.83	1	193	response to growth factor	BP	1	NPNT	up_APUL_EC
GO:1903599	0.531	0.842	1	8	positive regulation of autophagy of	BP	1	HIF1A	up_VCAV_EC
GO:1905476	0.531	0.839	1	9	negative regulation of protein localization to	BP	1	PPP2R5A	up_VCAV_EC
GO:2000696	0.531	0.842	1	8	regulation of epithelial cell differentiation involved in kidney	BP	1	GATA3	up_VCAV_EC
GO:0070371	0.531	0.828	1	91	ERK1 and ERK2 cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0000003	0.531	0.833	1	295	reproduction	BP	1	CYP26B1	up_VPOR_VSMC
GO:1901700	0.531	0.834	1	364	response to oxygen-containing compound	BP	1	SLIT2	up_VPUL_VSMC
GO:0019941	0.531195686	0.62255	7	258	modification-dependent protein catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,TP53INP2,RNF114,UBE2H	up_ACOR_EC
GO:0040014	0.531610648	0.82941	1	27	regulation of multicellular organism growth	BP	1	PLS1	up_ACOR_EC
GO:0010556	0.532	0.553	27	1137	regulation of macromolecule biosynthetic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0009141	0.532	0.606	9	110	nucleoside triphosphate metabolic process	BP	1	RAN,CDK1,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,NUDT1,CTPS1,ATP5F1D	down_ACOR_VSMC
GO:0042391	0.532	0.65	5	81	regulation of membrane potential	BP	1	WDR1,KIF5B,GNAQ,BNIP3,YWHAH	down_VSAP_EC
GO:0030162	0.532	0.648	5	202	regulation of proteolysis	BP	1	GAS1,CRYAB,F3,CLEC16A,RECK	up_AFEM_EC
GO:0001823	0.532	0.672	4	45	mesonephros development	BP	1	GREM1,ARG2,HOXB7,SIX4	down_ACOR_VSMC
GO:0042274	0.532	0.672	4	47	ribosomal small subunit biogenesis	BP	1	NOC4L,NOP14,EMG1,NOB1	down_ACOR_VSMC
GO:0061013	0.532	0.702	3	32	regulation of mRNA catabolic process	BP	1	HNRNPD,THRAP3,FASTKD3	down_ACOR_VSMC
GO:0044419	0.532	0.696	3	117	interspecies interaction between organisms	BP	1	LRRC15,RAB7A,NAPEPLD	up_AFEM_EC
GO:0050678	0.532	0.695	3	117	regulation of epithelial cell proliferation	BP	1	LEP,F3,ADAM17	up_AFEM_EC
GO:1902882	0.532	0.702	3	29	regulation of response to oxidative stress	BP	1	FZD1,SESN1,FBXO7	up_VSAP_EC
GO:0034766	0.532	0.749	2	19	negative regulation of ion transmembrane transport	BP	1	ACTN2,KCNE3	up_ACOR_VSMC
GO:0002534	0.532	0.75	2	18	cytokine production involved in inflammatory	BP	1	IL17RC,MYD88	up_VSAP_EC
GO:0048146	0.532	0.749	2	18	positive regulation of fibroblast proliferation	BP	1	DDR2,MYC	up_VSAP_EC
GO:0035116	0.532	0.833	1	15	embryonic hindlimb morphogenesis	BP	1	ZBTB16	down_VCAV_EC
GO:0051926	0.532	0.833	1	14	negative regulation of calcium ion transport	BP	1	PACSIN3	down_VCAV_EC
GO:0044319	0.532	0.835	1	12	wound healing, spreading of cells	BP	1	ADAM17	down_VSAP_EC
GO:0090504	0.532	0.835	1	12	epiboly	BP	1	ADAM17	down_VSAP_EC
GO:0090505	0.532	0.835	1	12	epiboly involved in wound healing	BP	1	ADAM17	down_VSAP_EC
GO:0032689	0.532	0.841	1	8	negative regulation of interferon-gamma	BP	1	CD274	up_ACOR_VSMC
GO:1903428	0.532	0.841	1	8	positive regulation of reactive oxygen species biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0007155	0.532	0.832	1	324	cell adhesion	BP	1	CTNNAL1	up_AORT_EC
GO:0010562	0.532	0.832	1	312	positive regulation of phosphorus metabolic	BP	1	TAOK1	up_AORT_EC
GO:0045937	0.532	0.832	1	312	positive regulation of phosphate metabolic	BP	1	TAOK1	up_AORT_EC
GO:0072215	0.532	0.841	1	8	regulation of metanephros	BP	1	PDGFB	up_VCAV_EC
GO:0097345	0.532	0.837	1	10	mitochondrial outer membrane	BP	1	SH3GLB1	up_VCAV_EC
GO:0045944	0.532	0.831	1	287	positive regulation of transcription by RNA polymerase II	BP	1	NKX2-5	up_VPOR_VSMC

GO:0055085	0.532	0.832	1	284	transmembrane transport	BP	1	NETO1	up_VFEM_VSMC
GO:0031498	0.532	0.841	1	8	chromatin disassembly	BP	1	SMARCD2	up_VSAP_EC
GO:0000904	0.532	0.828	1	181	cell morphogenesis involved in differentiation	BP	1	SHOX2	up_VSAP_VSMC
GO:0006355	0.532554662	0.55278	26	974	regulation of transcription, DNA-templated	BP	1	NR1H4,GATA4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0009314	0.532624818	0.66675	4	143	response to radiation	BP	1	BRSK1,AQP1,FIGNL1,MFAP4	up_ACOR_EC
GO:0009108	0.532981688	0.73925	2	68	coenzyme biosynthetic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0043170	0.533	0.613	13	2980	macromolecule metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CYP26B1,CDC42EP5,CHST7	up_VFEM_EC
GO:1903530	0.533	0.597	10	165	regulation of secretion by cell	BP	1	NR1H4,PTPN11,HIF1A,LYN,GSK3B,SDC4,REST,RAB11FIP1,INHBA,RHBDF2	down_VSAP_EC
GO:0006355	0.533	0.618	8	974	regulation of transcription, DNA-	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG0000000020 15,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0048584	0.533	0.65	5	592	positive regulation of response to stimulus	BP	1	C3AR1,ENSCAFG00000002015,ACVR2A,MTDH,ENSCAFG00000032731	up_VPOR_EC
GO:0019318	0.533	0.668	4	75	hexose metabolic process	BP	1	AKT2,H6PD,POFUT1,B4GALT1	down_VCAV_EC
GO:1905269	0.533	0.7	3	32	positive regulation of chromatin organization	BP	1	SREBF1,BRCA1,TADA2A	down_ACOR_VSMC
GO:1900046	0.533	0.747	2	21	regulation of hemostasis	BP	1	TFPI,CAV1	down_ACOR_VSMC
GO:0030193	0.533	0.747	2	21	regulation of blood coagulation	BP	1	TFPI,CAV1	down_ACOR_VSMC
GO:0040014	0.533	0.744	2	27	regulation of multicellular organism growth	BP	1	CELF1,PTPN11	down_VSAP_EC
GO:0042127	0.533	0.744	2	452	regulation of cell proliferation	BP	1	TBX5,HOXA3	up_APUL_EC
GO:0010718	0.533	0.747	2	21	positive regulation of epithelial to mesenchymal	BP	1	MTOR,BMP2	up_VCAV_EC
GO:0048708	0.533	0.748	2	20	astrocyte differentiation	BP	1	TLR4,BMP2	up_VCAV_EC
GO:0006096	0.533	0.749	2	18	glycolytic process	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0006165	0.533	0.749	2	18	nucleoside diphosphate phosphorylation	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0006757	0.533	0.749	2	18	ATP generation from ADP	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0042866	0.533	0.749	2	18	pyruvate biosynthetic process	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0036295	0.533	0.838	1	9	cellular response to increased oxygen levels	BP	1	CAV1	down_ACOR_VSMC
GO:0036296	0.533	0.838	1	9	response to increased oxygen levels	BP	1	CAV1	down_ACOR_VSMC
GO:0008152	0.533	1	1	3714	metabolic process	BP	1	GATA5	down_AFEM_VSMC
GO:0070849	0.533	0.832	1	15	response to epidermal growth factor	BP	1	ZFP36L1	down_VCAV_EC
GO:2000772	0.533	0.832	1	15	regulation of cellular senescence	BP	1	BMPR1A	down_VCAV_EC
GO:0009059	0.533	0.872	1	1563	macromolecule biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0097734	0.533	0.834	1	13	extracellular exosome biogenesis	BP	1	SDC4	down_VSAP_EC
GO:1990182	0.533	0.834	1	13	exosomal secretion	BP	1	SDC4	down_VSAP_EC
GO:0034661	0.533	0.835	1	12	ncRNA catabolic process	BP	1	SND1	down_VSAP_EC
GO:1901031	0.533	0.835	1	12	regulation of response to reactive oxygen species	BP	1	SESN2	down_VSAP_EC
GO:2000036	0.533	0.835	1	12	regulation of stem cell population maintenance	BP	1	KDM3A	down_VSAP_EC
GO:0045737	0.533	0.841	1	8	positive regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CCNT1	up_ACOR_VSMC
GO:0046174	0.533	0.84	1	8	polyol catabolic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0060999	0.533	0.843	1	7	positive regulation of dendritic spine	BP	1	PSEN1	up_ACOR_VSMC
GO:0002886	0.533	0.837	1	10	regulation of myeloid leukocyte mediated	BP	1	FES	up_VCAV_EC

GO:0051348	0.533	0.827	1	90	negative regulation of transferase activity	BP	1	ASPN	up_VPOR_EC
GO:0035050	0.533343907	0.82794	1	28	embryonic heart tube development	BP	1	FOXC2	up_ACOR_EC
GO:0045833	0.533736742	0.82748	1	29	negative regulation of lipid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0002702	0.5339116	0.82752	1	28	positive regulation of production of molecular mediator of immune	BP	1	FZD5	up_ACOR_EC
GO:0010605	0.534	0.537	37	745	negative regulation of macromolecule metabolic process	BP	1	CST3,NOTCH2,KIRREL1,DCN,NAB2,PRNP,BGN,KANK2,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,ASPN,LRPAP1,THY1,CC2D1A,GLI3,PARK7,ZFP36L1,CLEC16A,LOXL3,SPRED1,A2M,TSC22D3,GLIS2,SHC1,PYM1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0008154	0.534	0.622	7	81	actin polymerization or depolymerization	BP	1	CAPG,LIMA1,PDXP,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0070663	0.534	0.651	5	50	regulation of leukocyte proliferation	BP	1	CD274,MYD88,PNP,NCK1,TGFBR2	up_VSAP_EC
GO:0031344	0.534	0.666	4	161	regulation of cell projection organization	BP	1	PLXNA4,CYLD,CDC42EP5,KANK1	up_AFEM_EC
GO:0051302	0.534	0.697	3	47	regulation of cell division	BP	1	VEGFA,PLK3,CALM1	down_VSAP_EC
GO:0042102	0.534	0.747	2	19	positive regulation of T cell proliferation	BP	1	LEP,PTPN22	up_ACOR_VSMC
GO:0002275	0.534	0.748	2	18	myeloid cell activation involved in immune	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0000470	0.534	0.837	1	9	maturation of LSU-rRNA	BP	1	RSL1D1	down_ACOR_VSMC
GO:0060429	0.534	0.832	1	341	epithelium development	BP	1	SRSF6	down_AFEM_EC
GO:0002762	0.534	0.831	1	15	negative regulation of myeloid leukocyte	BP	1	FBN1	down_VCAV_EC
GO:0002082	0.534	0.84	1	8	regulation of oxidative phosphorylation	BP	1	PARK7	up_ACOR_VSMC
GO:0022610	0.534	0.83	1	326	biological adhesion	BP	1	CTNNAL1	up_AORT_EC
GO:0044766	0.534	0.838	1	9	multi-organism transport	BP	1	THOC1	up_VCAV_EC
GO:0050706	0.534	0.838	1	9	regulation of interleukin-1 beta secretion	BP	1	ARG2	up_VCAV_EC
GO:0051569	0.534	0.838	1	9	regulation of histone H3-K4 methylation	BP	1	GATA3	up_VCAV_EC
GO:1902579	0.534	0.838	1	9	multi-organism localization	BP	1	THOC1	up_VCAV_EC
GO:0060485	0.534	0.826	1	93	mesenchyme development	BP	1	SEMA3A	up_VPOR_EC
GO:0040008	0.534	0.827	1	179	regulation of growth	BP	1	SIX1	up_VFEM_EC
GO:0060548	0.534	0.83	1	294	negative regulation of cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0022008	0.53407802	0.5907	11	406	neurogenesis	BP	1	SH3TC2,BRSK1,SOX9,DIXDC1,RGMA,PAK3,DCLK2,MAPK8IP2,LRP4,NRP1,DBNDD2	up_ACOR_EC
GO:0031338	0.534502397	0.82708	1	28	regulation of vesicle fusion	BP	1	VPS16	up_ACOR_EC
GO:0006643	0.534853246	0.7376	2	68	membrane lipid metabolic process	BP	1	PIGS,PRKCD	up_ACOR_EC
GO:0044773	0.534924359	0.82677	1	28	mitotic DNA damage checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0031347	0.535	0.578	14	144	regulation of defense response	BP	1	NAPEPLD,IL17RC,TRAFD1,F2RL1,MYD88,NLRX1,TKFC,RNF216,MAPKBP1,CYBA,PQBP1,UNC93B1,FLOT1,MAVS	up_VSAP_EC
GO:0010631	0.535	0.631	6	118	epithelial cell migration	BP	1	DCN,GLIPR2,KANK2,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0090132	0.535	0.631	6	118	epithelium migration	BP	1	DCN,GLIPR2,KANK2,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0022407	0.535	0.632	6	96	regulation of cell-cell adhesion	BP	1	SOCS5,FAM49B,PTPN2,TFRC,LYN,SDC4	down_VSAP_EC
GO:0043535	0.535	0.669	4	45	regulation of blood vessel endothelial cell migration	BP	1	HMGB1,PRCP,NUS1,AMOTL1	down_ACOR_VSMC
GO:0045995	0.535	0.67	4	40	regulation of embryonic development	BP	1	FZD1,HNF4A,DLL1,OSR1	up_VSAP_EC
GO:0021675	0.535	0.7	3	29	nerve development	BP	1	EPHB1,CHD7,NAV2	up_VCAV_EC
GO:0048646	0.535	0.694	3	349	anatomical structure formation involved in	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0006356	0.535	0.745	2	20	regulation of transcription by RNA polymerase I	BP	1	DHX33,NCL	down_ACOR_VSMC

GO:0009987	0.535	1	2	5086	cellular process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0031397	0.535	0.742	2	30	negative regulation of protein ubiquitination	BP	1	NXN,SPOPL	down_VSAP_EC
GO:0007528	0.535	0.748	2	17	neuromuscular junction development	BP	1	CACNB3,APP	up_ACOR_VSMC
GO:0051155	0.535	0.747	2	18	positive regulation of striated muscle cell	BP	1	BMP4,EDN1	up_ACOR_VSMC
GO:0071559	0.535	0.737	2	75	response to transforming growth factor beta	BP	1	NR3C1,ADAM17	up_AFEM_EC
GO:0030036	0.535	0.738	2	223	actin cytoskeleton organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0043299	0.535	0.747	2	18	leukocyte degranulation	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0006144	0.535	0.837	1	9	purine nucleobase metabolic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0090311	0.535	0.831	1	15	regulation of protein deacetylation	BP	1	SPRED1	down_VCAV_EC
GO:2000249	0.535	0.833	1	12	regulation of actin cytoskeleton	BP	1	NRP1	down_VSAP_EC
GO:0044003	0.535	0.837	1	9	modification by symbiont of host morphology or	BP	1	TNIP1	up_VCAV_EC
GO:0071168	0.535	0.837	1	9	protein localization to chromatin	BP	1	RAD21	up_VCAV_EC
GO:0045948	0.535	0.837	1	9	positive regulation of translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0019693	0.535	0.827	1	172	ribose phosphate metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0001525	0.535	0.826	1	173	angiogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:0046660	0.535642685	0.82623	1	28	female sex differentiation	BP	1	LHX9	up_ACOR_EC
GO:0051153	0.535700318	0.82619	1	28	regulation of striated muscle cell differentiation	BP	1	RBM38	up_ACOR_EC
GO:0010035	0.535755443	0.69179	3	107	response to inorganic substance	BP	1	AQP1,GUCY1B1,PRKCD	up_ACOR_EC
GO:1902600	0.535855113	0.82559	1	31	proton transmembrane transport	BP	1	PM20D1	up_ACOR_EC
GO:0048699	0.536	0.537	35	371	generation of neurons	BP	1	THRB,EMX2,PEX7,CDON,WNT11,AMIGO1,IRX5,SLIT2,HOXD3,ABL1,DLL1,PLXNA4,IRX3,ZEB1,SHOX2,RTN4RL1,HOXC10,LRP4,DPYSL2,GDPD5,DAGLB,FBXO7,NTN4,NR2F6,NFIB,CYB5D2,CDNF,PQBP1,TTL,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:1901700	0.536	0.563	18	364	response to oxygen-containing compound	BP	1	GPAM,LRP1,PRNP,ADCY6,SLC10A3,KANK2,COL6A1,ENSCAFG00000014978,AKT2,NR3C1,ENSCAFG00000013404,TMEM161A,PARK7,ZFP36L1,SASH1,MPV17,RAB31,SHC1	down_VCAV_EC
GO:0009100	0.536	0.59	11	139	glycoprotein metabolic process	BP	1	ST8SIA6,TNIP1,ST6GAL1,B3GNT5,BMP2,CHST7,ST3GAL6,GALNT18,MFNG,HIF1A,TET2	up_VCAV_EC
GO:0090287	0.536	0.604	9	91	regulation of cellular response to growth factor	BP	1	SMAD6,FERMT1,BMP4,FGFR2,CITED2,TMEM108,FGF18,CDKN2B,NPNT	up_ACOR_VSMC
GO:0050657	0.536	0.648	5	51	nucleic acid transport	BP	1	ZFP36L1,NUP98,SNUPN,FLOT1,TGFBR2	up_VSAP_EC
GO:0050658	0.536	0.648	5	51	RNA transport	BP	1	ZFP36L1,NUP98,SNUPN,FLOT1,TGFBR2	up_VSAP_EC
GO:0051236	0.536	0.648	5	51	establishment of RNA localization	BP	1	ZFP36L1,NUP98,SNUPN,FLOT1,TGFBR2	up_VSAP_EC
GO:0007568	0.536	0.649	5	50	aging	BP	1	ABL1,MORC3,FBXO4,YPEL3,PRELP	up_VSAP_EC
GO:1900180	0.536	0.649	5	50	regulation of protein localization to nucleus	BP	1	CDH1,GLIS2,PIK3R1,FBXO4,MAVS	up_VSAP_EC
GO:0090090	0.536	0.669	4	44	negative regulation of canonical Wnt signaling	BP	1	CAV1,GREM1,GLI1,AMER1	down_ACOR_VSMC
GO:0046661	0.536	0.668	4	45	male sex differentiation	BP	1	KIT,GATA3,ARID4B,ATRX	up_VCAV_EC
GO:0051262	0.536	0.669	4	40	protein tetramerization	BP	1	ACACB,HSD17B8,SBF2,PCBD1	up_VSAP_EC
GO:1901991	0.536	0.693	3	56	negative regulation of mitotic cell cycle phase	BP	1	KANK2,ZFP36L1,BRSK1	down_VCAV_EC
GO:0006112	0.536	0.698	3	30	energy reserve metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0046626	0.536	0.746	2	18	regulation of insulin receptor signaling	BP	1	SESN3,INPP5K	up_ACOR_VSMC
GO:0032922	0.536	0.745	2	19	circadian regulation of gene expression	BP	1	TOP1,KDM5A	up_VCAV_EC
GO:0002444	0.536	0.746	2	18	myeloid leukocyte mediated immunity	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0046887	0.536	0.746	2	18	positive regulation of hormone secretion	BP	1	STX4,PPP3CB	up_VSAP_EC

GO:0048662	0.536	0.746	2	18	negative regulation of smooth muscle cell	BP	1	MFN2,HMOX1	up_VSAP_EC
GO:0002682	0.536	0.83	1	343	regulation of immune system process	BP	1	GABPA	down_AFEM_EC
GO:0030520	0.536	0.83	1	15	intracellular estrogen receptor signaling	BP	1	KANK2	down_VCAV_EC
GO:1900408	0.536	0.83	1	15	negative regulation of cellular response to	BP	1	PARK7	down_VCAV_EC
GO:1903202	0.536	0.83	1	15	negative regulation of oxidative stress-induced	BP	1	PARK7	down_VCAV_EC
GO:0031571	0.536	0.838	1	8	mitotic G1 DNA damage checkpoint	BP	1	CDKN1A	up_ACOR_VSMC
GO:0031646	0.536	0.841	1	7	positive regulation of neurological system	BP	1	WASF3	up_ACOR_VSMC
GO:0044783	0.536	0.838	1	8	G1 DNA damage checkpoint	BP	1	CDKN1A	up_ACOR_VSMC
GO:0044819	0.536	0.838	1	8	mitotic G1/S transition checkpoint	BP	1	CDKN1A	up_ACOR_VSMC
GO:0051657	0.536	0.84	1	7	maintenance of organelle location	BP	1	POLR2M	up_ACOR_VSMC
GO:0060074	0.536	0.841	1	7	synapse maturation	BP	1	DISC1	up_ACOR_VSMC
GO:0060628	0.536	0.838	1	8	regulation of ER to Golgi vesicle-mediated	BP	1	SEC24B	up_ACOR_VSMC
GO:0019933	0.536	0.825	1	32	cAMP-mediated signaling	BP	1	PTHLH	up_AFEM_EC
GO:0015833	0.536	0.835	1	521	peptide transport	BP	1	TLR2	up_AFEM_VSMC
GO:0006110	0.536	0.836	1	9	regulation of glycolytic process	BP	1	HIF1A	up_VCAV_EC
GO:0030811	0.536	0.836	1	9	regulation of nucleotide catabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0043470	0.536	0.836	1	9	regulation of carbohydrate catabolic	BP	1	HIF1A	up_VCAV_EC
GO:0097035	0.536	0.836	1	9	regulation of membrane lipid distribution	BP	1	ATP8A1	up_VCAV_EC
GO:2000279	0.536	0.836	1	9	negative regulation of DNA biosynthetic process	BP	1	DCP2	up_VCAV_EC
GO:0043436	0.536	0.829	1	303	oxoacid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0000122	0.536	0.826	1	218	negative regulation of transcription by RNA polymerase II	BP	1	NR1H4	up_VPUL_EC
GO:0071379	0.536	0.838	1	8	cellular response to prostaglandin stimulus	BP	1	PTGFR	up_VSAP_EC
GO:0043086	0.536	0.826	1	170	negative regulation of catalytic activity	BP	1	CAV1	up_VSAP_VSMC
GO:0061005	0.536336804	0.82571	1	28	cell differentiation involved in kidney	BP	1	FOXC2	up_ACOR_EC
GO:0018212	0.537	0.611	8	81	peptidyl-tyrosine modification	BP	1	LEP,TPST2,NRP1,PRKCE,PARP9,APP,PSEN1,DUSP22	up_ACOR_VSMC
GO:1903506	0.537	0.614	8	977	regulation of nucleic acid-templated transcription	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0007033	0.537	0.611	8	82	vacuole organization	BP	1	TPCN2,AMBRA1,MFN2,HPS4,PIP4K2B,VPS11,UBQLN2,NPRL3	up_VSAP_EC
GO:0006644	0.537	0.691	3	118	phospholipid metabolic process	BP	1	GPAM,NAPEPLD,AGPAT2	up_AFEM_EC
GO:0043255	0.537	0.698	3	29	regulation of carbohydrate biosynthetic	BP	1	C1QTNF2,PDK2,PASK	up_VSAP_EC
GO:0044272	0.537	0.738	2	35	sulfur compound biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:0032615	0.537	0.746	2	18	interleukin-12 production	BP	1	LEP,TLR3	up_ACOR_VSMC
GO:0009890	0.537	0.739	2	420	negative regulation of biosynthetic process	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0051781	0.537	0.745	2	18	positive regulation of cell division	BP	1	FGF7,LBH	up_VSAP_EC
GO:0002931	0.537	0.835	1	9	response to ischemia	BP	1	CAV1	down_ACOR_VSMC
GO:0034340	0.537	0.83	1	15	response to type I interferon	BP	1	MAVS	down_VCAV_EC
GO:0006749	0.537	0.83	1	14	glutathione metabolic process	BP	1	ENSCAFG00000028814	down_VSAP_EC
GO:0060602	0.537	0.832	1	12	branch elongation of an epithelium	BP	1	SIX4	down_VSAP_EC
GO:2000108	0.537	0.831	1	12	positive regulation of leukocyte apoptotic	BP	1	LYN	down_VSAP_EC
GO:0009892	0.537	0.844	1	835	negative regulation of metabolic process	BP	1	GATA5	down_VSAP_VSMC

GO:0050798	0.537	0.837	1	8	activated T cell proliferation	BP	1	CD274	up_ACOR_VSMC
GO:0042592	0.537	0.834	1	522	homeostatic process	BP	1	HOXC10	up_AFEM_VSMC
GO:0015936	0.537	0.834	1	10	coenzyme A metabolic process	BP	1	PANK3	up_VCAV_EC
GO:0009891	0.537	0.834	1	521	positive regulation of biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0071214	0.537	0.823	1	93	cellular response to abiotic stimulus	BP	1	ARHGEF2	up_VPOR_EC
GO:0104004	0.537	0.823	1	93	cellular response to environmental stimulus	BP	1	ARHGEF2	up_VPOR_EC
GO:0061430	0.537	0.838	1	8	bone trabecula morphogenesis	BP	1	PPARGC1B	up_VSAP_EC
GO:0045822	0.537	0.838	1	8	negative regulation of heart contraction	BP	1	KCNE3	up_VSAP_EC
GO:0007169	0.537	0.825	1	178	transmembrane receptor protein tyrosine kinase	BP	1	FGF5	up_VSAP_VSMC
GO:0048736	0.537136158	0.73568	2	66	appendage development	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0060173	0.537136158	0.73568	2	66	limb development	BP	1	TBX5,LRP4	up_ACOR_EC
GO:0050890	0.537171894	0.7356	2	67	cognition	BP	1	BRSK1,MAPK8IP2	up_ACOR_EC
GO:0006360	0.537920068	0.82452	1	28	transcription by RNA polymerase I	BP	1	RASL11A	up_ACOR_EC
GO:0003007	0.538	0.601	9	94	heart morphogenesis	BP	1	FZD1,WNT11,AXIN2,DLL1,SAV1,SHOX2,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0032970	0.538	0.607	8	130	regulation of actin filament-based process	BP	1	MYH9,FSCN1,WDR1,ACTR3,TWF1,PLEKHG2,CAPG,NRP1	down_VSAP_EC
GO:0006006	0.538	0.631	6	61	glucose metabolic process	BP	1	ACACB,C1QTNF2,PDK2,PASK,PC,NCOA2	up_VSAP_EC
GO:0001678	0.538	0.697	3	29	cellular glucose homeostasis	BP	1	PRKAA2,PRKCE,RAB11B	up_ACOR_VSMC
GO:0033559	0.538	0.743	2	21	unsaturated fatty acid metabolic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0002429	0.538	0.738	2	35	immune response-activating cell surface receptor signaling	BP	1	PRNP,THY1	down_VCAV_EC
GO:0042770	0.538	0.738	2	35	signal transduction in response to DNA damage	BP	1	SPRED1,FOXO3	down_VCAV_EC
GO:0032465	0.538	0.739	2	29	regulation of cytokinesis	BP	1	PLK3,CALM1	down_VSAP_EC
GO:0043280	0.538	0.738	2	33	positive regulation of cysteine-type endopeptidase activity	BP	1	FAM162A,REST	down_VSAP_EC
GO:0019318	0.538	0.735	2	75	hexose metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0009966	0.538	0.749	2	868	regulation of signal transduction	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0034470	0.538	0.824	1	154	ncRNA processing	BP	1	WDR12	down_ACOR_EC
GO:0051345	0.538	0.824	1	151	positive regulation of hydrolase activity	BP	1	LYN	down_ACOR_EC
GO:0002053	0.538	0.829	1	15	positive regulation of mesenchymal cell	BP	1	BMPR1A	down_VCAV_EC
GO:0019748	0.538	0.83	1	13	secondary metabolic process	BP	1	PGAM1	down_VSAP_EC
GO:0032620	0.538	0.836	1	8	interleukin-17 production	BP	1	NOD2	up_ACOR_VSMC
GO:0071071	0.538	0.837	1	8	regulation of phospholipid biosynthetic process	BP	1	HTR2B	up_ACOR_VSMC
GO:0034332	0.538	0.824	1	32	adherens junction organization	BP	1	GREM1	up_AFEM_EC
GO:0034644	0.538	0.824	1	32	cellular response to UV	BP	1	MFAP4	up_AFEM_EC
GO:0070498	0.538	0.835	1	9	interleukin-1-mediated signaling pathway	BP	1	OTUD4	up_VCAV_EC
GO:0006576	0.538	0.833	1	10	cellular biogenic amine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0031103	0.538	0.835	1	9	axon regeneration	BP	1	APOD	up_VCAV_EC
GO:1902622	0.538	0.831	1	11	regulation of neutrophil migration	BP	1	CXCL8	up_VCAV_EC
GO:0006082	0.538	0.827	1	305	organic acid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0030155	0.538	0.824	1	180	regulation of cell adhesion	BP	1	HOXA7	up_VFEM_EC
GO:0040017	0.538	0.824	1	180	positive regulation of locomotion	BP	1	TIAM1	up_VFEM_EC

GO:0045859	0.538	0.825	1	219	regulation of protein kinase activity	BP	1	FLRT3	up_VPUL_EC
GO:0098609	0.538	0.824	1	181	cell-cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0070167	0.538186582	0.82415	1	29	regulation of biomineral tissue development	BP	1	SOX9	up_ACOR_EC
GO:1903827	0.539	0.573	14	164	regulation of cellular protein localization	BP	1	ACSL3,SREBF1,SLC29A1,RAN,INSIG1,CDK1,NF2,MMP14,PLK3,NDC80,NUP62,DMAP1,EZR,CCT4	down_ACOR_VSMC
GO:0006357	0.539	0.577	13	547	regulation of transcription by RNA polymerase II	BP	1	HOXA9,LEP,HOXA7,DLL1,LMCD1,THRB,TMEM100,GREM1,NFE2L1,GREM2,MYBL1,NR3C1,PPARGC1A	up_AFEM_EC
GO:0044238	0.539	0.645	9	3383	primary metabolic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0060326	0.539	0.609	8	84	cell chemotaxis	BP	1	VEGFD,HRH1,FGF18,F2RL1,NRP1,CCL5,JAM3,ENSCAFG00000029553	up_ACOR_VSMC
GO:0002573	0.539	0.619	7	71	myeloid leukocyte differentiation	BP	1	RASSF2,BMP4,CITED2,F2RL1,CLSTN1,APP,PSEN1	up_ACOR_VSMC
GO:0000725	0.539	0.631	6	58	recombinational repair	BP	1	CDC7,TP53BP1,ZNF365,DMC1,WDR48,FAN1	up_ACOR_VSMC
GO:0009150	0.539	0.66	4	161	purine ribonucleotide metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0006487	0.539	0.694	3	34	protein N-linked glycosylation	BP	1	MPDU1,B4GALT1,NUS1	down_ACOR_VSMC
GO:0033138	0.539	0.697	3	28	positive regulation of peptidyl-serine	BP	1	APP,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:1901888	0.539	0.696	3	29	regulation of cell junction assembly	BP	1	NRP1,DUSP22,FAM107A	up_ACOR_VSMC
GO:0072332	0.539	0.696	3	29	intrinsic apoptotic signaling pathway by p53	BP	1	PDK2,KRCC1,DDIT4	up_VSAP_EC
GO:0030521	0.539	0.743	2	19	androgen receptor signaling pathway	BP	1	SMARCA4,KDM3A	up_VCAV_EC
GO:0070169	0.539	0.744	2	18	positive regulation of biomineral tissue	BP	1	OSR2,OSR1	up_VSAP_EC
GO:0009259	0.539	0.823	1	166	ribonucleotide metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0043537	0.539	0.828	1	15	negative regulation of blood vessel endothelial	BP	1	SPRED1	down_VCAV_EC
GO:0046718	0.539	0.829	1	13	viral entry into host cell	BP	1	P4HB	down_VSAP_EC
GO:0006805	0.539	0.836	1	8	xenobiotic metabolic process	BP	1	NCEH1	up_ACOR_VSMC
GO:0006851	0.539	0.836	1	8	mitochondrial calcium ion transmembrane transport	BP	1	MICU2	up_ACOR_VSMC
GO:0030851	0.539	0.836	1	8	granulocyte differentiation	BP	1	CITED2	up_ACOR_VSMC
GO:0051570	0.539	0.839	1	7	regulation of histone H3-K9 methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0035821	0.539	0.823	1	32	modification of morphology or physiology	BP	1	NAPEPLD	up_AFEM_EC
GO:1903076	0.539	0.823	1	32	regulation of protein localization to plasma	BP	1	LRRC15	up_AFEM_EC
GO:1903363	0.539	0.823	1	32	negative regulation of cellular protein catabolic	BP	1	CLEC16A	up_AFEM_EC
GO:0036474	0.539	0.834	1	9	cell death in response to hydrogen peroxide	BP	1	RIPK1	up_VCAV_EC
GO:0006895	0.539	0.836	1	8	Golgi to endosome transport	BP	1	DOP1B	up_VCAV_EC
GO:0010831	0.539	0.834	1	9	positive regulation of myotube differentiation	BP	1	MTOR	up_VCAV_EC
GO:1905331	0.539	0.834	1	9	negative regulation of morphogenesis of an	BP	1	GATA3	up_VCAV_EC
GO:0040012	0.539	0.827	1	303	regulation of locomotion	BP	1	C3AR1	up_VPOR_VSMC
GO:0006163	0.539	0.823	1	174	purine nucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0003006	0.539	0.824	1	180	developmental process involved in reproduction	BP	1	HOXA9	up_VFEM_EC
GO:0048699	0.539	0.829	1	371	generation of neurons	BP	1	SLIT2	up_VPUL_VSMC
GO:0014829	0.539	0.836	1	8	vascular smooth muscle contraction	BP	1	CHRM1	up_VSAP_EC
GO:0045671	0.539	0.836	1	8	negative regulation of osteoclast differentiation	BP	1	PIK3R1	up_VSAP_EC
GO:0010770	0.539048093	0.8235	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	NRP1	up_ACOR_EC

GO:1903506	0.539265263	0.54606	26	977	regulation of nucleic acid-templated transcription	BP	1	NR1H4,GATA4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0043473	0.539878354	0.82305	1	28	pigmentation	BP	1	CDH3	up_ACOR_EC
GO:0060070	0.54	0.593	10	105	canonical Wnt signaling pathway	BP	1	FZD1,WNT11,AXIN2,RECK,PLPP3,FAM53B,SULF2,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0010035	0.54	0.599	9	107	response to inorganic substance	BP	1	PPP1R15B,CAV1,RAD51,TIMELESS,EZH2,SLC30A1,IQGAP1,SIGMAR1,BAP1	down_ACOR_VSMC
GO:2001141	0.54	0.611	8	979	regulation of RNA biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0018212	0.54	0.617	7	81	peptidyl-tyrosine modification	BP	1	CAV1,NF2,GREM1,RAP2C,TTK,MELK,ARHGEF2	down_ACOR_VSMC
GO:0032989	0.54	0.614	7	292	cellular component morphogenesis	BP	1	PLXNA4,GREM1,CAMK2A,BVES,CDC42EP5,LRRN2,KANK1	up_AFEM_EC
GO:0010721	0.54	0.618	7	73	negative regulation of cell development	BP	1	THRB,SLIT2,DLL1,IRX3,RTN4RL1,LRP4,FBLN1	up_VSAP_EC
GO:0016054	0.54	0.629	6	61	organic acid catabolic process	BP	1	LEP,ENOSF1,ENSCAFG00000002977,ACAD11,SARDH,PCYOX1	up_ACOR_VSMC
GO:0046395	0.54	0.629	6	61	carboxylic acid catabolic process	BP	1	LEP,ENOSF1,ENSCAFG00000002977,ACAD11,SARDH,PCYOX1	up_ACOR_VSMC
GO:0002764	0.54	0.642	5	80	immune response-regulating signaling	BP	1	NR1H4,PTPN2,EIF2B1,SKAP2,LYN	down_VSAP_EC
GO:0008360	0.54	0.664	4	46	regulation of cell shape	BP	1	KIT,ARAP3,FES,FMNL3	up_VCAV_EC
GO:0060560	0.54	0.69	3	58	developmental growth involved in	BP	1	NDN,TRPV2,RDH10	down_VCAV_EC
GO:0090090	0.54	0.692	3	44	negative regulation of canonical Wnt signaling	BP	1	PRICKLE1,APOE,DDIT3	down_VSAP_EC
GO:0006950	0.54	0.704	3	1102	response to stress	BP	1	ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0048864	0.54	0.738	2	29	stem cell development	BP	1	HIF1A,NRP1	down_VSAP_EC
GO:0031057	0.54	0.743	2	18	negative regulation of histone modification	BP	1	KDM5A,KDM3A	up_VCAV_EC
GO:0010894	0.54	0.833	1	9	negative regulation of steroid biosynthetic	BP	1	INSIG1	down_ACOR_VSMC
GO:0045939	0.54	0.833	1	9	negative regulation of steroid metabolic process	BP	1	INSIG1	down_ACOR_VSMC
GO:0048199	0.54	0.833	1	9	vesicle targeting, to, from or within Golgi	BP	1	PREB	down_ACOR_VSMC
GO:1905521	0.54	0.833	1	9	regulation of macrophage migration	BP	1	MMP14	down_ACOR_VSMC
GO:0050654	0.54	0.827	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	DCN	down_VCAV_EC
GO:0031441	0.54	0.838	1	7	negative regulation of mRNA 3'-end processing	BP	1	CCNT1	up_ACOR_VSMC
GO:1900364	0.54	0.838	1	7	negative regulation of mRNA polyadenylation	BP	1	CCNT1	up_ACOR_VSMC
GO:0042886	0.54	0.831	1	527	amide transport	BP	1	TLR2	up_AFEM_VSMC
GO:1902531	0.54	0.832	1	536	regulation of intracellular signal transduction	BP	1	TLR2	up_AFEM_VSMC
GO:0051649	0.54	0.836	1	630	establishment of localization in cell	BP	1	WNT7A	up_AORT_VSMC
GO:0009268	0.54	0.832	1	10	response to pH	BP	1	GPR4	up_VCAV_EC
GO:0033158	0.54	0.835	1	8	regulation of protein import into nucleus,	BP	1	TMEM173	up_VCAV_EC
GO:1900101	0.54	0.83	1	11	regulation of endoplasmic reticulum unfolded protein response	BP	1	NCK1	up_VCAV_EC
GO:0015833	0.54	0.832	1	521	peptide transport	BP	1	CA2	up_VCAV_VSMC
GO:0042592	0.54	0.832	1	522	homeostatic process	BP	1	CA2	up_VCAV_VSMC
GO:0009895	0.54	0.821	1	94	negative regulation of catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0048589	0.54	0.823	1	188	developmental growth	BP	1	SIX1	up_VFEM_EC
GO:0006812	0.54	0.824	1	222	cation transport	BP	1	HOXA3	up_VPUL_EC
GO:0120036	0.54	0.828	1	373	plasma membrane bounded cell projection	BP	1	SLIT2	up_VPUL_VSMC
GO:0006308	0.54	0.835	1	8	DNA catabolic process	BP	1	DFFB	up_VSAP_EC
GO:0006895	0.54	0.835	1	8	Golgi to endosome transport	BP	1	DOP1B	up_VSAP_EC

GO:2000696	0.54	0.836	1	8	regulation of epithelial cell differentiation involved in kidney	BP	1	OSR1	up_VSAP_EC
GO:0061318	0.54	0.835	1	8	renal filtration cell differentiation	BP	1	KLF15	up_VSAP_EC
GO:0072010	0.54	0.835	1	8	glomerular epithelium development	BP	1	KLF15	up_VSAP_EC
GO:0072112	0.54	0.835	1	8	glomerular visceral epithelial cell	BP	1	KLF15	up_VSAP_EC
GO:0072311	0.54	0.835	1	8	glomerular epithelial cell differentiation	BP	1	KLF15	up_VSAP_EC
GO:0002824	0.540190103	0.82264	1	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	FZD5	up_ACOR_EC
GO:0048699	0.540515994	0.5899	10	371	generation of neurons	BP	1	BRSK1,SOX9,DIXDC1,RGMA,PAK3,DCLK2,MAPK8IP2,LRP4,NRP1,DBNDD2	up_ACOR_EC
GO:0035556	0.541	0.555	20	845	intracellular signal transduction	BP	1	CMKLR1,LEP,F3,FIBIN,MLLT11,LMCD1,TMEM100,PLAGL2,GREM1,CAMK2A,CLEC16A,CYLD,RASGEF1B,LRRC15,PTHLH,TBXA2R,CCL5,CDC42EP5,DMPK,KANK1	up_AFEM_EC
GO:0010977	0.541	0.693	3	33	negative regulation of neuron projection	BP	1	IFRD1,PPP3CA,RAPGEF2	up_VCAV_EC
GO:0016441	0.541	0.694	3	30	posttranscriptional gene silencing	BP	1	ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0035194	0.541	0.694	3	30	posttranscriptional gene silencing by RNA	BP	1	ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0071248	0.541	0.735	2	35	cellular response to metal ion	BP	1	PRNP,MT2A	down_VCAV_EC
GO:0070585	0.541	0.735	2	34	protein localization to mitochondrion	BP	1	DDIT3,SH3GLB1	down_VSAP_EC
GO:0031328	0.541	0.738	2	512	positive regulation of cellular biosynthetic	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0033674	0.541	0.822	1	144	positive regulation of kinase activity	BP	1	LYN	down_ACOR_EC
GO:0034103	0.541	0.829	1	12	regulation of tissue remodeling	BP	1	TFRC	down_VSAP_EC
GO:0003333	0.541	0.828	1	12	amino acid transmembrane transport	BP	1	SLC38A1	down_VSAP_EC
GO:0060008	0.541	0.837	1	7	Sertoli cell differentiation	BP	1	ATRX	up_ACOR_VSMC
GO:0030182	0.541	0.825	1	327	neuron differentiation	BP	1	HOXC10	up_AORT_EC
GO:0072673	0.541	0.835	1	8	lamellipodium morphogenesis	BP	1	SNX2	up_VCAV_EC
GO:0090190	0.541	0.831	1	10	positive regulation of branching involved in ureteric bud	BP	1	HOXB7	up_VCAV_EC
GO:0010632	0.541	0.821	1	95	regulation of epithelial cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0051129	0.541	0.823	1	221	negative regulation of cellular component	BP	1	ARHGEF2	up_VPUL_EC
GO:0034453	0.541	0.835	1	8	microtubule anchoring	BP	1	CEP19	up_VSAP_EC
GO:0033158	0.541	0.835	1	8	regulation of protein import into nucleus,	BP	1	MAVS	up_VSAP_EC
GO:0051046	0.541	0.822	1	174	regulation of secretion	BP	1	TLR2	up_VSAP_VSMC
GO:0071479	0.541504573	0.82164	1	29	cellular response to ionizing radiation	BP	1	FIGNL1	up_ACOR_EC
GO:0030031	0.542	0.574	13	155	cell projection assembly	BP	1	FSCN1,ANLN,CFAP298,CAV1,POC1A,RAC1,EMP2,CDC42EP4,EZR,ENSCAFG00000010224,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0008284	0.542	0.577	12	238	positive regulation of cell proliferation	BP	1	GPAM,PDGFRB,SLC35F6,BMPR1A,OSMR,AKT2,B4GALT1,GLI3,MYDGF,DDR2,GREM1,RAC2	down_VCAV_EC
GO:0090407	0.542	0.595	9	177	organophosphate biosynthetic process	BP	1	GPAM,ADCY6,LCAT,ATP5MC1,PIGS,ADK,AMPD2,ACSS2,ACAT1	down_VCAV_EC
GO:0051054	0.542	0.614	7	81	positive regulation of DNA metabolic process	BP	1	PDGFB,HMBOX1,PRKD2,TIMELESS,OTUD4,HMGB1,ATRX	up_VCAV_EC
GO:0033036	0.542	0.617	7	852	macromolecule localization	BP	1	MZT1,HOOK3,XPOT,ENSCAFG00000002015,GCC2,ABHD5,SRP54	up_VPOR_EC
GO:1901657	0.542	0.663	4	43	glycosyl compound metabolic process	BP	1	ENPP4,PTGDR,ENSCAFG00000018611,NT5C2	up_ACOR_VSMC
GO:0002699	0.542	0.663	4	46	positive regulation of immune effector process	BP	1	TLR4,GATA3,NECTIN2,FES	up_VCAV_EC
GO:0006664	0.542	0.691	3	37	glycolipid metabolic process	BP	1	KIT,CREM,ST3GAL6	up_VCAV_EC

GO:1903509	0.542	0.691	3	37	liposaccharide metabolic process	BP	1	KIT,CREM,ST3GAL6	up_VCAV_EC
GO:0019362	0.542	0.734	2	35	pyridine nucleotide metabolic process	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0046496	0.542	0.734	2	35	nicotinamide nucleotide metabolic process	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0006821	0.542	0.741	2	18	chloride transport	BP	1	SLC26A7,CLCN3	up_ACOR_VSMC
GO:0006959	0.542	0.739	2	21	humoral immune response	BP	1	MEF2C,GATA3	up_VCAV_EC
GO:0006414	0.542	0.826	1	15	translational elongation	BP	1	EEF2	down_VCAV_EC
GO:0032371	0.542	0.826	1	15	regulation of sterol transport	BP	1	SCP2	down_VCAV_EC
GO:0032374	0.542	0.826	1	15	regulation of cholesterol transport	BP	1	SCP2	down_VCAV_EC
GO:0046825	0.542	0.825	1	16	regulation of protein export from nucleus	BP	1	PARK7	down_VCAV_EC
GO:0050849	0.542	0.826	1	15	negative regulation of calcium-mediated	BP	1	PRNP	down_VCAV_EC
GO:0003401	0.542	0.825	1	15	axis elongation	BP	1	RDH10	down_VCAV_EC
GO:1902235	0.542	0.826	1	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:1902895	0.542	0.826	1	15	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	1	BMPR1A	down_VCAV_EC
GO:2000113	0.542	0.826	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	HDAC7	down_VPOR_EC
GO:0072283	0.542	0.828	1	12	metanephric renal vesicle morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0051353	0.542	0.827	1	13	positive regulation of oxidoreductase activity	BP	1	APOE	down_VSAP_EC
GO:0070232	0.542	0.827	1	13	regulation of T cell apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:0035556	0.542	0.84	1	845	intracellular signal transduction	BP	1	TGFBR1	down_VSAP_VSMC
GO:1903747	0.542	0.832	1	9	regulation of establishment of protein localization to	BP	1	SH3GLB1	up_VCAV_EC
GO:0006486	0.542	0.82	1	91	protein glycosylation	BP	1	OSTC	up_VPOR_EC
GO:0043413	0.542	0.82	1	91	macromolecule glycosylation	BP	1	OSTC	up_VPOR_EC
GO:0051347	0.542	0.821	1	182	positive regulation of transferase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0090407	0.542	0.821	1	177	organophosphate biosynthetic process	BP	1	ADCY3	up_VFEM_EC
GO:0071800	0.542	0.834	1	8	podosome assembly	BP	1	ARHGEF5	up_VSAP_EC
GO:0050767	0.542	0.821	1	184	regulation of neurogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0045785	0.542647477	0.68533	3	107	positive regulation of cell adhesion	BP	1	DUSP26,FOXC2,NRP1	up_ACOR_EC
GO:0043067	0.543	0.544	24	479	regulation of programmed cell death	BP	1	GPAM,SLC35F6,PRNP,KANK2,CLIP3,AKT2,ENSCAFG00000013404,TMEM161A,ARHGAP10,B4GALT1,GLI3,PARK7,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,ZBTB16	down_VCAV_EC
GO:0031329	0.543	0.546	23	241	regulation of cellular catabolic process	BP	1	AXIN2,PLEKHF1,ACACB,TPCN2,TENT5C,MFN2,ZFP36L1,POLDIP2,FBXO7,RNF166,LONP2,PIP4K2B,OSBPL7,SAMD4B,ZFP36L2,TIMP2,IDH1,UBQLN2,HTRA2,TNRC6C,HMOX1,NPRL3,DDIT4	up_VSAP_EC
GO:0010948	0.543	0.604	8	96	negative regulation of cell cycle process	BP	1	TAOK1,BLM,RAD21,RAD17,ZW10,ATRX,TOPBP1,FBXO5	up_VCAV_EC
GO:0050794	0.543	0.643	8	3075	regulation of cellular process	BP	1	EYA1,HOXA10,HOXA9,NETO1,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0003002	0.543	0.612	7	118	regionalization	BP	1	PRKACB,TMED2,CHSY1,HOXB7,CTNNB1,DDIT3,NRP1	down_VSAP_EC
GO:0031338	0.543	0.693	3	28	regulation of vesicle fusion	BP	1	USP6NL,EVI5L,SGSM2	up_ACOR_VSMC
GO:0031401	0.543	0.733	2	358	positive regulation of protein modification	BP	1	ACVRL1,LYN	down_ACOR_EC
GO:0006360	0.543	0.735	2	28	transcription by RNA polymerase I	BP	1	SMARCA4,GTF2H1	down_VSAP_EC
GO:0043473	0.543	0.735	2	28	pigmentation	BP	1	SHROOM2,SPARC	down_VSAP_EC

GO:0006879	0.543	0.737	2	23	cellular iron ion homeostasis	BP	1	CP,HIF1A	up_VCAV_EC
GO:0003143	0.543	0.737	2	22	embryonic heart tube morphogenesis	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0001732	0.543	0.831	1	9	formation of cytoplasmic translation initiation	BP	1	EIF3M	down_ACOR_VSMC
GO:0045616	0.543	0.831	1	9	regulation of keratinocyte differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:0019076	0.543	0.825	1	15	viral release from host cell	BP	1	TRIM8	down_VCAV_EC
GO:0035890	0.543	0.825	1	15	exit from host	BP	1	TRIM8	down_VCAV_EC
GO:0035891	0.543	0.825	1	15	exit from host cell	BP	1	TRIM8	down_VCAV_EC
GO:0051591	0.543	0.824	1	16	response to cAMP	BP	1	ZFP36L1	down_VCAV_EC
GO:0052126	0.543	0.825	1	15	movement in host environment	BP	1	TRIM8	down_VCAV_EC
GO:0052192	0.543	0.825	1	15	movement in environment of other organism involved in	BP	1	TRIM8	down_VCAV_EC
GO:1902743	0.543	0.824	1	16	regulation of lamellipodium	BP	1	RAC2	down_VCAV_EC
GO:0023052	0.543	0.866	1	1602	signaling	BP	1	PLCL1	down_VFEM_EC
GO:0000290	0.543	0.833	1	8	deadenylation-dependent decapping of nuclear-transcribed mRNA	BP	1	DCP1B	up_ACOR_VSMC
GO:0007039	0.543	0.836	1	7	protein catabolic process in the vacuole	BP	1	LAMP2	up_ACOR_VSMC
GO:2000515	0.543	0.833	1	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	CD274	up_ACOR_VSMC
GO:0048013	0.543	0.828	1	11	ephrin receptor signaling pathway	BP	1	NCK1	up_VCAV_EC
GO:0048705	0.543	0.819	1	95	skeletal system morphogenesis	BP	1	HOXA3	up_VPOR_EC
GO:0110053	0.543	0.818	1	98	regulation of actin filament organization	BP	1	TWF1	up_VPOR_EC
GO:0003299	0.543	0.833	1	8	muscle hypertrophy in response to stress	BP	1	KLF15	up_VSAP_EC
GO:0014887	0.543	0.833	1	8	cardiac muscle adaptation	BP	1	KLF15	up_VSAP_EC
GO:0014898	0.543	0.833	1	8	cardiac muscle hypertrophy in response	BP	1	KLF15	up_VSAP_EC
GO:0006606	0.543026184	0.73036	2	67	protein import into nucleus	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0060688	0.543130571	0.8204	1	29	regulation of morphogenesis of a	BP	1	SOX9	up_ACOR_EC
GO:0035239	0.54343059	0.60122	8	299	tube morphogenesis	BP	1	SOX9,AQP1,ENSCAFG00000004331,FZD5,ESM1,FOXC2,CLSTN1,NRP1	up_ACOR_EC
GO:2001141	0.543761304	0.54154	26	979	regulation of RNA biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC

GO:0071840	0.544	0.494	170	2059	cellular component organization or biogenesis	BP	1	EPHB1,PLK2,TEK,HCLS1,IL7R,GBP5,SELP,KIT,SELE,PRKCH,ARHGEF15,IFRD1,ENSCAFG00000007112,TIE1,CDA,ADAMTS9,ATP8A1,LRRC8D,MX2,AMOT,PDGFB,MALL,PODXL,BAIAP2L1,RELN,VWF,LAMC2,IWS1,OCLN,MEF2C,FERMT1,CHD7,RAPGEF1,TLR4,STC1,GATA3,EDN1,RAB11A,RALB,ARAP3,RAB27A,SMAD1,SNCAIP,PSME4,NEDD9,IRF8,SNAP91,ARHGAP28,TMOD1,FIGNL1,PPP3CA,NASP,MTSS1,NECTIN2,MTOR,ACPP,SAMD8,HOOK3,SNAP23,LRRC8C,TJP1,HHEX,LNX2,CAV2,PREX2,SLC12A7,SLK,CEP68,BMP2K,SCAF11,CNOT6,PDZD8,ABCA1,NCKAP1,GDPD5,MZT1,RIOK3,PROX1,UHRF2,IQGAP2,ENSCAFG00000010224,EPB41,ELMO1,ARID4B,STMN1,FLNB,SNX2,HMBOX1,BAZ1A,PAK2,PRKD2,SH3GLB1,SWAP70,SMARCA4,APOD,CENPC,NCK1,ESCO1,KCNJ2,EXOC5,LDB2,FES,NSD1,MRRF,HIST1H1A,TOP1,EHD4,RAPGEF2,PLCG2,CREB1,BCL10,SENP6,PAN3,GCC2,TAOK1,PRPF39,CTNNA1,CNOT7,FMNL3,STX11,SMG7,GCH1,SERAC1,VPS54,ASF1A,HMGB1,TBC1D1,PMAIP1,ARPC5L,BLM,NUP133,SPTBN4,RIPK1,SMC5,LSM14A,ITGA6,RAD21,MCU,DNAJC13,OLFML2A,ARHGDIB,ZW10,KDM5A,HIF1A,KDM3A,ARHGAP26,ALS2,IQUB,ATRX,HAUS3,ALDH1A3,HIST2H2AC,HP1BP3,ENSC	up_VCAV_EC
GO:0048878	0.544	0.538	27	283	chemical homeostasis	BP	1	HNF4A,C5AR2,LIPC,SLC8B1,ABL1,GOT1,CLDN1,ENSCAFG00000000071,F2RL1,RAB11B,PDK2,FXN,PIK3R1,SLC25A28,MYC,SCARA5,KCNB1,LCAT,FTL,RAF1,CYBA,STX4,PPP3CB,HMOX1,NCOA4,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0046649	0.544	0.586	10	162	lymphocyte activation	BP	1	SOCS5,FAM49B,MSN,PTPN2,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:2001242	0.544	0.625	6	62	regulation of intrinsic apoptotic signaling	BP	1	NACC2,SIAH1,SERINC3,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0044242	0.544	0.64	5	57	cellular lipid catabolic process	BP	1	ABHD5,PPARD,SGPL1,LIPC,ACADL	down_ACOR_VSMC
GO:0046890	0.544	0.641	5	51	regulation of lipid biosynthetic process	BP	1	LEP,HTR2B,ORMDL3,CCDC3,DKKL1	up_ACOR_VSMC
GO:0050794	0.544	0.756	3	3075	regulation of cellular process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0030879	0.544	0.69	3	34	mammary gland development	BP	1	GATA3,CREB1,HIF1A	up_VCAV_EC
GO:0098773	0.544	0.734	2	29	skin epidermis development	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0043412	0.544	0.752	2	1225	macromolecule modification	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0097061	0.544	0.737	2	21	dendritic spine organization	BP	1	EPHB1,RELN	up_VCAV_EC
GO:0070734	0.544	0.831	1	9	histone H3-K27 methylation	BP	1	EZH2	down_ACOR_VSMC
GO:0008542	0.544	0.826	1	13	visual learning	BP	1	HIF1A	down_VSAP_EC
GO:0042130	0.544	0.825	1	13	negative regulation of T cell proliferation	BP	1	SDC4	down_VSAP_EC
GO:0060795	0.544	0.827	1	12	cell fate commitment involved in formation of	BP	1	CTNNB1	down_VSAP_EC
GO:0002446	0.544	0.832	1	8	neutrophil mediated immunity	BP	1	F2RL1	up_ACOR_VSMC
GO:0006337	0.544	0.835	1	7	nucleosome disassembly	BP	1	SMARCD3	up_ACOR_VSMC
GO:0001573	0.544	0.832	1	8	ganglioside metabolic process	BP	1	NEU3	up_ACOR_VSMC
GO:0032770	0.544	0.832	1	8	positive regulation of monooxygenase activity	BP	1	HTR2B	up_ACOR_VSMC
GO:0032986	0.544	0.835	1	7	protein-DNA complex disassembly	BP	1	SMARCD3	up_ACOR_VSMC
GO:0034260	0.544	0.835	1	7	negative regulation of GTPase activity	BP	1	SH3BP4	up_ACOR_VSMC
GO:0045662	0.544	0.833	1	8	negative regulation of myoblast differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0010941	0.544	0.829	1	524	regulation of cell death	BP	1	EYA1	up_AFEM_VSMC
GO:0045683	0.544	0.83	1	9	negative regulation of epidermis development	BP	1	FERMT1	up_VCAV_EC
GO:0045945	0.544	0.839	1	6	positive regulation of transcription by RNA polymerase III	BP	1	MTOR	up_VCAV_EC
GO:0046164	0.544	0.827	1	11	alcohol catabolic process	BP	1	IMPA1	up_VCAV_EC

GO:0042886	0.544	0.829	1	527	amide transport	BP	1	CA2	up_VCAV_VSMC
GO:0030030	0.544	0.825	1	377	cell projection organization	BP	1	SLIT2	up_VPUL_VSMC
GO:1900363	0.544	0.833	1	8	regulation of mRNA polyadenylation	BP	1	CDK9	up_VSAP_EC
GO:0021561	0.544	0.832	1	8	facial nerve development	BP	1	PLXNA4	up_VSAP_EC
GO:0021610	0.544	0.832	1	8	facial nerve morphogenesis	BP	1	PLXNA4	up_VSAP_EC
GO:0030522	0.544336112	0.72918	2	67	intracellular receptor signaling pathway	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0031323	0.545	0.495	150	1788	regulation of cellular metabolic process	BP	1	ELK3,ACSL3,HMGB1,RNPS1,SREBF1,USP1,IRAK1,MCM7,ILF3,CBX5,PPRC1,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,HNRNPD,SREBF2,SMC1A,HINFP,UBE2S,NEDD4,SRSF2,MED17,U2AF2,SLC29A1,MTDH,HEY1,PPP1R15B,PARPBP,SRRT,CTDNEP1,NAB2,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,CDK1,RFC5,RFC3,RAD51,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,TCEA1,NF2,AURKB,NONO,HNRNPL,CDKN2C,ABHD5,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,HOXA7,ARG2,SF3B4,UHRF1,CKS2,PDCD2,RNF152,GMNN,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,E2F8,PRCP,TFRC,PPARD,RAP2C,YBX3,HNRNPF,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,FOSL1,IQGAP1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,SMC3,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,CLSPN,RBM14,RBM17,RAD23A,NOLC1,CDC20,HOXA10,ERF,TCERG1,PUM3,MAST2,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,KNL1,SUPT16H,TADA2A,WTAP,HAT1,HIST2H2AC,HOXA9,GLI1,TINF2,JMJD6,H2AFX,CDC5L,CCNB3,MIS18A,HMGN1,CCT4,SIX4,MTBP,NECAB3,SF3A1,MED16,ENSCAFG00000017103,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0007399	0.545	0.514	55	564	nervous system development	BP	1	SH3TC2,FGF13,VEGFD,LEP,EPYC,MBP,SHROOM3,FEZ1,ITM2C,BMP4,FGFR2,GJA1,ATRX,SEC24B,WASF3,CITED2,SPINT1,GLRB,ACSL6,ZNF365,LMO4,TMEM108,NDRG2,ATRN,CAMK2D,NRP1,GPM6A,ULK2,UNC5B,SMARCD3,SPINT2,SLITRK5,TBX20,FZD3,FRS2,RND1,DAG1,POMK,APP,PSEN1,SEMA6D,CHD7,SIPA1L1,CLN8,SSH3,ASAP1,JAM3,B2M,DISC1,TACC1,ATXN10,FEZ2,SUN1,WASL,CRKL	up_ACOR_VSMC
GO:0034097	0.545	0.575	12	238	response to cytokine	BP	1	PCOLCE,DCN,BGN,NUMBL,TIMP2,GFPT2,ASPN,ZFP36L1,MAVS,GSDME,RAB7B,FOXO3	down_VCAV_EC
GO:0090092	0.545	0.613	7	72	regulation of transmembrane receptor protein serine/threonine	BP	1	SMAD6,FERMT1,BMP4,CITED2,CDKN2B,NPNT,TBX20	up_ACOR_VSMC
GO:0019058	0.545	0.639	5	64	viral life cycle	BP	1	CXCL8,NECTIN2,PROX1,CNOT7,USP6NL	up_VCAV_EC
GO:0007204	0.545	0.66	4	46	positive regulation of cytosolic calcium ion	BP	1	HMGB1,CAV1,GSTO1,CORO1A	down_ACOR_VSMC
GO:0030100	0.545	0.657	4	70	regulation of endocytosis	BP	1	VEGFA,SERPINE1,APOE,LRRTM2	down_VSAP_EC
GO:0045927	0.545	0.657	4	61	positive regulation of growth	BP	1	CELF1,ZPR1,ADAM17,NRP1	down_VSAP_EC
GO:0051262	0.545	0.661	4	40	protein tetramerization	BP	1	ACTN2,PCBD1,EVL,SBF2	up_ACOR_VSMC
GO:0008406	0.545	0.685	3	57	gonad development	BP	1	IRX5,RDH10,FOXO3	down_VCAV_EC
GO:0045137	0.545	0.685	3	57	development of primary sexual characteristics	BP	1	IRX5,RDH10,FOXO3	down_VCAV_EC
GO:0048523	0.545	0.705	3	1399	negative regulation of cellular process	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0006338	0.545	0.687	3	45	chromatin remodeling	BP	1	SMARCA4,MORF4L2,CTNNB1	down_VSAP_EC
GO:0022612	0.545	0.687	3	44	gland morphogenesis	BP	1	SULF1,MSN,NRP1	down_VSAP_EC
GO:0060675	0.545	0.691	3	29	ureteric bud morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0051101	0.545	0.688	3	35	regulation of DNA binding	BP	1	GATA3,NSD1,HMGB1	up_VCAV_EC
GO:0006629	0.545	0.732	2	382	lipid metabolic process	BP	1	LYN,ACSL3	down_ACOR_EC
GO:0030163	0.545	0.732	2	365	protein catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC

GO:0034394	0.545	0.737	2	19	protein localization to cell surface	BP	1	ACTN2,RAB11B	up_ACOR_VSMC
GO:2000059	0.545	0.737	2	19	negative regulation of ubiquitin-dependent protein catabolic process	BP	1	PSEN1,PARK7	up_ACOR_VSMC
GO:0051279	0.545	0.738	2	19	regulation of release of sequestered calcium ion into cytosol	BP	1	ABL1,CYBA	up_VSAP_EC
GO:0033059	0.545	0.826	1	12	cellular pigmentation	BP	1	SHROOM2	down_VSAP_EC
GO:0045058	0.545	0.826	1	12	T cell selection	BP	1	PTPN2	down_VSAP_EC
GO:0045184	0.545	0.828	1	532	establishment of protein localization	BP	1	TLR2	up_AFEM_VSMC
GO:0070838	0.545	0.817	1	96	divalent metal ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0048589	0.545	0.818	1	188	developmental growth	BP	1	HOXA11	up_VSAP_VSMC
GO:0006996	0.546	0.506	78	1301	organelle organization	BP	1	ARHGEF2,SIPA1L1,MYH9,NR1H4,FMNL3,PLK3,ACTN1,VASP,SEC24D,TPM4,EXOC5,CORO1C,FSCN1,FLNB,SEC23A,MZT1,DPYSL3,HOOK3,ENSCAFG00000007260,PPP1R12A,SMARCA4,SESN2,WDR1,MSN,RPGR,KIF5B,LMAN1,HIF1A,DYNLL1,TUBB,IWS1,TNIK,NAA10,ZPR1,MORF4L2,TMSB10,SMG7,USO1,BRD2,CNOT7,ACTR3,PALLD,CTNNB1,KPNB1,BNIP3,TWF1,PDS5B,FAM162A,PLEKHG2,TLN1,PLS3,GSK3B,NEXN,CDC37,DAAM1,CCSER2,SH3GLB1,SDC4,HTT,REST,ENSCAFG00000017326,ZMYND8,EIF2S1,PRMT1,DISC1,PAK2,CAPG,SIX4,RSL24D1,SLC25A46,NRP1,ENSCAFG00000030508,BLZF1,TNFAIP1,SEC13,KDM3A,MYBPC2,MID1	down_VSAP_EC
GO:0007369	0.546	0.624	6	63	gastrulation	BP	1	HOXA11,WNT11,HNF4A,OSR1,PLPP3,TGFBR2	up_VSAP_EC
GO:0030041	0.546	0.624	6	62	actin filament polymerization	BP	1	FAM107A,SLIT2,CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:0016051	0.546	0.637	5	63	carbohydrate biosynthetic process	BP	1	PDGFB,ATF3,FAM3C,ENSCAFG00000010596,IMPA1	up_VCAV_EC
GO:0016197	0.546	0.655	4	78	endosomal transport	BP	1	SNX18,MICALL2,RAB7B,ARHGAP1	down_VCAV_EC
GO:0010565	0.546	0.659	4	40	regulation of cellular ketone metabolic process	BP	1	PPARGC1A,PRKCE,DKKL1,PARK7	up_ACOR_VSMC
GO:0009893	0.546	0.665	4	995	positive regulation of metabolic process	BP	1	NR1H4,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0060411	0.546	0.688	3	33	cardiac septum morphogenesis	BP	1	CHD7,PROX1,JAG1	up_VCAV_EC
GO:0007260	0.546	0.736	2	19	tyrosine phosphorylation of STAT protein	BP	1	LEP,PARP9	up_ACOR_VSMC
GO:0070861	0.546	0.829	1	9	regulation of protein exit from endoplasmic	BP	1	INSIG1	down_ACOR_VSMC
GO:1903747	0.546	0.829	1	9	regulation of establishment of protein localization to	BP	1	SREBF1	down_ACOR_VSMC
GO:0048260	0.546	0.822	1	15	positive regulation of receptor-mediated	BP	1	GREM1	down_VCAV_EC
GO:1903727	0.546	0.822	1	16	positive regulation of phospholipid metabolic	BP	1	PDGFRB	down_VCAV_EC
GO:0006739	0.546	0.824	1	13	NADP metabolic process	BP	1	PGAM1	down_VSAP_EC
GO:0035561	0.546	0.825	1	12	regulation of chromatin binding	BP	1	CTNNB1	down_VSAP_EC
GO:0042531	0.546	0.824	1	13	positive regulation of tyrosine phosphorylation	BP	1	LYN	down_VSAP_EC
GO:0009261	0.546	0.831	1	8	ribonucleotide catabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:0010447	0.546	0.831	1	8	response to acidic pH	BP	1	RAB11B	up_ACOR_VSMC
GO:0032309	0.546	0.829	1	9	icosanoid secretion	BP	1	NOS2	up_VCAV_EC
GO:0072503	0.546	0.816	1	97	cellular divalent inorganic cation homeostasis	BP	1	C3AR1	up_VPOR_EC
GO:0033081	0.546	0.831	1	8	regulation of T cell differentiation in thymus	BP	1	ZEB1	up_VSAP_EC
GO:0072673	0.546	0.831	1	8	lamellipodium morphogenesis	BP	1	ENPP2	up_VSAP_EC
GO:0030155	0.546	0.818	1	180	regulation of cell adhesion	BP	1	CAV1	up_VSAP_VSMC
GO:0051223	0.546	0.818	1	181	regulation of protein transport	BP	1	TLR2	up_VSAP_VSMC

GO:0048524	0.546756884	0.81745	1	30	positive regulation of viral process	BP	1	CHMP4B	up_ACOR_EC
GO:1903052	0.547	0.638	5	51	positive regulation of proteolysis involved in cellular protein catabolic	BP	1	SH3RF2,RNF19A,PSEN1,DISC1,HERPUD1	up_ACOR_VSMC
GO:0051346	0.547	0.654	4	78	negative regulation of hydrolase activity	BP	1	CST3,RECK,PARK7,SPRED1	down_VCAV_EC
GO:0071236	0.547	0.659	4	39	cellular response to antibiotic	BP	1	TP53INP1,ADCY6,PRKCE,PARK7	up_ACOR_VSMC
GO:2000377	0.547	0.659	4	41	regulation of reactive oxygen species metabolic	BP	1	F2RL1,BNIP3,CDKN1A,PARK7	up_ACOR_VSMC
GO:0030072	0.547	0.657	4	48	peptide hormone secretion	BP	1	CHD7,EDN1,MCU,HIF1A	up_VCAV_EC
GO:0030216	0.547	0.688	3	29	keratinocyte differentiation	BP	1	EXPH5,LATS2,FOSL2	up_ACOR_VSMC
GO:0016441	0.547	0.688	3	30	posttranscriptional gene silencing	BP	1	MOV10,PPP3CA,TUT7	up_VCAV_EC
GO:0035194	0.547	0.688	3	30	posttranscriptional gene silencing by RNA	BP	1	MOV10,PPP3CA,TUT7	up_VCAV_EC
GO:0032872	0.547	0.726	2	77	regulation of stress-activated MAPK cascade	BP	1	LEP,CYLD	up_AFEM_EC
GO:0007565	0.547	0.733	2	23	female pregnancy	BP	1	PTGS2,ARHGDIB	up_VCAV_EC
GO:0072525	0.547	0.733	2	24	pyridine-containing compound biosynthetic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:2000736	0.547	0.735	2	21	regulation of stem cell differentiation	BP	1	JAG1,KDM3A	up_VCAV_EC
GO:0045664	0.547	0.817	1	144	regulation of neuron differentiation	BP	1	LYN	down_ACOR_EC
GO:0035988	0.547	0.829	1	9	chondrocyte proliferation	BP	1	MMP14	down_ACOR_VSMC
GO:1902236	0.547	0.828	1	9	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling	BP	1	TXNDC12	down_ACOR_VSMC
GO:0030260	0.547	0.822	1	15	entry into host cell	BP	1	TRIM8	down_VCAV_EC
GO:0035329	0.547	0.821	1	16	hippo signaling	BP	1	TEAD1	down_VCAV_EC
GO:0038083	0.547	0.821	1	16	peptidyl-tyrosine autophosphorylation	BP	1	GREM1	down_VCAV_EC
GO:0044409	0.547	0.822	1	15	entry into host	BP	1	TRIM8	down_VCAV_EC
GO:0051806	0.547	0.822	1	15	entry into cell of other organism involved in	BP	1	TRIM8	down_VCAV_EC
GO:0051828	0.547	0.822	1	15	entry into other organism involved in symbiotic	BP	1	TRIM8	down_VCAV_EC
GO:0009719	0.547	0.823	1	395	response to endogenous stimulus	BP	1	CITED2	down_VPOR_EC
GO:0010558	0.547	0.823	1	392	negative regulation of macromolecule biosynthetic process	BP	1	HDAC7	down_VPOR_EC
GO:0002714	0.547	0.824	1	12	positive regulation of B cell mediated immunity	BP	1	TFRC	down_VSAP_EC
GO:0002891	0.547	0.824	1	12	positive regulation of immunoglobulin mediated immune	BP	1	TFRC	down_VSAP_EC
GO:0006974	0.547	0.821	1	333	cellular response to DNA damage stimulus	BP	1	TAOK1	up_AORT_EC
GO:0008285	0.547	0.817	1	201	negative regulation of cell proliferation	BP	1	TBX5	up_APUL_EC
GO:0030206	0.547	0.828	1	9	chondroitin sulfate biosynthetic process	BP	1	CHST7	up_VCAV_EC
GO:0050790	0.547	0.827	1	532	regulation of catalytic activity	BP	1	LIMK1	up_VCAV_VSMC
GO:1903959	0.547	0.83	1	8	regulation of anion transmembrane transport	BP	1	OSR1	up_VSAP_EC
GO:1902188	0.547	0.83	1	8	positive regulation of viral release from host cell	BP	1	PC	up_VSAP_EC
GO:0040017	0.547	0.817	1	180	positive regulation of locomotion	BP	1	CAV1	up_VSAP_VSMC
GO:0043632	0.547114168	0.60686	7	262	modification-dependent macromolecule catabolic	BP	1	EDEM2,KLHL25,PIAS1,CLU,TP53INP2,RNF114,UBE2H	up_ACOR_EC
GO:0002250	0.547388345	0.72637	2	68	adaptive immune response	BP	1	FZD5,PRKCD	up_ACOR_EC

GO:0006355	0.548	0.498	94	974	regulation of transcription, DNA-templated	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,FGFR2,TP53BP1,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0060548	0.548	0.533	28	294	negative regulation of cell death	BP	1	SMAD6,PLCG2,BCL2,HTR2B,PRKAA2,BMP4,TM7SF3,FGFR2,SH3RF2,PPARGC1A,CITED2,AR,PLAC8B,KLHL20,LIMS2,DAPK1,BNIP3,NRP1,LRPAP1,UNC5B,SH3RF1,FZD3,PSEN1,CLN8,OXR1,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0043069	0.548	0.542	22	262	negative regulation of programmed cell death	BP	1	SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,FAM129B,AURKB,GREM1,PLK3,ARG2,DHCR24,NOC2L,NUP62,HMGB2,ENSCAFG00000005299,CORO1A,TXNDC12,CTH,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0060322	0.548	0.555	17	193	head development	BP	1	PTCHD1,RELN,CHD7,TIPARP,HOOK3,BMP2,HHEX,GDPD5,PROX1,ENSCAFG00000010224,APOD,RAPGEF2,CREB1,HIF1A,ATRX,ALDH1A3,CDON	up_VCAV_EC
GO:0048534	0.548	0.567	13	262	hematopoietic or lymphoid organ development	BP	1	NOTCH2,FBN1,LMO4,TFE3,CLSTN1,GLI3,EEF2,ZFP36L1,LOXL3,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0031329	0.548	0.572	12	241	regulation of cellular catabolic process	BP	1	LRP1,DCN,TIMP2,AKT2,PSMF1,SAMD4B,POLDIP2,PARK7,ZFP36L1,CLEC16A,LONP2,PACSIN3	down_VCAV_EC
GO:0032956	0.548	0.578	11	116	regulation of actin cytoskeleton organization	BP	1	WNT11,FAM107A,ARHGEF5,SLIT2,ABL1,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,NCK1,BAG4	up_VSAP_EC
GO:0006869	0.548	0.609	7	81	lipid transport	BP	1	ACSL3,SREBF2,PRELID1,LIMA1,PPARD,LIPC,NUS1	down_ACOR_VSMC
GO:0043406	0.548	0.621	6	62	positive regulation of MAP kinase activity	BP	1	ARHGEF5,MAP3K5,PDGFD,C1QTNF2,TRAF7,SASH1	up_VSAP_EC
GO:0048523	0.548	0.648	5	1399	negative regulation of cellular process	BP	1	TBX5,NR1H4,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:1903034	0.548	0.658	4	40	regulation of response to wounding	BP	1	F2RL1,ENPP4,PRKCE,RREB1	up_ACOR_VSMC
GO:0048588	0.548	0.683	3	44	developmental cell growth	BP	1	IFRD1,CTNNB1,NRP1	down_VSAP_EC
GO:0071695	0.548	0.684	3	45	anatomical structure maturation	BP	1	HIF1A,CTNNB1,DDIT3	down_VSAP_EC
GO:0001819	0.548	0.68	3	120	positive regulation of cytokine production	BP	1	LEP,ADAM17,AGPAT2	up_AFEM_EC
GO:0030316	0.548	0.687	3	31	osteoclast differentiation	BP	1	MTOR,CREB1,TJP2	up_VCAV_EC
GO:0000041	0.548	0.729	2	31	transition metal ion transport	BP	1	SLC39A7,TFRC	down_VSAP_EC
GO:0061387	0.548	0.736	2	18	regulation of extent of cell growth	BP	1	NRP1,ULK2	up_ACOR_VSMC
GO:0007154	0.548	0.863	1	1622	cell communication	BP	1	PLCL1	down_VFEM_EC
GO:0032331	0.548	0.83	1	8	negative regulation of chondrocyte	BP	1	BMP4	up_ACOR_VSMC
GO:0061037	0.548	0.83	1	8	negative regulation of cartilage development	BP	1	BMP4	up_ACOR_VSMC
GO:0010977	0.548	0.816	1	33	negative regulation of neuron projection	BP	1	KANK1	up_AFEM_EC
GO:1900182	0.548	0.816	1	33	positive regulation of protein localization to	BP	1	LEP	up_AFEM_EC
GO:1904589	0.548	0.816	1	33	regulation of protein import	BP	1	LEP	up_AFEM_EC
GO:0009605	0.548	0.826	1	538	response to external stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:1990748	0.548	0.83	1	8	cellular detoxification	BP	1	SESN1	up_VSAP_EC
GO:0006956	0.548	0.83	1	8	complement activation	BP	1	CFD	up_VSAP_EC

GO:0061298	0.548	0.83	1	8	retina vasculature development in camera-	BP	1	ACVRL1	up_VSAP_EC
GO:0030216	0.548165726	0.81653	1	29	keratinocyte differentiation	BP	1	CDH3	up_ACOR_EC
GO:0048522	0.548330497	0.52441	39	1484	positive regulation of cellular process	BP	1	CDH3,NR1H4,GATA4,PKIB,CALY,SOX9,PTH1R,AQP1,ENSCAFG00000004331,SYNPO2,EDEM2,FZD5,CCDC3,SEMA6D,DUSP26,DIXDC1,RASL11A,NOD2,SMAD6,ACTN2,ESM1,PAK3,TNFRSF19,PTGER4,PIAS1,MAVS,FOXC2,LRRC15,IFIT2,TBX5,LRP4,CLSTN1,SH3RF3,CLU,TP53INP2,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0034220	0.549	0.551	18	188	ion transmembrane transport	BP	1	AMIGO1,CALHM2,SLC8B1,ABL1,KCNE3,OSR1,CLIC5,KLHL24,SLC25A12,SLC25A28,SCARA5,CLCN2,STEAP3,KCNB1,ENSCAFG00000013366,CYBA,FXYD1,KCNC4	up_VSAP_EC
GO:0043604	0.549	0.555	16	288	amide biosynthetic process	BP	1	ASNS,CARS,SARS,AARS,PUM3,UGCG,SESN2,MRPL1,YARS,TARS,NARS,EIF4EBP1,CNOT7,EIF5,EIF2S1,RSL24D1	down_VSAP_EC
GO:0044267	0.549	0.576	13	1583	cellular protein metabolic process	BP	1	OSTC,OGA,ARHGEF2,ASPN,ACVR2A,RSL24D1,RPL10L,KLHL28,PUM3,EIF5,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0050769	0.549	0.59	9	95	positive regulation of neurogenesis	BP	1	CDON,HOXD3,IRX3,ZEB1,SHOX2,GDPD5,CYB5D2,NCK1,MAP2K2	up_VSAP_EC
GO:0051641	0.549	0.611	7	858	cellular localization	BP	1	MZT1,HOOK3,XPOT,ENSCAFG00000005494,GCC2,SRP54,TMEM87B	up_VPOR_EC
GO:0034599	0.549	0.633	5	81	cellular response to oxidative stress	BP	1	P4HB,SESN2,HIF1A,CTNNB1,EIF2S1	down_VSAP_EC
GO:0071902	0.549	0.652	4	79	positive regulation of protein serine/threonine	BP	1	CSPG4,SASH1,MAPRE3,SHC1	down_VCAV_EC
GO:0032465	0.549	0.687	3	29	regulation of cytokinesis	BP	1	PKP4,PRKCE,PIK3C3	up_ACOR_VSMC
GO:0006626	0.549	0.687	3	29	protein targeting to mitochondrion	BP	1	MFN2,FBXO7,BAG4	up_VSAP_EC
GO:0032233	0.549	0.732	2	21	positive regulation of actin filament bundle	BP	1	NF2,RAC1	down_ACOR_VSMC
GO:0048513	0.549	0.74	2	906	animal organ development	BP	1	CITED2,TBX15	down_VPOR_EC
GO:0000184	0.549	0.735	2	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	PNRC1,CTIF	up_ACOR_VSMC
GO:0043367	0.549	0.735	2	18	CD4-positive, alpha-beta T cell differentiation	BP	1	CD83,IL18R1	up_ACOR_VSMC
GO:0046939	0.549	0.734	2	19	nucleotide phosphorylation	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:0006812	0.549	0.725	2	222	cation transport	BP	1	HOXA3,ENSCAFG00000005494	up_VPOR_EC
GO:0009067	0.549	0.827	1	9	aspartate family amino acid biosynthetic process	BP	1	CTH	down_ACOR_VSMC
GO:0031114	0.549	0.826	1	9	regulation of microtubule depolymerization	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0031639	0.549	0.827	1	9	plasminogen activation	BP	1	DHCR24	down_ACOR_VSMC
GO:0032733	0.549	0.827	1	9	positive regulation of interleukin-10 production	BP	1	HMGB1	down_ACOR_VSMC
GO:0034122	0.549	0.827	1	9	negative regulation of toll-like receptor signaling	BP	1	CACTIN	down_ACOR_VSMC
GO:0048873	0.549	0.827	1	9	homeostasis of number of cells within a tissue	BP	1	CORO1A	down_ACOR_VSMC
GO:0035295	0.549	0.82	1	356	tube development	BP	1	SRSF6	down_AFEM_EC
GO:0009968	0.549	0.821	1	392	negative regulation of signal transduction	BP	1	HDAC7	down_VPOR_EC
GO:0051726	0.549	0.821	1	393	regulation of cell cycle	BP	1	CITED2	down_VPOR_EC
GO:2001222	0.549	0.823	1	11	regulation of neuron migration	BP	1	ARHGEF2	down_VSAP_EC
GO:0051187	0.549	0.822	1	13	cofactor catabolic process	BP	1	ALDH1L2	down_VSAP_EC
GO:0072202	0.549	0.822	1	13	cell differentiation involved in metanephros	BP	1	CTNNB1	down_VSAP_EC
GO:0035518	0.549	0.829	1	8	histone H2A monoubiquitination	BP	1	PCGF5	up_ACOR_VSMC
GO:1902806	0.549	0.815	1	33	regulation of cell cycle G1/S phase transition	BP	1	DCUN1D3	up_AFEM_EC
GO:0048645	0.549	0.815	1	33	animal organ formation	BP	1	AXIN2	up_AFEM_EC
GO:0006468	0.549	0.825	1	544	protein phosphorylation	BP	1	TLR2	up_AFEM_VSMC
GO:0006952	0.549	0.819	1	319	defense response	BP	1	BPI	up_AORT_EC

GO:0002724	0.549	0.827	1	9	regulation of T cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:0061001	0.549	0.829	1	8	regulation of dendritic spine morphogenesis	BP	1	RELN	up_VCAV_EC
GO:0010573	0.549	0.827	1	9	vascular endothelial growth factor production	BP	1	HIF1A	up_VCAV_EC
GO:0010574	0.549	0.827	1	9	regulation of vascular endothelial growth factor	BP	1	HIF1A	up_VCAV_EC
GO:0072511	0.549	0.814	1	97	divalent inorganic cation transport	BP	1	HOXA3	up_VPOR_EC
GO:0051493	0.549	0.816	1	188	regulation of cytoskeleton organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0043171	0.549	0.829	1	8	peptide catabolic process	BP	1	RNPEP	up_VSAP_EC
GO:0071711	0.549	0.829	1	8	basement membrane organization	BP	1	CTSS	up_VSAP_EC
GO:0014912	0.549	0.829	1	8	negative regulation of smooth muscle cell	BP	1	SLIT2	up_VSAP_EC
GO:0120036	0.55	0.522	35	373	plasma membrane bounded cell projection organization	BP	1	WASF3,AMIGO1,ENPP2,SLIT2,ABL1,EMP2,CDC42EP5,FUZ,PLXNA4,RILPL2,CDC42EP2,F2RL1,SHOX2,FGD4,RTN4RL1,LRP4,DPYSL2,GDPD5,E2F4,KIF27,FBXO7,TMEM17,NFIB,CDNF,PQBP1,TTL,TTC8,EMP3,FLOT1,NCK1,ULK1,CEP19,MAP2K2,OGN,BAG4	up_VSAP_EC
GO:0030029	0.55	0.545	20	239	actin filament-based process	BP	1	FSCN1,FLNB,FMNL3,CAPG,CAV1,LIMA1,NF2,STMN1,GAS2L3,RAC1,EMP2,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,PHACTR4,ARPC1B,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0043069	0.55	0.564	13	262	negative regulation of programmed cell death	BP	1	GPAM,SLC35F6,PRNP,KANK2,AKT2,TMEM161A,ARHGAP10,GLI3,PARK7,MYDGF,TSC22D3,SHC1,GREM1	down_VCAV_EC
GO:0006873	0.55	0.595	8	160	cellular ion homeostasis	BP	1	PRNP,ENSCAFG00000018277,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0006644	0.55	0.616	6	118	phospholipid metabolic process	BP	1	GPAM,PDGFRB,ENSCAFG00000014978,LCAT,PIGS,NAPEPLD	down_VCAV_EC
GO:0071902	0.55	0.632	5	79	positive regulation of protein serine/threonine	BP	1	VEGFA,PTPN11,TNIK,MAGED1,MADD	down_VSAP_EC
GO:0051224	0.55	0.654	4	47	negative regulation of protein transport	BP	1	SREBF1,INSIG1,ARG2,EZR	down_ACOR_VSMC
GO:1904950	0.55	0.654	4	47	negative regulation of establishment of protein localization	BP	1	SREBF1,INSIG1,ARG2,EZR	down_ACOR_VSMC
GO:0006807	0.55	0.717	4	3221	nitrogen compound metabolic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0000082	0.55	0.68	3	57	G1/S transition of mitotic cell cycle	BP	1	KANK2,LSM10,EIF4EBP1	down_VCAV_EC
GO:0000462	0.55	0.731	2	22	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	NOC4L,EMG1	down_ACOR_VSMC
GO:0010812	0.55	0.733	2	19	negative regulation of cell-substrate adhesion	BP	1	DUSP22,FAM107A	up_ACOR_VSMC
GO:0021795	0.55	0.733	2	20	cerebral cortex cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0009891	0.55	0.73	2	521	positive regulation of biosynthetic process	BP	1	NR1H4,ARHGEF2	up_VPUL_EC
GO:0032504	0.55	0.814	1	152	multicellular organism reproduction	BP	1	ACSL4	down_ACOR_EC
GO:0048609	0.55	0.814	1	152	multicellular organismal reproductive process	BP	1	ACSL4	down_ACOR_EC
GO:0010002	0.55	0.826	1	9	cardioblast differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0010224	0.55	0.826	1	9	response to UV-B	BP	1	HMGN1	down_ACOR_VSMC
GO:0010831	0.55	0.826	1	9	positive regulation of myotube differentiation	BP	1	MMP14	down_ACOR_VSMC
GO:0034138	0.55	0.826	1	9	toll-like receptor 3 signaling pathway	BP	1	CAV1	down_ACOR_VSMC
GO:0046040	0.55	0.826	1	9	IMP metabolic process	BP	1	PFAS	down_ACOR_VSMC
GO:1905331	0.55	0.826	1	9	negative regulation of morphogenesis of an	BP	1	GREM1	down_ACOR_VSMC
GO:0097242	0.55	0.831	1	7	amyloid-beta clearance	BP	1	LRPAP1	up_ACOR_VSMC
GO:0045639	0.55	0.814	1	33	positive regulation of myeloid cell	BP	1	EVI2B	up_AFEM_EC
GO:0044283	0.55	0.815	1	201	small molecule biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0010656	0.55	0.828	1	8	negative regulation of muscle cell apoptotic	BP	1	RGL2	up_VCAV_EC

GO:0035313	0.55	0.831	1	7	wound healing, spreading of epidermal cells	BP	1	MTOR	up_VCAV_EC
GO:0046907	0.550391438	0.56134	14	536	intracellular transport	BP	1	SH3TC2,CDH3,CALY,KCNB1,EDEM2,DYNC1I1,ACTN2,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD	up_ACOR_EC
GO:0007275	0.551	0.583	11	1370	multicellular organism development	BP	1	C3AR1,BARX1,HOOK3,HOXA3,ARHGEF2,SEMA3A,ASPN,ACVR2A,MTDH,HOXA2,RNF6	up_VPOR_EC
GO:0050801	0.551	0.579	10	200	ion homeostasis	BP	1	GPAM,DCN,PRNP,ENSCAFG00000018277,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0010876	0.551	0.596	8	92	lipid localization	BP	1	OSBPL9,ATP8A1,PDZD8,ABCA1,OSBPL6,SLCO3A1,APOD,NOS2	up_VCAV_EC
GO:0006479	0.551	0.654	4	45	protein methylation	BP	1	PRMT1,EZH2,FBL,PRMT5	down_ACOR_VSMC
GO:0008213	0.551	0.654	4	45	protein alkylation	BP	1	PRMT1,EZH2,FBL,PRMT5	down_ACOR_VSMC
GO:0031333	0.551	0.654	4	46	negative regulation of protein complex assembly	BP	1	HMGB1,CAPG,INSIG1,STMN1	down_ACOR_VSMC
GO:0002274	0.551	0.655	4	40	myeloid leukocyte activation	BP	1	F2RL1,BATF2,STX4,TGFBR2	up_VSAP_EC
GO:2001243	0.551	0.683	3	33	negative regulation of intrinsic apoptotic	BP	1	NOC2L,TXNDC12,ARHGEF2	down_ACOR_VSMC
GO:0006996	0.551	0.697	3	1301	organelle organization	BP	1	GPSM2,NDUFA10,FSCN1	down_AFEM_EC
GO:0007006	0.551	0.726	2	35	mitochondrial membrane organization	BP	1	SLC35F6,PEX5	down_VCAV_EC
GO:0043393	0.551	0.723	2	77	regulation of protein binding	BP	1	GREM2,CYLD	up_AFEM_EC
GO:0019693	0.551	0.814	1	172	ribose phosphate metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0030003	0.551	0.813	1	157	cellular cation homeostasis	BP	1	LYN	down_ACOR_EC
GO:0048596	0.551	0.825	1	9	embryonic camera-type eye morphogenesis	BP	1	PHACTR4	down_ACOR_VSMC
GO:0070233	0.551	0.825	1	9	negative regulation of T cell apoptotic process	BP	1	ARG2	down_ACOR_VSMC
GO:0071168	0.551	0.825	1	9	protein localization to chromatin	BP	1	EZH2	down_ACOR_VSMC
GO:0021602	0.551	0.818	1	16	cranial nerve morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0140112	0.551	0.819	1	15	extracellular vesicle biogenesis	BP	1	SDC4	down_VCAV_EC
GO:0061384	0.551	0.821	1	12	heart trabecula morphogenesis	BP	1	FHL2	down_VSAP_EC
GO:0050772	0.551	0.82	1	13	positive regulation of axonogenesis	BP	1	NRP1	down_VSAP_EC
GO:0006677	0.551	0.828	1	8	glycosylceramide metabolic process	BP	1	UGCG	up_ACOR_VSMC
GO:0034315	0.551	0.827	1	8	regulation of Arp2/3 complex-mediated actin	BP	1	WASL	up_ACOR_VSMC
GO:0097094	0.551	0.828	1	8	craniofacial suture morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:1902532	0.551	0.815	1	204	negative regulation of intracellular signal	BP	1	NR1H4	up_APUL_EC
GO:0036035	0.551	0.83	1	7	osteoclast development	BP	1	TJP2	up_VCAV_EC
GO:0009605	0.551	0.823	1	538	response to external stimulus	BP	1	C6	up_VCAV_VSMC
GO:0051271	0.551	0.813	1	98	negative regulation of cellular component	BP	1	SEMA3A	up_VPOR_EC
GO:0043009	0.551	0.815	1	227	chordate embryonic development	BP	1	HOXA3	up_VPUL_EC
GO:0046856	0.551	0.827	1	8	phosphatidylinositol dephosphorylation	BP	1	INPP5E	up_VSAP_EC
GO:1900087	0.551	0.828	1	8	positive regulation of G1/S transition of mitotic	BP	1	LSM10	up_VSAP_EC
GO:0046605	0.551614991	0.81367	1	30	regulation of centrosome cycle	BP	1	CHMP4B	up_ACOR_EC
GO:0045944	0.552	0.559	14	287	positive regulation of transcription by RNA polymerase II	BP	1	DCN,LUM,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,MYDGF,MAVS,GREM1,THRB	down_VCAV_EC
GO:0000209	0.552	0.596	8	83	protein polyubiquitination	BP	1	DDB2,RBCK1,RNF24,SASH1,FBXO4,RNF166,RNF216,CDC26	up_VSAP_EC
GO:0061041	0.552	0.682	3	34	regulation of wound healing	BP	1	TFPI,CAV1,PPARD	down_ACOR_VSMC
GO:0031324	0.552	0.685	3	735	negative regulation of cellular metabolic process	BP	1	NR1H4,PCSK1N,LZTS1	up_APUL_EC
GO:0019222	0.552	0.711	3	1934	regulation of metabolic process	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC

GO:0046824	0.552	0.683	3	30	positive regulation of nucleocytoplasmic	BP	1	CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0006900	0.552	0.73	2	21	vesicle budding from membrane	BP	1	INSIG1,PREB	down_ACOR_VSMC
GO:0048016	0.552	0.731	2	19	inositol phosphate-mediated signaling	BP	1	C28H10orf71,EDN1	up_ACOR_VSMC
GO:0006810	0.552	0.745	2	1244	transport	BP	1	TLR2,SLC16A12	up_AFEM_VSMC
GO:0002381	0.552	0.732	2	19	immunoglobulin production involved in immunoglobulin	BP	1	THOC1,SWAP70	up_VCAV_EC
GO:0021872	0.552	0.731	2	19	forebrain generation of neurons	BP	1	PROX1,RAPGEF2	up_VCAV_EC
GO:0043009	0.552	0.723	2	227	chordate embryonic development	BP	1	HOXA3,ACVR2A	up_VPOR_EC
GO:0007010	0.552	0.726	2	441	cytoskeleton organization	BP	1	CDC42EP5,MTSS1	up_VFEM_EC
GO:0000096	0.552	0.825	1	9	sulfur amino acid metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0032732	0.552	0.825	1	9	positive regulation of interleukin-1 production	BP	1	HMGB1	down_ACOR_VSMC
GO:0032728	0.552	0.818	1	16	positive regulation of interferon-beta	BP	1	MAVS	down_VCAV_EC
GO:0033962	0.552	0.82	1	12	cytoplasmic mRNA processing body assembly	BP	1	CNOT7	down_VSAP_EC
GO:0045911	0.552	0.82	1	12	positive regulation of DNA recombination	BP	1	TFRC	down_VSAP_EC
GO:0070528	0.552	0.819	1	13	protein kinase C signaling	BP	1	VEGFA	down_VSAP_EC
GO:2000514	0.552	0.819	1	13	regulation of CD4-positive, alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:0009966	0.552	0.833	1	868	regulation of signal transduction	BP	1	GATA5	down_VSAP_VSMC
GO:0044273	0.552	0.827	1	8	sulfur compound catabolic process	BP	1	PCYOX1	up_ACOR_VSMC
GO:0045923	0.552	0.826	1	8	positive regulation of fatty acid metabolic process	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0072074	0.552	0.827	1	8	kidney mesenchyme development	BP	1	BMP4	up_ACOR_VSMC
GO:0043280	0.552	0.813	1	33	positive regulation of cysteine-type endopeptidase activity	BP	1	F3	up_AFEM_EC
GO:0071514	0.552	0.827	1	8	genetic imprinting	BP	1	ARID4B	up_VCAV_EC
GO:0045671	0.552	0.827	1	8	negative regulation of osteoclast differentiation	BP	1	TJP2	up_VCAV_EC
GO:0046685	0.552	0.823	1	10	response to arsenic-containing substance	BP	1	MAPK13	up_VCAV_EC
GO:0033993	0.552	0.814	1	186	response to lipid	BP	1	CYP26B1	up_VFEM_EC
GO:0071498	0.552	0.827	1	8	cellular response to fluid shear stress	BP	1	ASS1	up_VSAP_EC
GO:0048512	0.552	0.827	1	8	circadian behavior	BP	1	NCOA2	up_VSAP_EC
GO:2000113	0.553	0.543	19	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	NAB2,KANK2,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,ZFP36L1,LOXL3,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0051962	0.553	0.574	11	112	positive regulation of nervous system	BP	1	BMP4,WASF3,ZNF365,NRP1,SMARCD3,SLITRK5,FZD3,APP,PSEN1,DISC1,CRKL	up_ACOR_VSMC
GO:0043412	0.553	0.585	10	1225	macromolecule modification	BP	1	OSTC,OGA,ARHGEF2,ASPN,ACVR2A,KLHL28,PUM3,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0048731	0.553	0.586	10	1247	system development	BP	1	C3AR1,BARX1,HOOK3,HOXA3,ARHGEF2,SEMA3A,ASPN,ACVR2A,MTDH,RNF6	up_VPOR_EC
GO:0051347	0.553	0.584	9	182	positive regulation of transferase activity	BP	1	PDGFRB,PRNP,LMO4,CSPG4,SASH1,MAPRE3,DDR2,SHC1,GREM1	down_VCAV_EC
GO:0060255	0.553	0.62	7	1782	regulation of macromolecule metabolic	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0051171	0.553	0.632	6	1697	regulation of nitrogen compound metabolic	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0030900	0.553	0.628	5	101	forebrain development	BP	1	BMPR1A,NUMBL,PEX5,GLI3,CDH2	down_VCAV_EC
GO:0071346	0.553	0.652	4	41	cellular response to interferon-gamma	BP	1	DAPK1,EVL,PARP9,CCL5	up_ACOR_VSMC
GO:0031325	0.553	0.657	4	914	positive regulation of cellular metabolic process	BP	1	EYA1,HOXA9,MAP2K6,SIX1	up_VFEM_EC
GO:0007286	0.553	0.681	3	34	spermatid development	BP	1	TRIP13,HMGB2,TTLL1	down_ACOR_VSMC
GO:1903169	0.553	0.681	3	34	regulation of calcium ion transmembrane transport	BP	1	GSTO1,CORO1A,REM1	down_ACOR_VSMC

GO:0050773	0.553	0.683	3	29	regulation of dendrite development	BP	1	PSEN1,SIPA1L1,ASAP1	up_ACOR_VSMC
GO:0035295	0.553	0.678	3	356	tube development	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0010923	0.553	0.683	3	30	negative regulation of phosphatase activity	BP	1	SH2D4A,TMEM225B,BAG4	up_VSAP_EC
GO:0072171	0.553	0.683	3	30	mesonephric tubule morphogenesis	BP	1	HOXA11,WNT11,OSR1	up_VSAP_EC
GO:0051341	0.553	0.729	2	22	regulation of oxidoreductase activity	BP	1	CAV1,NUS1	down_ACOR_VSMC
GO:0007417	0.553	0.721	2	235	central nervous system development	BP	1	HOOK3,SEMA3A	up_VPOR_EC
GO:0032735	0.553	0.824	1	9	positive regulation of interleukin-12 production	BP	1	HMGB1	down_ACOR_VSMC
GO:0036474	0.553	0.823	1	9	cell death in response to hydrogen peroxide	BP	1	SIGMAR1	down_ACOR_VSMC
GO:0046676	0.553	0.824	1	9	negative regulation of insulin secretion	BP	1	SREBF1	down_ACOR_VSMC
GO:0097035	0.553	0.824	1	9	regulation of membrane lipid distribution	BP	1	PRELID1	down_ACOR_VSMC
GO:0033013	0.553	0.817	1	15	tetrapyrrole metabolic process	BP	1	UROS	down_VCAV_EC
GO:0043392	0.553	0.817	1	16	negative regulation of DNA binding	BP	1	CLSTN1	down_VCAV_EC
GO:0045913	0.553	0.818	1	15	positive regulation of carbohydrate metabolic	BP	1	AKT2	down_VCAV_EC
GO:0021517	0.553	0.82	1	12	ventral spinal cord development	BP	1	VLDLR	down_VSAP_EC
GO:0048745	0.553	0.826	1	8	smooth muscle tissue development	BP	1	BMP4	up_ACOR_VSMC
GO:2001024	0.553	0.826	1	8	negative regulation of response to drug	BP	1	PARK7	up_ACOR_VSMC
GO:0000278	0.553	0.816	1	331	mitotic cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0003159	0.553	0.824	1	9	morphogenesis of an endothelium	BP	1	DLL4	up_VCAV_EC
GO:0061154	0.553	0.824	1	9	endothelial tube morphogenesis	BP	1	DLL4	up_VCAV_EC
GO:0009725	0.553	0.813	1	188	response to hormone	BP	1	AVPR1A	up_VFEM_EC
GO:0070647	0.553	0.815	1	311	protein modification by small protein conjugation	BP	1	EYA1	up_VFEM_VSMC
GO:0030318	0.553	0.826	1	8	melanocyte differentiation	BP	1	HPS4	up_VSAP_EC
GO:0002076	0.553	0.826	1	8	osteoblast development	BP	1	LIMD1	up_VSAP_EC
GO:1990126	0.553	0.826	1	8	retrograde transport, endosome to plasma	BP	1	RAB11B	up_VSAP_EC
GO:0046456	0.553	0.826	1	8	icosanoid biosynthetic process	BP	1	PTGES	up_VSAP_EC
GO:0090087	0.553	0.812	1	185	regulation of peptide transport	BP	1	TLR2	up_VSAP_VSMC
GO:0002821	0.553060516	0.81254	1	30	positive regulation of adaptive immune	BP	1	FZD5	up_ACOR_EC
GO:0031099	0.553507675	0.81218	1	30	regeneration	BP	1	RGMA	up_ACOR_EC
GO:0021675	0.55364582	0.81224	1	29	nerve development	BP	1	NRP1	up_ACOR_EC
GO:0060255	0.554	0.518	42	1782	regulation of macromolecule metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ACACB,PPARGC1A,CCL5,CTIF,ADAM17,SAMD4B,TNC	up_AFEM_EC
GO:0070925	0.554	0.532	24	293	organelle assembly	BP	1	PLK2,MEF2C,EDN1,RAB11A,RALB,TMOD1,NECTIN2,CNOT6,MZT1,PROX1,SH3GLB1,CENPC,EXOC5,SENP6,PAN3,CNOT7,LSM14A,IQUB,HAUS3,SPATA6,TMOD3,FSCN1,FBXO5,SASS6	up_VCAV_EC
GO:0002683	0.554	0.568	12	126	negative regulation of immune system process	BP	1	TMEM176B,TMEM176A,BMP4,ELF1,PDE5A,CD274,F2RL1,PTPN22,DUSP22,WASL,PAG1,TAPBPL	up_ACOR_VSMC
GO:0044265	0.554	0.576	10	423	cellular macromolecule catabolic process	BP	1	CTSS,TENT5C,CLEC16A,CYLD,RAB7A,AXIN2,CTIF,FAP,SAMD4B,RNF181	up_AFEM_EC
GO:0016042	0.554	0.628	5	80	lipid catabolic process	BP	1	SESN2,PLCL1,APOE,ABHD5,YWHAH	down_VSAP_EC
GO:0016579	0.554	0.632	5	49	protein deubiquitination	BP	1	ZRANB1,USP53,USP20,WDR48,PARK7	up_ACOR_VSMC

GO:0031099	0.554	0.682	3	30	regeneration	BP	1	SULF2,RTN4RL1,MAP2K2	up_VSAP_EC
GO:0002687	0.554	0.723	2	36	positive regulation of leukocyte migration	BP	1	THY1,RAC2	down_VCAV_EC
GO:0000187	0.554	0.725	2	28	activation of MAPK activity	BP	1	PTPN11,MADD	down_VSAP_EC
GO:0043154	0.554	0.727	2	23	negative regulation of cysteine-type endopeptidase activity	BP	1	PAK2,PTGS2	up_VCAV_EC
GO:0034622	0.554	0.724	2	421	cellular protein-containing complex assembly	BP	1	TRIM9,CDC42EP5	up_VFEM_EC
GO:0048016	0.554	0.729	2	19	inositol phosphate-mediated signaling	BP	1	TBC1D10C,PPP3CB	up_VSAP_EC
GO:0006163	0.554	0.811	1	174	purine nucleotide metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0036297	0.554	0.823	1	9	interstrand cross-link repair	BP	1	RAD51	down_ACOR_VSMC
GO:0086004	0.554	0.821	1	10	regulation of cardiac muscle cell contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0006721	0.554	0.817	1	14	terpenoid metabolic process	BP	1	RDH11	down_VSAP_EC
GO:0031268	0.554	0.823	1	9	pseudopodium organization	BP	1	F2RL1	up_ACOR_VSMC
GO:0031269	0.554	0.823	1	9	pseudopodium assembly	BP	1	F2RL1	up_ACOR_VSMC
GO:2001028	0.554	0.825	1	8	positive regulation of endothelial cell	BP	1	FGF18	up_ACOR_VSMC
GO:0030162	0.554	0.812	1	202	regulation of proteolysis	BP	1	PCSK1N	up_APUL_EC
GO:0070734	0.554	0.823	1	9	histone H3-K27 methylation	BP	1	GATA3	up_VCAV_EC
GO:0090185	0.554	0.821	1	10	negative regulation of kidney development	BP	1	GATA3	up_VCAV_EC
GO:0090344	0.554	0.825	1	8	negative regulation of cell aging	BP	1	ABL1	up_VSAP_EC
GO:2001024	0.554	0.825	1	8	negative regulation of response to drug	BP	1	OSR1	up_VSAP_EC
GO:1904467	0.554	0.825	1	8	regulation of tumor necrosis factor secretion	BP	1	MAVS	up_VSAP_EC
GO:0006950	0.554445485	0.52702	29	1102	response to stress	BP	1	NR1H4,BRSK1,PCSK1N,FNDC4,AQP1,EDEM2,FZD5,NOD2,IL33,RGMA,SMAD6,PAK3,GUCY1B1,TRIM8,TNFRSF19,PTGER4,MAPK8IP2,MAVS,FOXC2,FIGNL1,IFIT2,CLSTN1,SH3RF3,CLU,RARRES2,AGBL5,PRKACA,HM13,PRKCD	up_ACOR_EC
GO:0046632	0.554551557	0.81153	1	29	alpha-beta T cell differentiation	BP	1	PTGER4	up_ACOR_EC
GO:0007399	0.554915855	0.55336	15	564	nervous system development	BP	1	SH3TC2,BRSK1,SOX9,NDRG2,AQP1,SEMA6D,DIXDC1,RGMA,PAK3,DCLK2,MAPK8IP2,LRP4,NRP1,PYGO2,DBNDD2	up_ACOR_EC
GO:0008150	0.555	0.49	455	5646	biological_process	BP	1	GNGT2,ACKR1,EPHB1,PLK2,EDNRB,HOXB7,TEK,RASGRP3,HCLS1,PCDH12,IL7R,GBP5,NPR1,ADGRF5,SELP,ST8SIA6,RGS16,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PANK3,F8,PTCHD1,PRKCH,ARHGEF15,IFRD1,LAPTM5,SHE,CP,CXCR4,EMCN,OSBPL9,FGD5,FRMD4B,ENSCAFG00000007112,DOCK4,CLEC14A,IL6,CALCRL,FLI1,TIE1,CDA,TNFAIP3,PCDH1,ADAMTS9,PPARG,ADGRL2,MAP3K11,ATP8A1,TNIP1,LRRC8D,MX2,AMOT,PDGFB,BCL6B,P2RX7,MALL,KIF21B,PODXL,STK10,SH2D3C,BAIAP2L1,TMEM173,DSC2,ATP2B1,TSPAN8,EXOC3L2,RELN,VWF,CD34,ST6GAL1,SELL,FGD6,CTSC,LAMC2,KDR,CXHXorf36,PDE4D,MOV10,IWS1,OCLN,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,SLC35A3,TLR4,NOS3,NLRC5,QKI,LYVE1,GPR4,TSPAN15,STC1,CDH5,EIF2B2,GK5,ESAM,GATA3,MMP28,USP33,COL4A5,EDN1,HOXB8,RAB11A,RALB,KIF3C,APLNR,ARAP3,RAB27A,TCF4,SLC39A8,SMAD1,EXOC6,CTTNBP2NL,NTN4,SNCAIP,FOXN2,MEOX1,HOMER3,SLC49A3,PIPOX,PTGS1,TNFAIP8,TFPI,ENSCAFG00000017103,ZDHHC22,IGSF3,PSME4,ENSCAFG00000003530,NEDD9,IRF8,SNAP91,SLCO2A1,ARHGAP28,SOX18,PIK3C2A,TMOD1,EGFL7,FIGNL1,PELI1,PPP3CA,NASP,PTPRB,SERIN	up_VCAV_EC
GO:0009895	0.555	0.585	9	94	negative regulation of catabolic process	BP	1	AXIN2,ACACB,TENT5C,POLDIP2,AZIN2,TIMP2,HTRA2,HMOX1,DDIT4	up_VSAP_EC
GO:0055074	0.555	0.592	8	95	calcium ion homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC

GO:1902105	0.555	0.627	5	80	regulation of leukocyte differentiation	BP	1	SOCS5,PTPN2,EVI2B,CTNNB1,LYN	down_VSAP_EC
GO:0051716	0.555	0.765	2	2001	cellular response to stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC
GO:0070302	0.555	0.719	2	78	regulation of stress-activated protein kinase	BP	1	LEP,CYLD	up_AFEM_EC
GO:0072666	0.555	0.728	2	21	establishment of protein localization to vacuole	BP	1	TNFAIP3,GCC2	up_VCAV_EC
GO:0001885	0.555	0.729	2	19	endothelial cell development	BP	1	F2RL1,MYD88	up_VSAP_EC
GO:0031648	0.555	0.728	2	19	protein destabilization	BP	1	PEX2,FBXO4	up_VSAP_EC
GO:0016477	0.555	0.723	2	426	cell migration	BP	1	EMX2,CAV1	up_VSAP_VSMC
GO:1901616	0.555	0.815	1	15	organic hydroxy compound catabolic	BP	1	MAOA	down_VCAV_EC
GO:1904035	0.555	0.815	1	16	regulation of epithelial cell apoptotic process	BP	1	ZFP36L1	down_VCAV_EC
GO:0070229	0.555	0.817	1	13	negative regulation of lymphocyte apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0099024	0.555	0.817	1	13	plasma membrane invagination	BP	1	MYH9	down_VSAP_EC
GO:0019048	0.555	0.824	1	8	modulation by virus of host morphology or	BP	1	DAG1	up_ACOR_VSMC
GO:0006955	0.555	0.814	1	327	immune response	BP	1	BPI	up_AORT_EC
GO:0051172	0.555	0.824	1	663	negative regulation of nitrogen compound	BP	1	ESR1	up_AORT_VSMC
GO:0065008	0.555	0.836	1	1056	regulation of biological quality	BP	1	HOXA3	up_APUL_VSMC
GO:0005975	0.555	0.811	1	183	carbohydrate metabolic process	BP	1	CHST7	up_VFEM_EC
GO:0032940	0.555	0.812	1	231	secretion by cell	BP	1	NR1H4	up_VPUL_EC
GO:0008207	0.555	0.825	1	8	C21-steroid hormone metabolic process	BP	1	DHRS9	up_VSAP_EC
GO:0001782	0.555	0.825	1	8	B cell homeostasis	BP	1	ABL1	up_VSAP_EC
GO:0033036	0.556	0.497	71	852	macromolecule localization	BP	1	ACSL3,HMGB1,SREBF1,RPA1,DDX39A,STXBP6,USP4,SREBF2,HINFP,NEDD4,ZW10,CENPA,SLC29A1,NDC1,RRBP1,TIMM44,POLA2,CTDNEP1,HSPA9,RAN,PRELID1,HM13,BIRC5,INSIG1,CAV1,CDK1,LIMA1,NF2,AURKB,MMP14,ABHD5,EZH2,FBL,PLK3,ARG2,DHCR24,ENSCAFG00000011598,PREB,TFRC,PPARD,TRAM1,NDC80,IPO4,ARHGDIA,YWHAB,NUP62,EMP2,NUP188,HASPIN,RSL1D1,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,MIOS,TTK,NOP58,KNL1,PMPCA,TINF2,MRPL18,LIPC,NUS1,CCT4,SIX4,MTBP	down_ACOR_VSMC
GO:0022008	0.556	0.514	38	406	neurogenesis	BP	1	THRB,EMX2,PEX7,CDON,WNT11,WASF3,AMIGO1,IRX5,SLIT2,HOXD3,ABL1,DLL1,KLF15,PLXNA4,PLPP3,IRX3,ZEB1,SHOX2,RTN4RL1,HOXC10,LRP4,DPYSL2,GDPD5,DAGLB,FBXO7,NTN4,NR2F6,NFIB,CYB5D2,CDNF,PQBP1,TTL,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0048522	0.556	0.573	12	1484	positive regulation of cellular process	BP	1	C3AR1,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,MTDH,ABHD5,CCAR1,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0051258	0.556	0.584	9	94	protein polymerization	BP	1	FGF13,TUBB4A,MX1,JMY,EVL,PRKCE,TTC17,FAM107A,WASL	up_ACOR_VSMC
GO:0006605	0.556	0.59	8	99	protein targeting	BP	1	SREBF1,NEDD4,TIMM44,TRAM1,YWHAB,TOMM34,SAMM50,PMPCA	down_ACOR_VSMC
GO:1901653	0.556	0.591	8	84	cellular response to peptide	BP	1	GOT1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0010467	0.556	0.617	7	1787	gene expression	BP	1	NR1H4,MAPK10,HOXA3,PCSK1N,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0070085	0.556	0.6	7	95	glycosylation	BP	1	ST8SIA6,ST6GAL1,B3GNT5,ST3GAL6,GALNT18,MFNG,TET2	up_VCAV_EC
GO:0044843	0.556	0.613	6	62	cell cycle G1/S phase transition	BP	1	FAM107A,CRADD,E2F4,FBXO7,LSM10,LATS2	up_VSAP_EC
GO:0019222	0.556	0.652	5	1934	regulation of metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0097479	0.556	0.65	4	41	synaptic vesicle localization	BP	1	FBXL20,STX11,PSEN1,PREPL	up_ACOR_VSMC
GO:0030330	0.556	0.725	2	25	DNA damage response, signal transduction by p53 class mediator	BP	1	PMAIP1,ATRX	up_VCAV_EC

GO:0008610	0.556	0.809	1	177	lipid biosynthetic process	BP	1	ACSL3	down_ACOR_EC
GO:0016578	0.556	0.821	1	9	histone deubiquitination	BP	1	BAP1	down_ACOR_VSMC
GO:0050706	0.556	0.821	1	9	regulation of interleukin-1 beta secretion	BP	1	ARG2	down_ACOR_VSMC
GO:0048546	0.556	0.815	1	16	digestive tract morphogenesis	BP	1	GLI3	down_VCAV_EC
GO:0048641	0.556	0.814	1	16	regulation of skeletal muscle tissue	BP	1	TSC22D3	down_VCAV_EC
GO:0001759	0.556	0.816	1	13	organ induction	BP	1	CTNNB1	down_VSAP_EC
GO:0032370	0.556	0.816	1	13	positive regulation of lipid transport	BP	1	APOE	down_VSAP_EC
GO:1904292	0.556	0.816	1	13	regulation of ERAD pathway	BP	1	USP14	down_VSAP_EC
GO:0031018	0.556	0.824	1	8	endocrine pancreas development	BP	1	BMP4	up_ACOR_VSMC
GO:0060333	0.556	0.823	1	8	interferon-gamma-mediated signaling	BP	1	PARP9	up_ACOR_VSMC
GO:0006357	0.556	0.82	1	547	regulation of transcription by RNA polymerase II	BP	1	GATA5	up_VCAV_VSMC
GO:0010562	0.556	0.813	1	312	positive regulation of phosphorus metabolic	BP	1	ANKRD6	up_VPOR_VSMC
GO:0045937	0.556	0.813	1	312	positive regulation of phosphate metabolic	BP	1	ANKRD6	up_VPOR_VSMC
GO:0015807	0.556	0.823	1	8	L-amino acid transport	BP	1	CTNS	up_VSAP_EC
GO:0035162	0.556	0.824	1	8	embryonic hemopoiesis	BP	1	TGFBR2	up_VSAP_EC
GO:0072074	0.556	0.823	1	8	kidney mesenchyme development	BP	1	OSR1	up_VSAP_EC
GO:0097094	0.556	0.824	1	8	craniofacial suture morphogenesis	BP	1	INSIG2	up_VSAP_EC
GO:1902894	0.556	0.823	1	8	negative regulation of pri-miRNA transcription by RNA polymerase II	BP	1	NFIB	up_VSAP_EC
GO:0001817	0.556	0.81	1	182	regulation of cytokine production	BP	1	TLR2	up_VSAP_VSMC
GO:0051173	0.556104833	0.53359	23	874	positive regulation of nitrogen compound metabolic process	BP	1	NR1H4,GATA4,PKIB,SOX9,ENSCAFG00000004331,EDEM2,FZD5,DUSP26,RASL11A,NOD2,SMAD6,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,TP53INP2,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0006367	0.556641958	0.8094	1	32	transcription initiation from RNA polymerase II	BP	1	CLSTN1	up_ACOR_EC
GO:0030097	0.557	0.562	12	244	hemopoiesis	BP	1	NOTCH2,FBN1,TFE3,CLSTN1,GLI3,EEF2,ZFP36L1,LOXL3,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0031323	0.557	0.616	7	1788	regulation of cellular metabolic process	BP	1	NR1H4,PLCL1,PCSK1N,LZTS1,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0010468	0.557	0.637	5	1270	regulation of gene expression	BP	1	NR1H4,MAPK10,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0043123	0.557	0.648	4	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	IRAK1,MTDH,NUP62,CTH	down_ACOR_VSMC
GO:0034329	0.557	0.673	3	60	cell junction assembly	BP	1	RHOD,THY1,GREM1	down_VCAV_EC
GO:0031122	0.557	0.725	2	21	cytoplasmic microtubule organization	BP	1	PLK3,EZR	down_ACOR_VSMC
GO:0007165	0.557	0.749	2	1496	signal transduction	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0055094	0.557	0.821	1	9	response to lipoprotein particle	BP	1	SREBF2	down_ACOR_VSMC
GO:0030163	0.557	0.814	1	365	protein catabolic process	BP	1	USP33	down_AFEM_EC
GO:0007035	0.557	0.814	1	16	vacuolar acidification	BP	1	ATP6V0C	down_VCAV_EC
GO:2001057	0.557	0.813	1	16	reactive nitrogen species metabolic process	BP	1	SUOX	down_VCAV_EC
GO:0000212	0.557	0.826	1	7	meiotic spindle organization	BP	1	ATRX	up_ACOR_VSMC
GO:0035313	0.557	0.825	1	7	wound healing, spreading of epidermal cells	BP	1	RREB1	up_ACOR_VSMC
GO:0008283	0.557	0.819	1	545	cell proliferation	BP	1	EYA1	up_AFEM_VSMC
GO:0060284	0.557	0.81	1	212	regulation of cell development	BP	1	NTRK2	up_APUL_EC
GO:0010518	0.557	0.821	1	9	positive regulation of phospholipase activity	BP	1	SELE	up_VCAV_EC

GO:0050982	0.557	0.821	1	9	detection of mechanical stimulus	BP	1	KIT	up_VCAV_EC
GO:0070085	0.557	0.808	1	95	glycosylation	BP	1	OSTC	up_VPOR_EC
GO:0009792	0.557	0.81	1	231	embryo development ending in birth or egg	BP	1	HOXA3	up_VPUL_EC
GO:0045923	0.557	0.823	1	8	positive regulation of fatty acid metabolic process	BP	1	C1QTNF2	up_VSAP_EC
GO:0050685	0.557	0.823	1	8	positive regulation of mRNA processing	BP	1	NUP98	up_VSAP_EC
GO:0032331	0.557	0.823	1	8	negative regulation of chondrocyte	BP	1	RARG	up_VSAP_EC
GO:0061037	0.557	0.823	1	8	negative regulation of cartilage development	BP	1	RARG	up_VSAP_EC
GO:0090103	0.557	0.823	1	8	cochlea morphogenesis	BP	1	ZEB1	up_VSAP_EC
GO:0033993	0.55722651	0.62309	5	186	response to lipid	BP	1	NR1H4,AQP1,PTGIR,NOD2,PTGER4	up_ACOR_EC
GO:0015718	0.557804659	0.80878	1	30	monocarboxylic acid transport	BP	1	CFI	up_ACOR_EC
GO:0098609	0.558	0.544	17	181	cell-cell adhesion	BP	1	PCDH19,SERPINB8,CD274,LIMS2,CDH1,ABL1,CLDN1,ZBTB16,PLPP3,ZFP36L1,CD83,PNP,AS S1,FLOT1,NCK1,TGFBR2,CITED2	up_VSAP_EC
GO:0048667	0.558	0.559	13	140	cell morphogenesis involved in neuron	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,NFI B,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0098655	0.558	0.568	11	142	cation transmembrane transport	BP	1	RELN,PDE4D,MEF2C,CHD7,APLNR,SLC39A8,K CNJ3,KCNJ2,SLC25A25,PLCG2,MCU	up_VCAV_EC
GO:0071407	0.558	0.588	8	129	cellular response to organic cyclic compound	BP	1	SMARCA4,MSN,CTNNB1,UBA5,REST,PAK2,Y WHAH,KDM3A	down_VSAP_EC
GO:0019058	0.558	0.611	6	64	viral life cycle	BP	1	USP6NL,MX1,ISG15,CTSB,ATG16L2,INPP5K	up_ACOR_VSMC
GO:0019538	0.558	0.627	6	1713	protein metabolic process	BP	1	NR1H4,STK32B,CCL24,PTGER2,FLRT3,ARHGE F2	up_VPUL_EC
GO:0016053	0.558	0.624	5	97	organic acid biosynthetic process	BP	1	UROS,THNSL2,PARK7,RDH10,GLS2	down_VCAV_EC
GO:0046394	0.558	0.624	5	97	carboxylic acid biosynthetic process	BP	1	UROS,THNSL2,PARK7,RDH10,GLS2	down_VCAV_EC
GO:0071356	0.558	0.673	3	57	cellular response to tumor necrosis factor	BP	1	ZFP36L1,GSDME,FOXO3	down_VCAV_EC
GO:0035282	0.558	0.721	2	30	segmentation	BP	1	TMED2,NRP1	down_VSAP_EC
GO:0010171	0.558	0.727	2	18	body morphogenesis	BP	1	DAG1,ARID5B	up_ACOR_VSMC
GO:0032663	0.558	0.726	2	19	regulation of interleukin-2 production	BP	1	CD83,MAP3K7	up_ACOR_VSMC
GO:0016197	0.558	0.717	2	78	endosomal transport	BP	1	BVES,RAB7A	up_AFEM_EC
GO:0042981	0.558	0.721	2	471	regulation of apoptotic process	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0051341	0.558	0.724	2	22	regulation of oxidoreductase activity	BP	1	EDN1,GCH1	up_VCAV_EC
GO:0021515	0.558	0.82	1	9	cell differentiation in spinal cord	BP	1	HOXC10	down_ACOR_VSMC
GO:0070498	0.558	0.82	1	9	interleukin-1-mediated signaling pathway	BP	1	IRAK1	down_ACOR_VSMC
GO:0010324	0.558	0.812	1	16	membrane invagination	BP	1	SNX18	down_VCAV_EC
GO:1903313	0.558	0.813	1	16	positive regulation of mRNA metabolic process	BP	1	ZFP36L1	down_VCAV_EC
GO:0002068	0.558	0.822	1	8	glandular epithelial cell development	BP	1	BMP4	up_ACOR_VSMC
GO:0014902	0.558	0.808	1	34	myotube differentiation	BP	1	DMPK	up_AFEM_EC
GO:0032366	0.558	0.822	1	8	intracellular sterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0032367	0.558	0.822	1	8	intracellular cholesterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0045577	0.558	0.82	1	9	regulation of B cell differentiation	BP	1	ATP11C	up_VCAV_EC
GO:0060135	0.558	0.818	1	10	maternal process involved in female pregnancy	BP	1	PTGS2	up_VCAV_EC
GO:0008283	0.558	0.818	1	545	cell proliferation	BP	1	TGFBI	up_VCAV_VSMC
GO:0016053	0.558	0.807	1	97	organic acid biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0046394	0.558	0.807	1	97	carboxylic acid biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0009968	0.558	0.814	1	392	negative regulation of signal transduction	BP	1	SLIT2	up_VPUL_VSMC

GO:0001893	0.558	0.822	1	8	maternal placenta development	BP	1	CITED2	up_VSAP_EC
GO:0002089	0.558	0.822	1	8	lens morphogenesis in camera-type eye	BP	1	CITED2	up_VSAP_EC
GO:0003044	0.558	0.822	1	8	regulation of systemic arterial blood pressure mediated by a chemical	BP	1	F2RL1	up_VSAP_EC
GO:0045933	0.558	0.822	1	8	positive regulation of muscle contraction	BP	1	TBXA2R	up_VSAP_EC
GO:0050884	0.558	0.822	1	8	neuromuscular process controlling posture	BP	1	FXN	up_VSAP_EC
GO:2000352	0.558	0.822	1	8	negative regulation of endothelial cell apoptotic	BP	1	ABL1	up_VSAP_EC
GO:0071071	0.558	0.822	1	8	regulation of phospholipid biosynthetic process	BP	1	IDH1	up_VSAP_EC
GO:0098657	0.558	0.808	1	181	import into cell	BP	1	CAV1	up_VSAP_VSMC
GO:0070201	0.558	0.809	1	187	regulation of establishment of protein	BP	1	TLR2	up_VSAP_VSMC
GO:0051865	0.55839457	0.80815	1	31	protein autoubiquitination	BP	1	SH3RF3	up_ACOR_EC
GO:0051170	0.558442837	0.71619	2	69	import into nucleus	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0010923	0.558782714	0.808	1	30	negative regulation of phosphatase activity	BP	1	PPP1R26	up_ACOR_EC
GO:1901135	0.559	0.512	36	390	carbohydrate derivative metabolic process	BP	1	GALNT3,GALNT10,ST3GAL5,B3GALNT2,ITM2C,B3GNT7,CCDC126,PPARGC1A,PIGN,PDE5A,PIGS,UGCG,PFKM,ADCY6,PIGG,ENPP4,MAGT1,STT3B,PTGDR,FUT11,FUT8,ENSCAFG00000018611,POMK,PSEN1,PCSK6,ALDOC,DDIT4,EOGT,NEU3,EXTL2,PFKL,NT5C2,NMNAT1,PARK7,ELOVL7,LMF1	up_ACOR_VSMC
GO:0019219	0.559	0.525	27	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,PPARGC1A,SAMD4B	up_AFEM_EC
GO:0009144	0.559	0.574	10	103	purine nucleoside triphosphate metabolic process	BP	1	COQ9,NDUFS1,ENSCAFG00000004260,FXN,GALK1,CTNS,NDUFS2,ENSCAFG00000013366,NDUFV1,DDIT4	up_VSAP_EC
GO:0008610	0.559	0.578	9	177	lipid biosynthetic process	BP	1	GPAM,LCAT,HSD3B7,SCP2,CYB5R3,THNSL2,PIGS,ORMDL3,RDH10	down_VCAV_EC
GO:0016485	0.559	0.598	7	73	protein processing	BP	1	PSEN2,ERO1B,SCG5,PSEN1,PCSK6,PERP,NCSTN	up_ACOR_VSMC
GO:0002221	0.559	0.646	4	46	pattern recognition receptor signaling	BP	1	HMGB1,IRAK1,CAV1,CACTIN	down_ACOR_VSMC
GO:0002758	0.559	0.646	4	46	innate immune response-activating signal	BP	1	HMGB1,IRAK1,CAV1,CACTIN	down_ACOR_VSMC
GO:0032990	0.559	0.641	4	167	cell part morphogenesis	BP	1	PLXNA4,CAMK2A,LRRN2,KANK1	up_AFEM_EC
GO:0030879	0.559	0.676	3	34	mammary gland development	BP	1	CAV1,B4GALT1,HOXA9	down_ACOR_VSMC
GO:0043487	0.559	0.676	3	33	regulation of RNA stability	BP	1	HNRNPD,THRAP3,FASTKD3	down_ACOR_VSMC
GO:0009749	0.559	0.676	3	34	response to glucose	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:1903670	0.559	0.677	3	30	regulation of sprouting angiogenesis	BP	1	NRP1,SYNJ2BP,PIK3C2A	up_ACOR_VSMC
GO:0070972	0.559	0.723	2	23	protein localization to endoplasmic reticulum	BP	1	INSIG1,TRAM1	down_ACOR_VSMC
GO:0017156	0.559	0.719	2	32	calcium ion regulated exocytosis	BP	1	GSK3B,REST	down_VSAP_EC
GO:0060113	0.559	0.726	2	18	inner ear receptor cell differentiation	BP	1	BMP4,SEC24B	up_ACOR_VSMC
GO:0051704	0.559	0.721	2	476	multi-organism process	BP	1	NR1H4,BPI	up_APUL_EC
GO:1901216	0.559	0.725	2	19	positive regulation of neuron death	BP	1	ABL1,MAP3K5	up_VSAP_EC
GO:0060037	0.559	0.819	1	9	pharyngeal system development	BP	1	SIX4	down_ACOR_VSMC
GO:0009948	0.559	0.812	1	16	anterior/posterior axis specification	BP	1	PCSK6	down_VCAV_EC
GO:0032655	0.559	0.811	1	16	regulation of interleukin-12 production	BP	1	MAST2	down_VCAV_EC
GO:1902883	0.559	0.812	1	16	negative regulation of response to oxidative	BP	1	PARK7	down_VCAV_EC
GO:0006414	0.559	0.812	1	15	translational elongation	BP	1	AARS	down_VSAP_EC

GO:1902894	0.559	0.822	1	8	negative regulation of pri-miRNA transcription by RNA polymerase II	BP	1	BMP4	up_ACOR_VSMC
GO:0000422	0.559	0.807	1	34	autophagy of mitochondrion	BP	1	CLEC16A	up_AFEM_EC
GO:0009749	0.559	0.807	1	34	response to glucose	BP	1	GPAM	up_AFEM_EC
GO:0032675	0.559	0.807	1	34	regulation of interleukin-6 production	BP	1	BPI	up_AFEM_EC
GO:0043244	0.559	0.808	1	34	regulation of protein complex disassembly	BP	1	CLEC16A	up_AFEM_EC
GO:0061041	0.559	0.807	1	34	regulation of wound healing	BP	1	KANK1	up_AFEM_EC
GO:0061726	0.559	0.807	1	34	mitochondrion disassembly	BP	1	CLEC16A	up_AFEM_EC
GO:0040013	0.559	0.806	1	100	negative regulation of locomotion	BP	1	SEMA3A	up_VPOR_EC
GO:0006760	0.559	0.821	1	8	folic acid-containing compound metabolic	BP	1	ENSCAFG00000013986	up_VSAP_EC
GO:2000050	0.559	0.822	1	8	regulation of non-canonical Wnt signaling	BP	1	ABL1	up_VSAP_EC
GO:0032703	0.559	0.821	1	8	negative regulation of interleukin-2 production	BP	1	HDAC7	up_VSAP_EC
GO:0050869	0.559	0.821	1	8	negative regulation of B cell activation	BP	1	TBC1D10C	up_VSAP_EC
GO:0060628	0.559	0.821	1	8	regulation of ER to Golgi vesicle-mediated	BP	1	GAS1	up_VSAP_EC
GO:0009725	0.559	0.808	1	188	response to hormone	BP	1	CAV1	up_VSAP_VSMC
GO:0033993	0.559	0.808	1	186	response to lipid	BP	1	CAV1	up_VSAP_VSMC
GO:0042552	0.559292438	0.80759	1	30	myelination	BP	1	SH3TC2	up_ACOR_EC
GO:0031325	0.559598647	0.52844	24	914	positive regulation of cellular metabolic process	BP	1	CDH3,NR1H4,GATA4,PKIB,SOX9,ENSCAFG00000004331,EDEM2,FZD5,DUSP26,RASL11A,NOD2,SMAD6,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,TP53INP2,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0031623	0.559723227	0.80709	1	31	receptor internalization	BP	1	CALY	up_ACOR_EC
GO:0051099	0.559897699	0.71479	2	70	positive regulation of binding	BP	1	PLCL1,PYGO2	up_ACOR_EC
GO:0042886	0.56	0.523	26	527	amide transport	BP	1	GPAM,SNX18,PRNP,FOLR2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,GLI3,PARK7,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0016053	0.56	0.587	8	97	organic acid biosynthetic process	BP	1	SCD,BCAT1,INSIG1,BRCA1,ELOVL1,ELOVL6,CTH,LIPC	down_ACOR_VSMC
GO:0046394	0.56	0.587	8	97	carboxylic acid biosynthetic process	BP	1	SCD,BCAT1,INSIG1,BRCA1,ELOVL1,ELOVL6,CTH,LIPC	down_ACOR_VSMC
GO:0044238	0.56	0.648	7	3383	primary metabolic process	BP	1	CST3,HDAC7,CITED2,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0009755	0.56	0.626	5	52	hormone-mediated signaling pathway	BP	1	PPARGC1B,CREBRF,PRMT2,LBH,LATS2	up_VSAP_EC
GO:0002757	0.56	0.642	4	78	immune response-activating signal	BP	1	PRNP,THY1,CYBA,RAB7B	down_VCAV_EC
GO:0031401	0.56	0.671	3	358	positive regulation of protein modification	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0051172	0.56	0.676	3	663	negative regulation of nitrogen compound	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0000726	0.56	0.723	2	21	non-recombinational repair	BP	1	POLA1,RBBP8	down_ACOR_VSMC
GO:1903363	0.56	0.718	2	32	negative regulation of cellular protein catabolic	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0065009	0.56	0.726	2	735	regulation of molecular function	BP	1	HOXA3,BAMBI	up_VPOR_VSMC
GO:0098586	0.56	0.724	2	19	cellular response to virus	BP	1	NLRX1,TKFC	up_VSAP_EC
GO:0006873	0.56	0.807	1	160	cellular ion homeostasis	BP	1	LYN	down_ACOR_EC
GO:0071417	0.56	0.807	1	142	cellular response to organonitrogen	BP	1	IGF1R	down_ACOR_EC
GO:0030206	0.56	0.818	1	9	chondroitin sulfate biosynthetic process	BP	1	XYLT1	down_ACOR_VSMC
GO:0032365	0.56	0.818	1	9	intracellular lipid transport	BP	1	NUS1	down_ACOR_VSMC
GO:0045063	0.56	0.819	1	9	T-helper 1 cell differentiation	BP	1	HMGB1	down_ACOR_VSMC

GO:1901700	0.56	0.811	1	364	response to oxygen-containing compound	BP	1	GABPA	down_AFEM_EC
GO:0017145	0.56	0.814	1	13	stem cell division	BP	1	ARHGEF2	down_VSAP_EC
GO:0071526	0.56	0.814	1	12	semaphorin-plexin signaling pathway	BP	1	NRP1	down_VSAP_EC
GO:0070296	0.56	0.82	1	8	sarcoplasmic reticulum calcium ion transport	BP	1	CHD7	up_ACOR_VSMC
GO:0071482	0.56	0.806	1	34	cellular response to light stimulus	BP	1	MFAP4	up_AFEM_EC
GO:0071887	0.56	0.807	1	34	leukocyte apoptotic process	BP	1	GPAM	up_AFEM_EC
GO:0010971	0.56	0.816	1	10	positive regulation of G2/M transition of mitotic	BP	1	RAB11A	up_VCAV_EC
GO:2000479	0.56	0.821	1	8	regulation of cAMP-dependent protein kinase	BP	1	RAPGEF2	up_VCAV_EC
GO:0006779	0.56	0.82	1	8	porphyrin-containing compound biosynthetic	BP	1	CPOX	up_VSAP_EC
GO:0006783	0.56	0.82	1	8	heme biosynthetic process	BP	1	CPOX	up_VSAP_EC
GO:0032480	0.56	0.82	1	8	negative regulation of type I interferon	BP	1	NLRX1	up_VSAP_EC
GO:0033014	0.56	0.82	1	8	tetrapyrrole biosynthetic process	BP	1	CPOX	up_VSAP_EC
GO:0086010	0.56	0.821	1	8	membrane depolarization during action potential	BP	1	TPCN2	up_VSAP_EC
GO:1902916	0.56	0.821	1	8	positive regulation of protein polyubiquitination	BP	1	FBXO4	up_VSAP_EC
GO:0044774	0.560301916	0.80678	1	30	mitotic DNA integrity checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0044057	0.56070988	0.66799	3	110	regulation of system process	BP	1	AQP1,GNAO1,RNLS	up_ACOR_EC
GO:0006366	0.561	0.501	49	583	transcription by RNA polymerase II	BP	1	ELK3,HMGB1,SREBF1,CBX5,PPRC1,ATAD2,SREBF2,NEDD4,MED17,MTDH,INSIG1,CAV1,TIMELESS,THRAP3,AURKB,EZH2,GREM1,SMARCC1,PLK3,HOXA7,UHRF1,CKS2,BRCA1,NOC2L,E2F8,PPARD,NCL,FOSL1,SUV39H1,ZNF367,HMGB2,DMAP1,CDK2,SMARCB1,EZR,RBM14,ERF,TCERG1,SMARCAL1,ELF4,PSMC1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,CDC5L,HMGN1,ENSCAFG00000017103	down_ACOR_VSMC
GO:0050867	0.561	0.595	7	83	positive regulation of cell activation	BP	1	HMGB1,CAV1,MMP14,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0030041	0.561	0.608	6	62	actin filament polymerization	BP	1	JMY,EVL,PRKCE,TTC17,FAM107A,WASL	up_ACOR_VSMC
GO:0007346	0.561	0.619	5	210	regulation of mitotic cell cycle	BP	1	GAS1,OVOL1,CYLD,DCUN1D3,FAP	up_AFEM_EC
GO:1903531	0.561	0.645	4	41	negative regulation of secretion by cell	BP	1	LEP,F2RL1,PTPN22,PFKL	up_ACOR_VSMC
GO:0022612	0.561	0.644	4	44	gland morphogenesis	BP	1	TNFAIP3,NTN4,PROX1,BTBD7	up_VCAV_EC
GO:0043039	0.561	0.674	3	33	tRNA aminoacylation	BP	1	VARS,FARSA,RARS	down_ACOR_VSMC
GO:0045931	0.561	0.671	3	49	positive regulation of mitotic cell cycle	BP	1	ASNS,PTPN11,EIF4EBP1	down_VSAP_EC
GO:1903828	0.561	0.673	3	38	negative regulation of cellular protein	BP	1	PPP2R5A,FERMT1,APOD	up_VCAV_EC
GO:2000112	0.561	0.685	3	1119	regulation of cellular macromolecule biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0015718	0.561	0.675	3	30	monocarboxylic acid transport	BP	1	SLC16A12,ABCB11,SLC27A6	up_VSAP_EC
GO:0034767	0.561	0.718	2	31	positive regulation of ion transmembrane transport	BP	1	HTT,CALM1	down_VSAP_EC
GO:0010092	0.561	0.724	2	19	specification of animal organ identity	BP	1	HOXA11,AXIN2	up_VSAP_EC
GO:0002828	0.561	0.817	1	9	regulation of type 2 immune response	BP	1	ARG2	down_ACOR_VSMC
GO:0071320	0.561	0.818	1	9	cellular response to cAMP	BP	1	EZR	down_ACOR_VSMC
GO:0086003	0.561	0.816	1	10	cardiac muscle cell contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0009048	0.561	0.818	1	9	dosage compensation by inactivation of X	BP	1	BRCA1	down_ACOR_VSMC
GO:0071495	0.561	0.811	1	365	cellular response to endogenous stimulus	BP	1	GABPA	down_AFEM_EC
GO:0046427	0.561	0.81	1	16	positive regulation of JAK-STAT cascade	BP	1	ARL2BP	down_VCAV_EC
GO:0045893	0.561	0.812	1	413	positive regulation of transcription, DNA-	BP	1	CITED2	down_VPOR_EC

GO:0045934	0.561	0.812	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	HDAC7	down_VPOR_EC
GO:0048518	0.561	0.855	1	1676	positive regulation of biological process	BP	1	MOSPD1	down_VFEM_EC
GO:2000758	0.561	0.82	1	8	positive regulation of peptidyl-lysine acetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0050851	0.561	0.806	1	34	antigen receptor-mediated signaling	BP	1	CYLD	up_AFEM_EC
GO:0110110	0.561	0.806	1	34	positive regulation of animal organ	BP	1	GREM1	up_AFEM_EC
GO:0006458	0.561	0.816	1	10	'de novo' protein folding	BP	1	SH3GLB1	up_VCAV_EC
GO:0034113	0.561	0.816	1	10	heterotypic cell-cell adhesion	BP	1	CD200	up_VCAV_EC
GO:0060986	0.561	0.816	1	10	endocrine hormone secretion	BP	1	GATA3	up_VCAV_EC
GO:0006390	0.561	0.82	1	8	mitochondrial transcription	BP	1	PPARGC1B	up_VSAP_EC
GO:0006851	0.561	0.82	1	8	mitochondrial calcium ion transmembrane transport	BP	1	SLC8B1	up_VSAP_EC
GO:0031365	0.561	0.82	1	8	N-terminal protein amino acid modification	BP	1	NAA60	up_VSAP_EC
GO:0086091	0.561	0.82	1	8	regulation of heart rate by cardiac conduction	BP	1	KCNE3	up_VSAP_EC
GO:0032620	0.561	0.82	1	8	interleukin-17 production	BP	1	MYD88	up_VSAP_EC
GO:0034767	0.561152328	0.80594	1	31	positive regulation of ion transmembrane transport	BP	1	ACTN2	up_ACOR_EC
GO:0010389	0.561272214	0.806	1	30	regulation of G2/M transition of mitotic cell	BP	1	BRSK1	up_ACOR_EC
GO:0050954	0.561445145	0.80586	1	30	sensory perception of mechanical stimulus	BP	1	USP53	up_ACOR_EC
GO:0010594	0.561868657	0.7129	2	71	regulation of endothelial cell migration	BP	1	FOXC2,NRP1	up_ACOR_EC
GO:0016477	0.562	0.506	40	426	cell migration	BP	1	EMX2,HOXA7,PEX7,TWIST2,WNT11,FAM107A,ARHGEF5,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,IL17RC,FUZ,PDGFD,HSD3B7,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,SASH1,MYD88,LIMD1,ZNF580,STX4,ZFAND5,ACVRL1,NCK1,HMOX1,TGFBR2,SAA1,BAG4	up_VSAP_EC
GO:0008283	0.562	0.52	27	545	cell proliferation	BP	1	GPAM,PDGFRB,SLC35F6,NDN,PRNP,SDC4,KANK2,BMPR1A,NUMBL,OSMR,AKT2,CLSTN1,CSPG4,ENSCAFG00000013404,B4GALT1,GLI3,ZFP36L1,MYDGF,IFT57,CDH2,GSDME,DDR2,SHC1,GREM1,RAC2,FOXO3,ZBTB16	down_VCAV_EC
GO:0010876	0.562	0.578	9	92	lipid localization	BP	1	LEP,LCAT,ABCA1,APOL6,ABCA4,SCP2,OSBPL1A,PLIN2,CFI	up_ACOR_VSMC
GO:0009126	0.562	0.584	8	100	purine nucleoside monophosphate metabolic process	BP	1	CDK1,PFAS,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0009167	0.562	0.584	8	100	purine ribonucleoside monophosphate metabolic process	BP	1	CDK1,PFAS,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D,NUDT3	down_ACOR_VSMC
GO:0045637	0.562	0.596	7	73	regulation of myeloid cell differentiation	BP	1	RASSF2,ISG15,FAM210B,P4HTM,CLSTN1,B2M,CNOT4	up_ACOR_VSMC
GO:0090130	0.562	0.604	6	121	tissue migration	BP	1	DCN,GLIPR2,KANK2,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0071216	0.562	0.608	6	61	cellular response to biotic stimulus	BP	1	TLR1,ABCA1,SASH1,ANKRD1,PRKCE,NOD2	up_ACOR_VSMC
GO:0043066	0.562	0.604	6	253	negative regulation of apoptotic process	BP	1	ANGPT4,DLL1,CRYAB,GPAM,GREM1,PPARGC1A	up_AFEM_EC
GO:0016525	0.562	0.715	2	38	negative regulation of angiogenesis	BP	1	DCN,SPRED1	down_VCAV_EC
GO:2000181	0.562	0.715	2	38	negative regulation of blood vessel	BP	1	DCN,SPRED1	down_VCAV_EC
GO:0007006	0.562	0.716	2	35	mitochondrial membrane organization	BP	1	BNIP3,SH3GLB1	down_VSAP_EC
GO:0014033	0.562	0.717	2	30	neural crest cell differentiation	BP	1	HIF1A,NRP1	down_VSAP_EC
GO:0001885	0.562	0.723	2	19	endothelial cell development	BP	1	ARHGEF26,F2RL1	up_ACOR_VSMC
GO:0051049	0.562	0.718	2	479	regulation of transport	BP	1	NR1H4,HOXA3	up_APUL_EC
GO:0071621	0.562	0.718	2	27	granulocyte chemotaxis	BP	1	CXCL8,PDE4D	up_VCAV_EC
GO:0009792	0.562	0.713	2	231	embryo development ending in birth or egg	BP	1	HOXA3,ACVR2A	up_VPOR_EC

GO:0044093	0.562	0.717	2	437	positive regulation of molecular function	BP	1	MAP2K6,TIAM1	up_VFEM_EC
GO:0006614	0.562	0.815	1	10	SRP-dependent cotranslational protein	BP	1	TRAM1	down_ACOR_VSMC
GO:0008053	0.562	0.815	1	10	mitochondrial fusion	BP	1	CHCHD3	down_ACOR_VSMC
GO:1905276	0.562	0.817	1	9	regulation of epithelial tube formation	BP	1	SIX4	down_ACOR_VSMC
GO:0007589	0.562	0.81	1	16	body fluid secretion	BP	1	CYBA	down_VCAV_EC
GO:0001755	0.562	0.81	1	16	neural crest cell migration	BP	1	SEMA3C	down_VCAV_EC
GO:1900117	0.562	0.819	1	8	regulation of execution phase of apoptosis	BP	1	FZD3	up_ACOR_VSMC
GO:0006915	0.562	0.815	1	550	apoptotic process	BP	1	EYA1	up_AFEM_VSMC
GO:0006811	0.562	0.809	1	330	ion transport	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0042474	0.562	0.814	1	11	middle ear morphogenesis	BP	1	EDN1	up_VCAV_EC
GO:0042060	0.562	0.804	1	103	wound healing	BP	1	SLC7A11	up_VPOR_EC
GO:0001573	0.562	0.819	1	8	ganglioside metabolic process	BP	1	B3GALT4	up_VSAP_EC
GO:0010447	0.562	0.819	1	8	response to acidic pH	BP	1	RAB11B	up_VSAP_EC
GO:0031571	0.562	0.819	1	8	mitotic G1 DNA damage checkpoint	BP	1	CRADD	up_VSAP_EC
GO:0043029	0.562	0.819	1	8	T cell homeostasis	BP	1	PPP3CB	up_VSAP_EC
GO:0043928	0.562	0.819	1	8	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-	BP	1	EXOSC7	up_VSAP_EC
GO:0044783	0.562	0.819	1	8	G1 DNA damage checkpoint	BP	1	CRADD	up_VSAP_EC
GO:0044819	0.562	0.819	1	8	mitotic G1/S transition checkpoint	BP	1	CRADD	up_VSAP_EC
GO:2000515	0.562	0.819	1	8	negative regulation of CD4-positive, alpha-beta T cell activation	BP	1	CD274	up_VSAP_EC
GO:0031629	0.562	0.819	1	8	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	STX4	up_VSAP_EC
GO:0045662	0.562	0.819	1	8	negative regulation of myoblast differentiation	BP	1	DLL1	up_VSAP_EC
GO:0099500	0.562	0.819	1	8	vesicle fusion to plasma membrane	BP	1	STX4	up_VSAP_EC
GO:0002705	0.562175292	0.80511	1	31	positive regulation of leukocyte mediated	BP	1	FZD5	up_ACOR_EC
GO:0055082	0.562671712	0.61764	5	189	cellular chemical homeostasis	BP	1	NR1H4,PTH1R,KCNB1,SLC9A9,PRKACA	up_ACOR_EC
GO:0002443	0.562788798	0.71205	2	71	leukocyte mediated immunity	BP	1	FZD5,PRKCD	up_ACOR_EC
GO:0009166	0.562948508	0.80449	1	31	nucleotide catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0042221	0.563	0.499	50	1012	response to chemical	BP	1	PCOLCE,GPAM,PDGFRB,SMAD9,LRP1,DCN,NDN,PRNP,MT2A,FOLR2,VASN,FBN1,ADCY6,BGN,SLC10A3,KANK2,COL6A1,NUMBL,ENSCAFG00000014978,AKT1S1,CHRDL1,TIMP2,AKT2,NR3C1,HSD3B7,ENSCAFG00000013404,EPHX1,ANXA11,TMEM161A,GFPT2,SEMA3C,ASPN,CYP1B1,GLI3,PARK7,ZFP36L1,SASH1,MAVS,MPV17,GSDME,FUT8,RAB7B,SEC61B,RAB31,HM13,SHC1,GREM1,RAC2,FOXO3,RGMA	down_VCAV_EC
GO:0006952	0.563	0.515	30	319	defense response	BP	1	TLR1,LEP,CD83,FBXL20,COCH,MX1,HRH1,TLR3,ISG15,PLAC8B,F2RL1,DAPK1,BNIP3,C1S,CLSTN1,PTPN22,EVL,PTGDR,PRKCE,PARP9,APP,PSEN1,CCL5,NOD2,DDIT4,JAM3,SERINC3,TNFRSF11B,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0031400	0.563	0.541	16	205	negative regulation of protein modification process	BP	1	TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,CDYL,HMG20A,HHEX,PREX2,SH3BP5,SWAP70,NCK1,KDM5A,KDM3A,IVNS1ABP	up_VCAV_EC
GO:0032535	0.563	0.558	12	128	regulation of cellular component size	BP	1	PRR16,SLIT2,ABL1,CDC42EP5,PLXNA4,CDC42EP2,F2RL1,DPYSL2,E2F4,TTL,NCK1,BAG4	up_VSAP_EC
GO:0009199	0.563	0.583	8	100	ribonucleoside triphosphate metabolic	BP	1	RAN,CDK1,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,CTPS1,ATP5F1D	down_ACOR_VSMC

GO:0043122	0.563	0.606	6	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	HTR2B,TLR3,F2RL1,PRKCE,NOD2,MAP3K7	up_ACOR_VSMC
GO:0048839	0.563	0.622	5	50	inner ear development	BP	1	BMP4,FGFR2,SEC24B,FZD3,CHD7	up_ACOR_VSMC
GO:0042221	0.563	0.648	4	1012	response to chemical	BP	1	NR1H4,SLITRK5,NPNT,NTRK2	up_APUL_EC
GO:0060021	0.563	0.672	3	34	roof of mouth development	BP	1	INSIG1,SGPL1,MSC	down_ACOR_VSMC
GO:0010822	0.563	0.673	3	31	positive regulation of mitochondrion	BP	1	PPARGC1A,MARCH5,BNIP3	up_ACOR_VSMC
GO:0030316	0.563	0.673	3	31	osteoclast differentiation	BP	1	PPARGC1B,PIK3R1,TFE3	up_VSAP_EC
GO:0051279	0.563	0.722	2	19	regulation of release of sequestered calcium ion into cytosol	BP	1	PRKCE,CHD7	up_ACOR_VSMC
GO:0031668	0.563	0.712	2	79	cellular response to extracellular stimulus	BP	1	CLEC16A,POSTN	up_AFEM_EC
GO:0006984	0.563	0.722	2	19	ER-nucleus signaling pathway	BP	1	INSIG2,NCK1	up_VSAP_EC
GO:0045599	0.563	0.722	2	19	negative regulation of fat cell differentiation	BP	1	ZADH2,ZFP36L2	up_VSAP_EC
GO:0046939	0.563	0.721	2	19	nucleotide phosphorylation	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0015909	0.563	0.809	1	16	long-chain fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:0034314	0.563	0.809	1	16	Arp2/3 complex-mediated actin nucleation	BP	1	ACTR3B	down_VCAV_EC
GO:0042073	0.563	0.808	1	16	intraciliary transport	BP	1	IFT57	down_VCAV_EC
GO:0010648	0.563	0.81	1	407	negative regulation of cell communication	BP	1	HDAC7	down_VPOR_EC
GO:1902680	0.563	0.81	1	415	positive regulation of RNA biosynthetic process	BP	1	CITED2	down_VPOR_EC
GO:1903508	0.563	0.81	1	415	positive regulation of nucleic acid-templated	BP	1	CITED2	down_VPOR_EC
GO:0045843	0.563	0.811	1	13	negative regulation of striated muscle tissue	BP	1	SIX4	down_VSAP_EC
GO:0050710	0.563	0.811	1	13	negative regulation of cytokine secretion	BP	1	NR1H4	down_VSAP_EC
GO:2000171	0.563	0.819	1	8	negative regulation of dendrite development	BP	1	ASAP1	up_ACOR_VSMC
GO:0019216	0.563	0.803	1	101	regulation of lipid metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:0072521	0.563	0.804	1	185	purine-containing compound metabolic	BP	1	ADCY3	up_VFEM_EC
GO:0006974	0.563	0.808	1	333	cellular response to DNA damage stimulus	BP	1	EYA1	up_VFEM_VSMC
GO:0051050	0.563	0.806	1	235	positive regulation of transport	BP	1	NR1H4	up_VPUL_EC
GO:0002446	0.563	0.819	1	8	neutrophil mediated immunity	BP	1	F2RL1	up_VSAP_EC
GO:0015937	0.563	0.819	1	8	coenzyme A biosynthetic process	BP	1	DCAKD	up_VSAP_EC
GO:0030851	0.563	0.818	1	8	granulocyte differentiation	BP	1	CITED2	up_VSAP_EC
GO:0032689	0.563	0.819	1	8	negative regulation of interferon-gamma	BP	1	CD274	up_VSAP_EC
GO:0050829	0.563	0.819	1	8	defense response to Gram-negative bacterium	BP	1	F2RL1	up_VSAP_EC
GO:0051817	0.563796695	0.8038	1	31	modification of morphology or physiology of other organism	BP	1	AQP1	up_ACOR_EC
GO:0010833	0.563813163	0.80395	1	30	telomere maintenance via telomere lengthening	BP	1	PKIB	up_ACOR_EC
GO:0043414	0.563864155	0.71109	2	70	macromolecule methylation	BP	1	NR1H4,PYGO2	up_ACOR_EC
GO:0071702	0.564	0.49	65	687	organic substance transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,SLC26A7,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,LCAT,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,SLC2A5,STX11,ANKRD1,F2RL1,APOL6,SLC17A5,CDKN1A,ABCA4,PTPN22,TCN2,OS9,SCP2,OSBPL1A,SLCO1A2,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,CHD7,LAMP2,JUP,CCL5,CLN8,RAB11B,EDN1,SLC25A20,NOD2,LMTK2,AP2B1,PLIN2,SCAMP5,SAR1B,HERPUD1,CFI,VPS26A,INPP5K,FAF2,RAB5C,PFKL,AZIN2,RPAIN,SLC25A12,PARK7,SLC2A12,LMF1,PTPN14	up_ACOR_VSMC

GO:0051093	0.564	0.519	26	273	negative regulation of developmental process	BP	1	TMEM176B,TMEM176A,SMAD6,LBH,ITM2C,FERMT1,BMP4,TP53INP1,ZNF365,PLAC8B,LIMS2,MARCH5,BNIP3,NRP1,ULK2,TBX5,FZD3,FRS2,APP,PSEN1,SYNJ2BP,WWC2,ASAP1,B2M,TNFRSF11B,STC2	up_ACOR_VSMC
GO:0048666	0.564	0.522	24	258	neuron development	BP	1	THRB,AMIGO1,IRX5,SLIT2,ABL1,PLXNA4,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,NTN4,NR2F6,NFIB,CDNF,PQBP1,TTL,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0006629	0.564	0.573	9	382	lipid metabolic process	BP	1	LEP,GPAM,PLAGL2,SDR42E1,RAB7A,ACACB,NAPEPLD,PPARGC1A,AGPAT2	up_AFEM_EC
GO:0060541	0.564	0.604	6	73	respiratory system development	BP	1	CHD7,HHEX,PROX1,TIMELESS,CREB1,ALDH1A3	up_VCAV_EC
GO:0030833	0.564	0.62	5	59	regulation of actin filament polymerization	BP	1	CAPG,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0010212	0.564	0.62	5	60	response to ionizing radiation	BP	1	GATA3,FIGNL1,USP28,BLM,TOPBP1	up_VCAV_EC
GO:0022898	0.564	0.641	4	48	regulation of transmembrane	BP	1	NEDD4,CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0009259	0.564	0.636	4	166	ribonucleotide metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0051607	0.564	0.667	3	58	defense response to virus	BP	1	GPAM,RNF216,MAVS	down_VCAV_EC
GO:0050896	0.564	0.714	3	2346	response to stimulus	BP	1	WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0032612	0.564	0.719	2	22	interleukin-1 production	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0007368	0.564	0.713	2	37	determination of left/right symmetry	BP	1	IFT57,PCSK6	down_VCAV_EC
GO:0042273	0.564	0.714	2	35	ribosomal large subunit biogenesis	BP	1	MRPL1,RSL24D1	down_VSAP_EC
GO:0032270	0.564	0.716	2	479	positive regulation of cellular protein metabolic	BP	1	NPNT,NTRK2	up_APUL_EC
GO:0046928	0.564	0.718	2	23	regulation of neurotransmitter	BP	1	MEF2C,SNCAIP	up_VCAV_EC
GO:0030593	0.564	0.72	2	19	neutrophil chemotaxis	BP	1	C5AR2,SLIT2	up_VSAP_EC
GO:0045646	0.564	0.72	2	19	regulation of erythrocyte differentiation	BP	1	ANKRD54,ZFP36L1	up_VSAP_EC
GO:0003416	0.564	0.816	1	9	endochondral bone growth	BP	1	POC1A	down_ACOR_VSMC
GO:0030890	0.564	0.816	1	9	positive regulation of B cell proliferation	BP	1	TFRC	down_ACOR_VSMC
GO:0035725	0.564	0.808	1	16	sodium ion transmembrane transport	BP	1	FXYD1	down_VCAV_EC
GO:0043330	0.564	0.808	1	16	response to exogenous dsRNA	BP	1	MAVS	down_VCAV_EC
GO:0070884	0.564	0.808	1	16	regulation of calcineurin-NFAT signaling cascade	BP	1	PRNP	down_VCAV_EC
GO:0106056	0.564	0.808	1	16	regulation of calcineurin-mediated signaling	BP	1	PRNP	down_VCAV_EC
GO:0062009	0.564	0.818	1	8	secondary palate development	BP	1	CHD7	up_ACOR_VSMC
GO:0090022	0.564	0.815	1	9	regulation of neutrophil chemotaxis	BP	1	JAM3	up_ACOR_VSMC
GO:0071800	0.564	0.817	1	8	podosome assembly	BP	1	FSCN1	up_VCAV_EC
GO:0097028	0.564	0.812	1	11	dendritic cell differentiation	BP	1	HMGB1	up_VCAV_EC
GO:1905276	0.564	0.815	1	9	regulation of epithelial tube formation	BP	1	GATA3	up_VCAV_EC
GO:0016072	0.564	0.802	1	102	rRNA metabolic process	BP	1	RRP15	up_VPOR_EC
GO:0051260	0.564	0.802	1	100	protein homooligomerization	BP	1	FBP1	up_VPOR_EC
GO:0062012	0.564	0.802	1	100	regulation of small molecule metabolic	BP	1	FBP1	up_VPOR_EC
GO:0001914	0.564	0.817	1	8	regulation of T cell mediated cytotoxicity	BP	1	PPP3CB	up_VSAP_EC
GO:0030497	0.564	0.818	1	8	fatty acid elongation	BP	1	HACD4	up_VSAP_EC
GO:0046174	0.564	0.817	1	8	polyol catabolic process	BP	1	INPP5E	up_VSAP_EC
GO:0048340	0.564	0.817	1	8	paraxial mesoderm morphogenesis	BP	1	WNT11	up_VSAP_EC
GO:0060055	0.564	0.818	1	8	angiogenesis involved in wound healing	BP	1	HPSE	up_VSAP_EC
GO:0030307	0.564123788	0.80354	1	31	positive regulation of cell growth	BP	1	NRP1	up_ACOR_EC

GO:0048644	0.564164019	0.8035	1	31	muscle organ morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:2001021	0.564263399	0.80359	1	30	negative regulation of response to DNA damage	BP	1	CLU	up_ACOR_EC
GO:0008277	0.564445265	0.80327	1	31	regulation of G protein-coupled receptor signaling	BP	1	RGS1	up_ACOR_EC
GO:0009968	0.565	0.506	37	392	negative regulation of signal transduction	BP	1	FZD1,WNT11,ACKR3,AXIN2,TBC1D10C,SLIT2,ABL1,HDAC7,EPN2,SESN1,F2RL1,GLIS2,MFN2,MYC,PIK3IP1,SULF2,HIC1,RTN4RL1,CREBRF,LRP4,GDPD5,CASTOR1,LIMD1,NLRX1,TKFC,FBLN1,RAF1,MAPKBP1,QARS,ARHGAP12,UBQLN2,NCK1,HMOX1,NPRL3,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0010941	0.565	0.518	26	524	regulation of cell death	BP	1	GPAM,SLC35F6,LRP1,PRNP,KANK2,CLIP3,AKT2,ENSCAFG00000013404,TMEM161A,LRPAP1,ARHGAP10,B4GALT1,GLI3,PARK7,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,ZBTB16	down_VCAV_EC
GO:0071417	0.565	0.547	14	142	cellular response to organonitrogen compound	BP	1	ACTN2,CASTOR1,ADCY6,AKAP6,UBR1,PTPN22,APLP1,SESN3,APP,PSEN1,JUP,NOD2,INPP5K,SH3BP4	up_ACOR_VSMC
GO:0007389	0.565	0.58	8	137	pattern specification process	BP	1	PRKACB,TMED2,CHSY1,HOXB7,HIF1A,CTNNB1,DDIT3,NRP1	down_VSAP_EC
GO:0006914	0.565	0.589	7	141	autophagy	BP	1	DCN,GABARAP,POLDIP2,WDR45,CLEC16A,RETREG1,EMC6	down_VCAV_EC
GO:0061919	0.565	0.589	7	141	process utilizing autophagic mechanism	BP	1	DCN,GABARAP,POLDIP2,WDR45,CLEC16A,RETREG1,EMC6	down_VCAV_EC
GO:0007050	0.565	0.62	5	53	cell cycle arrest	BP	1	TP53INP1,CDKN2B,CDKN1A,JMY,CRLF3	up_ACOR_VSMC
GO:0055123	0.565	0.642	4	40	digestive system development	BP	1	GATA5,GATA4,BMP4,FGFR2	up_ACOR_VSMC
GO:0009166	0.565	0.671	3	31	nucleotide catabolic process	BP	1	PDE5A,ALDOC,DDIT4	up_ACOR_VSMC
GO:0015718	0.565	0.671	3	30	monocarboxylic acid transport	BP	1	LEP,PLIN2,CFI	up_ACOR_VSMC
GO:0072171	0.565	0.671	3	30	mesonephric tubule morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0016043	0.565	0.7	3	1973	cellular component organization	BP	1	SLITRK5,LIMK1,TGFBI	up_VCAV_VSMC
GO:0030048	0.565	0.717	2	23	actin filament-based movement	BP	1	CAV1,EMP2	down_ACOR_VSMC
GO:0035556	0.565	0.724	2	845	intracellular signal transduction	BP	1	GPSM2,IVNS1ABP	down_AFEM_EC
GO:0097191	0.565	0.71	2	79	extrinsic apoptotic signaling pathway	BP	1	MLLT11,CYLD	up_AFEM_EC
GO:0010468	0.565	0.734	2	1270	regulation of gene expression	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0033043	0.565	0.714	2	446	regulation of organelle organization	BP	1	TRIM9,CDC42EP5	up_VFEM_EC
GO:0034766	0.565	0.72	2	19	negative regulation of ion transmembrane transport	BP	1	KCNE3,OSR1	up_VSAP_EC
GO:0032205	0.565	0.815	1	9	negative regulation of telomere maintenance	BP	1	TINF2	down_ACOR_VSMC
GO:0010830	0.565	0.807	1	16	regulation of myotube differentiation	BP	1	RBM38	down_VCAV_EC
GO:0030219	0.565	0.807	1	16	megakaryocyte differentiation	BP	1	RAB7B	down_VCAV_EC
GO:0002183	0.565	0.807	1	16	cytoplasmic translational initiation	BP	1	EIF3K	down_VCAV_EC
GO:1901570	0.565	0.808	1	16	fatty acid derivative biosynthetic process	BP	1	ACAT1	down_VCAV_EC
GO:0023057	0.565	0.809	1	409	negative regulation of signaling	BP	1	HDAC7	down_VPOR_EC
GO:0043408	0.565	0.803	1	211	regulation of MAPK cascade	BP	1	NPNT	up_APUL_EC
GO:0031399	0.565	0.813	1	559	regulation of protein modification process	BP	1	LIMK1	up_VCAV_VSMC
GO:0098542	0.565	0.802	1	100	defense response to other organism	BP	1	OAS3	up_VPOR_EC
GO:0000165	0.565	0.804	1	236	MAPK cascade	BP	1	CCL24	up_VPUL_EC
GO:0034312	0.565	0.817	1	8	diol biosynthetic process	BP	1	PCBD1	up_VSAP_EC
GO:0043248	0.565	0.817	1	8	proteasome assembly	BP	1	PSMD9	up_VSAP_EC
GO:0097201	0.565	0.817	1	8	negative regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	NCK1	up_VSAP_EC

GO:0045321	0.565	0.803	1	191	leukocyte activation	BP	1	CAV1	up_VSAP_VSMC
GO:0009719	0.566	0.504	37	395	response to endogenous stimulus	BP	1	FZD1,FAM107A,PTGFR,PPARGC1B,SLIT2,CDH1,FGF7,ABL1,GOT1,CHRM1,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,SULF2,CREBRF,MYD88,LRP4,STK16,CASTOR1,PRMT2,ZFP36L2,HPGD,NCOA2,TIMP2,ACVRL1,NCK1,BGLAP,TGFBR2,CITED2,BAG4,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0006351	0.566	0.521	25	1069	transcription, DNA-templated	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC
GO:0060541	0.566	0.592	7	73	respiratory system development	BP	1	BMP4,FGFR2,SEC24B,FGF18,TBX5,DAG1,CHD7	up_ACOR_VSMC
GO:0000086	0.566	0.619	5	52	G2/M transition of mitotic cell cycle	BP	1	CDC7,SKP2,CDKN2B,CDKN1A,APP	up_ACOR_VSMC
GO:0000302	0.566	0.619	5	52	response to reactive oxygen species	BP	1	EGLN1,SESN3,SESN1,CAT,PARK7	up_ACOR_VSMC
GO:0042770	0.566	0.669	3	35	signal transduction in response to DNA damage	BP	1	CASP2,DTL,CDC5L	down_ACOR_VSMC
GO:0003151	0.566	0.669	3	34	outflow tract morphogenesis	BP	1	MEF2C,JAG1,HIF1A	up_VCAV_EC
GO:0009892	0.566	0.674	3	835	negative regulation of metabolic process	BP	1	NR1H4,PTGER2,FLRT3	up_VPUL_EC
GO:0018193	0.566	0.712	2	368	peptidyl-amino acid modification	BP	1	LYN,IGF1R	down_ACOR_EC
GO:0002768	0.566	0.712	2	37	immune response-regulating cell surface receptor signaling	BP	1	PRNP,THY1	down_VCAV_EC
GO:1904888	0.566	0.713	2	31	cranial skeletal system development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:1901564	0.566	0.756	2	2053	organonitrogen compound metabolic	BP	1	AK5,ENSCAFG00000028814	down_VSAP_VSMC
GO:1901880	0.566	0.718	2	19	negative regulation of protein depolymerization	BP	1	FGF13,MID1	up_ACOR_VSMC
GO:0009132	0.566	0.715	2	25	nucleoside diphosphate metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0032206	0.566	0.716	2	23	positive regulation of telomere maintenance	BP	1	HMBOX1,ATRX	up_VCAV_EC
GO:0120036	0.566	0.807	1	373	plasma membrane bounded cell projection	BP	1	FSCN1	down_AFEM_EC
GO:0031327	0.566	0.808	1	412	negative regulation of cellular biosynthetic	BP	1	HDAC7	down_VPOR_EC
GO:0090304	0.566	0.852	1	1694	nucleic acid metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0007215	0.566	0.808	1	13	glutamate receptor signaling pathway	BP	1	GNAQ	down_VSAP_EC
GO:0009112	0.566	0.808	1	14	nucleobase metabolic process	BP	1	CMPK1	down_VSAP_EC
GO:0001953	0.566	0.808	1	14	negative regulation of cell-matrix adhesion	BP	1	SERPINE1	down_VSAP_EC
GO:0021544	0.566	0.816	1	8	subpallium development	BP	1	SLITRK5	up_ACOR_VSMC
GO:1990138	0.566	0.802	1	35	neuron projection extension	BP	1	PLXNA4	up_AFEM_EC
GO:0071702	0.566	0.816	1	687	organic substance transport	BP	1	ARG2	up_AORT_VSMC
GO:0001523	0.566	0.809	1	12	retinoid metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0045892	0.566	0.805	1	328	negative regulation of transcription, DNA-	BP	1	SHOX2	up_VFEM_VSMC
GO:0006325	0.566	0.803	1	234	chromatin organization	BP	1	NR1H4	up_VPUL_EC
GO:0042981	0.567	0.498	44	471	regulation of apoptotic process	BP	1	SMAD6,CASP10,MAP3K8,BCL2,HTR2B,RASSF2,SKP2,NACC2,PRKAA2,ITM2C,BMP4,FGFR2,SH3RF2,PPARGC1A,LATS2,CITED2,TP53INP1,CD274,AR,PLAC8B,KLHL20,LIMS2,ANKRD1,DAPK1,BNIP3,JMY,NRP1,UNC5B,SH3RF1,FZD3,DKKL1,FRS2,PSEN1,SPINK2,CLN8,SIAH1,OXR1,NOD2,SERINC3,TNFRSF11B,KLF11,HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0016482	0.567	0.602	6	63	cytosolic transport	BP	1	KLHL20,SGSM2,PIK3C3,AKTIP,LMTK2,VPS26A	up_ACOR_VSMC
GO:0034329	0.567	0.603	6	60	cell junction assembly	BP	1	ACTN2,PKP4,NRP1,JUP,DUSP22,FAM107A	up_ACOR_VSMC
GO:0010595	0.567	0.618	5	52	positive regulation of endothelial cell migration	BP	1	BMP4,SASH1,FGF18,NRP1,PIK3C2A	up_ACOR_VSMC

GO:0002696	0.567	0.635	4	80	positive regulation of leukocyte activation	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:1902904	0.567	0.711	2	38	negative regulation of supramolecular fiber	BP	1	CLIP3,PLEKHH2	down_VCAV_EC
GO:0042542	0.567	0.712	2	31	response to hydrogen peroxide	BP	1	CRYAB,KPNA4	down_VSAP_EC
GO:0043067	0.567	0.713	2	479	regulation of programmed cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0031324	0.567	0.719	2	735	negative regulation of cellular metabolic process	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:0021783	0.567	0.813	1	9	preganglionic parasympathetic fiber	BP	1	NAV2	down_ACOR_VSMC
GO:1901838	0.567	0.813	1	9	positive regulation of transcription of nucleolar large rRNA by RNA	BP	1	NCL	down_ACOR_VSMC
GO:0019233	0.567	0.806	1	16	sensory perception of pain	BP	1	NDN	down_VCAV_EC
GO:1902116	0.567	0.806	1	16	negative regulation of organelle assembly	BP	1	EVI5L	down_VCAV_EC
GO:0032720	0.567	0.808	1	13	negative regulation of tumor necrosis factor	BP	1	NR1H4	down_VSAP_EC
GO:0043949	0.567	0.808	1	13	regulation of cAMP-mediated signaling	BP	1	CALM1	down_VSAP_EC
GO:0045746	0.567	0.807	1	14	negative regulation of Notch signaling pathway	BP	1	HIF1AN	down_VSAP_EC
GO:0045806	0.567	0.806	1	15	negative regulation of endocytosis	BP	1	LRRTM2	down_VSAP_EC
GO:0043032	0.567	0.815	1	8	positive regulation of macrophage activation	BP	1	APP	up_ACOR_VSMC
GO:2000781	0.567	0.815	1	8	positive regulation of double-strand break	BP	1	PARP9	up_ACOR_VSMC
GO:0071867	0.567	0.813	1	9	response to monoamine	BP	1	PDE4D	up_VCAV_EC
GO:0071868	0.567	0.813	1	9	cellular response to monoamine stimulus	BP	1	PDE4D	up_VCAV_EC
GO:0071869	0.567	0.813	1	9	response to catecholamine	BP	1	PDE4D	up_VCAV_EC
GO:0071870	0.567	0.813	1	9	cellular response to catecholamine stimulus	BP	1	PDE4D	up_VCAV_EC
GO:0050896	0.568	0.629	6	2346	response to stimulus	BP	1	EYA1,GATM,NETO1,FBP1,EMX2,SHOX2	up_VFEM_VSMC
GO:0002285	0.568	0.617	5	50	lymphocyte activation involved in immune	BP	1	PLCG2,TP53BP1,F2RL1,PSEN1,IL18R1	up_ACOR_VSMC
GO:0006575	0.568	0.636	4	53	cellular modified amino acid metabolic process	BP	1	GATA3,PIPOX,SERINC5,GCH1	up_VCAV_EC
GO:0031047	0.568	0.667	3	33	gene silencing by RNA	BP	1	SRRT,RAN,RBM14	down_ACOR_VSMC
GO:1904375	0.568	0.667	3	35	regulation of protein localization to cell	BP	1	ACSL3,MMP14,EZR	down_ACOR_VSMC
GO:0043547	0.568	0.662	3	61	positive regulation of GTPase activity	BP	1	SNX18,AKT2,EVI5L	down_VCAV_EC
GO:0016049	0.568	0.66	3	124	cell growth	BP	1	PLXNA4,DCUN1D3,ADAM17	up_AFEM_EC
GO:0051641	0.568	0.721	2	858	cellular localization	BP	1	ANKRD50,GPSM2	down_AFEM_EC
GO:0030838	0.568	0.71	2	37	positive regulation of actin filament	BP	1	KIRREL1,ACTR3B	down_VCAV_EC
GO:0036294	0.568	0.71	2	37	cellular response to decreased oxygen levels	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0071456	0.568	0.71	2	37	cellular response to hypoxia	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0042303	0.568	0.712	2	30	molting cycle	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0042633	0.568	0.712	2	30	hair cycle	BP	1	CTNNB1,INHBA	down_VSAP_EC
GO:0032414	0.568	0.716	2	21	positive regulation of ion transmembrane transporter activity	BP	1	RELN,PLCG2	up_VCAV_EC
GO:0015748	0.568	0.805	1	16	organophosphate ester transport	BP	1	SCP2	down_VCAV_EC
GO:0006903	0.568	0.806	1	14	vesicle targeting	BP	1	MYH9	down_VSAP_EC
GO:0007632	0.568	0.806	1	14	visual behavior	BP	1	HIF1A	down_VSAP_EC
GO:0021532	0.568	0.807	1	13	neural tube patterning	BP	1	PRKACB	down_VSAP_EC
GO:0050994	0.568	0.806	1	14	regulation of lipid catabolic process	BP	1	ABHD5	down_VSAP_EC
GO:0014912	0.568	0.815	1	8	negative regulation of smooth muscle cell	BP	1	SEMA6D	up_ACOR_VSMC

GO:0033081	0.568	0.814	1	8	regulation of T cell differentiation in thymus	BP	1	BMP4	up_ACOR_VSMC
GO:0002706	0.568	0.8	1	35	regulation of lymphocyte mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0048562	0.568	0.799	1	102	embryonic organ morphogenesis	BP	1	HOXA3	up_VPOR_EC
GO:0007267	0.568	0.803	1	332	cell-cell signaling	BP	1	NETO1	up_VFEM_VSMC
GO:1902679	0.568	0.804	1	329	negative regulation of RNA biosynthetic process	BP	1	SHOX2	up_VFEM_VSMC
GO:1903507	0.568	0.804	1	329	negative regulation of nucleic acid-templated	BP	1	SHOX2	up_VFEM_VSMC
GO:1904888	0.568288271	0.80013	1	31	cranial skeletal system development	BP	1	FOXC2	up_ACOR_EC
GO:0030307	0.569	0.711	2	31	positive regulation of cell growth	BP	1	ADAM17,NRP1	down_VSAP_EC
GO:0030032	0.569	0.716	2	19	lamellipodium assembly	BP	1	WASF3,SSH3	up_ACOR_VSMC
GO:1902893	0.569	0.716	2	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:0031297	0.569	0.717	2	18	replication fork processing	BP	1	ATRX,ZNF365	up_ACOR_VSMC
GO:0060350	0.569	0.713	2	23	endochondral bone morphogenesis	BP	1	MEF2C,STC1	up_VCAV_EC
GO:1905114	0.569	0.799	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	SULF1	down_ACOR_EC
GO:0015012	0.569	0.811	1	9	heparan sulfate proteoglycan biosynthetic	BP	1	XYLT1	down_ACOR_VSMC
GO:0010569	0.569	0.803	1	17	regulation of double-strand break repair via homologous	BP	1	FBH1	down_VCAV_EC
GO:0016925	0.569	0.804	1	16	protein sumoylation	BP	1	PARK7	down_VCAV_EC
GO:0000460	0.569	0.805	1	15	maturation of 5.8S rRNA	BP	1	PDCD11	down_VSAP_EC
GO:0046456	0.569	0.813	1	8	icosanoid biosynthetic process	BP	1	EDN1	up_ACOR_VSMC
GO:0046856	0.569	0.814	1	8	phosphatidylinositol dephosphorylation	BP	1	INPP5K	up_ACOR_VSMC
GO:0002244	0.569	0.799	1	35	hematopoietic progenitor cell differentiation	BP	1	BVES	up_AFEM_EC
GO:0045580	0.569	0.799	1	35	regulation of T cell differentiation	BP	1	CYLD	up_AFEM_EC
GO:0012501	0.569	0.81	1	561	programmed cell death	BP	1	EYA1	up_AFEM_VSMC
GO:0046040	0.569	0.811	1	9	IMP metabolic process	BP	1	ADSS	up_VCAV_EC
GO:0051704	0.57	0.494	45	476	multi-organism process	BP	1	HOXA11,THRB,NAPEPLD,HOXA9,MAP3K14,PTGFR,SLC6A4,ABL1,EMP2,ZNF449,IL17RC,HERPUD2,ZBTB16,RECK,PATZ1,F2RL1,BATF2,PLA2G6,TBXA2R,CFAP69,SASH1,MYD88,MON1B,WIPF1,CFD,NLRX1,TKFC,PC,KDM2B,RNF216,EIF3G,HPGD,MAPKBP1,CYBA,CA5B,EIF3L,PQBP1,EIF3D,PPP3CB,NCK1,MAVS,ULK1,CITED2,JCHAIN,DDIT4	up_VSAP_EC
GO:0002252	0.57	0.56	10	166	immune effector process	BP	1	SOCS5,FAM49B,WDR1,PVR,CNOT7,TFRC,LYN,BNIP3,A2M,BTK	down_VSAP_EC
GO:0071496	0.57	0.577	8	97	cellular response to external stimulus	BP	1	SREBF1,SREBF2,CASP2,RNF152,PDXP,FOSL1,MIOS,NUDT1	down_ACOR_VSMC
GO:0008064	0.57	0.587	7	72	regulation of actin polymerization or	BP	1	ACTN2,F2RL1,JMY,EVL,PRKCE,SSH3,WASL	up_ACOR_VSMC
GO:0030832	0.57	0.587	7	72	regulation of actin filament length	BP	1	ACTN2,F2RL1,JMY,EVL,PRKCE,SSH3,WASL	up_ACOR_VSMC
GO:0043412	0.57	0.607	6	1225	macromolecule modification	BP	1	ACVRL1,LYN,IGF1R,PRKAR2A,USP28,ASPN	down_ACOR_EC
GO:0009108	0.57	0.613	5	68	coenzyme biosynthetic process	BP	1	PANK3,ELOVL7,ENSCAFG00000024323,GCH1,HIF1A	up_VCAV_EC
GO:0060993	0.57	0.636	4	42	kidney morphogenesis	BP	1	HOXA11,WNT11,OSR1,IRX3	up_VSAP_EC
GO:0051058	0.57	0.713	2	21	negative regulation of small GTPase mediated signal transduction	BP	1	STMN1,NUP62	down_ACOR_VSMC
GO:0045935	0.57	0.711	2	491	positive regulation of nucleobase-containing compound metabolic	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0016445	0.57	0.714	2	20	somatic diversification of immunoglobulins	BP	1	THOC1,SWAP70	up_VCAV_EC

GO:0016447	0.57	0.714	2	20	somatic recombination of immunoglobulin gene	BP	1	THOC1,SWAP70	up_VCAV_EC
GO:0002637	0.57	0.714	2	20	regulation of immunoglobulin	BP	1	STAT6,STX4	up_VSAP_EC
GO:0042987	0.57	0.809	1	10	amyloid precursor protein catabolic process	BP	1	DHCR24	down_ACOR_VSMC
GO:0030030	0.57	0.804	1	377	cell projection organization	BP	1	FSCN1	down_AFEM_EC
GO:0022602	0.57	0.806	1	13	ovulation cycle process	BP	1	INHBA	down_VSAP_EC
GO:0072077	0.57	0.806	1	13	renal vesicle morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0072273	0.57	0.806	1	13	metanephric nephron morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0090344	0.57	0.813	1	8	negative regulation of cell aging	BP	1	MARCH5	up_ACOR_VSMC
GO:0009746	0.57	0.799	1	35	response to hexose	BP	1	GPAM	up_AFEM_EC
GO:0034284	0.57	0.799	1	35	response to monosaccharide	BP	1	GPAM	up_AFEM_EC
GO:1904375	0.57	0.798	1	35	regulation of protein localization to cell	BP	1	LRRC15	up_AFEM_EC
GO:0046486	0.57	0.797	1	102	glycerolipid metabolic process	BP	1	ABHD5	up_VPOR_EC
GO:1901652	0.57	0.797	1	105	response to peptide	BP	1	ARHGEF2	up_VPOR_EC
GO:0045724	0.57	0.811	1	9	positive regulation of cilium assembly	BP	1	FUZ	up_VSAP_EC
GO:0045446	0.570548921	0.79812	1	32	endothelial cell differentiation	BP	1	ARHGEF26	up_ACOR_EC
GO:0045926	0.570860549	0.7044	2	72	negative regulation of growth	BP	1	TBX5,NRP1	up_ACOR_EC
GO:0010975	0.571	0.562	10	103	regulation of neuron projection development	BP	1	ITM2C,ZNF365,NRP1,ULK2,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1	up_ACOR_VSMC
GO:0110053	0.571	0.596	6	98	regulation of actin filament organization	BP	1	WDR1,ACTR3,TWF1,PLEKHG2,CAPG,NRP1	down_VSAP_EC
GO:0002687	0.571	0.664	3	36	positive regulation of leukocyte migration	BP	1	HMGB1,MMP14,RAC1	down_ACOR_VSMC
GO:0034767	0.571	0.665	3	31	positive regulation of ion transmembrane transport	BP	1	AMIGO1,ABL1,FXYD1	up_VSAP_EC
GO:0007405	0.571	0.713	2	21	neuroblast proliferation	BP	1	ASPM,ARHGEF2	down_ACOR_VSMC
GO:0032649	0.571	0.712	2	23	regulation of interferon-gamma production	BP	1	HMGB1,FAM49B	down_ACOR_VSMC
GO:0048844	0.571	0.709	2	30	artery morphogenesis	BP	1	APOE,NRP1	down_VSAP_EC
GO:1902803	0.571	0.714	2	20	regulation of synaptic vesicle transport	BP	1	FBXL20,PREPL	up_ACOR_VSMC
GO:2000300	0.571	0.714	2	20	regulation of synaptic vesicle exocytosis	BP	1	FBXL20,PREPL	up_ACOR_VSMC
GO:0008202	0.571	0.704	2	80	steroid metabolic process	BP	1	LEP,SDR42E1	up_AFEM_EC
GO:0051234	0.571	0.729	2	1283	establishment of localization	BP	1	TLR2,SLC16A12	up_AFEM_VSMC
GO:0010557	0.571	0.71	2	492	positive regulation of macromolecule biosynthetic process	BP	1	NPNT,HOXA1	up_APUL_EC
GO:0016567	0.571	0.705	2	232	protein ubiquitination	BP	1	KLHL28,RNF6	up_VPOR_EC
GO:0032870	0.571	0.798	1	162	cellular response to hormone stimulus	BP	1	NEDD4	down_ACOR_EC
GO:0051052	0.571	0.798	1	145	regulation of DNA metabolic process	BP	1	ACVRL1	down_ACOR_EC
GO:0072521	0.571	0.797	1	185	purine-containing compound metabolic	BP	1	TNRC6B	down_ACOR_EC
GO:0031343	0.571	0.808	1	10	positive regulation of cell killing	BP	1	FAM49B	down_ACOR_VSMC
GO:0003197	0.571	0.802	1	16	endocardial cushion development	BP	1	BMPR1A	down_VCAV_EC
GO:0030501	0.571	0.802	1	16	positive regulation of bone mineralization	BP	1	BMPR1A	down_VCAV_EC
GO:0048854	0.571	0.805	1	13	brain morphogenesis	BP	1	UCHL5	down_VSAP_EC
GO:0060740	0.571	0.805	1	13	prostate gland epithelium morphogenesis	BP	1	SULF1	down_VSAP_EC
GO:0061298	0.571	0.813	1	8	retina vasculature development in camera-	BP	1	NRP1	up_ACOR_VSMC
GO:0090075	0.571	0.812	1	8	relaxation of muscle	BP	1	PDE5A	up_ACOR_VSMC

GO:0035270	0.571	0.797	1	35	endocrine system development	BP	1	DLL1	up_AFEM_EC
GO:0002429	0.571	0.797	1	35	immune response-activating cell surface receptor signaling	BP	1	CYLD	up_AFEM_EC
GO:0043467	0.571	0.797	1	35	regulation of generation of precursor metabolites	BP	1	PPARGC1A	up_AFEM_EC
GO:0062014	0.571	0.798	1	35	negative regulation of small molecule metabolic	BP	1	ACACB	up_AFEM_EC
GO:0048646	0.571	0.802	1	349	anatomical structure formation involved in	BP	1	DUSP2	up_AORT_EC
GO:0044091	0.571	0.808	1	10	membrane biogenesis	BP	1	CAV2	up_VCAV_EC
GO:0032259	0.571057506	0.70427	2	71	methylation	BP	1	NR1H4,PYGO2	up_ACOR_EC
GO:0007272	0.571213845	0.79772	1	31	ensheathment of neurons	BP	1	SH3TC2	up_ACOR_EC
GO:0008366	0.571213845	0.79772	1	31	axon ensheathment	BP	1	SH3TC2	up_ACOR_EC
GO:0044248	0.572	0.501	34	691	cellular catabolic process	BP	1	LRP1,DCN,MAOA,CHID1,GABARAP,TIMP2,AKT2,PSMF1,SAMD4B,ACAA1,EPHX1,ENTPD3,THNSL2,POLDIP2,RNF216,WDR45,PEX5,PARK7,ZFP36L1,CLEC16A,RETREG1,RNPEP,EMC6,ENSCAFG00000002977,ENSCAFG00000017708,SEC61B,HM13,PYM1,FBH1,LONP2,GLS2,PACSIN3,BCKDHB,ACAT1	down_VCAV_EC
GO:0097659	0.572	0.515	25	1072	nucleic acid-templated transcription	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC
GO:0015980	0.572	0.594	6	106	energy derivation by oxidation of organic	BP	1	ENPP1,ENSCAFG00000007260,HIF1A,PPP1R3C,BNIP3,GSK3B	down_VSAP_EC
GO:0019362	0.572	0.663	3	35	pyridine nucleotide metabolic process	BP	1	NNT,PDHA1,PGD	down_ACOR_VSMC
GO:0046496	0.572	0.663	3	35	nicotinamide nucleotide metabolic process	BP	1	NNT,PDHA1,PGD	down_ACOR_VSMC
GO:0051817	0.572	0.664	3	31	modification of morphology or physiology of other organism	BP	1	F2RL1,DAG1,INPP5K	up_ACOR_VSMC
GO:1902903	0.572	0.656	3	125	regulation of supramolecular fiber	BP	1	CRYAB,CDC42EP5,KANK1	up_AFEM_EC
GO:0010556	0.572	0.674	3	1137	regulation of macromolecule	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0006368	0.572	0.711	2	22	transcription elongation from RNA polymerase II	BP	1	EZH2,SUPT16H	down_ACOR_VSMC
GO:0035710	0.572	0.712	2	22	CD4-positive, alpha-beta T cell activation	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0006664	0.572	0.706	2	37	glycolipid metabolic process	BP	1	PIGS,ENSCAFG00000017708	down_VCAV_EC
GO:1903509	0.572	0.706	2	37	liposaccharide metabolic process	BP	1	PIGS,ENSCAFG00000017708	down_VCAV_EC
GO:0009311	0.572	0.711	2	21	oligosaccharide metabolic process	BP	1	ST3GAL5,NEU3	up_ACOR_VSMC
GO:0042035	0.572	0.713	2	20	regulation of cytokine biosynthetic process	BP	1	TLR1,TLR3	up_ACOR_VSMC
GO:0009152	0.572	0.703	2	80	purine ribonucleotide biosynthetic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0003229	0.572	0.801	1	17	ventricular cardiac muscle tissue development	BP	1	BMPR1A	down_VCAV_EC
GO:0007338	0.572	0.802	1	16	single fertilization	BP	1	B4GALT1	down_VCAV_EC
GO:0007528	0.572	0.801	1	17	neuromuscular junction development	BP	1	CACNB3	down_VCAV_EC
GO:0043388	0.572	0.801	1	16	positive regulation of DNA binding	BP	1	PARK7	down_VCAV_EC
GO:0048247	0.572	0.801	1	16	lymphocyte chemotaxis	BP	1	HSD3B7	down_VCAV_EC
GO:0043266	0.572	0.803	1	14	regulation of potassium ion transport	BP	1	KIF5B	down_VSAP_EC
GO:0019674	0.572	0.809	1	9	NAD metabolic process	BP	1	NMNAT1	up_ACOR_VSMC
GO:0034453	0.572	0.811	1	8	microtubule anchoring	BP	1	DAG1	up_ACOR_VSMC
GO:0000038	0.572	0.805	1	12	very long-chain fatty acid metabolic process	BP	1	ELOVL7	up_VCAV_EC
GO:0010648	0.572	0.803	1	407	negative regulation of cell communication	BP	1	SLIT2	up_VPUL_VSMC
GO:0022008	0.572	0.803	1	406	neurogenesis	BP	1	SLIT2	up_VPUL_VSMC

GO:0008104	0.573	0.482	62	763	protein localization	BP	1	HCLS1,GBP5,PPP2R5A,TNFAIP3,AMOT,MALL,TMEM173,EXOC3L2,RELN,IWS1,FERMT1,TLR4,TSPAN15,GATA3,RAB11A,RAB27A,EXOC6,ZDHHC22,PPP3CA,ARG2,HOOK3,TSPAN14,HHEX,CEP68,SCAMP1,ABCA1,MZT1,EPB41,SNX2,MCC,THOC1,SH3GLB1,SWAP70,AKAP12,APOD,EXOC5,CD200,MMD,RAPGEF2,CTDSPL2,PAN3,GCC2,CTNNA1,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,SPTBN4,RAD21,MCU,ZW10,HIF1A,IPO11,ALS2,LMTK2,ATRX,ENSCAFG00000002015,SHROOM2,RABGAP1,USP6NL	up_VCAV_EC
GO:0007154	0.573	0.597	7	1622	cell communication	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2,FGF5,GJB5	up_VSAP_VSMC
GO:0060402	0.573	0.662	3	35	calcium ion transport into cytosol	BP	1	CAV1,GSTO1,CORO1A	down_ACOR_VSMC
GO:0061333	0.573	0.661	3	35	renal tubule morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0030833	0.573	0.657	3	59	regulation of actin filament polymerization	BP	1	KIRREL1,ENSCAFG00000014978,ACTR3B	down_VCAV_EC
GO:0006367	0.573	0.662	3	32	transcription initiation from RNA polymerase II	BP	1	MED14,CLSTN1,GTF2A1L	up_ACOR_VSMC
GO:0072359	0.573	0.658	3	368	circulatory system development	BP	1	C3AR1,HOXA3,MTDH	up_VPOR_EC
GO:0010508	0.573	0.705	2	38	positive regulation of autophagy	BP	1	DCN,CLEC16A	down_VCAV_EC
GO:0010833	0.573	0.707	2	30	telomere maintenance via telomere lengthening	BP	1	SMG7,CTNNB1	down_VSAP_EC
GO:0046649	0.573	0.796	1	162	lymphocyte activation	BP	1	LYN	down_ACOR_EC
GO:0050877	0.573	0.796	1	164	nervous system process	BP	1	HOXA1	down_ACOR_EC
GO:0006695	0.573	0.8	1	16	cholesterol biosynthetic process	BP	1	CYB5R3	down_VCAV_EC
GO:0001954	0.573	0.8	1	17	positive regulation of cell-matrix adhesion	BP	1	THY1	down_VCAV_EC
GO:0060760	0.573	0.8	1	17	positive regulation of response to cytokine	BP	1	MAVS	down_VCAV_EC
GO:1902653	0.573	0.8	1	16	secondary alcohol biosynthetic process	BP	1	CYB5R3	down_VCAV_EC
GO:0009890	0.573	0.802	1	420	negative regulation of biosynthetic process	BP	1	HDAC7	down_VPOR_EC
GO:0048247	0.573	0.801	1	16	lymphocyte chemotaxis	BP	1	ADAM17	down_VSAP_EC
GO:0072012	0.573	0.809	1	9	glomerulus vasculature development	BP	1	BMP4	up_ACOR_VSMC
GO:0072673	0.573	0.811	1	8	lamellipodium morphogenesis	BP	1	RREB1	up_ACOR_VSMC
GO:0035418	0.573	0.808	1	9	protein localization to synapse	BP	1	RELN	up_VCAV_EC
GO:0010458	0.573	0.804	1	12	exit from mitosis	BP	1	ZW10	up_VCAV_EC
GO:0090102	0.573	0.807	1	10	cochlea development	BP	1	ZEB1	up_VCAV_EC
GO:1902745	0.573	0.808	1	9	positive regulation of lamellipodium	BP	1	ENPP2	up_VSAP_EC
GO:0090092	0.573042297	0.70233	2	72	regulation of transmembrane receptor protein serine/threonine	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:1901342	0.573246368	0.65563	3	114	regulation of vasculature development	BP	1	AQP1,FOXC2,NRP1	up_ACOR_EC
GO:0035821	0.573751106	0.79545	1	32	modification of morphology or physiology	BP	1	AQP1	up_ACOR_EC
GO:0071702	0.574	0.48	65	687	organic substance transport	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,LIPC,SLC8B1,TBC1D10C,TBC1D2B,CDH1,SLC6A4,ABL1,PEX2,SLC16A12,OSR1,IL17RC,SCAMP4,KLF15,C1QTNF2,ANXA4,RILPL2,ABCB11,VPS36,SLC25A12,APOL5,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,ZFP36L1,PIK3R1,SLC27A6,CTNS,SLC10A6,PASK,NUP98,AZIN2,HPS4,ABCA9,STEAP3,FBXO7,KCNB1,LCAT,LONP2,SNUPN,OSBPL7,SCAMP2,RAF1,PNP,MAPKBP1,CYBA,STX4,VPS11,FLOT1,PPP3CB,PEX6,MAVS,TGFBR2,BAG4,NCOA4,NAGPA,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0032774	0.574	0.513	25	1073	RNA biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A	up_AFEM_EC

GO:0070482	0.574	0.584	7	75	response to oxygen levels	BP	1	VEGFD,ITPR1,BNIP3,EGLN1,PRKCE,EDN1,DDIT4	up_ACOR_VSMC
GO:0001936	0.574	0.631	4	49	regulation of endothelial cell proliferation	BP	1	HMGB1,CAV1,NRAS,HMGB2	down_ACOR_VSMC
GO:0048638	0.574	0.627	4	82	regulation of developmental growth	BP	1	GPAM,BMPR1A,TRPV2,PEX5	down_VCAV_EC
GO:0008654	0.574	0.657	3	58	phospholipid biosynthetic process	BP	1	GPAM,LCAT,PIGS	down_VCAV_EC
GO:0106106	0.574	0.658	3	48	cold-induced thermogenesis	BP	1	PLCL1,DDIT3,KDM3A	down_VSAP_EC
GO:0120161	0.574	0.658	3	48	regulation of cold-induced thermogenesis	BP	1	PLCL1,DDIT3,KDM3A	down_VSAP_EC
GO:0070665	0.574	0.662	3	31	positive regulation of leukocyte proliferation	BP	1	LEP,CDKN1A,PTPN22	up_ACOR_VSMC
GO:0005976	0.574	0.661	3	34	polysaccharide metabolic process	BP	1	PCDH12,PDGFB,PPP1CB	up_VCAV_EC
GO:0072524	0.574	0.704	2	37	pyridine-containing compound metabolic	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0010646	0.574	0.716	2	945	regulation of cell communication	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0030183	0.574	0.706	2	30	B cell differentiation	BP	1	PTPN2,BTK	down_VSAP_EC
GO:0070228	0.574	0.71	2	20	regulation of lymphocyte apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0009566	0.574	0.709	2	24	fertilization	BP	1	NECTIN2,SPTBN4	up_VCAV_EC
GO:0006766	0.574	0.8	1	16	vitamin metabolic process	BP	1	VKORC1	down_VCAV_EC
GO:0051568	0.574	0.799	1	17	histone H3-K4 methylation	BP	1	PRMT6	down_VCAV_EC
GO:0061951	0.574	0.8	1	16	establishment of protein localization to plasma	BP	1	RAB31	down_VCAV_EC
GO:0090317	0.574	0.8	1	16	negative regulation of intracellular protein	BP	1	PARK7	down_VCAV_EC
GO:0050702	0.574	0.802	1	13	interleukin-1 beta secretion	BP	1	GBP5	down_VSAP_EC
GO:0090200	0.574	0.805	1	10	positive regulation of release of cytochrome c	BP	1	BNIP3	up_ACOR_VSMC
GO:0007006	0.574	0.795	1	35	mitochondrial membrane organization	BP	1	CAMK2A	up_AFEM_EC
GO:0001775	0.574	0.796	1	219	cell activation	BP	1	BPI	up_APUL_EC
GO:0002097	0.574	0.804	1	11	tRNA wobble base modification	BP	1	TRMT9B	up_VCAV_EC
GO:0031935	0.574	0.81	1	8	regulation of chromatin silencing	BP	1	UHRF2	up_VCAV_EC
GO:0002369	0.574	0.806	1	10	T cell cytokine production	BP	1	GATA3	up_VCAV_EC
GO:0003416	0.574	0.807	1	9	endochondral bone growth	BP	1	STC1	up_VCAV_EC
GO:0061036	0.574	0.804	1	11	positive regulation of cartilage development	BP	1	BMP2	up_VCAV_EC
GO:0023057	0.574	0.801	1	409	negative regulation of signaling	BP	1	SLIT2	up_VPUL_VSMC
GO:0008152	0.574330264	0.4851	97	3714	metabolic process	BP	1	C7,CDH3,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,CALY,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PCSK1N,ENSCAFG00000002230,PHF20,ATG16L2,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,CCDC3,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,BTD,LHX9,ENSCAFG00000028814,SMAD6,B3GNT7,KLHL25,PLCE1,ZMYND8,NIT2,PTGDS,PAK3,CFI,GUCY1B1,FMO3,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,CHPT1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,ARSK,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,RBM38,CLU,SFMBT2,ALDOC,ZNF229,CHMP4B,TP53INP2,RARRES2,VPS16,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,PRKCD,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,ENSCAFG00000010493,CCNYL1,MFAP4,TLE2	up_ACOR_EC
GO:0015031	0.575	0.509	25	510	protein transport	BP	1	GPAM,SNX18,PRNP,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,GLI3,PARK7,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0120039	0.575	0.537	14	158	plasma membrane bounded cell projection morphogenesis	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,PPP3CA,PREX2,ENSCAFG00000010224,STMN1,SNX2,RAPGEF2,CREB1,SPTBN4,ALS2	up_VCAV_EC

GO:0017144	0.575	0.555	10	199	drug metabolic process	BP	1	MAOA,VKORC1,CHID1,NT5C2,ATP5MC1,UQCR10,ADK,PARK7,ACSS2,ACAT1	down_VCAV_EC
GO:0006810	0.575	0.563	10	1244	transport	BP	1	HOOK3,XPOT,HOXA3,SLC7A11,ENSCAFG00000005494,GOLT1B,GCC2,SLC25A16,SRP54,TMEM87B	up_VPOR_EC
GO:0051047	0.575	0.572	8	84	positive regulation of secretion	BP	1	CD274,ABL1,IL17RC,F2RL1,CYBA,STX4,PPP3CB,MAVS	up_VSAP_EC
GO:0010921	0.575	0.63	4	46	regulation of phosphatase activity	BP	1	MEF2C,BMP2,PPP1R2,FKBP15	up_VCAV_EC
GO:0009913	0.575	0.657	3	47	epidermal cell differentiation	BP	1	ERRFI1,CASP3,FLNB	down_VSAP_EC
GO:0043433	0.575	0.657	3	49	negative regulation of DNA-binding transcription factor activity	BP	1	NR1H4,BHLHE40,DDIT3	down_VSAP_EC
GO:0034248	0.575	0.654	3	125	regulation of cellular amide metabolic process	BP	1	PRR16,CTIF,SAMD4B	up_AFEM_EC
GO:0060021	0.575	0.66	3	34	roof of mouth development	BP	1	MEF2C,CHD7,TIPARP	up_VCAV_EC
GO:0055024	0.575	0.708	2	22	regulation of cardiac muscle tissue	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0051239	0.575	0.714	2	859	regulation of multicellular organismal process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0071236	0.575	0.703	2	39	cellular response to antibiotic	BP	1	ADCY6,PARK7	down_VCAV_EC
GO:0006354	0.575	0.705	2	30	DNA-templated transcription, elongation	BP	1	IWS1,DDX39B	down_VSAP_EC
GO:1905954	0.575	0.71	2	19	positive regulation of lipid localization	BP	1	ABCA1,SCP2	up_ACOR_VSMC
GO:0006869	0.575	0.7	2	81	lipid transport	BP	1	LEP,CRY2	up_AFEM_EC
GO:0030029	0.575	0.701	2	239	actin filament-based process	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0006379	0.575	0.805	1	10	mRNA cleavage	BP	1	WDR33	down_ACOR_VSMC
GO:0002052	0.575	0.807	1	9	positive regulation of neuroblast proliferation	BP	1	ASPM	down_ACOR_VSMC
GO:0033137	0.575	0.805	1	10	negative regulation of peptidyl-serine	BP	1	CAV1	down_ACOR_VSMC
GO:0045745	0.575	0.805	1	10	positive regulation of G protein-coupled receptor signaling pathway	BP	1	PRMT5	down_ACOR_VSMC
GO:0002228	0.575	0.807	1	9	natural killer cell mediated immunity	BP	1	LEP	up_ACOR_VSMC
GO:0042267	0.575	0.807	1	9	natural killer cell mediated cytotoxicity	BP	1	LEP	up_ACOR_VSMC
GO:0043201	0.575	0.812	1	7	response to leucine	BP	1	UBR1	up_ACOR_VSMC
GO:0051966	0.575	0.809	1	8	regulation of synaptic transmission,	BP	1	PSEN1	up_ACOR_VSMC
GO:0071233	0.575	0.812	1	7	cellular response to leucine	BP	1	UBR1	up_ACOR_VSMC
GO:0007166	0.575	0.809	1	686	cell surface receptor signaling pathway	BP	1	WNT7A	up_AORT_VSMC
GO:1903010	0.575	0.809	1	8	regulation of bone development	BP	1	TJP2	up_VCAV_EC
GO:0031498	0.575	0.809	1	8	chromatin disassembly	BP	1	SMARCA4	up_VCAV_EC
GO:0051281	0.575	0.805	1	10	positive regulation of release of sequestered calcium ion into cytosol	BP	1	APLNR	up_VCAV_EC
GO:0045892	0.575	0.798	1	328	negative regulation of transcription, DNA-	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010498	0.575	0.795	1	194	proteasomal protein catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:0071560	0.575014944	0.70045	2	72	cellular response to transforming growth	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:0097305	0.575127063	0.79446	1	31	response to alcohol	BP	1	PTGER4	up_ACOR_EC
GO:0006955	0.576	0.527	16	327	immune response	BP	1	LRP1,CFD,PRNP,BMPR1A,TFE3,TRIM8,ENSCAFG00000013404,THY1,PARK7,BPI,CYBA,MAVS,LOXL3,RAB7B,A2M,RAC2	down_VCAV_EC
GO:1901988	0.576	0.593	6	63	negative regulation of cell cycle phase transition	BP	1	FAM107A,CRADD,ZFP36L1,FBXO7,ZFP36L2,TPRA1	up_VSAP_EC
GO:0019216	0.576	0.605	5	101	regulation of lipid metabolic process	BP	1	PDGFRB,ENSCAFG00000014978,AKT2,ORMDL3,LONP2	down_VCAV_EC
GO:0097529	0.576	0.609	5	52	myeloid leukocyte migration	BP	1	ARHGEF5,C5AR2,SLIT2,IL17RC,MYD88	up_VSAP_EC
GO:0022900	0.576	0.629	4	46	electron transport chain	BP	1	PPARGC1A,SLC25A12,NDUFA4L2,PARK7	up_ACOR_VSMC

GO:0090276	0.576	0.658	3	36	regulation of peptide hormone secretion	BP	1	CHD7,MCU,HIF1A	up_VCAV_EC
GO:0007045	0.576	0.707	2	23	cell-substrate adherens junction assembly	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0048041	0.576	0.707	2	23	focal adhesion assembly	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0030038	0.576	0.704	2	31	contractile actin filament bundle assembly	BP	1	NRP1,TNFAIP1	down_VSAP_EC
GO:0043149	0.576	0.704	2	31	stress fiber assembly	BP	1	NRP1,TNFAIP1	down_VSAP_EC
GO:0008154	0.576	0.699	2	81	actin polymerization or depolymerization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0000245	0.576	0.706	2	24	spliceosomal complex assembly	BP	1	SCAF11,PRPF39	up_VCAV_EC
GO:0080135	0.576	0.7	2	240	regulation of cellular response to stress	BP	1	CXHXorf57,ARHGEF2	up_VPOR_EC
GO:0005975	0.576	0.793	1	183	carbohydrate metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0009163	0.576	0.798	1	16	nucleoside biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0002287	0.576	0.797	1	17	alpha-beta T cell activation involved in	BP	1	LOXL3	down_VCAV_EC
GO:0002292	0.576	0.797	1	17	T cell differentiation involved in immune	BP	1	LOXL3	down_VCAV_EC
GO:0002293	0.576	0.797	1	17	alpha-beta T cell differentiation involved in	BP	1	LOXL3	down_VCAV_EC
GO:0002294	0.576	0.797	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	LOXL3	down_VCAV_EC
GO:0042093	0.576	0.797	1	17	T-helper cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0042455	0.576	0.798	1	16	ribonucleoside biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:1903146	0.576	0.798	1	17	regulation of autophagy of mitochondrion	BP	1	CLEC16A	down_VCAV_EC
GO:0046638	0.576	0.801	1	13	positive regulation of alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:0006895	0.576	0.808	1	8	Golgi to endosome transport	BP	1	KLHL20	up_ACOR_VSMC
GO:0072215	0.576	0.809	1	8	regulation of metanephros	BP	1	BMP4	up_ACOR_VSMC
GO:0032205	0.576	0.806	1	9	negative regulation of telomere maintenance	BP	1	DCP2	up_VCAV_EC
GO:0043616	0.576	0.805	1	10	keratinocyte proliferation	BP	1	FERMT1	up_VCAV_EC
GO:0043921	0.576	0.804	1	10	modulation by host of viral transcription	BP	1	SMARCA4	up_VCAV_EC
GO:0048599	0.576	0.804	1	10	oocyte development	BP	1	FBXO5	up_VCAV_EC
GO:0048678	0.576	0.804	1	10	response to axon injury	BP	1	APOD	up_VCAV_EC
GO:0052312	0.576	0.804	1	10	modulation of transcription in other organism involved in	BP	1	SMARCA4	up_VCAV_EC
GO:0052472	0.576	0.804	1	10	modulation by host of symbiont transcription	BP	1	SMARCA4	up_VCAV_EC
GO:1902679	0.576	0.797	1	329	negative regulation of RNA biosynthetic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:1903507	0.576	0.797	1	329	negative regulation of nucleic acid-templated	BP	1	NKX2-5	up_VPOR_VSMC
GO:0031327	0.577	0.517	20	412	negative regulation of cellular biosynthetic process	BP	1	NAB2,KANK2,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,ZFP36L1,LOXL3,ORMDL3,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0010558	0.577	0.518	19	392	negative regulation of macromolecule biosynthetic process	BP	1	NAB2,KANK2,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,ZFP36L1,LOXL3,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0031330	0.577	0.571	8	85	negative regulation of cellular catabolic process	BP	1	AXIN2,ACACB,TENT5C,POLDIP2,TIMP2,HTRA2,HMOX1,DDIT4	up_VSAP_EC
GO:0080090	0.577	0.609	6	1734	regulation of primary metabolic process	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0030177	0.577	0.609	5	51	positive regulation of Wnt signaling pathway	BP	1	LGR6,ZRANB1,MLLT3,FGFR2,DISC1	up_ACOR_VSMC
GO:0051054	0.577	0.699	2	81	positive regulation of DNA metabolic process	BP	1	GREM1,PPARGC1A	up_AFEM_EC
GO:0030511	0.577	0.803	1	10	positive regulation of transforming growth factor beta receptor	BP	1	SLC29A1	down_ACOR_VSMC

GO:0030866	0.577	0.804	1	10	cortical actin cytoskeleton organization	BP	1	EZR	down_ACOR_VSMC
GO:1903846	0.577	0.803	1	10	positive regulation of cellular response to transforming growth	BP	1	SLC29A1	down_ACOR_VSMC
GO:0006629	0.577	0.798	1	382	lipid metabolic process	BP	1	ETFA	down_AFEM_EC
GO:0060325	0.577	0.8	1	13	face morphogenesis	BP	1	PTPN11	down_VSAP_EC
GO:0035337	0.577	0.805	1	9	fatty-acyl-CoA metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034501	0.577	0.805	1	9	protein localization to kinetochore	BP	1	ZW10	up_VCAV_EC
GO:0000902	0.577008708	0.57672	7	266	cell morphogenesis	BP	1	BRSK1,RHOU,PAK3,MAPK8IP2,LRP4,NRP1,ARHGEF26	up_ACOR_EC
GO:0030968	0.577244768	0.79237	1	33	endoplasmic reticulum unfolded protein	BP	1	EDEM2	up_ACOR_EC
GO:0000018	0.577967919	0.79208	1	31	regulation of DNA recombination	BP	1	FIGNL1	up_ACOR_EC
GO:0031324	0.578	0.478	61	735	negative regulation of cellular metabolic process	BP	1	ELK3,HMGB1,RNPS1,SREBF1,ILF3,CBX5,USP4,ATAD2,HMGA1,EIF4A3,HMGCR,SREBF2,SMC1A,NEDD4,U2AF2,SLC29A1,MTDH,PPP1R15B,PARPBP,NAB2,BIRC5,INSIG1,CAV1,TIMELESS,THRAP3,FAM129B,NF2,AURKB,CDKN2C,EZH2,GREM1,SMARCC1,PLK3,HOXA7,UHRF1,GMNN,DHCR24,BRCA1,NOC2L,PPARD,YWHAB,NCL,NUP62,IQGAP1,SUV39H1,CACTIN,HMGB2,DMAP1,SMC3,CDK2,ENSCAFG00000005299,EZR,RBM14,ERF,TCERG1,KNL1,HAT1,HIST2H2AC,TINF2,H2AFX,SIX4	down_ACOR_VSMC
GO:1901566	0.578	0.479	57	598	organonitrogen compound biosynthetic process	BP	1	PRR16,NECAB3,MRPL37,ACACB,NADK,GOT1,GLUL,GALNT15,ENSCAFG00000013986,CERS4,WARS2,ENSCAFG00000000071,PYM1,LMF1,PDK2,ZFP36L1,GALK1,FKRP,HACD4,EEF2,ENSCAFG00000016140,LARP6,RPL13,ANKHD1,AZIN2,GALNT11,MOCOS,ZDHHC8,FARS2,LCAT,PCBD1,UBA52,RPUSD4,RPL15,ACSS2,PNPO,DCAKD,EIF3G,SAMD4B,ZFP36L2,CPOX,ENSCAFG00000013366,PNP,EIF3K,EIF3L,QARS,EIF3D,ASS1,TNRC6C,COA1,NCK1,MRPL4,CHST7,LARS2,B3GALT4,DDIT4,SOAT1	up_VSAP_EC
GO:0030030	0.578	0.494	35	377	cell projection organization	BP	1	WASF3,AMIGO1,ENPP2,SLIT2,ABL1,EMP2,CDC42EP5,FUZ,PLXNA4,RILPL2,CDC42EP2,F2RL1,SHOX2,FGD4,RTN4RL1,LRP4,DPYSL2,GDPD5,E2F4,KIF27,FBXO7,TMEM17,NFIB,CDNF,PQBP1,TTL,TTC8,EMP3,FLOT1,NCK1,ULK1,CEP19,MAP2K2,OGN,BAG4	up_VSAP_EC
GO:0050790	0.578	0.504	26	532	regulation of catalytic activity	BP	1	CST3,PDGFRB,SNX18,DCN,PRNP,BGN,LMO4,RECK,ENSCAFG00000014978,AKT1S1,TIMP2,AKT2,SYDE1,CSPG4,ASPN,THY1,PARK7,SASH1,IFT57,SPRED1,MAPRE3,ARHGAP1,DDR2,SHC1,GREM1,EVI5L	down_VCAV_EC
GO:0051222	0.578	0.603	5	103	positive regulation of protein transport	BP	1	PRNP,ENSCAFG00000014978,AKT2,GLI3,MAVS	down_VCAV_EC
GO:0001657	0.578	0.628	4	42	ureteric bud development	BP	1	HOXA11,WNT11,SLIT2,OSR1	up_VSAP_EC
GO:0072163	0.578	0.628	4	42	mesonephric epithelium development	BP	1	HOXA11,WNT11,SLIT2,OSR1	up_VSAP_EC
GO:0072164	0.578	0.628	4	42	mesonephric tubule development	BP	1	HOXA11,WNT11,SLIT2,OSR1	up_VSAP_EC
GO:0033108	0.578	0.655	3	39	mitochondrial respiratory chain complex assembly	BP	1	FASTKD3,SAMM50,FOXRED1	down_ACOR_VSMC
GO:0042306	0.578	0.702	2	31	regulation of protein import into nucleus	BP	1	ZPR1,CDKN1A	down_VSAP_EC
GO:1901214	0.578	0.697	2	81	regulation of neuron death	BP	1	PPARGC1A,CCL5	up_AFEM_EC
GO:0061383	0.578	0.707	2	20	trabecula morphogenesis	BP	1	CHD7,DLL4	up_VCAV_EC
GO:0000291	0.578	0.803	1	10	nuclear-transcribed mRNA catabolic process,	BP	1	EXOSC5	down_ACOR_VSMC
GO:0015936	0.578	0.803	1	10	coenzyme A metabolic process	BP	1	HMGCR	down_ACOR_VSMC
GO:0051254	0.578	0.798	1	431	positive regulation of RNA metabolic process	BP	1	CITED2	down_VPOR_EC
GO:0001961	0.578	0.799	1	13	positive regulation of cytokine-mediated	BP	1	ADAM17	down_VSAP_EC
GO:0006636	0.578	0.798	1	14	unsaturated fatty acid biosynthetic process	BP	1	PTGS2	down_VSAP_EC

GO:0021952	0.578	0.799	1	13	central nervous system projection neuron	BP	1	CDH11	down_VSAP_EC
GO:0021561	0.578	0.807	1	8	facial nerve development	BP	1	NRP1	up_ACOR_VSMC
GO:0021610	0.578	0.807	1	8	facial nerve morphogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0002092	0.578	0.804	1	9	positive regulation of receptor internalization	BP	1	PLCG2	up_ACOR_VSMC
GO:0035459	0.578	0.807	1	8	cargo loading into vesicle	BP	1	SEC24B	up_ACOR_VSMC
GO:0090110	0.578	0.807	1	8	cargo loading into COPII-coated vesicle	BP	1	SEC24B	up_ACOR_VSMC
GO:2000042	0.578	0.807	1	8	negative regulation of double-strand break repair via homologous	BP	1	TP53BP1	up_ACOR_VSMC
GO:0050864	0.578	0.792	1	36	regulation of B cell activation	BP	1	CYLD	up_AFEM_EC
GO:0043933	0.578	0.806	1	698	protein-containing complex subunit	BP	1	ESR1	up_AORT_VSMC
GO:0000122	0.578	0.793	1	218	negative regulation of transcription by RNA polymerase II	BP	1	NR1H4	up_APUL_EC
GO:0009165	0.578	0.79	1	104	nucleotide biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0030111	0.578	0.791	1	108	regulation of Wnt signaling pathway	BP	1	BARX1	up_VPOR_EC
GO:0043549	0.578	0.793	1	244	regulation of kinase activity	BP	1	FLRT3	up_VPUL_EC
GO:0019725	0.578	0.794	1	245	cellular homeostasis	BP	1	NR1H4	up_VPUL_EC
GO:0032727	0.578	0.805	1	9	positive regulation of interferon-alpha	BP	1	MAVS	up_VSAP_EC
GO:0071320	0.578	0.805	1	9	cellular response to cAMP	BP	1	ZFP36L1	up_VSAP_EC
GO:0006753	0.579	0.516	20	211	nucleoside phosphate metabolic process	BP	1	ACSM3,ACACB,NADK,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,ENTPD3,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,PNP,NDUFV1,DDIT4	up_VSAP_EC
GO:0001817	0.579	0.528	15	182	regulation of cytokine production	BP	1	HMGB1,IRAK1,SLC29A1,DHX33,ARG2,FAM49B,RAC1,IQGAP1,CACTIN,HMGB2,EZR,POLR3F,BAP1,MAST2,ARHGEF2	down_ACOR_VSMC
GO:0002764	0.579	0.623	4	80	immune response-regulating signaling	BP	1	PRNP,THY1,CYBA,RAB7B	down_VCAV_EC
GO:0007259	0.579	0.627	4	42	JAK-STAT cascade	BP	1	LEP,CRLF3,PARP9,LRRC4	up_ACOR_VSMC
GO:0016241	0.579	0.627	4	41	regulation of macroautophagy	BP	1	FEZ1,PRKAA2,BNIP3,FEZ2	up_ACOR_VSMC
GO:0050870	0.579	0.627	4	42	positive regulation of T cell activation	BP	1	LEP,CD83,CD274,PTPN22	up_ACOR_VSMC
GO:0071241	0.579	0.627	4	42	cellular response to inorganic substance	BP	1	PRKAA2,ATRX,BNIP3,B2M	up_ACOR_VSMC
GO:0090090	0.579	0.627	4	44	negative regulation of canonical Wnt signaling	BP	1	FERMT1,RAPGEF1,BMP2,MCC	up_VCAV_EC
GO:0009746	0.579	0.656	3	35	response to hexose	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0034284	0.579	0.656	3	35	response to monosaccharide	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0032879	0.579	0.659	3	767	regulation of localization	BP	1	NR1H4,TBX5,HOXA3	up_APUL_EC
GO:0009798	0.579	0.658	3	31	axis specification	BP	1	DLL1,LRP4,CITED2	up_VSAP_EC
GO:0015908	0.579	0.704	2	23	fatty acid transport	BP	1	SLCO3A1,NOS2	up_VCAV_EC
GO:1901655	0.579	0.706	2	20	cellular response to ketone	BP	1	PTGFR,DDIT4	up_VSAP_EC
GO:1905517	0.579	0.802	1	10	macrophage migration	BP	1	MMP14	down_ACOR_VSMC
GO:0098930	0.579	0.795	1	17	axonal transport	BP	1	MGARP	down_VCAV_EC
GO:0000027	0.579	0.796	1	16	ribosomal large subunit assembly	BP	1	RSL24D1	down_VSAP_EC
GO:0045655	0.579	0.803	1	9	regulation of monocyte differentiation	BP	1	CLSTN1	up_ACOR_VSMC
GO:0070131	0.579	0.804	1	9	positive regulation of mitochondrial translation	BP	1	NGRN	up_ACOR_VSMC
GO:0008286	0.579	0.79	1	36	insulin receptor signaling pathway	BP	1	KANK1	up_AFEM_EC
GO:0017148	0.579	0.791	1	36	negative regulation of translation	BP	1	SAMD4B	up_AFEM_EC

GO:0071705	0.579	0.802	1	582	nitrogen compound transport	BP	1	TLR2	up_AFEM_VSMC
GO:0006778	0.579	0.799	1	12	porphyrin-containing compound metabolic	BP	1	BLVRA	up_VCAV_EC
GO:0040020	0.579	0.802	1	10	regulation of meiotic nuclear division	BP	1	FBXO5	up_VCAV_EC
GO:0042168	0.579	0.799	1	12	heme metabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0060317	0.579	0.8	1	11	cardiac epithelial to mesenchymal transition	BP	1	BMP2	up_VCAV_EC
GO:0006366	0.579	0.801	1	583	transcription by RNA polymerase II	BP	1	GATA5	up_VCAV_VSMC
GO:0006281	0.579	0.791	1	208	DNA repair	BP	1	EYA1	up_VFEM_EC
GO:0030097	0.579	0.793	1	244	hemopoiesis	BP	1	EVI2B	up_VPUL_EC
GO:0001932	0.579	0.797	1	416	regulation of protein phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0045893	0.579	0.797	1	413	positive regulation of transcription, DNA-	BP	1	GATA5	up_VPUL_VSMC
GO:0021783	0.579	0.804	1	9	preganglionic parasympathetic fiber	BP	1	PLXNA4	up_VSAP_EC
GO:0034694	0.579	0.803	1	9	response to prostaglandin	BP	1	PTGFR	up_VSAP_EC
GO:0001816	0.579	0.791	1	194	cytokine production	BP	1	TLR2	up_VSAP_VSMC
GO:1902533	0.579035243	0.57461	7	271	positive regulation of intracellular signal	BP	1	SOX9,FZD5,NOD2,TNFRSF19,SH3RF3,CLU,NRP1	up_ACOR_EC
GO:0016567	0.579298329	0.58595	6	232	protein ubiquitination	BP	1	NOD2,KLHL25,KLHDC8B,SH3RF3,RNF114,UBE2H	up_ACOR_EC
GO:0045639	0.579408844	0.79054	1	33	positive regulation of myeloid cell	BP	1	CLSTN1	up_ACOR_EC
GO:0010605	0.58	0.472	71	745	negative regulation of macromolecule metabolic process	BP	1	SMAD6,LEP,GATA5,RASSF2,RECK,NACC2,PRKAA2,ITM2C,FERMT1,BMP4,PNRC1,FGFR2,TP53BP1,EIF4A2,GJA1,ATRX,TRPS1,SH3RF2,LATS2,TP53INP1,ATXN2,ISG15,AR,PTPN3,NDRG2,CST3,ZNF174,ANKRD1,F2RL1,FAM129A,DAPK1,CDKN1A,ENSCAFG00000006238,DCP1B,CLSTN1,PTPN22,LRPAP1,OS9,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,DAG1,PARP9,APP,PSEN1,SYNJ2BP,MXI1,SPINK2,NR3C1,WWC2,DUSP22,EDN1,OXR1,DUSP26,CBX7,LRRC4,KLF11,INPP5K,CNOT4,WFS1,AZIN2,CTIF,ENSCAFG00000029553,ID3,PARK7,STC2,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0051050	0.58	0.51	22	235	positive regulation of transport	BP	1	CD274,ARHGEF5,AMIGO1,CDH1,ABL1,CHRM1,DLL1,IL17RC,KLF15,C1QTNF2,F2RL1,ICE1,PIK3R1,AZIN2,KCNB1,CYBA,ZNF205,FXYD1,STX4,FLOT1,PPP3CB,MAVS	up_VSAP_EC
GO:0048585	0.58	0.545	11	475	negative regulation of response to stimulus	BP	1	LEP,LBH,CRY2,GREM1,GREM2,CYLD,LRRC15,RAB7A,AXIN2,ADAM17,KANK1	up_AFEM_EC
GO:0043254	0.58	0.565	8	164	regulation of protein complex assembly	BP	1	KIRREL1,LMO4,CLIP3,ENSCAFG00000014978,LCAT,CLSTN1,NCLN,ACTR3B	down_VCAV_EC
GO:0050877	0.58	0.565	8	164	nervous system process	BP	1	NDN,PRNP,LUM,PEX5,ENSCAFG00000017708,RDH10,THRB,BRSK1	down_VCAV_EC
GO:0019827	0.58	0.604	5	59	stem cell population maintenance	BP	1	SMC1A,MED17,SRRT,SMC3,ASPM	down_ACOR_VSMC
GO:0042180	0.58	0.603	5	61	cellular ketone metabolic process	BP	1	SREBF1,INSIG1,CAV1,BRCA1,PDSS1	down_ACOR_VSMC
GO:0070372	0.58	0.602	5	85	regulation of ERK1 and ERK2 cascade	BP	1	PTPN11,PTPN2,LYN,ATF3,NRP1	down_VSAP_EC
GO:0043065	0.58	0.79	1	188	positive regulation of apoptotic process	BP	1	LYN	down_ACOR_EC
GO:0006743	0.58	0.801	1	10	ubiquinone metabolic process	BP	1	PDSS1	down_ACOR_VSMC
GO:0006744	0.58	0.801	1	10	ubiquinone biosynthetic process	BP	1	PDSS1	down_ACOR_VSMC
GO:0090185	0.58	0.8	1	10	negative regulation of kidney development	BP	1	GREM1	down_ACOR_VSMC
GO:1901663	0.58	0.801	1	10	quinone biosynthetic process	BP	1	PDSS1	down_ACOR_VSMC
GO:1903541	0.58	0.801	1	10	regulation of exosomal secretion	BP	1	SDC1	down_ACOR_VSMC
GO:1903543	0.58	0.801	1	10	positive regulation of exosomal secretion	BP	1	SDC1	down_ACOR_VSMC
GO:0051094	0.58	0.795	1	388	positive regulation of developmental process	BP	1	SRSF6	down_AFEM_EC
GO:0007029	0.58	0.795	1	16	endoplasmic reticulum organization	BP	1	PEX5	down_VCAV_EC

GO:0048709	0.58	0.795	1	17	oligodendrocyte differentiation	BP	1	GLI3	down_VCAV_EC
GO:0007029	0.58	0.795	1	16	endoplasmic reticulum organization	BP	1	LMAN1	down_VSAP_EC
GO:0032371	0.58	0.795	1	15	regulation of sterol transport	BP	1	APOE	down_VSAP_EC
GO:0032374	0.58	0.795	1	15	regulation of cholesterol transport	BP	1	APOE	down_VSAP_EC
GO:0051443	0.58	0.795	1	15	positive regulation of ubiquitin-protein	BP	1	TRIB3	down_VSAP_EC
GO:0071514	0.58	0.805	1	8	genetic imprinting	BP	1	PCGF5	up_ACOR_VSMC
GO:0030036	0.58	0.791	1	223	actin cytoskeleton organization	BP	1	PDLIM3	up_APUL_EC
GO:0051129	0.58	0.791	1	221	negative regulation of cellular component	BP	1	TUBB4A	up_APUL_EC
GO:0006305	0.58	0.803	1	9	DNA alkylation	BP	1	MTA2	up_VCAV_EC
GO:0006306	0.58	0.803	1	9	DNA methylation	BP	1	MTA2	up_VCAV_EC
GO:0048820	0.58	0.803	1	9	hair follicle maturation	BP	1	FERMT1	up_VCAV_EC
GO:0060674	0.58	0.798	1	12	placenta blood vessel development	BP	1	VASH1	up_VCAV_EC
GO:0045785	0.58	0.789	1	107	positive regulation of cell adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0007155	0.58	0.795	1	324	cell adhesion	BP	1	COL4A5	up_VPOR_VSMC
GO:0006259	0.58	0.794	1	354	DNA metabolic process	BP	1	EYA1	up_VFEM_VSMC
GO:0034622	0.58	0.796	1	421	cellular protein-containing complex assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:1902680	0.58	0.796	1	415	positive regulation of RNA biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:1903508	0.58	0.796	1	415	positive regulation of nucleic acid-templated	BP	1	GATA5	up_VPUL_VSMC
GO:0055094	0.58	0.803	1	9	response to lipoprotein particle	BP	1	MYD88	up_VSAP_EC
GO:0007267	0.581	0.495	31	332	cell-cell signaling	BP	1	GPR1,FZD1,WNT11,HNF4A,FAM107A,AXIN2,SLC8B1,SLC6A4,FGF7,ABL1,CHRM1,DLL1,RECK,PLPP3,RAB11B,FAM53B,SULF2,SLC12A6,HIC1,LRP4,PASK,KCNB1,WISP2,LIMD1,RAF1,STX4,KCNC4,FLOT1,PPP3CB,RAB11FIP2,LATS2	up_VSAP_EC
GO:0034613	0.581	0.498	28	576	cellular protein localization	BP	1	LRP1,PRNP,TLN2,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,TRIM8,CLTB,SSR3,WDR45,PEX5,GLI3,PARK7,ARL2BP,MAVS,CDH2,TOM1,SEC61B,GLIS2,RAB31,HM13,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0010942	0.581	0.523	16	200	positive regulation of cell death	BP	1	HMGB1,RNPS1,MNDA,PRELID1,CAV1,CASP2,MAP3K20,TRIM35,BID,PDCD2,EIF5A,B4GALT1,CYCS,MELK,AIFM1,PIK3CD	down_ACOR_VSMC
GO:0032956	0.581	0.574	7	116	regulation of actin cytoskeleton organization	BP	1	FSCN1,WDR1,ACTR3,TWF1,PLEKHG2,CAPG,NRP1	down_VSAP_EC
GO:0002237	0.581	0.601	5	85	response to molecule of bacterial origin	BP	1	NR1H4,SERPINE1,MTDH,ADAM17,LYN	down_VSAP_EC
GO:0070646	0.581	0.622	4	63	protein modification by small protein removal	BP	1	USP12,UCHL5,USP48,USP14	down_VSAP_EC
GO:0002705	0.581	0.655	3	31	positive regulation of leukocyte mediated	BP	1	STAT6,F2RL1,STX4	up_VSAP_EC
GO:1902117	0.581	0.654	3	32	positive regulation of organelle assembly	BP	1	ARHGEF5,FUZ,PIP4K2B	up_VSAP_EC
GO:0015914	0.581	0.8	1	10	phospholipid transport	BP	1	PRELID1	down_ACOR_VSMC
GO:0080134	0.581	0.794	1	386	regulation of response to stress	BP	1	SRSF6	down_AFEM_EC
GO:2000113	0.581	0.795	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0031057	0.581	0.793	1	18	negative regulation of histone modification	BP	1	PRMT6	down_VCAV_EC
GO:0090342	0.581	0.794	1	17	regulation of cell aging	BP	1	BMPR1A	down_VCAV_EC
GO:2001239	0.581	0.796	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	INHBA	down_VSAP_EC
GO:0006796	0.581	0.811	1	938	phosphate-containing compound metabolic	BP	1	AK5	down_VSAP_VSMC
GO:0010894	0.581	0.802	1	9	negative regulation of steroid biosynthetic	BP	1	DKKL1	up_ACOR_VSMC

GO:0045939	0.581	0.802	1	9	negative regulation of steroid metabolic process	BP	1	DKKL1	up_ACOR_VSMC
GO:0002931	0.581	0.802	1	9	response to ischemia	BP	1	BVES	up_ACOR_VSMC
GO:0006941	0.581	0.788	1	36	striated muscle contraction	BP	1	DMPK	up_AFEM_EC
GO:1904659	0.581	0.789	1	36	glucose transmembrane transport	BP	1	LEP	up_AFEM_EC
GO:0006896	0.581	0.8	1	10	Golgi to vacuole transport	BP	1	VPS54	up_VCAV_EC
GO:0016311	0.581	0.788	1	106	dephosphorylation	BP	1	FBP1	up_VPOR_EC
GO:0072160	0.581	0.802	1	9	nephron tubule epithelial cell differentiation	BP	1	OSR1	up_VSAP_EC
GO:0008637	0.581123555	0.78881	1	35	apoptotic mitochondrial changes	BP	1	IFI6	up_ACOR_EC
GO:0048858	0.582	0.53	14	159	cell projection morphogenesis	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,PPP3CA,PREX2,ENSCAFG00000010224,STMN1,SNX2,RAPGEF2,CREB1,SPTBN4,ALS2	up_VCAV_EC
GO:2001233	0.582	0.53	14	149	regulation of apoptotic signaling pathway	BP	1	ACKR3,PLEKHF1,CRADD,TRAF7,RBCK1,PTPMT1,RAF1,ZNF205,STX4,QARS,HTRA2,NCK1,HMOX1,DEDD2	up_VSAP_EC
GO:0044260	0.582	0.568	11	2593	cellular macromolecule metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CDC42EP5,CHST7	up_VFEM_EC
GO:0045637	0.582	0.586	6	73	regulation of myeloid cell differentiation	BP	1	HSPA9,PRMT1,HMGB3,HOXA7,HMGB2,HOXA9	down_ACOR_VSMC
GO:0045055	0.582	0.603	5	52	regulated exocytosis	BP	1	F2RL1,RAB11B,STX4,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0071241	0.582	0.624	4	42	cellular response to inorganic substance	BP	1	ENSCAFG00000009113,CDH1,MT2A,HMOX1	up_VSAP_EC
GO:0043038	0.582	0.653	3	34	amino acid activation	BP	1	VARS,FARSA,RARS	down_ACOR_VSMC
GO:0003279	0.582	0.65	3	48	cardiac septum development	BP	1	LTBP1,ADAMTS6,NRP1	down_VSAP_EC
GO:0042306	0.582	0.654	3	31	regulation of protein import into nucleus	BP	1	CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0014068	0.582	0.702	2	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	NEDD4,PPARD	down_ACOR_VSMC
GO:0051281	0.582	0.799	1	10	positive regulation of release of sequestered calcium ion into cytosol	BP	1	GSTO1	down_ACOR_VSMC
GO:0031297	0.582	0.792	1	18	replication fork processing	BP	1	FBH1	down_VCAV_EC
GO:1900015	0.582	0.793	1	17	regulation of cytokine production involved in inflammatory response	BP	1	CHID1	down_VCAV_EC
GO:0051642	0.582	0.796	1	13	centrosome localization	BP	1	KIF5B	down_VSAP_EC
GO:0061842	0.582	0.796	1	13	microtubule organizing center localization	BP	1	KIF5B	down_VSAP_EC
GO:0090313	0.582	0.794	1	14	regulation of protein targeting to membrane	BP	1	MYO1C	down_VSAP_EC
GO:2001023	0.582	0.795	1	14	regulation of response to drug	BP	1	PTPN11	down_VSAP_EC
GO:0061318	0.582	0.803	1	8	renal filtration cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0072010	0.582	0.803	1	8	glomerular epithelium development	BP	1	BMP4	up_ACOR_VSMC
GO:0072112	0.582	0.803	1	8	glomerular visceral epithelial cell	BP	1	BMP4	up_ACOR_VSMC
GO:0072311	0.582	0.803	1	8	glomerular epithelial cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0006379	0.582	0.799	1	10	mRNA cleavage	BP	1	MOV10	up_VCAV_EC
GO:0003203	0.582	0.798	1	11	endocardial cushion morphogenesis	BP	1	BMP2	up_VCAV_EC
GO:0097120	0.582	0.801	1	9	receptor localization to synapse	BP	1	RELN	up_VCAV_EC
GO:0030511	0.582	0.799	1	10	positive regulation of transforming growth factor beta receptor	BP	1	FERMT1	up_VCAV_EC
GO:0043300	0.582	0.797	1	11	regulation of leukocyte degranulation	BP	1	FES	up_VCAV_EC
GO:0072678	0.582	0.799	1	10	T cell migration	BP	1	APOD	up_VCAV_EC
GO:1903846	0.582	0.799	1	10	positive regulation of cellular response to transforming growth	BP	1	FERMT1	up_VCAV_EC

GO:0071705	0.582	0.799	1	582	nitrogen compound transport	BP	1	CA2	up_VCAV_VSMC
GO:0022610	0.582	0.792	1	326	biological adhesion	BP	1	COL4A5	up_VPOR_VSMC
GO:0060384	0.582	0.801	1	9	innervation	BP	1	SULF2	up_VSAP_EC
GO:0043065	0.582	0.788	1	188	positive regulation of apoptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:0043170	0.583	0.562	13	2980	macromolecule metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0071496	0.583	0.556	9	97	cellular response to external stimulus	BP	1	WNT11,FAM107A,MAP3K14,CRADD,SESN1,MAP3K5,PDK2,CASTOR1,NPRL3	up_VSAP_EC
GO:0008015	0.583	0.571	7	120	blood circulation	BP	1	PRCP,PTGS2,HTR7,ACTA2,APOE,PLOD3,CALM1	down_VSAP_EC
GO:0051048	0.583	0.623	4	42	negative regulation of secretion	BP	1	LEP,F2RL1,PTPN22,PFKL	up_ACOR_VSMC
GO:0019219	0.583	0.664	3	1151	regulation of nucleobase-containing compound metabolic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0034446	0.583	0.7	2	23	substrate adhesion-dependent cell spreading	BP	1	RAC1,RADIL	down_ACOR_VSMC
GO:1902041	0.583	0.7	2	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	HMGB2,ARHGEF2	down_ACOR_VSMC
GO:0050688	0.583	0.702	2	20	regulation of defense response to virus	BP	1	PTPN22,PARP9	up_ACOR_VSMC
GO:0006865	0.583	0.7	2	23	amino acid transport	BP	1	LRRC8D,SLC38A1	up_VCAV_EC
GO:0061180	0.583	0.702	2	20	mammary gland epithelium development	BP	1	STAT6,LBH	up_VSAP_EC
GO:0050853	0.583	0.799	1	10	B cell receptor signaling pathway	BP	1	MNDA	down_ACOR_VSMC
GO:0046782	0.583	0.792	1	17	regulation of viral transcription	BP	1	TRIM8	down_VCAV_EC
GO:0019068	0.583	0.793	1	15	virion assembly	BP	1	APOE	down_VSAP_EC
GO:1903556	0.583	0.794	1	14	negative regulation of tumor necrosis factor superfamily cytokine	BP	1	NR1H4	down_VSAP_EC
GO:0043171	0.583	0.802	1	8	peptide catabolic process	BP	1	ERAP1	up_ACOR_VSMC
GO:1900543	0.583	0.8	1	9	negative regulation of purine nucleotide	BP	1	DDIT4	up_ACOR_VSMC
GO:1903579	0.583	0.8	1	9	negative regulation of ATP metabolic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0006754	0.583	0.788	1	36	ATP biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0009048	0.583	0.8	1	9	dosage compensation by inactivation of X	BP	1	CDYL	up_VCAV_EC
GO:0043201	0.583	0.806	1	7	response to leucine	BP	1	MTOR	up_VCAV_EC
GO:0071233	0.583	0.806	1	7	cellular response to leucine	BP	1	MTOR	up_VCAV_EC
GO:0051130	0.583	0.791	1	342	positive regulation of cellular component	BP	1	NKX2-5	up_VPOR_VSMC
GO:0023014	0.583	0.789	1	248	signal transduction by protein phosphorylation	BP	1	CCL24	up_VPUL_EC
GO:0043368	0.583	0.8	1	9	positive T cell selection	BP	1	STAT6	up_VSAP_EC
GO:0043277	0.583	0.8	1	9	apoptotic cell clearance	BP	1	XKR8	up_VSAP_EC
GO:0120031	0.583015817	0.61704	4	154	plasma membrane bounded cell projection	BP	1	ACTN2,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0060541	0.583839167	0.6919	2	73	respiratory system development	BP	1	ADAMTSL2,TBX5	up_ACOR_EC
GO:0043009	0.584	0.54	11	227	chordate embryonic development	BP	1	SDC4,BMPR1A,LMO4,TBX15,SEMA3C,GLI3,ZFP36L1,IFT57,IRX5,PRKCSH,RDH10	down_VCAV_EC
GO:1901653	0.584	0.572	7	84	cellular response to peptide	BP	1	SREBF1,CAV1,TIMELESS,CDK4,SMARCC1,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0043547	0.584	0.586	6	61	positive regulation of GTPase activity	BP	1	USP6NL,EVI5L,PKP4,F2RL1,SGSM2,CCL5	up_ACOR_VSMC
GO:0006796	0.584	0.626	4	938	phosphate-containing compound metabolic	BP	1	EYA1,MAP2K6,CDC42EP5,ADCY3	up_VFEM_EC
GO:0090276	0.584	0.651	3	36	regulation of peptide hormone secretion	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0016070	0.584	0.668	3	1479	RNA metabolic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0097530	0.584	0.652	3	33	granulocyte migration	BP	1	HRH1,CCL5,JAM3	up_ACOR_VSMC

GO:0042542	0.584	0.652	3	31	response to hydrogen peroxide	BP	1	ABL1,MAP3K5,ZNF580	up_VSAP_EC
GO:0051817	0.584	0.652	3	31	modification of morphology or physiology of other organism	BP	1	NAPEPLD,F2RL1,PC	up_VSAP_EC
GO:0055007	0.584	0.696	2	31	cardiac muscle cell differentiation	BP	1	FHL2,NEXN	down_VSAP_EC
GO:1903672	0.584	0.701	2	20	positive regulation of sprouting angiogenesis	BP	1	NRP1,PIK3C2A	up_ACOR_VSMC
GO:0002027	0.584	0.701	2	20	regulation of heart rate	BP	1	IRX5,KCNE3	up_VSAP_EC
GO:1903201	0.584	0.701	2	20	regulation of oxidative stress-induced cell death	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:0043068	0.584	0.787	1	190	positive regulation of programmed cell death	BP	1	LYN	down_ACOR_EC
GO:0033688	0.584	0.797	1	10	regulation of osteoblast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:0033555	0.584	0.794	1	13	multicellular organismal response to stress	BP	1	APOE	down_VSAP_EC
GO:0072111	0.584	0.8	1	9	cell proliferation involved in kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:1903053	0.584	0.798	1	10	regulation of extracellular matrix organization	BP	1	FSCN1	up_VCAV_EC
GO:0008285	0.584	0.787	1	201	negative regulation of cell proliferation	BP	1	MTSS1	up_VFEM_EC
GO:1900449	0.584	0.799	1	9	regulation of glutamate receptor signaling	BP	1	KLHL24	up_VSAP_EC
GO:0070647	0.584199269	0.55992	8	311	protein modification by small protein conjugation	BP	1	NOD2,KLHL25,PIAS1,USP53,KLHDC8B,SH3RF3,RNF114,UBE2H	up_ACOR_EC
GO:1901222	0.584930773	0.78598	1	32	regulation of NIK/NF-kappaB signaling	BP	1	NOD2	up_ACOR_EC
GO:0045184	0.585	0.497	26	532	establishment of protein localization	BP	1	GPAM,SNX18,PRNP,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,GLI3,PARK7,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0009896	0.585	0.536	12	127	positive regulation of catabolic process	BP	1	PRKAA2,SH3RF2,TP53INP1,DAPK1,BNIP3,PRKCE,RNF19A,PSEN1,DISC1,HERPUD1,SH3BP4,ENSCAFG00000029553	up_ACOR_VSMC
GO:0070372	0.585	0.562	8	85	regulation of ERK1 and ERK2 cascade	BP	1	ACKR3,C5AR2,TBC1D10C,ABL1,PDGFD,F2RL1,FBLN1,RAF1	up_VSAP_EC
GO:0033157	0.585	0.571	7	82	regulation of intracellular protein transport	BP	1	HCLS1,TMEM173,IWS1,FERMT1,APOD,CTDSPL2,GCC2	up_VCAV_EC
GO:1901564	0.585	0.592	7	2053	organonitrogen compound metabolic	BP	1	NR1H4,STK32B,ENSCAFG00000028814,CCL24,PTGER2,FLRT3,ARHGEF2	up_VPUL_EC
GO:0051179	0.585	0.601	6	1747	localization	BP	1	TBX5,HOXA3,NR1H4,CCL24,FLRT3,ARHGEF2	up_VPUL_EC
GO:0007281	0.585	0.598	5	60	germ cell development	BP	1	TRIP13,FBXO5,HMGB2,ASPM,TTLL1	down_ACOR_VSMC
GO:0061024	0.585	0.595	5	215	membrane organization	BP	1	RAB20,CAMK2A,REEP2,RAB7A,DMPK	up_AFEM_EC
GO:0045088	0.585	0.617	4	81	regulation of innate immune response	BP	1	CYBA,MAVS,RAB7B,A2M	down_VCAV_EC
GO:0051716	0.585	0.645	4	2001	cellular response to stimulus	BP	1	HDAC7,CITED2,RAB11B,HSD3B7	down_VPOR_EC
GO:1903363	0.585	0.651	3	32	negative regulation of cellular protein catabolic	BP	1	OS9,PSEN1,PARK7	up_ACOR_VSMC
GO:0006487	0.585	0.694	2	34	protein N-linked glycosylation	BP	1	STT3A,RPN1	down_VSAP_EC
GO:0032091	0.585	0.694	2	34	negative regulation of protein binding	BP	1	GSK3B,DISC1	down_VSAP_EC
GO:0030148	0.585	0.696	2	28	sphingolipid biosynthetic process	BP	1	SPTLC2,SAMD8	up_VCAV_EC
GO:0017144	0.585	0.786	1	199	drug metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0021680	0.585	0.796	1	10	cerebellar Purkinje cell layer development	BP	1	ARCN1	down_ACOR_VSMC
GO:0048821	0.585	0.797	1	10	erythrocyte development	BP	1	JMJD6	down_ACOR_VSMC
GO:0097345	0.585	0.797	1	10	mitochondrial outer membrane	BP	1	SLC25A5	down_ACOR_VSMC
GO:0030042	0.585	0.79	1	17	actin filament depolymerization	BP	1	PLEKHH2	down_VCAV_EC
GO:0030834	0.585	0.79	1	17	regulation of actin filament depolymerization	BP	1	PLEKHH2	down_VCAV_EC
GO:1904894	0.585	0.79	1	17	positive regulation of STAT cascade	BP	1	ARL2BP	down_VCAV_EC
GO:0140112	0.585	0.791	1	15	extracellular vesicle biogenesis	BP	1	SDC4	down_VSAP_EC

GO:0043687	0.585	0.792	1	14	post-translational protein modification	BP	1	STT3A	down_VSAP_EC
GO:1902476	0.585	0.793	1	13	chloride transmembrane transport	BP	1	CLCN3	down_VSAP_EC
GO:2000001	0.585	0.793	1	13	regulation of DNA damage checkpoint	BP	1	DDX39B	down_VSAP_EC
GO:0006793	0.585	0.808	1	948	phosphorus metabolic process	BP	1	AK5	down_VSAP_VSMC
GO:0010646	0.585	0.808	1	945	regulation of cell communication	BP	1	GATA5	down_VSAP_VSMC
GO:0031401	0.585	0.79	1	358	positive regulation of protein modification	BP	1	TAOK1	up_AORT_EC
GO:0006812	0.585	0.787	1	222	cation transport	BP	1	HOXA3	up_APUL_EC
GO:0051797	0.585	0.797	1	10	regulation of hair follicle development	BP	1	FERMT1	up_VCAV_EC
GO:0044087	0.585	0.79	1	339	regulation of cellular component biogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0032958	0.585	0.799	1	9	inositol phosphate biosynthetic process	BP	1	PPIP5K1	up_VSAP_EC
GO:0070885	0.585	0.798	1	9	negative regulation of calcineurin-NFAT signaling	BP	1	TBC1D10C	up_VSAP_EC
GO:0106057	0.585	0.798	1	9	negative regulation of calcineurin-mediated	BP	1	TBC1D10C	up_VSAP_EC
GO:0048485	0.585	0.798	1	9	sympathetic nervous system development	BP	1	PLXNA4	up_VSAP_EC
GO:0019637	0.586	0.496	26	342	organophosphate metabolic process	BP	1	TEK,NPR1,ADGRF5,PANK3,CDA,PDGFB,GK5,PIPOX,SERINC5,ADSS,GUCY1A1,SPTLC2,ACPP,SAMD8,ITPKB,SH3GLB1,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,PLCG2,DCK,NOS2,IMPA1,PIP5K1B,HIF1A	up_VCAV_EC
GO:0010563	0.586	0.544	10	203	negative regulation of phosphorus metabolic	BP	1	KIRREL1,DCN,PRNP,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1,GREM1	down_VCAV_EC
GO:0045936	0.586	0.544	10	203	negative regulation of phosphate metabolic	BP	1	KIRREL1,DCN,PRNP,BGN,AKT1S1,ASPN,THY1,PARK7,SPRED1,GREM1	down_VCAV_EC
GO:0010468	0.586	0.552	10	1270	regulation of gene expression	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:0002252	0.586	0.558	8	166	immune effector process	BP	1	GPAM,LRP1,CFD,RNF216,MAVS,LOXL3,A2M,RAC2	down_VCAV_EC
GO:0051090	0.586	0.559	8	134	regulation of DNA-binding transcription factor	BP	1	ARHGEF2,VEGFA,NR1H4,BHLHE40,SMARCA4,MTDH,CTNNB1,DDIT3	down_VSAP_EC
GO:0030324	0.586	0.583	6	64	lung development	BP	1	BMP4,FGFR2,SEC24B,FGF18,TBX5,DAG1	up_ACOR_VSMC
GO:0051649	0.586	0.598	5	630	establishment of localization in cell	BP	1	HOOK3,XPOT,GCC2,SRP54,TMEM87B	up_VPOR_EC
GO:0006888	0.586	0.618	4	49	ER to Golgi vesicle-mediated transport	BP	1	ZW10,INSIG1,PREB,TRAPPC6A	down_ACOR_VSMC
GO:0009306	0.586	0.642	3	127	protein secretion	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:0010033	0.586	0.652	3	772	response to organic substance	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0014855	0.586	0.698	2	22	striated muscle cell proliferation	BP	1	PPARD,GLI1	down_ACOR_VSMC
GO:0008630	0.586	0.692	2	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	TMEM161A,FBH1	down_VCAV_EC
GO:0034644	0.586	0.694	2	32	cellular response to UV	BP	1	EIF2S1,CDKN1A	down_VSAP_EC
GO:0042490	0.586	0.7	2	19	mechanoreceptor differentiation	BP	1	BMP4,SEC24B	up_ACOR_VSMC
GO:0048483	0.586	0.7	2	19	autonomic nervous system development	BP	1	NRP1,FZD3	up_ACOR_VSMC
GO:0007033	0.586	0.69	2	82	vacuole organization	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0033692	0.586	0.699	2	20	cellular polysaccharide biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:1901224	0.586	0.699	2	20	positive regulation of NIK/NF-kappaB signaling	BP	1	RBCK1,SASH1	up_VSAP_EC
GO:0045428	0.586	0.796	1	10	regulation of nitric oxide biosynthetic process	BP	1	CAV1	down_ACOR_VSMC
GO:0003337	0.586	0.796	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	GREM1	down_ACOR_VSMC
GO:0010558	0.586	0.791	1	392	negative regulation of macromolecule biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0051726	0.586	0.79	1	393	regulation of cell cycle	BP	1	GPSM2	down_AFEM_EC

GO:0031663	0.586	0.79	1	17	lipopolysaccharide-mediated signaling	BP	1	SASH1	down_VCAV_EC
GO:0033173	0.586	0.789	1	17	calcineurin-NFAT signaling cascade	BP	1	PRNP	down_VCAV_EC
GO:0045604	0.586	0.79	1	17	regulation of epidermal cell differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0097720	0.586	0.789	1	17	calcineurin-mediated signaling	BP	1	PRNP	down_VCAV_EC
GO:0120163	0.586	0.789	1	17	negative regulation of cold-induced	BP	1	PLCL1	down_VCAV_EC
GO:0001945	0.586	0.797	1	9	lymph vessel development	BP	1	PTPN14	up_ACOR_VSMC
GO:0001946	0.586	0.797	1	9	lymphangiogenesis	BP	1	PTPN14	up_ACOR_VSMC
GO:0033233	0.586	0.798	1	9	regulation of protein sumoylation	BP	1	PARK7	up_ACOR_VSMC
GO:0036230	0.586	0.798	1	9	granulocyte activation	BP	1	F2RL1	up_ACOR_VSMC
GO:0036303	0.586	0.797	1	9	lymph vessel morphogenesis	BP	1	PTPN14	up_ACOR_VSMC
GO:1900363	0.586	0.801	1	8	regulation of mRNA polyadenylation	BP	1	CCNT1	up_ACOR_VSMC
GO:0046627	0.586	0.796	1	10	negative regulation of insulin receptor signaling	BP	1	NCK1	up_VCAV_EC
GO:0010035	0.586	0.783	1	107	response to inorganic substance	BP	1	FBP1	up_VPOR_EC
GO:0034472	0.586	0.798	1	9	snRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0043068	0.586	0.785	1	190	positive regulation of programmed cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0009889	0.586238079	0.49244	31	1190	regulation of biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,PKIB,SOX9,PKNOX2,FZD5,CCDC3,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0009059	0.587	0.454	126	1563	macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,ST8SIA6,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,ST6GAL1,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,ZDHHC22,IRF8,SOX18,PELI1,PPP3CA,YES1,B3GNT5,TARSL2,MTOR,SAMD8,ELF4,HHAT,BMP2,HMG20A,HHEX,CHST7,CREM,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,GALNT18,PRKD2,THOC1,SMARCA4,TLR3,MFNG,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,MRRF,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZDHHC6,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC
GO:0032501	0.587	0.535	14	1782	multicellular organismal process	BP	1	C3AR1,BARX1,HTR7,HOOK3,HOXA3,ARHGEF2,SLC7A11,SEMA3A,ASPN,ACVR2A,MTDH,RPL10L,HOXA2,RNF6	up_VPOR_EC
GO:0071417	0.587	0.529	13	142	cellular response to organonitrogen compound	BP	1	SLIT2,CDH1,GOT1,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,CASTOR1,NCK1,BGLAP	up_VSAP_EC
GO:1904951	0.587	0.551	9	108	positive regulation of establishment of protein localization	BP	1	HCLS1,TMEM173,FERMT1,GATA3,SH3GLB1,CTDSPL2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0006139	0.587	0.576	8	1909	nucleobase-containing compound metabolic	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0060491	0.587	0.597	5	62	regulation of cell projection assembly	BP	1	FSCN1,ANLN,CAV1,RAC1,CDC42EP4	down_ACOR_VSMC
GO:0120032	0.587	0.597	5	62	regulation of plasma membrane bounded cell	BP	1	FSCN1,ANLN,CAV1,RAC1,CDC42EP4	down_ACOR_VSMC
GO:0009913	0.587	0.618	4	47	epidermal cell differentiation	BP	1	FLNB,EZH2,HOXA7,GLI1	down_ACOR_VSMC
GO:0034341	0.587	0.619	4	43	response to interferon-gamma	BP	1	DAPK1,EVL,PARP9,CCL5	up_ACOR_VSMC
GO:0014070	0.587	0.613	4	172	response to organic cyclic compound	BP	1	LBH,CRY2,FIBIN,NR3C1	up_AFEM_EC

GO:0007229	0.587	0.649	3	32	integrin-mediated signaling pathway	BP	1	LIMS2,ABL1,EMP2	up_VSAP_EC
GO:0034614	0.587	0.691	2	39	cellular response to reactive oxygen species	BP	1	PARK7,MPV17	down_VCAV_EC
GO:0006303	0.587	0.699	2	19	double-strand break repair via nonhomologous	BP	1	TP53BP1,PARP9	up_ACOR_VSMC
GO:0040011	0.587	0.694	2	505	locomotion	BP	1	TBX5,NTRK2	up_APUL_EC
GO:0014855	0.587	0.697	2	22	striated muscle cell proliferation	BP	1	EPHB1,MEF2C	up_VCAV_EC
GO:0002684	0.587	0.69	2	239	positive regulation of immune system process	BP	1	C3AR1,ACVR2A	up_VPOR_EC
GO:0010646	0.587	0.705	2	945	regulation of cell communication	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0042059	0.587	0.795	1	10	negative regulation of epidermal growth factor receptor signaling	BP	1	NUP62	down_ACOR_VSMC
GO:0051894	0.587	0.795	1	10	positive regulation of focal adhesion assembly	BP	1	RAC1	down_ACOR_VSMC
GO:0070527	0.587	0.795	1	10	platelet aggregation	BP	1	ITGB3	down_ACOR_VSMC
GO:0009968	0.587	0.79	1	392	negative regulation of signal transduction	BP	1	IVNS1ABP	down_AFEM_EC
GO:2000142	0.587	0.788	1	17	regulation of DNA-templated transcription,	BP	1	CLSTN1	down_VCAV_EC
GO:0032501	0.587	0.838	1	1782	multicellular organismal process	BP	1	PLCL1	down_VFEM_EC
GO:0000154	0.587	0.789	1	15	rRNA modification	BP	1	MRPL1	down_VSAP_EC
GO:0072528	0.587	0.79	1	14	pyrimidine-containing compound biosynthetic	BP	1	CMPK1	down_VSAP_EC
GO:0097150	0.587	0.791	1	13	neuronal stem cell population maintenance	BP	1	HOOK3	down_VSAP_EC
GO:0032897	0.587	0.797	1	9	negative regulation of viral transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0035988	0.587	0.797	1	9	chondrocyte proliferation	BP	1	DDR2	up_ACOR_VSMC
GO:0046579	0.587	0.797	1	9	positive regulation of Ras protein signal	BP	1	F2RL1	up_ACOR_VSMC
GO:0048699	0.587	0.788	1	371	generation of neurons	BP	1	HOXC10	up_AORT_EC
GO:0006376	0.587	0.794	1	11	mRNA splice site selection	BP	1	PRPF39	up_VCAV_EC
GO:0021696	0.587	0.795	1	10	cerebellar cortex morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0043403	0.587	0.794	1	11	skeletal muscle tissue regeneration	BP	1	IFRD1	up_VCAV_EC
GO:0048286	0.587	0.793	1	11	lung alveolus development	BP	1	CREB1	up_VCAV_EC
GO:0046040	0.587	0.797	1	9	IMP metabolic process	BP	1	NT5C2	up_VSAP_EC
GO:0010212	0.588	0.596	5	60	response to ionizing radiation	BP	1	INTS7,RAD54L,RAD51,TOPBP1,MAP3K20	down_ACOR_VSMC
GO:0055067	0.588	0.617	4	42	monovalent inorganic cation homeostasis	BP	1	SLC26A7,DMXL1,EDN1,SLC8A1	up_ACOR_VSMC
GO:0002706	0.588	0.647	3	35	regulation of lymphocyte mediated immunity	BP	1	HMGB1,TFRC,FAM49B	down_ACOR_VSMC
GO:0031623	0.588	0.648	3	31	receptor internalization	BP	1	ACKR3,UBQLN2,FLOT1	up_VSAP_EC
GO:0051865	0.588	0.648	3	31	protein autoubiquitination	BP	1	DDB2,KLHL24,SASH1	up_VSAP_EC
GO:0048144	0.588	0.696	2	23	fibroblast proliferation	BP	1	CDK4,RNASEH2B	down_ACOR_VSMC
GO:0048145	0.588	0.696	2	23	regulation of fibroblast proliferation	BP	1	CDK4,RNASEH2B	down_ACOR_VSMC
GO:0048259	0.588	0.695	2	24	regulation of receptor-mediated endocytosis	BP	1	GREM1,HIST1H1A	down_ACOR_VSMC
GO:0006892	0.588	0.69	2	39	post-Golgi vesicle-mediated transport	BP	1	MYO1B,RAB31	down_VCAV_EC
GO:0033135	0.588	0.69	2	40	regulation of peptidyl-serine phosphorylation	BP	1	PLCL1,PARK7	down_VCAV_EC
GO:0006476	0.588	0.692	2	31	protein deacetylation	BP	1	MORF4L2,REST	down_VSAP_EC
GO:0046824	0.588	0.693	2	30	positive regulation of nucleocytoplasmic	BP	1	ZPR1,GSK3B	down_VSAP_EC
GO:1903321	0.588	0.692	2	33	negative regulation of protein modification by small protein conjugation	BP	1	NXN,SPOPL	down_VSAP_EC
GO:0008284	0.588	0.688	2	238	positive regulation of cell proliferation	BP	1	HOXA3,CCAR1	up_VPOR_EC

GO:0006793	0.588	0.704	2	948	phosphorus metabolic process	BP	1	PHEX,SLIT2	up_VPUL_VSMC
GO:0021695	0.588	0.697	2	20	cerebellar cortex development	BP	1	SEZ6L,DLL1	up_VSAP_EC
GO:0014070	0.588	0.783	1	172	response to organic cyclic compound	BP	1	NEDD4	down_ACOR_EC
GO:0006929	0.588	0.794	1	10	substrate-dependent cell migration	BP	1	ITGA2	down_ACOR_VSMC
GO:0030195	0.588	0.794	1	10	negative regulation of blood coagulation	BP	1	TFPI	down_ACOR_VSMC
GO:0050918	0.588	0.795	1	10	positive chemotaxis	BP	1	CORO1A	down_ACOR_VSMC
GO:1900047	0.588	0.794	1	10	negative regulation of hemostasis	BP	1	TFPI	down_ACOR_VSMC
GO:0046148	0.588	0.787	1	17	pigment biosynthetic process	BP	1	UROS	down_VCAV_EC
GO:0010467	0.588	0.837	1	1787	gene expression	BP	1	MOSPD1	down_VFEM_EC
GO:0006826	0.588	0.789	1	15	iron ion transport	BP	1	TFRC	down_VSAP_EC
GO:0010677	0.588	0.789	1	14	negative regulation of cellular carbohydrate	BP	1	ENPP1	down_VSAP_EC
GO:0014910	0.588	0.791	1	13	regulation of smooth muscle cell migration	BP	1	SERPINE1	down_VSAP_EC
GO:0060445	0.588	0.79	1	13	branching involved in salivary gland	BP	1	NRP1	down_VSAP_EC
GO:0070072	0.588	0.798	1	8	vacuolar proton-transporting V-type	BP	1	DMXL1	up_ACOR_VSMC
GO:0070070	0.588	0.798	1	8	proton-transporting V-type ATPase complex	BP	1	DMXL1	up_ACOR_VSMC
GO:0070071	0.588	0.798	1	8	proton-transporting two-sector ATPase complex	BP	1	DMXL1	up_ACOR_VSMC
GO:0140014	0.588	0.782	1	110	mitotic nuclear division	BP	1	MZT1	up_VPOR_EC
GO:0051130	0.588	0.787	1	342	positive regulation of cellular component	BP	1	SHOX2	up_VFEM_VSMC
GO:0045063	0.588	0.796	1	9	T-helper 1 cell differentiation	BP	1	STAT6	up_VSAP_EC
GO:1905952	0.588272069	0.78293	1	33	regulation of lipid localization	BP	1	PRKCD	up_ACOR_EC
GO:0006936	0.588376096	0.68742	2	74	muscle contraction	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0030031	0.588496736	0.61144	4	155	cell projection assembly	BP	1	ACTN2,NRP1,ARHGEF26,PRKCD	up_ACOR_EC
GO:0045087	0.589	0.519	15	161	innate immune response	BP	1	ABL1,TRAFD1,CDC42EP2,F2RL1,MYD88,CFD,NLRX1,TKFC,CYBA,STX4,PQBP1,UNC93B1,FLOT1,MAVS,JCHAIN	up_VSAP_EC
GO:0033993	0.589	0.547	9	186	response to lipid	BP	1	ADCY6,SLC10A3,KANK2,NR3C1,ENSCAFG00000013404,TMEM161A,PARK7,ZFP36L1,SASH1	down_VCAV_EC
GO:0090596	0.589	0.558	8	84	sensory organ morphogenesis	BP	1	BMP4,FGFR2,SEC24B,CITED2,FZD3,FRS2,CHD7,EDN1	up_ACOR_VSMC
GO:0031647	0.589	0.567	7	87	regulation of protein stability	BP	1	LSS,SREBF1,USP4,NF2,RAD23A,TADA2A,CCT4	down_ACOR_VSMC
GO:0009126	0.589	0.592	5	100	purine nucleoside monophosphate metabolic process	BP	1	NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2	down_VCAV_EC
GO:0009167	0.589	0.592	5	100	purine ribonucleoside monophosphate metabolic process	BP	1	NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2	down_VCAV_EC
GO:0001935	0.589	0.615	4	50	endothelial cell proliferation	BP	1	HMGB1,CAV1,NRAS,HMGB2	down_ACOR_VSMC
GO:0018210	0.589	0.644	3	48	peptidyl-threonine modification	BP	1	GALNT1,GSK3B,CAMK2D	down_VSAP_EC
GO:0070887	0.589	0.649	3	775	cellular response to chemical stimulus	BP	1	NR1H4,NPNT,NTRK2	up_APUL_EC
GO:0000018	0.589	0.647	3	31	regulation of DNA recombination	BP	1	FIGNL1,THOC1,BLM	up_VCAV_EC
GO:0042476	0.589	0.646	3	36	odontogenesis	BP	1	CD34,BMP2,ITGA6	up_VCAV_EC
GO:0097553	0.589	0.647	3	32	calcium ion transmembrane import	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0097306	0.589	0.695	2	22	cellular response to alcohol	BP	1	RAD51,CDK4	down_ACOR_VSMC
GO:1990823	0.589	0.69	2	39	response to leukemia inhibitory factor	BP	1	PCOLCE,GFPT2	down_VCAV_EC
GO:1990830	0.589	0.69	2	39	cellular response to leukemia inhibitory factor	BP	1	PCOLCE,GFPT2	down_VCAV_EC
GO:0003073	0.589	0.697	2	20	regulation of systemic arterial blood pressure	BP	1	EMP2,F2RL1	up_VSAP_EC

GO:0051897	0.589	0.697	2	20	positive regulation of protein kinase B signaling	BP	1	HPSE,BAG4	up_VSAP_EC
GO:0048870	0.589	0.691	2	451	cell motility	BP	1	EMX2,CAV1	up_VSAP_VSMC
GO:0051674	0.589	0.691	2	451	localization of cell	BP	1	EMX2,CAV1	up_VSAP_VSMC
GO:0031670	0.589	0.793	1	10	cellular response to nutrient	BP	1	PDXP	down_ACOR_VSMC
GO:2000725	0.589	0.794	1	10	regulation of cardiac muscle cell differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0032786	0.589	0.79	1	13	positive regulation of DNA-templated transcription, elongation	BP	1	DDX39B	down_VSAP_EC
GO:0072087	0.589	0.788	1	14	renal vesicle development	BP	1	CTNNB1	down_VSAP_EC
GO:0023051	0.589	0.805	1	954	regulation of signaling	BP	1	GATA5	down_VSAP_VSMC
GO:0046329	0.589	0.795	1	9	negative regulation of JNK cascade	BP	1	F2RL1	up_ACOR_VSMC
GO:0008203	0.589	0.781	1	37	cholesterol metabolic process	BP	1	LEP	up_AFEM_EC
GO:0015850	0.589	0.782	1	37	organic hydroxy compound transport	BP	1	LEP	up_AFEM_EC
GO:0035305	0.589	0.782	1	37	negative regulation of dephosphorylation	BP	1	MYO1D	up_AFEM_EC
GO:0006767	0.589	0.79	1	12	water-soluble vitamin metabolic process	BP	1	ACPP	up_VCAV_EC
GO:1902930	0.589	0.794	1	10	regulation of alcohol biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0002682	0.589	0.786	1	343	regulation of immune system process	BP	1	HOXA9	up_VFEM_VSMC
GO:0051606	0.589390731	0.78196	1	33	detection of stimulus	BP	1	NOD2	up_ACOR_EC
GO:0040007	0.59	0.498	23	276	growth	BP	1	IFRD1,CDA,PDE4D,MEF2C,CHD7,STC1,GATA3,EDN1,RAB11A,IRF8,MTOR,HHEX,PROX1,SMARCA4,APOD,SLC25A25,CREB1,VPS54,SPTBN4,HIF1A,ATRX,RBBP6,GINS4	up_VCAV_EC
GO:0009893	0.59	0.6	5	995	positive regulation of metabolic process	BP	1	ACVRL1,LYN,HOXA1,ACSL3,NEDD4	down_ACOR_EC
GO:0098742	0.59	0.615	4	44	cell-cell adhesion via plasma-membrane	BP	1	PCDH19,CDH1,CLDN1,TGFBR2	up_VSAP_EC
GO:0031398	0.59	0.642	3	51	positive regulation of protein ubiquitination	BP	1	PRICKLE1,HSPA5,TRIB3	down_VSAP_EC
GO:0032922	0.59	0.696	2	19	circadian regulation of gene expression	BP	1	PPARGC1A,RBM4B	up_ACOR_VSMC
GO:0042493	0.59	0.781	1	178	response to drug	BP	1	PDPN	down_ACOR_EC
GO:0071604	0.59	0.793	1	10	transforming growth factor beta production	BP	1	SLC29A1	down_ACOR_VSMC
GO:0071634	0.59	0.793	1	10	regulation of transforming growth factor beta	BP	1	SLC29A1	down_ACOR_VSMC
GO:0009719	0.59	0.787	1	395	response to endogenous stimulus	BP	1	GABPA	down_AFEM_EC
GO:0042116	0.59	0.785	1	18	macrophage activation	BP	1	BPI	down_VCAV_EC
GO:0061387	0.59	0.785	1	18	regulation of extent of cell growth	BP	1	TRPV2	down_VCAV_EC
GO:0043044	0.59	0.788	1	14	ATP-dependent chromatin remodeling	BP	1	SMARCA4	down_VSAP_EC
GO:0003148	0.59	0.788	1	13	outflow tract septum morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0032735	0.59	0.794	1	9	positive regulation of interleukin-12 production	BP	1	TLR3	up_ACOR_VSMC
GO:0090162	0.59	0.794	1	9	establishment of epithelial cell polarity	BP	1	FERMT1	up_ACOR_VSMC
GO:0001570	0.59	0.781	1	37	vasculogenesis	BP	1	TMEM100	up_AFEM_EC
GO:0002065	0.59	0.781	1	37	columnar/cuboidal epithelial cell	BP	1	DLL1	up_AFEM_EC
GO:0030866	0.59	0.793	1	10	cortical actin cytoskeleton organization	BP	1	EPB41	up_VCAV_EC
GO:2001026	0.59	0.793	1	10	regulation of endothelial cell chemotaxis	BP	1	PRKD2	up_VCAV_EC
GO:0070734	0.59	0.795	1	9	histone H3-K27 methylation	BP	1	PHF1	up_VSAP_EC
GO:1902532	0.59	0.782	1	204	negative regulation of intracellular signal	BP	1	CAV1	up_VSAP_VSMC

GO:0019219	0.590302815	0.4893	30	1151	regulation of nucleobase-containing compound metabolic process	BP	1	NR1H4,GATA4,TRPS1,PKIB,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0006672	0.590653243	0.78086	1	33	ceramide metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0007178	0.591	0.54	10	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FZD1,HNF4A,ABL1,ZEB1,LRP4,NCEH1,HPGD,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0072175	0.591	0.593	5	60	epithelial tube formation	BP	1	PODXL,GATA3,BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0023052	0.591	0.63	4	1602	signaling	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0035821	0.591	0.645	3	32	modification of morphology or physiology	BP	1	F2RL1,DAG1,INPP5K	up_ACOR_VSMC
GO:0032204	0.591	0.644	3	35	regulation of telomere maintenance	BP	1	HMBOX1,ATRX,DCP2	up_VCAV_EC
GO:0046849	0.591	0.692	2	23	bone remodeling	BP	1	GREM1,TFRC	down_ACOR_VSMC
GO:0006355	0.591	0.701	2	974	regulation of transcription, DNA-pathway-restricted SMAD protein phosphorylation	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0060389	0.591	0.693	2	21	positive regulation of protein metabolic process	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:0051247	0.591	0.691	2	502	glutamine family amino acid metabolic process	BP	1	NPNT,NTRK2	up_APUL_EC
GO:0009064	0.591	0.692	2	23	keratinocyte proliferation	BP	1	ARG2,AADAT	up_VCAV_EC
GO:0043616	0.591	0.792	1	10	negative regulation of insulin receptor signaling	BP	1	PPARD	down_ACOR_VSMC
GO:0046627	0.591	0.792	1	10	endocrine hormone secretion	BP	1	NCOA5	down_ACOR_VSMC
GO:0060986	0.591	0.792	1	10	hematopoietic stem cell proliferation	BP	1	FAM129B	down_ACOR_VSMC
GO:0071425	0.591	0.792	1	10	regulation of sodium ion transmembrane transporter activity	BP	1	PDCD2	down_ACOR_VSMC
GO:2000649	0.591	0.79	1	11	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	NEDD4	down_ACOR_VSMC
GO:0000184	0.591	0.784	1	18	positive regulation of signal transduction	BP	1	PYM1	down_VCAV_EC
GO:0009967	0.591	0.787	1	435	regulation of dendritic spine development	BP	1	CITED2	down_VPOR_EC
GO:0060998	0.591	0.787	1	14	lysosome localization	BP	1	APOE	down_VSAP_EC
GO:0032418	0.591	0.785	1	17	regulation of endocrine process	BP	1	LYN	down_VSAP_EC
GO:0044060	0.591	0.793	1	9	potassium ion transport	BP	1	F2RL1	up_ACOR_VSMC
GO:0006813	0.591	0.78	1	37	determination of left/right symmetry	BP	1	KCNC4	up_AFEM_EC
GO:0007368	0.591	0.78	1	37	hexose transmembrane transport	BP	1	DLL1	up_AFEM_EC
GO:0008645	0.591	0.78	1	37	monosaccharide transmembrane transport	BP	1	LEP	up_AFEM_EC
GO:0015749	0.591	0.78	1	37	positive regulation of actin filament	BP	1	LEP	up_AFEM_EC
GO:0030838	0.591	0.78	1	37	carbohydrate transmembrane transport	BP	1	CDC42EP5	up_AFEM_EC
GO:0034219	0.591	0.78	1	37	immune response-regulating cell surface receptor signaling	BP	1	LEP	up_AFEM_EC
GO:0002768	0.591	0.78	1	37	lipid homeostasis	BP	1	CYLD	up_AFEM_EC
GO:0055088	0.591	0.78	1	37	regulation of DNA biosynthetic process	BP	1	GPAM	up_AFEM_EC
GO:2000278	0.591	0.78	1	37	chromatin organization	BP	1	GREM1	up_AFEM_EC
GO:0006325	0.591	0.781	1	234	regulation of osteoblast proliferation	BP	1	NR1H4	up_APUL_EC
GO:0033688	0.591	0.792	1	10	positive regulation of viral transcription	BP	1	BMP2	up_VCAV_EC
GO:0050434	0.591	0.792	1	10	defense response to Gram-positive bacterium	BP	1	SMARCA4	up_VCAV_EC
GO:0050830	0.591	0.789	1	12	positive regulation of organelle organization	BP	1	LYZ	up_VCAV_EC
GO:0010638	0.591	0.781	1	207		BP	1	CDC42EP5	up_VFEM_EC

GO:0046903	0.591	0.782	1	255	secretion	BP	1	NR1H4	up_VPUL_EC
GO:0010800	0.591	0.793	1	9	positive regulation of peptidyl-threonine	BP	1	TNKS1BP1	up_VSAP_EC
GO:2000637	0.591	0.794	1	9	positive regulation of gene silencing by miRNA	BP	1	LIMD1	up_VSAP_EC
GO:0051453	0.591403609	0.7802	1	33	regulation of intracellular pH	BP	1	SLC9A9	up_ACOR_EC
GO:0007186	0.592	0.562	7	124	G protein-coupled receptor signaling	BP	1	PRKACB,RGS2,PLCL1,AGRN,GNAQ,APOE,RDH11	down_VSAP_EC
GO:0003013	0.592	0.562	7	121	circulatory system process	BP	1	PRCP,PTGS2,HTR7,ACTA2,APOE,PLOD3,CALM1	down_VSAP_EC
GO:0016485	0.592	0.576	6	73	protein processing	BP	1	BIRC5,CASP2,MMP14,DHCR24,ENSCAFG00000005299,PMPCA	down_ACOR_VSMC
GO:0052548	0.592	0.609	4	80	regulation of endopeptidase activity	BP	1	CST3,RECK,PARK7,IFT57	down_VCAV_EC
GO:0097237	0.592	0.614	4	42	cellular response to toxic substance	BP	1	TP53INP1,PRKCE,SESN1,PARK7	up_ACOR_VSMC
GO:0019693	0.592	0.608	4	172	ribose phosphate metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0002244	0.592	0.643	3	35	hematopoietic progenitor cell differentiation	BP	1	ANLN,HSPA9,PDCD2	down_ACOR_VSMC
GO:0009260	0.592	0.684	2	83	ribonucleotide biosynthetic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0046390	0.592	0.684	2	83	ribose phosphate biosynthetic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0006356	0.592	0.693	2	20	regulation of transcription by RNA polymerase I	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0006458	0.592	0.791	1	10	'de novo' protein folding	BP	1	CCT4	down_ACOR_VSMC
GO:0038179	0.592	0.791	1	10	neurotrophin signaling pathway	BP	1	CORO1A	down_ACOR_VSMC
GO:0042558	0.592	0.789	1	11	pteridine-containing compound metabolic	BP	1	GGH	down_ACOR_VSMC
GO:0060428	0.592	0.784	1	17	lung epithelium development	BP	1	THRB	down_VCAV_EC
GO:0071599	0.592	0.793	1	9	otic vesicle development	BP	1	FGFR2	up_ACOR_VSMC
GO:0036294	0.592	0.78	1	37	cellular response to decreased oxygen levels	BP	1	ANGPT4	up_AFEM_EC
GO:0071456	0.592	0.78	1	37	cellular response to hypoxia	BP	1	ANGPT4	up_AFEM_EC
GO:0070198	0.592	0.791	1	10	protein localization to chromosome, telomeric	BP	1	ATRX	up_VCAV_EC
GO:0043279	0.592	0.791	1	10	response to alkaloid	BP	1	BLM	up_VCAV_EC
GO:0006820	0.592	0.778	1	109	anion transport	BP	1	SLC7A11	up_VPOR_EC
GO:0045893	0.593	0.491	25	413	positive regulation of transcription, DNA-templated	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0060541	0.593	0.575	6	73	respiratory system development	BP	1	TIMELESS,MMP14,GLI1,JMJD6,MSC,SIX4	down_ACOR_VSMC
GO:0018209	0.593	0.572	6	125	peptidyl-serine modification	BP	1	DCN,AKT2,PLCL1,PARK7,MAST2,CAMK2D	down_VCAV_EC
GO:0008104	0.593	0.577	6	763	protein localization	BP	1	MZT1,HOOK3,XPOT,ENSCAFG00000002015,GCC2,SRP54	up_VPOR_EC
GO:0072073	0.593	0.591	5	60	kidney epithelium development	BP	1	GREM1,ARG2,HOXB7,IQGAP1,SIX4	down_ACOR_VSMC
GO:0010817	0.593	0.588	5	102	regulation of hormone levels	BP	1	CYP1B1,RETSAT,PARK7,RDH10,PCSK6	down_VCAV_EC
GO:0072009	0.593	0.611	4	48	nephron epithelium development	BP	1	GREM1,HOXB7,IQGAP1,SIX4	down_ACOR_VSMC
GO:0051225	0.593	0.639	3	49	spindle assembly	BP	1	MZT1,TUBB,KPNB1	down_VSAP_EC
GO:1905477	0.593	0.643	3	32	positive regulation of protein localization to	BP	1	LRP4,KCNB1,STX4	up_VSAP_EC
GO:1903506	0.593	0.699	2	977	regulation of nucleic acid-templated transcription	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0021766	0.593	0.693	2	20	hippocampus development	BP	1	FGF13,TMEM108	up_ACOR_VSMC
GO:0061614	0.593	0.693	2	20	pri-miRNA transcription by RNA polymerase II	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:1901019	0.593	0.692	2	20	regulation of calcium ion transmembrane transporter activity	BP	1	PLCG2,CACNB3	up_ACOR_VSMC
GO:0001658	0.593	0.69	2	24	branching involved in ureteric bud	BP	1	HOXB7,BMP2	up_VCAV_EC

GO:0023051	0.593	0.699	2	954	regulation of signaling	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:1902622	0.593	0.788	1	11	regulation of neutrophil migration	BP	1	RAC1	down_ACOR_VSMC
GO:0007435	0.593	0.782	1	18	salivary gland morphogenesis	BP	1	SEMA3C	down_VCAV_EC
GO:1901862	0.593	0.785	1	14	negative regulation of muscle tissue	BP	1	SIX4	down_VSAP_EC
GO:2000242	0.593	0.784	1	15	negative regulation of reproductive process	BP	1	SULF1	down_VSAP_EC
GO:0007263	0.593	0.795	1	8	nitric oxide mediated signal transduction	BP	1	PDE5A	up_ACOR_VSMC
GO:0031498	0.593	0.794	1	8	chromatin disassembly	BP	1	SMARCD3	up_ACOR_VSMC
GO:0072359	0.593	0.783	1	368	circulatory system development	BP	1	SGCD	up_AORT_EC
GO:0033554	0.593	0.794	1	708	cellular response to stress	BP	1	ARG2	up_AORT_VSMC
GO:0032365	0.593	0.792	1	9	intracellular lipid transport	BP	1	ABCA1	up_VCAV_EC
GO:0042462	0.593	0.792	1	9	eye photoreceptor cell development	BP	1	THRB	up_VSAP_EC
GO:0045717	0.593	0.792	1	9	negative regulation of fatty acid biosynthetic	BP	1	INSIG2	up_VSAP_EC
GO:0098754	0.593	0.792	1	9	detoxification	BP	1	SESN1	up_VSAP_EC
GO:0008285	0.593	0.779	1	201	negative regulation of cell proliferation	BP	1	CAV1	up_VSAP_VSMC
GO:0048645	0.593252849	0.77857	1	33	animal organ formation	BP	1	TBX5	up_ACOR_EC
GO:0090263	0.593952626	0.77795	1	33	positive regulation of canonical Wnt signaling	BP	1	CDH3	up_ACOR_EC
GO:0010648	0.594	0.475	38	407	negative regulation of cell communication	BP	1	FZD1,WNT11,ACKR3,AXIN2,TBC1D10C,SLIT2,ABL1,HDAC7,EPN2,SESN1,F2RL1,GLIS2,MFN2,MYC,PIK3IP1,SULF2,HIC1,RTN4RL1,CREBRF,LRP4,GDPD5,CASTOR1,KCNB1,LIMD1,NLRX1,TKFC,FBLN1,RAF1,MAPKBP1,QARS,ARHGAP12,UBQLN2,NCK1,HMOX1,NPRL3,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0080134	0.594	0.476	36	386	regulation of response to stress	BP	1	FZD1,NAPEPLD,ACKR3,ARHGEF5,AXIN2,ABL1,KLKB1,SESN1,MAP3K5,IL17RC,TRAFD1,HPSE,F2RL1,PIK3R1,MYC,RTN4RL1,SASH1,FBXO4,MYD88,NPAS2,FBXO7,NLRX1,TKFC,CDK9,RNF216,YPEL3,MAPKBP1,CYBA,PQBP1,QARS,UBQLN2,UNC93B1,FLOT1,NCK1,MAVS,MAP2K2	up_VSAP_EC
GO:0044087	0.594	0.481	32	339	regulation of cellular component biogenesis	BP	1	SYNPO2L,SMAD6,ARHGAP28,FEZ1,PRKAA2,LCAT,EVI5L,SYNPO2,TUBB4A,SEC24B,ATXN2,LMO4,F2RL1,JMY,CLSTN1,NRP1,ORMDL3,EVL,SLITRK5,TBX20,PRKCE,DAG1,APP,DUSP22,SSH3,EDN1,ASAP1,FAM107A,KIF9,FEZ2,INPP5K,WASL	up_ACOR_VSMC
GO:0044092	0.594	0.497	21	270	negative regulation of molecular function	BP	1	PPP2R5A,TNFAIP3,AMOT,PDGFB,NLRC5,RALB,CTTNBP2NL,ARHGAP28,PELI1,PPP3CA,HHEX,PREX2,SH3BP5,PROX1,ENSCAFG00000010596,STMN1,PAK2,CD200,PTGS2,KDM5A,FKBP15	up_VCAV_EC
GO:0032502	0.594	0.531	13	1661	developmental process	BP	1	C3AR1,BARX1,PTK7,HOOK3,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,MTDH,HOXA2,RNF6	up_VPOR_EC
GO:0043010	0.594	0.544	9	96	camera-type eye development	BP	1	BMP4,GJA1,CITED2,NRP1,GPM6A,SMARCD3,FRS2,CHD7,CLN8	up_ACOR_VSMC
GO:0044237	0.594	0.592	9	3491	cellular metabolic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0009144	0.594	0.551	8	103	purine nucleoside triphosphate metabolic	BP	1	RAN,CDK1,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,NUDT1,ATP5F1D	down_ACOR_VSMC
GO:0046486	0.594	0.551	8	102	glycerolipid metabolic process	BP	1	PDGFB,GK5,SERINC5,ENSCAFG00000010596,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0046486	0.594	0.572	6	102	glycerolipid metabolic process	BP	1	NR1H4,PTPN11,SEL1L,APOE,SH3GLB1,ABHD5	down_VSAP_EC
GO:0030178	0.594	0.591	5	52	negative regulation of Wnt signaling pathway	BP	1	MLLT3,FERMT1,LATS2,ZNRF3,CLSTN1	up_ACOR_VSMC
GO:0006793	0.594	0.616	4	948	phosphorus metabolic process	BP	1	EYA1,MAP2K6,CDC42EP5,ADCY3	up_VFEM_EC
GO:0046631	0.594	0.641	3	35	alpha-beta T cell activation	BP	1	HMGB1,ARG2,ELF4	down_ACOR_VSMC
GO:0048515	0.594	0.641	3	36	spermatid differentiation	BP	1	TRIP13,HMGB2,TTLL1	down_ACOR_VSMC
GO:0072088	0.594	0.641	3	36	nephron epithelium morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC

GO:0031929	0.594	0.636	3	62	TOR signaling	BP	1	AKT1S1,CLEC16A,EIF4EBP1	down_VCAV_EC
GO:0071407	0.594	0.635	3	129	cellular response to organic cyclic compound	BP	1	LBH,CRY2,NR3C1	up_AFEM_EC
GO:0072088	0.594	0.641	3	36	nephron epithelium morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:2001141	0.594	0.698	2	979	regulation of RNA biosynthetic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0006493	0.594	0.692	2	20	protein O-linked glycosylation	BP	1	FKRP,GALNT11	up_VSAP_EC
GO:0032418	0.594	0.782	1	17	lysosome localization	BP	1	RAC2	down_VCAV_EC
GO:0042509	0.594	0.782	1	17	regulation of tyrosine phosphorylation of STAT	BP	1	ARL2BP	down_VCAV_EC
GO:0034629	0.594	0.785	1	14	cellular protein-containing complex localization	BP	1	MZT1	down_VSAP_EC
GO:0061647	0.594	0.785	1	13	histone H3-K9 modification	BP	1	KDM3A	down_VSAP_EC
GO:0009593	0.594	0.787	1	11	detection of chemical stimulus	BP	1	P2RX2	up_VCAV_EC
GO:0043555	0.594	0.789	1	10	regulation of translation in response to stress	BP	1	NCK1	up_VCAV_EC
GO:0071622	0.594	0.785	1	13	regulation of granulocyte chemotaxis	BP	1	CXCL8	up_VCAV_EC
GO:0007346	0.594	0.778	1	210	regulation of mitotic cell cycle	BP	1	MAP2K6	up_VFEM_EC
GO:0046579	0.594	0.791	1	9	positive regulation of Ras protein signal	BP	1	F2RL1	up_VSAP_EC
GO:0046850	0.594	0.791	1	9	regulation of bone remodeling	BP	1	PPARGC1B	up_VSAP_EC
GO:0050982	0.594	0.791	1	9	detection of mechanical stimulus	BP	1	DENND5A	up_VSAP_EC
GO:0046676	0.594	0.791	1	9	negative regulation of insulin secretion	BP	1	KCNB1	up_VSAP_EC
GO:0050678	0.594271153	0.63445	3	117	regulation of epithelial cell proliferation	BP	1	CDH3,SOX9,PYGO2	up_ACOR_EC
GO:1901292	0.594816691	0.77704	1	34	nucleoside phosphate catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0030534	0.594902927	0.77711	1	33	adult behavior	BP	1	TMOD1	up_ACOR_EC
GO:0050866	0.595	0.61	4	48	negative regulation of cell activation	BP	1	HMGB1,MNDA,HMGB3,ARG2	down_ACOR_VSMC
GO:0106106	0.595	0.609	4	48	cold-induced thermogenesis	BP	1	CAV1,ADIPOR2,HOXC10,ELOVL6	down_ACOR_VSMC
GO:0120161	0.595	0.609	4	48	regulation of cold-induced thermogenesis	BP	1	CAV1,ADIPOR2,HOXC10,ELOVL6	down_ACOR_VSMC
GO:0043406	0.595	0.635	3	62	positive regulation of MAP kinase activity	BP	1	CSPG4,SASH1,SHC1	down_VCAV_EC
GO:0031326	0.595	0.652	3	1176	regulation of cellular biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0010717	0.595	0.641	3	32	regulation of epithelial to mesenchymal transition	BP	1	AXIN2,TIAM1,TGFBR2	up_VSAP_EC
GO:0099173	0.595	0.683	2	40	postsynapse organization	BP	1	PRNP,CDH2	down_VCAV_EC
GO:0021872	0.595	0.691	2	19	forebrain generation of neurons	BP	1	FGFR2,NRP1	up_ACOR_VSMC
GO:0003156	0.595	0.691	2	20	regulation of animal organ formation	BP	1	HOXA11,CITED2	up_VSAP_EC
GO:0043370	0.595	0.789	1	10	regulation of CD4-positive, alpha-beta T cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0048806	0.595	0.788	1	10	genitalia development	BP	1	DHCR24	down_ACOR_VSMC
GO:0090181	0.595	0.789	1	10	regulation of cholesterol metabolic process	BP	1	SREBF1	down_ACOR_VSMC
GO:0090278	0.595	0.789	1	10	negative regulation of peptide hormone	BP	1	SREBF1	down_ACOR_VSMC
GO:0006919	0.595	0.782	1	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	IFT57	down_VCAV_EC
GO:0010972	0.595	0.781	1	18	negative regulation of G2/M transition of mitotic	BP	1	BRSK1	down_VCAV_EC
GO:0030260	0.595	0.782	1	15	entry into host cell	BP	1	P4HB	down_VSAP_EC
GO:0031960	0.595	0.783	1	15	response to corticosteroid	BP	1	REST	down_VSAP_EC
GO:0036465	0.595	0.784	1	13	synaptic vesicle recycling	BP	1	CANX	down_VSAP_EC
GO:0043954	0.595	0.783	1	14	cellular component maintenance	BP	1	APOE	down_VSAP_EC

GO:0044409	0.595	0.782	1	15	entry into host	BP	1	P4HB	down_VSAP_EC
GO:0048635	0.595	0.784	1	14	negative regulation of muscle organ	BP	1	SIX4	down_VSAP_EC
GO:0051384	0.595	0.783	1	15	response to glucocorticoid	BP	1	REST	down_VSAP_EC
GO:0051806	0.595	0.782	1	15	entry into cell of other organism involved in	BP	1	P4HB	down_VSAP_EC
GO:0051828	0.595	0.782	1	15	entry into other organism involved in symbiotic	BP	1	P4HB	down_VSAP_EC
GO:2000826	0.595	0.784	1	14	regulation of heart morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0019377	0.595	0.79	1	9	glycolipid catabolic process	BP	1	NEU3	up_ACOR_VSMC
GO:0032732	0.595	0.79	1	9	positive regulation of interleukin-1 production	BP	1	NOD2	up_ACOR_VSMC
GO:0046479	0.595	0.79	1	9	glycosphingolipid catabolic process	BP	1	NEU3	up_ACOR_VSMC
GO:0046514	0.595	0.79	1	9	ceramide catabolic process	BP	1	NEU3	up_ACOR_VSMC
GO:0070861	0.595	0.79	1	9	regulation of protein exit from endoplasmic	BP	1	OS9	up_ACOR_VSMC
GO:0060341	0.595	0.779	1	255	regulation of cellular localization	BP	1	NR1H4	up_VPUL_EC
GO:0051254	0.595	0.784	1	431	positive regulation of RNA metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0032479	0.595917704	0.77621	1	33	regulation of type I interferon production	BP	1	MAVS	up_ACOR_EC
GO:0006508	0.596	0.468	45	483	proteolysis	BP	1	MBP,ZRANB1,RECK,SKP2,CPXM1,SH3RF2,ISG15,ZNRF3,CTSS,PTPN3,USP53,CST3,KLHL20,PSEN2,ERO1B,DAPK1,CTSB,UBR1,OS9,STT3B,UBE2H,SH3RF1,RNF24,RNF19A,SCG5,DAG1,PSEN1,PCSK6,SPINK2,PERP,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,NCSTN,WFS1,WDR48,DZIP3,ERAP1,PARK7	up_ACOR_VSMC
GO:0007389	0.596	0.528	11	137	pattern specification process	BP	1	HOXA3,GREM1,HOXA7,HOXC10,HOXB7,HOXC6,HOXB5,HOXC4,HOXA9,GLI1,RTTN	down_ACOR_VSMC
GO:0048523	0.596	0.537	11	1399	negative regulation of cellular process	BP	1	BARX1,CXHXorf57,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,FBP1,MTDH,TWF1,RNF6	up_VPOR_EC
GO:0048511	0.596	0.572	6	72	rhythmic process	BP	1	SREBF1,HNRNPD,TIMELESS,THRAP3,EZH2,SGPL1	down_ACOR_VSMC
GO:0048284	0.596	0.572	6	66	organelle fusion	BP	1	USP6NL,SYT16,EVI5L,STX11,BNIP3,SGSM2	up_ACOR_VSMC
GO:0043069	0.596	0.569	6	262	negative regulation of programmed cell death	BP	1	ANGPT4,DLL1,CRYAB,GPAM,GREM1,PPARGC1A	up_AFEM_EC
GO:0000122	0.596	0.584	5	218	negative regulation of transcription by RNA polymerase II	BP	1	LEP,HOXA7,LMCD1,THRB,NR3C1	up_AFEM_EC
GO:0007519	0.596	0.608	4	49	skeletal muscle tissue development	BP	1	FLNB,CAV1,MSC,SIX4	down_ACOR_VSMC
GO:0001101	0.596	0.606	4	65	response to acid chemical	BP	1	NR1H4,SESN2,YES1,LYN	down_VSAP_EC
GO:0044264	0.596	0.64	3	32	cellular polysaccharide metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0030010	0.596	0.682	2	41	establishment of cell polarity	BP	1	UST,BRSK1	down_VCAV_EC
GO:0070509	0.596	0.689	2	21	calcium ion import	BP	1	MICU2,SLC8A1	up_ACOR_VSMC
GO:1901653	0.596	0.68	2	84	cellular response to peptide	BP	1	CAMK2A,KANK1	up_AFEM_EC
GO:0044703	0.596	0.776	1	172	multi-organism reproductive process	BP	1	ACSL4	down_ACOR_EC
GO:0001702	0.596	0.788	1	10	gastrulation with mouth forming second	BP	1	UGDH	down_ACOR_VSMC
GO:0033198	0.596	0.787	1	10	response to ATP	BP	1	PDXP	down_ACOR_VSMC
GO:0043001	0.596	0.786	1	11	Golgi to plasma membrane protein	BP	1	ACSL3	down_ACOR_VSMC
GO:0010171	0.596	0.78	1	18	body morphogenesis	BP	1	CRISPLD2	down_VCAV_EC
GO:0060420	0.596	0.78	1	18	regulation of heart growth	BP	1	BMPR1A	down_VCAV_EC
GO:0042698	0.596	0.783	1	14	ovulation cycle	BP	1	INHBA	down_VSAP_EC
GO:0060512	0.596	0.783	1	14	prostate gland morphogenesis	BP	1	SULF1	down_VSAP_EC
GO:0000096	0.596	0.79	1	9	sulfur amino acid metabolic process	BP	1	PCYOX1	up_ACOR_VSMC

GO:0034122	0.596	0.79	1	9	negative regulation of toll-like receptor signaling	BP	1	F2RL1	up_ACOR_VSMC
GO:0036124	0.596	0.792	1	8	histone H3-K9 trimethylation	BP	1	ATRX	up_ACOR_VSMC
GO:0031324	0.596	0.792	1	735	negative regulation of cellular metabolic process	BP	1	ESR1	up_AORT_VSMC
GO:0016101	0.596	0.784	1	13	diterpenoid metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0060572	0.596	0.786	1	11	morphogenesis of an epithelial bud	BP	1	HHEX	up_VCAV_EC
GO:0097193	0.596	0.775	1	109	intrinsic apoptotic signaling pathway	BP	1	ARHGEF2	up_VPOR_EC
GO:0009967	0.596	0.783	1	435	positive regulation of signal transduction	BP	1	GATA5	up_VPUL_VSMC
GO:0006359	0.596	0.787	1	10	regulation of transcription by RNA polymerase III	BP	1	ICE1	up_VSAP_EC
GO:1903747	0.596	0.789	1	9	regulation of establishment of protein localization to	BP	1	BAG4	up_VSAP_EC
GO:0007622	0.596	0.789	1	9	rhythmic behavior	BP	1	NCOA2	up_VSAP_EC
GO:0000422	0.596834936	0.77525	1	34	autophagy of mitochondrion	BP	1	ENSCAFG00000010493	up_ACOR_EC
GO:0061726	0.596834936	0.77525	1	34	mitochondrion disassembly	BP	1	ENSCAFG00000010493	up_ACOR_EC
GO:0051649	0.596863343	0.50721	16	630	establishment of localization in cell	BP	1	SH3TC2,CDH3,NR1H4,BRSK1,CALY,KCNB1,EDEM2,DYNC1I1,ACTN2,PREB,MAVS,CHMP4B,VPS16,ABCB9,HM13,PRKCD	up_ACOR_EC
GO:0044271	0.597	0.445	120	1501	cellular nitrogen compound biosynthetic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NOS3,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,ODC1,SPTLC2,ARG2,TARSL2,MTOR,SAMD8,ELF4,BMP2,HMG20A,HHEX,CREM,CNOT6,RSC1A1,ENC1,CCAR1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,GUCY1B1,MRRF,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,GCH1,ENSCAFG00000002897,HMGB1,AHR,NOS2,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,ZNF354A,DCP2,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0042981	0.597	0.49	23	471	regulation of apoptotic process	BP	1	GPAM,SLC35F6,PRNP,CLIP3,AKT2,ENSCAFG00000013404,TMEM161A,ARHGAP10,B4GALT1,GLI3,PARK7,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,ZBTB16	down_VCAV_EC
GO:0050708	0.597	0.549	8	101	regulation of protein secretion	BP	1	FERMT1,TLR4,GATA3,ARG2,CD200,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0090304	0.597	0.573	7	1694	nucleic acid metabolic process	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0051128	0.597	0.611	4	790	regulation of cellular component organization	BP	1	ACVRL1,LYN,PDPN,NRP2	down_ACOR_EC
GO:0050867	0.597	0.604	4	83	positive regulation of cell activation	BP	1	GPAM,THY1,GLI3,ZBTB16	down_VCAV_EC
GO:1902106	0.597	0.64	3	31	negative regulation of leukocyte differentiation	BP	1	TMEM176B,TMEM176A,BMP4	up_ACOR_VSMC
GO:0046425	0.597	0.637	3	39	regulation of JAK-STAT cascade	BP	1	HCLS1,KIT,CNOT7	up_VCAV_EC
GO:0019933	0.597	0.683	2	32	cAMP-mediated signaling	BP	1	GNAQ,CALM1	down_VSAP_EC
GO:0001708	0.597	0.688	2	20	cell fate specification	BP	1	LMO4,PSEN1	up_ACOR_VSMC
GO:0014037	0.597	0.787	1	10	Schwann cell differentiation	BP	1	NAB2	down_ACOR_VSMC
GO:0021696	0.597	0.787	1	10	cerebellar cortex morphogenesis	BP	1	GLI1	down_ACOR_VSMC
GO:0032801	0.597	0.786	1	10	receptor catabolic process	BP	1	NEDD4	down_ACOR_VSMC
GO:1902930	0.597	0.786	1	10	regulation of alcohol biosynthetic process	BP	1	SREBF1	down_ACOR_VSMC

GO:0060563	0.597	0.779	1	18	neuroepithelial cell differentiation	BP	1	CDH2	down_VCAV_EC
GO:0009791	0.597	0.775	1	38	post-embryonic development	BP	1	PLAGL2	up_AFEM_EC
GO:0030163	0.597	0.779	1	365	protein catabolic process	BP	1	LNPEP	up_AORT_EC
GO:0065009	0.597	0.791	1	735	regulation of molecular function	BP	1	ESR1	up_AORT_VSMC
GO:0010862	0.597	0.784	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	BMP2	up_VCAV_EC
GO:0060291	0.597	0.786	1	11	long-term synaptic potentiation	BP	1	RELN	up_VCAV_EC
GO:1902110	0.597	0.784	1	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	SH3GLB1	up_VCAV_EC
GO:1902686	0.597	0.784	1	12	mitochondrial outer membrane permeabilization involved	BP	1	SH3GLB1	up_VCAV_EC
GO:0006732	0.597	0.774	1	107	coenzyme metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0044057	0.597	0.773	1	110	regulation of system process	BP	1	SEMA3A	up_VPOR_EC
GO:0006110	0.597	0.788	1	9	regulation of glycolytic process	BP	1	DDIT4	up_VSAP_EC
GO:0030811	0.597	0.788	1	9	regulation of nucleotide catabolic process	BP	1	DDIT4	up_VSAP_EC
GO:0043470	0.597	0.788	1	9	regulation of carbohydrate catabolic	BP	1	DDIT4	up_VSAP_EC
GO:0030194	0.597	0.789	1	9	positive regulation of blood coagulation	BP	1	HPSE	up_VSAP_EC
GO:1900048	0.597	0.789	1	9	positive regulation of hemostasis	BP	1	HPSE	up_VSAP_EC
GO:1905897	0.597049327	0.77506	1	34	regulation of response to endoplasmic reticulum	BP	1	EDEM2	up_ACOR_EC
GO:0050878	0.597232561	0.67862	2	75	regulation of body fluid levels	BP	1	AQP1,PRKCD	up_ACOR_EC
GO:0033036	0.598	0.455	69	852	macromolecule localization	BP	1	HCLS1,GBP5,PPP2R5A,OSBPL9,TNFAIP3,ATP8A1,AMOT,MALL,TMEM173,EXOC3L2,RELN,IWS1,FERMT1,TLR4,QKI,TSPAN15,GATA3,RAB11A,RAB27A,EXOC6,ZDHHC22,PPP3CA,ARG2,HOOK3,TSPAN14,HHEX,CEP68,SCAMP1,PDZD8,ABCA1,MZT1,OSBPL6,EPB41,SNX2,SLCO3A1,MCC,THOC1,SH3GLB1,SWAP70,AKAP12,APOD,EXOC5,CD200,MMD,RAPGEF2,CTDSPL2,PAN3,GCC2,CTNNA1,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,SPTBN4,RAD21,MCU,ZW10,HIF1A,IPO11,ALS2,LMTK2,ATRX,ENSCAFG00000002015,DCP2,SHROOM2,RABGAP1,USP6NL	up_VCAV_EC
GO:0051640	0.598	0.513	14	174	organelle localization	BP	1	ZW10,CENPA,RAN,BIRC5,KIF22,CDCA8,PREB,NDC80,NUP62,TRAK1,ENSCAFG00000005299,EZR,ASPM,CEP83	down_ACOR_VSMC
GO:0048871	0.598	0.527	11	120	multicellular organismal homeostasis	BP	1	NAPEPLD,PPARGC1B,ACACB,EBF2,DLL1,CLDN1,STAT6,MFN2,HOXC10,PASK,PRKAB1	up_VSAP_EC
GO:0051046	0.598	0.531	10	174	regulation of secretion	BP	1	NR1H4,PTPN11,HIF1A,LYN,GSK3B,SDC4,REST,RAB11FIP1,INHBA,RHBDF2	down_VSAP_EC
GO:0072001	0.598	0.533	10	104	renal system development	BP	1	SMAD6,BMP4,TBX18,FGFR2,CLSTN1,NRP1,NPNT,NID1,ARID5B,WFS1	up_ACOR_VSMC
GO:0061138	0.598	0.57	6	73	morphogenesis of a branching epithelium	BP	1	TIMELESS,MMP14,GREM1,HOXB7,B4GALT1,SIX4	down_ACOR_VSMC
GO:0097696	0.598	0.607	4	43	STAT cascade	BP	1	LEP,CRLF3,PARP9,LRRC4	up_ACOR_VSMC
GO:1903039	0.598	0.608	4	43	positive regulation of leukocyte cell-cell	BP	1	LEP,CD83,CD274,PTPN22	up_ACOR_VSMC
GO:0051640	0.598	0.602	4	174	organelle localization	BP	1	CHRM2,CAMK2A,BVES,KXD1	up_AFEM_EC
GO:0045995	0.598	0.681	2	40	regulation of embryonic development	BP	1	BMPR1A,LAMA3	down_VCAV_EC
GO:0043279	0.598	0.786	1	10	response to alkaloid	BP	1	RAD51	down_ACOR_VSMC
GO:0071402	0.598	0.786	1	10	cellular response to lipoprotein particle	BP	1	SREBF2	down_ACOR_VSMC
GO:0001941	0.598	0.781	1	14	postsynaptic membrane organization	BP	1	APOE	down_VSAP_EC
GO:0006919	0.598	0.778	1	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	FAM162A	down_VSAP_EC

GO:0030204	0.598	0.781	1	14	chondroitin sulfate metabolic process	BP	1	CHSY1	down_VSAP_EC
GO:0071398	0.598	0.781	1	14	cellular response to fatty acid	BP	1	NR1H4	down_VSAP_EC
GO:0036297	0.598	0.787	1	9	interstrand cross-link repair	BP	1	FAN1	up_ACOR_VSMC
GO:0006110	0.598	0.788	1	9	regulation of glycolytic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0030811	0.598	0.788	1	9	regulation of nucleotide catabolic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0043470	0.598	0.788	1	9	regulation of carbohydrate catabolic	BP	1	DDIT4	up_ACOR_VSMC
GO:0070986	0.598	0.788	1	9	left/right axis specification	BP	1	CITED2	up_ACOR_VSMC
GO:1905331	0.598	0.788	1	9	negative regulation of morphogenesis of an	BP	1	BMP4	up_ACOR_VSMC
GO:0019935	0.598	0.773	1	38	cyclic-nucleotide-mediated signaling	BP	1	PTHLH	up_AFEM_EC
GO:0010738	0.598	0.787	1	9	regulation of protein kinase A signaling	BP	1	AKAP12	up_VCAV_EC
GO:0031102	0.598	0.784	1	11	neuron projection regeneration	BP	1	APOD	up_VCAV_EC
GO:0044093	0.598	0.781	1	437	positive regulation of molecular function	BP	1	HOXA3	up_VPUL_VSMC
GO:1905276	0.598	0.788	1	9	regulation of epithelial tube formation	BP	1	FZD1	up_VSAP_EC
GO:0048199	0.598	0.788	1	9	vesicle targeting, to, from or within Golgi	BP	1	CEP19	up_VSAP_EC
GO:1990774	0.598	0.788	1	9	tumor necrosis factor secretion	BP	1	MAVS	up_VSAP_EC
GO:0030855	0.599	0.502	17	183	epithelial cell differentiation	BP	1	EXPH5,LBH,GATA5,GATA4,SHROOM3,BMP4,FGFR2,GJA1,ATRX,SEC24B,LATS2,ARHGEF26,F2RL1,CTSB,SPINT2,FRS2,FOSL2	up_ACOR_VSMC
GO:0006575	0.599	0.585	5	53	cellular modified amino acid metabolic process	BP	1	ENSCAFG00000013986,CTNS,IDH1,ASS1,ENSCAFG00000006478	up_VSAP_EC
GO:1901360	0.599	0.631	4	2016	organic cyclic compound metabolic process	BP	1	HDAC7,CITED2,HSD3B7,TBX15	down_VPOR_EC
GO:0036294	0.599	0.635	3	37	cellular response to decreased oxygen levels	BP	1	PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:0071456	0.599	0.635	3	37	cellular response to hypoxia	BP	1	PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:0051128	0.599	0.639	3	790	regulation of cellular component organization	BP	1	TUBB4A,SLITRK5,NTRK2	up_APUL_EC
GO:0071840	0.599	0.668	3	2059	cellular component organization or biogenesis	BP	1	SLITRK5,LIMK1,TGFBI	up_VCAV_VSMC
GO:0015908	0.599	0.684	2	23	fatty acid transport	BP	1	ACSL3,PPARD	down_ACOR_VSMC
GO:0097194	0.599	0.684	2	23	execution phase of apoptosis	BP	1	CASP2,AIFM1	down_ACOR_VSMC
GO:0051055	0.599	0.685	2	21	negative regulation of lipid biosynthetic process	BP	1	ORMDL3,DKKL1	up_ACOR_VSMC
GO:1903201	0.599	0.686	2	20	regulation of oxidative stress-induced cell death	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0023052	0.599	0.711	2	1602	signaling	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0019725	0.599	0.678	2	245	cellular homeostasis	BP	1	C3AR1,ENSCAFG00000005494	up_VPOR_EC
GO:0022402	0.599	0.779	1	407	cell cycle process	BP	1	GPSM2	down_AFEM_EC
GO:1901659	0.599	0.778	1	17	glycosyl compound biosynthetic process	BP	1	ADK	down_VCAV_EC
GO:0032615	0.599	0.777	1	18	interleukin-12 production	BP	1	MAST2	down_VCAV_EC
GO:0043367	0.599	0.778	1	18	CD4-positive, alpha-beta T cell differentiation	BP	1	LOXL3	down_VCAV_EC
GO:0060038	0.599	0.777	1	18	cardiac muscle cell proliferation	BP	1	BMPR1A	down_VCAV_EC
GO:0061951	0.599	0.778	1	16	establishment of protein localization to plasma	BP	1	BLZF1	down_VSAP_EC
GO:0097009	0.599	0.781	1	13	energy homeostasis	BP	1	PRCP	down_VSAP_EC
GO:0010002	0.599	0.787	1	9	cardioblast differentiation	BP	1	TBX5	up_ACOR_VSMC
GO:0030194	0.599	0.787	1	9	positive regulation of blood coagulation	BP	1	ENPP4	up_ACOR_VSMC
GO:0044003	0.599	0.787	1	9	modification by symbiont of host morphology or	BP	1	DAG1	up_ACOR_VSMC
GO:0045683	0.599	0.787	1	9	negative regulation of epidermis development	BP	1	FERMT1	up_ACOR_VSMC

GO:0050706	0.599	0.787	1	9	regulation of interleukin-1 beta secretion	BP	1	NOD2	up_ACOR_VSMC
GO:1900048	0.599	0.787	1	9	positive regulation of hemostasis	BP	1	ENPP4	up_ACOR_VSMC
GO:1905476	0.599	0.787	1	9	negative regulation of protein localization to	BP	1	INPP5K	up_ACOR_VSMC
GO:1902652	0.599	0.773	1	38	secondary alcohol metabolic process	BP	1	LEP	up_AFEM_EC
GO:0098815	0.599	0.787	1	9	modulation of excitatory postsynaptic potential	BP	1	RELN	up_VCAV_EC
GO:0043457	0.599	0.784	1	11	regulation of cellular respiration	BP	1	HIF1A	up_VCAV_EC
GO:0060441	0.599	0.783	1	11	epithelial tube branching involved in lung	BP	1	HHEX	up_VCAV_EC
GO:0060706	0.599	0.783	1	11	cell differentiation involved in embryonic	BP	1	MDFI	up_VCAV_EC
GO:0090189	0.599	0.782	1	12	regulation of branching involved in ureteric bud	BP	1	HOXB7	up_VCAV_EC
GO:0045948	0.599	0.787	1	9	positive regulation of translational initiation	BP	1	NCK1	up_VSAP_EC
GO:0003159	0.599	0.787	1	9	morphogenesis of an endothelium	BP	1	ACVRL1	up_VSAP_EC
GO:1900745	0.599	0.787	1	9	positive regulation of p38MAPK cascade	BP	1	SASH1	up_VSAP_EC
GO:0006541	0.599	0.787	1	9	glutamine metabolic process	BP	1	GLUL	up_VSAP_EC
GO:0061154	0.599	0.787	1	9	endothelial tube morphogenesis	BP	1	ACVRL1	up_VSAP_EC
GO:0007286	0.599449491	0.77291	1	34	spermatid development	BP	1	PYGO2	up_ACOR_EC
GO:0110110	0.599893144	0.77251	1	34	positive regulation of animal organ	BP	1	SOX9	up_ACOR_EC
GO:0043066	0.6	0.493	20	253	negative regulation of apoptotic process	BP	1	PLK2,HCLS1,IL7R,PRKCH,TNFAIP3,MEF2C,GATA3,FIGNL1,ARG2,ITPKB,PAK2,PTGS2,BCL10,CTNNA1,RIPK1,ITGA6,HIF1A,IVNS1ABP,RGL2,ARHGEF2	up_VCAV_EC
GO:0051301	0.6	0.538	9	117	cell division	BP	1	PDGFB,RAB11A,EPB41,STMN1,TOP1,PPP1CB,BLM,USP37,ARHGEF2	up_VCAV_EC
GO:1903320	0.6	0.545	8	102	regulation of protein modification by small protein conjugation or	BP	1	TNFAIP3,TNIP1,PELI1,HMG20A,OTUD4,BCL10,UBE2D1,IVNS1ABP	up_VCAV_EC
GO:0046777	0.6	0.601	4	86	protein autophosphorylation	BP	1	PDGFRB,EEF2K,DDR2,GREM1	down_VCAV_EC
GO:0007276	0.6	0.628	3	130	gamete generation	BP	1	HOXA9,OVOL1,SPATA6	up_AFEM_EC
GO:0022411	0.6	0.628	3	130	cellular component disassembly	BP	1	CTSS,CLEC16A,FAP	up_AFEM_EC
GO:0030168	0.6	0.684	2	23	platelet activation	BP	1	ITGB3,PIK3CD	down_ACOR_VSMC
GO:0051128	0.6	0.688	2	790	regulation of cellular component organization	BP	1	FBP1,SHOX2	up_VFEM_VSMC
GO:0032722	0.6	0.779	1	14	positive regulation of chemokine production	BP	1	ADAM17	down_VSAP_EC
GO:0001913	0.6	0.784	1	10	T cell mediated cytotoxicity	BP	1	B2M	up_ACOR_VSMC
GO:0036474	0.6	0.786	1	9	cell death in response to hydrogen peroxide	BP	1	PARK7	up_ACOR_VSMC
GO:0043516	0.6	0.784	1	10	regulation of DNA damage response, signal transduction by p53 class	BP	1	ANKRD1	up_ACOR_VSMC
GO:2000279	0.6	0.786	1	9	negative regulation of DNA biosynthetic process	BP	1	ANKRD1	up_ACOR_VSMC
GO:0010508	0.6	0.772	1	38	positive regulation of autophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0033045	0.6	0.772	1	38	regulation of sister chromatid segregation	BP	1	AXIN2	up_AFEM_EC
GO:0051250	0.6	0.772	1	38	negative regulation of lymphocyte activation	BP	1	CYLD	up_AFEM_EC
GO:0071459	0.6	0.784	1	10	protein localization to chromosome,	BP	1	ZW10	up_VCAV_EC
GO:0008284	0.600740713	0.56373	6	238	positive regulation of cell proliferation	BP	1	CDH3,SOX9,PTH1R,AQP1,ESM1,TBX5	up_ACOR_EC
GO:0050900	0.601	0.545	8	89	leukocyte migration	BP	1	VEGFD,HRH1,F2RL1,PTPN22,APP,CCL5,JAM3,WASL	up_ACOR_VSMC
GO:0030323	0.601	0.567	6	65	respiratory tube development	BP	1	BMP4,FGFR2,SEC24B,FGF18,TBX5,DAG1	up_ACOR_VSMC
GO:1901605	0.601	0.581	5	67	alpha-amino acid metabolic process	BP	1	PIPOX,ODC1,ARG2,AADAT,BCAT1	up_VCAV_EC
GO:0044238	0.601	0.671	4	3383	primary metabolic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC

GO:0031532	0.601	0.635	3	31	actin cytoskeleton reorganization	BP	1	NRP1,SIPA1L1,ATP2C1	up_ACOR_VSMC
GO:0034644	0.601	0.635	3	32	cellular response to UV	BP	1	MFAP4,TP53INP1,CDKN1A	up_ACOR_VSMC
GO:0044344	0.601	0.679	2	33	cellular response to fibroblast growth factor	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0071774	0.601	0.679	2	33	response to fibroblast growth factor	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0030193	0.601	0.683	2	21	regulation of blood coagulation	BP	1	F2RL1,ENPP4	up_ACOR_VSMC
GO:1900046	0.601	0.683	2	21	regulation of hemostasis	BP	1	F2RL1,ENPP4	up_ACOR_VSMC
GO:1905332	0.601	0.685	2	20	positive regulation of morphogenesis of an	BP	1	BMP4,RREB1	up_ACOR_VSMC
GO:0072666	0.601	0.684	2	21	establishment of protein localization to vacuole	BP	1	VPS36,NCOA4	up_VSAP_EC
GO:1903533	0.601	0.684	2	21	regulation of protein targeting	BP	1	KCNB1,BAG4	up_VSAP_EC
GO:0010648	0.601	0.777	1	407	negative regulation of cell communication	BP	1	IVNS1ABP	down_AFEM_EC
GO:1904427	0.601	0.775	1	18	positive regulation of calcium ion	BP	1	THY1	down_VCAV_EC
GO:0051898	0.601	0.777	1	15	negative regulation of protein kinase B signaling	BP	1	DDIT3	down_VSAP_EC
GO:0002639	0.601	0.778	1	14	positive regulation of immunoglobulin	BP	1	TFRC	down_VSAP_EC
GO:0010573	0.601	0.785	1	9	vascular endothelial growth factor production	BP	1	NDRG2	up_ACOR_VSMC
GO:0010574	0.601	0.785	1	9	regulation of vascular endothelial growth factor	BP	1	NDRG2	up_ACOR_VSMC
GO:0006633	0.601	0.771	1	38	fatty acid biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0042147	0.601	0.771	1	38	retrograde transport, endosome to Golgi	BP	1	RAB7A	up_AFEM_EC
GO:0060349	0.601	0.771	1	38	bone morphogenesis	BP	1	AXIN2	up_AFEM_EC
GO:0009648	0.601	0.781	1	11	photoperiodism	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0009994	0.601	0.781	1	11	oocyte differentiation	BP	1	FBXO5	up_VCAV_EC
GO:0043153	0.601	0.781	1	11	entrainment of circadian clock by photoperiod	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0060351	0.601	0.782	1	11	cartilage development involved in endochondral bone morphogenesis	BP	1	STC1	up_VCAV_EC
GO:0051253	0.601	0.775	1	359	negative regulation of RNA metabolic process	BP	1	SHOX2	up_VFEM_VSMC
GO:0031639	0.601	0.785	1	9	plasminogen activation	BP	1	KLKB1	up_VSAP_EC
GO:0002828	0.601	0.785	1	9	regulation of type 2 immune response	BP	1	STAT6	up_VSAP_EC
GO:0030206	0.601	0.786	1	9	chondroitin sulfate biosynthetic process	BP	1	CHST7	up_VSAP_EC
GO:0071248	0.60116983	0.77122	1	35	cellular response to metal ion	BP	1	AQP1	up_ACOR_EC
GO:0062014	0.601231475	0.77116	1	35	negative regulation of small molecule metabolic	BP	1	NR1H4	up_ACOR_EC
GO:0030879	0.601453136	0.77111	1	34	mammary gland development	BP	1	PYGO2	up_ACOR_EC
GO:0002224	0.601462076	0.7711	1	34	toll-like receptor signaling pathway	BP	1	NR1H4	up_ACOR_EC
GO:0030641	0.601923378	0.77068	1	34	regulation of cellular pH	BP	1	SLC9A9	up_ACOR_EC
GO:1902680	0.602	0.481	25	415	positive regulation of RNA biosynthetic process	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:1903508	0.602	0.481	25	415	positive regulation of nucleic acid-templated transcription	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0050768	0.602	0.566	6	66	negative regulation of neurogenesis	BP	1	THRB,SLIT2,DLL1,IRX3,RTN4RL1,LRP4	up_VSAP_EC
GO:0030041	0.602	0.582	5	62	actin filament polymerization	BP	1	CAPG,IQGAP2,CDC42EP4,CORO1A,ARPC1B	down_ACOR_VSMC
GO:0016310	0.602	0.581	5	641	phosphorylation	BP	1	ARHGEF2,ASPN,ACVR2A,FBP1,ENSCAFG00000032731	up_VPOR_EC

GO:0006163	0.602	0.598	4	174	purine nucleotide metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0046434	0.602	0.601	4	52	organophosphate catabolic process	BP	1	ENSCAFG00000024323,PLCG2,IMPA1,HIF1A	up_VCAV_EC
GO:1901799	0.602	0.681	2	24	negative regulation of proteasomal protein catabolic process	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC
GO:0009743	0.602	0.677	2	40	response to carbohydrate	BP	1	GPAM,ZFP36L1	down_VCAV_EC
GO:0030902	0.602	0.676	2	41	hindbrain development	BP	1	SMAD9,NAGLU	down_VCAV_EC
GO:0032784	0.602	0.683	2	21	regulation of DNA-templated transcription,	BP	1	IWS1,THOC1	up_VCAV_EC
GO:0007140	0.602	0.782	1	10	male meiotic nuclear division	BP	1	TRIP13	down_ACOR_VSMC
GO:0030317	0.602	0.78	1	11	flagellated sperm motility	BP	1	TTLL1	down_ACOR_VSMC
GO:0097722	0.602	0.78	1	11	sperm motility	BP	1	TTLL1	down_ACOR_VSMC
GO:0000281	0.602	0.775	1	18	mitotic cytokinesis	BP	1	SNX18	down_VCAV_EC
GO:0007338	0.602	0.776	1	16	single fertilization	BP	1	SPINK2	down_VSAP_EC
GO:0030520	0.602	0.777	1	15	intracellular estrogen receptor signaling	BP	1	UBA5	down_VSAP_EC
GO:0006541	0.602	0.785	1	9	glutamine metabolic process	BP	1	NIT2	up_ACOR_VSMC
GO:1903828	0.602	0.77	1	38	negative regulation of cellular protein	BP	1	LRRC15	up_AFEM_EC
GO:0008219	0.602	0.782	1	611	cell death	BP	1	EYA1	up_AFEM_VSMC
GO:0007212	0.602	0.781	1	11	dopamine receptor signaling pathway	BP	1	CAV2	up_VCAV_EC
GO:0015800	0.602	0.783	1	10	acidic amino acid transport	BP	1	LRRC8D	up_VCAV_EC
GO:0050691	0.602	0.78	1	11	regulation of defense response to virus by host	BP	1	TMEM173	up_VCAV_EC
GO:0050850	0.602	0.781	1	11	positive regulation of calcium-mediated	BP	1	PPP3CA	up_VCAV_EC
GO:0071345	0.602	0.771	1	210	cellular response to cytokine stimulus	BP	1	MME	up_VFEM_EC
GO:0034122	0.602	0.784	1	9	negative regulation of toll-like receptor signaling	BP	1	F2RL1	up_VSAP_EC
GO:1903523	0.602	0.782	1	10	negative regulation of blood circulation	BP	1	KCNE3	up_VSAP_EC
GO:2000279	0.602	0.785	1	9	negative regulation of DNA biosynthetic process	BP	1	ACVRL1	up_VSAP_EC
GO:0051960	0.602	0.771	1	216	regulation of nervous system development	BP	1	SHOX2	up_VSAP_VSMC
GO:0016052	0.602850835	0.76984	1	34	carbohydrate catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0019941	0.603	0.482	24	258	modification-dependent protein catabolic process	BP	1	ZRANB1,SKP2,SH3RF2,ISG15,ZNRF3,KLHL20,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,SIAH1,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0090087	0.603	0.504	15	185	regulation of peptide transport	BP	1	HCLS1,TMEM173,IWS1,FERMT1,CHD7,TLR4,GATA3,ARG2,APOD,CD200,CTDSPL2,GCC2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0050865	0.603	0.522	11	135	regulation of cell activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,MMP14,HMGB3,ARG2,TFRC,FAM49B,TOX,CORO1A	down_ACOR_VSMC
GO:0007186	0.603	0.563	6	124	G protein-coupled receptor signaling	BP	1	ADCY6,PLCL1,GNAZ,SPNS1,CRCP,RAC2	down_VCAV_EC
GO:0070507	0.603	0.564	6	73	regulation of microtubule cytoskeleton organization	BP	1	PLK2,STMN1,FES,SENP6,TAOK1,ARHGEF2	up_VCAV_EC
GO:0006486	0.603	0.578	5	91	protein glycosylation	BP	1	GALNT1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0043413	0.603	0.578	5	91	macromolecule glycosylation	BP	1	GALNT1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0007154	0.603	0.619	4	1622	cell communication	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0044271	0.603	0.649	3	1501	cellular nitrogen compound biosynthetic	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0009889	0.603	0.644	3	1190	regulation of biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0002274	0.603	0.676	2	40	myeloid leukocyte activation	BP	1	BPI,RAC2	down_VCAV_EC
GO:0051592	0.603	0.677	2	33	response to calcium ion	BP	1	CALM1,HOMER1	down_VSAP_EC
GO:0042089	0.603	0.682	2	21	cytokine biosynthetic process	BP	1	TLR1,TLR3	up_ACOR_VSMC

GO:0006536	0.603	0.781	1	10	glutamate metabolic process	BP	1	AADAT	down_ACOR_VSMC
GO:0007257	0.603	0.782	1	10	activation of JUN kinase activity	BP	1	MAP3K20	down_ACOR_VSMC
GO:0023057	0.603	0.776	1	409	negative regulation of signaling	BP	1	IVNS1ABP	down_AFEM_EC
GO:0060323	0.603	0.776	1	14	head morphogenesis	BP	1	PTPN11	down_VSAP_EC
GO:1905898	0.603	0.775	1	16	positive regulation of response to endoplasmic	BP	1	PTPN2	down_VSAP_EC
GO:2000785	0.603	0.775	1	16	regulation of autophagosome assembly	BP	1	SH3GLB1	down_VSAP_EC
GO:2001056	0.603	0.769	1	38	positive regulation of cysteine-type	BP	1	F3	up_AFEM_EC
GO:0051050	0.603	0.771	1	235	positive regulation of transport	BP	1	NR1H4	up_APUL_EC
GO:0048103	0.603	0.781	1	10	somatic stem cell division	BP	1	ARHGEF2	up_VCAV_EC
GO:0007010	0.603	0.776	1	441	cytoskeleton organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0090141	0.603	0.784	1	9	positive regulation of mitochondrial fission	BP	1	DDHD1	up_VSAP_EC
GO:1900543	0.603	0.783	1	9	negative regulation of purine nucleotide	BP	1	DDIT4	up_VSAP_EC
GO:1903579	0.603	0.783	1	9	negative regulation of ATP metabolic process	BP	1	DDIT4	up_VSAP_EC
GO:0097035	0.603	0.784	1	9	regulation of membrane lipid distribution	BP	1	XKR8	up_VSAP_EC
GO:0043408	0.603	0.77	1	211	regulation of MAPK cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0051347	0.604	0.497	17	182	positive regulation of transferase activity	BP	1	LEP,MAP3K8,HTR2B,RASSF2,BMP4,PDE5A,SASH1,LMO4,FGF18,CCNT1,FRS2,PSEN1,DDR2,EDN1,DCUN1D4,MAP3K7,HMBOX1	up_ACOR_VSMC
GO:0044262	0.604	0.551	7	89	cellular carbohydrate metabolic process	BP	1	PCDH12,GK5,FAM3C,ENSCAFG00000010596,PPP1CB,PMAIP1,IMPA1	up_VCAV_EC
GO:0055076	0.604	0.601	4	44	transition metal ion homeostasis	BP	1	EGLN1,ATP7A,APP,B2M	up_ACOR_VSMC
GO:0042789	0.604	0.781	1	10	mRNA transcription by RNA polymerase II	BP	1	SREBF1	down_ACOR_VSMC
GO:0048486	0.604	0.781	1	10	parasympathetic nervous system development	BP	1	NAV2	down_ACOR_VSMC
GO:0031327	0.604	0.775	1	412	negative regulation of cellular biosynthetic	BP	1	GABPA	down_AFEM_EC
GO:0002534	0.604	0.773	1	18	cytokine production involved in inflammatory	BP	1	CHID1	down_VCAV_EC
GO:0045661	0.604	0.773	1	18	regulation of myoblast differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0051155	0.604	0.773	1	18	positive regulation of striated muscle cell	BP	1	GREM1	down_VCAV_EC
GO:0044249	0.604	0.826	1	1851	cellular biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0070266	0.604	0.775	1	14	necroptotic process	BP	1	ARHGEF2	down_VSAP_EC
GO:0098661	0.604	0.776	1	14	inorganic anion transmembrane transport	BP	1	CLCN3	down_VSAP_EC
GO:0002828	0.604	0.783	1	9	regulation of type 2 immune response	BP	1	NOD2	up_ACOR_VSMC
GO:0003159	0.604	0.783	1	9	morphogenesis of an endothelium	BP	1	BMP4	up_ACOR_VSMC
GO:0061154	0.604	0.783	1	9	endothelial tube morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:1901137	0.604	0.77	1	232	carbohydrate derivative biosynthetic process	BP	1	GALNT17	up_APUL_EC
GO:0060384	0.604	0.783	1	9	innervation	BP	1	CHD7	up_VCAV_EC
GO:0019637	0.604	0.773	1	342	organophosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0009067	0.604	0.783	1	9	aspartate family amino acid biosynthetic process	BP	1	GOT1	up_VSAP_EC
GO:0046329	0.604	0.782	1	9	negative regulation of JNK cascade	BP	1	F2RL1	up_VSAP_EC
GO:0071276	0.604	0.783	1	9	cellular response to cadmium ion	BP	1	HMOX1	up_VSAP_EC
GO:0010894	0.604	0.783	1	9	negative regulation of steroid biosynthetic	BP	1	INSIG2	up_VSAP_EC
GO:0045939	0.604	0.783	1	9	negative regulation of steroid metabolic process	BP	1	INSIG2	up_VSAP_EC
GO:0060575	0.604	0.783	1	9	intestinal epithelial cell differentiation	BP	1	SAV1	up_VSAP_EC

GO:0010942	0.604	0.77	1	200	positive regulation of cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0045807	0.604285109	0.7684	1	35	positive regulation of endocytosis	BP	1	CALY	up_ACOR_EC
GO:0034097	0.60456451	0.55973	6	238	response to cytokine	BP	1	NR1H4,CCDC3,MAVS,LRRC15,IFIT2,LRRC4	up_ACOR_EC
GO:0042471	0.604597471	0.76826	1	34	ear morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0014902	0.604792644	0.76808	1	34	myotube differentiation	BP	1	RBM38	up_ACOR_EC
GO:0006355	0.605	0.444	81	974	regulation of transcription, DNA-templated	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,HOXA10,ERF,TCERG1,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:0007017	0.605	0.482	23	273	microtubule-based process	BP	1	PLK2,MAP3K11,KIF21B,RAB11A,KIF3C,HOOK3,SLK,CEP68,MZT1,ENSCAFG00000010224,STMN1,FES,SENP6,GCC2,TAOK1,ZW10,HIF1A,ATRX,HAUS3,GAS2L3,ARHGEF2,FBXO5,SASS6	up_VCAV_EC
GO:0006807	0.605	0.538	14	3221	nitrogen compound metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0061458	0.605	0.514	12	131	reproductive system development	BP	1	HOXA11,HOXA9,GJB5,IRX5,SLIT2,OSR1,RARG,PATZ1,DLX3,ZFP36L1,PLEKHA5,CITED2	up_VSAP_EC
GO:0018205	0.605	0.525	10	122	peptidyl-lysine modification	BP	1	IWS1,GATA3,HMG20A,ARID4B,ESCO1,NSD1,SENP6,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0009266	0.605	0.601	4	43	response to temperature stimulus	BP	1	SCARA5,NR2F6,HTRA2,HMOX1	up_VSAP_EC
GO:0006813	0.605	0.629	3	37	potassium ion transport	BP	1	NEDD4,CAV1,CDK2	down_ACOR_VSMC
GO:0007050	0.605	0.626	3	53	cell cycle arrest	BP	1	DDIT3,INHBA,CDKN1A	down_VSAP_EC
GO:1900180	0.605	0.626	3	50	regulation of protein localization to nucleus	BP	1	SESN2,ZPR1,CDKN1A	down_VSAP_EC
GO:1905475	0.605	0.626	3	52	regulation of protein localization to membrane	BP	1	MYO1C,KIF5B,SH3GLB1	down_VSAP_EC
GO:0043536	0.605	0.63	3	32	positive regulation of blood vessel endothelial	BP	1	FGF18,NRP1,PIK3C2A	up_ACOR_VSMC
GO:1901222	0.605	0.631	3	32	regulation of NIK/NF-kappaB signaling	BP	1	HDAC7,RBCK1,SASH1	up_VSAP_EC
GO:0035051	0.605	0.673	2	41	cardiocyte differentiation	BP	1	SEMA3C,GREM1	down_VCAV_EC
GO:0003006	0.605	0.768	1	180	developmental process involved in reproduction	BP	1	SULF1	down_ACOR_EC
GO:0007212	0.605	0.778	1	11	dopamine receptor signaling pathway	BP	1	PRMT5	down_ACOR_VSMC
GO:0071359	0.605	0.778	1	11	cellular response to dsRNA	BP	1	CAV1	down_ACOR_VSMC
GO:1903524	0.605	0.778	1	11	positive regulation of blood circulation	BP	1	CAV1	down_ACOR_VSMC
GO:0044260	0.605	0.862	1	2593	cellular macromolecule metabolic process	BP	1	CST3	down_AORT_EC
GO:0035307	0.605	0.772	1	18	positive regulation of protein	BP	1	PDGFRB	down_VCAV_EC
GO:0032729	0.605	0.774	1	15	positive regulation of interferon-gamma	BP	1	FAM49B	down_VSAP_EC
GO:0060037	0.605	0.782	1	9	pharyngeal system development	BP	1	BMP4	up_ACOR_VSMC
GO:0010605	0.605	0.784	1	745	negative regulation of macromolecule metabolic	BP	1	ESR1	up_AORT_VSMC
GO:0060765	0.605	0.779	1	10	regulation of androgen receptor signaling	BP	1	SMARCA4	up_VCAV_EC
GO:0071158	0.605	0.78	1	10	positive regulation of cell cycle arrest	BP	1	UHRF2	up_VCAV_EC
GO:0031401	0.605	0.772	1	358	positive regulation of protein modification	BP	1	ANKRD6	up_VPOR_VSMC
GO:0006515	0.605	0.782	1	9	protein quality control for misfolded or incompletely synthesized proteins	BP	1	LONP2	up_VSAP_EC

GO:0035988	0.605	0.782	1	9	chondrocyte proliferation	BP	1	DDR2	up_VSAP_EC
GO:0044060	0.605	0.782	1	9	regulation of endocrine process	BP	1	F2RL1	up_VSAP_EC
GO:0051290	0.605	0.782	1	9	protein heterotetramerization	BP	1	HSD17B8	up_VSAP_EC
GO:0072111	0.605	0.782	1	9	cell proliferation involved in kidney development	BP	1	OSR1	up_VSAP_EC
GO:0086001	0.605	0.782	1	9	cardiac muscle cell action potential	BP	1	KCNE3	up_VSAP_EC
GO:0072012	0.605	0.781	1	9	glomerulus vasculature development	BP	1	OSR1	up_VSAP_EC
GO:0010563	0.605	0.769	1	203	negative regulation of phosphorus metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0031400	0.605	0.768	1	205	negative regulation of protein modification	BP	1	CAV1	up_VSAP_VSMC
GO:0045936	0.605	0.769	1	203	negative regulation of phosphate metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0048732	0.605243545	0.6232	3	116	gland development	BP	1	SOX9,NRP1,PYGO2	up_ACOR_EC
GO:0001892	0.605682653	0.76712	1	35	embryonic placenta development	BP	1	FZD5	up_ACOR_EC
GO:0023014	0.606	0.481	23	248	signal transduction by protein phosphorylation	BP	1	CDON,ACKR3,MAP3K14,ARHGEF5,C5AR2,TBC1D10C,ABL1,OSR1,MAP3K5,CDC42EP5,PDGFD,C1QTNF2,F2RL1,ZFP36L1,TRAF7,MYC,SASH1,MYD88,FBLN1,ZFP36L2,RAF1,QARS,MAP2K2	up_VSAP_EC
GO:0006508	0.606	0.518	11	483	proteolysis	BP	1	USP54,GAS1,CRYAB,CTSS,F3,CLEC16A,CYLD,RECK,FAP,ADAM17,RNF181	up_AFEM_EC
GO:0050769	0.606	0.532	9	95	positive regulation of neurogenesis	BP	1	BMP4,ZNF365,NRP1,SMARCD3,FZD3,APP,PSEN1,DISC1,CRKL	up_ACOR_VSMC
GO:0044282	0.606	0.54	8	89	small molecule catabolic process	BP	1	LEP,ENOSF1,ENSCAFG00000002977,ACAD11,ENPP4,SARDH,PCYOX1,INPP5K	up_ACOR_VSMC
GO:0043901	0.606	0.599	4	44	negative regulation of multi-organism process	BP	1	PRDX4,MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0035601	0.606	0.629	3	36	protein deacylation	BP	1	SREBF1,RBM14,TADA2A	down_ACOR_VSMC
GO:0098732	0.606	0.629	3	36	macromolecule deacylation	BP	1	SREBF1,RBM14,TADA2A	down_ACOR_VSMC
GO:0044843	0.606	0.624	3	62	cell cycle G1/S phase transition	BP	1	KANK2,LSM10,EIF4EBP1	down_VCAV_EC
GO:0045446	0.606	0.629	3	32	endothelial cell differentiation	BP	1	BMP4,ARHGEF26,F2RL1	up_ACOR_VSMC
GO:0035821	0.606	0.629	3	32	modification of morphology or physiology	BP	1	NAPEPLD,F2RL1,PC	up_VSAP_EC
GO:0071887	0.606	0.673	2	34	leukocyte apoptotic process	BP	1	HIF1A,LYN	down_VSAP_EC
GO:0048708	0.606	0.68	2	20	astrocyte differentiation	BP	1	APP,PSEN1	up_ACOR_VSMC
GO:0030162	0.606	0.767	1	202	regulation of proteolysis	BP	1	LYN	down_ACOR_EC
GO:0002275	0.606	0.772	1	18	myeloid cell activation involved in immune	BP	1	RAC2	down_VCAV_EC
GO:0050873	0.606	0.771	1	18	brown fat cell differentiation	BP	1	NAPEPLD	down_VCAV_EC
GO:0003407	0.606	0.773	1	15	neural retina development	BP	1	SMARCA4	down_VSAP_EC
GO:0000002	0.606	0.781	1	9	mitochondrial genome maintenance	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0005979	0.606	0.781	1	9	regulation of glycogen biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0010962	0.606	0.781	1	9	regulation of glucan biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0070233	0.606	0.781	1	9	negative regulation of T cell apoptotic process	BP	1	BMP4	up_ACOR_VSMC
GO:0070873	0.606	0.781	1	9	regulation of glycogen metabolic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0014065	0.606	0.766	1	39	phosphatidylinositol 3-kinase signaling	BP	1	LEP	up_AFEM_EC
GO:0050770	0.606	0.767	1	39	regulation of axonogenesis	BP	1	PLXNA4	up_AFEM_EC
GO:0032956	0.606	0.765	1	116	regulation of actin cytoskeleton organization	BP	1	TWF1	up_VPOR_EC
GO:0009117	0.606	0.767	1	208	nucleotide metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0120036	0.606	0.771	1	373	plasma membrane bounded cell projection	BP	1	SHOX2	up_VFEM_VSMC
GO:0001912	0.606	0.781	1	9	positive regulation of leukocyte mediated	BP	1	F2RL1	up_VSAP_EC

GO:0070131	0.606	0.781	1	9	positive regulation of mitochondrial translation	BP	1	RPUSD4	up_VSAP_EC
GO:0051101	0.606898277	0.76601	1	35	regulation of DNA binding	BP	1	CLSTN1	up_ACOR_EC
GO:0023057	0.607	0.462	38	409	negative regulation of signaling	BP	1	FZD1,WNT11,ACKR3,AXIN2,TBC1D10C,SLIT2,ABL1,HDAC7,EPN2,SESN1,F2RL1,GLIS2,MFN2,MYC,PIK3IP1,SULF2,HIC1,RTN4RL1,CREBRF,LRP4,GDPD5,CASTOR1,KCNB1,LIMD1,NLRX1,TKFC,FBLN1,RAF1,MAPKBP1,QARS,ARHGAP12,UBQLN2,NCK1,HMOX1,NPRL3,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0051704	0.607	0.48	23	476	multi-organism process	BP	1	ADAMTS2,GPAM,CFD,RECK,SYDE1,TRIM8,ENSCAFG00000013404,WIPF1,FKBP5,RNF216,MEA1,B4GALT1,SASH1,BPI,CYBA,MAVS,GSDME,ENSCAFG00000017708,SHC1,NAPEPLD,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0009416	0.607	0.539	8	88	response to light stimulus	BP	1	MFAP4,HRH1,LRRN4,TP53INP1,RBM4B,CDKN1A,APP,GNAQ	up_ACOR_VSMC
GO:0044237	0.607	0.603	7	3491	cellular metabolic process	BP	1	CST3,HDAC7,CITED2,RAB11B,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:1901698	0.607	0.557	6	266	response to nitrogen compound	BP	1	LEP,CRY2,CHRM2,AVPR1A,CAMK2A,KANK1	up_AFEM_EC
GO:0006906	0.607	0.577	5	55	vesicle fusion	BP	1	USP6NL,SYT16,EVI5L,STX11,SGSM2	up_ACOR_VSMC
GO:0030041	0.607	0.623	3	62	actin filament polymerization	BP	1	KIRREL1,ENSCAFG00000014978,ACTR3B	down_VCAV_EC
GO:0042180	0.607	0.624	3	61	cellular ketone metabolic process	BP	1	AKT2,PARK7,LONP2	down_VCAV_EC
GO:0050789	0.607	0.703	3	3295	regulation of biological process	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0016444	0.607	0.677	2	23	somatic cell DNA recombination	BP	1	HMGB1,TFRC	down_ACOR_VSMC
GO:0002200	0.607	0.677	2	23	somatic diversification of immune receptors	BP	1	HMGB1,TFRC	down_ACOR_VSMC
GO:0002562	0.607	0.677	2	23	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	HMGB1,TFRC	down_ACOR_VSMC
GO:0048513	0.607	0.684	2	906	animal organ development	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0048645	0.607	0.673	2	33	animal organ formation	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:1904589	0.607	0.673	2	33	regulation of protein import	BP	1	ZPR1,CDKN1A	down_VSAP_EC
GO:0071156	0.607	0.678	2	21	regulation of cell cycle arrest	BP	1	CDKN1A,CRLF3	up_ACOR_VSMC
GO:0005996	0.607	0.669	2	85	monosaccharide metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0021782	0.607	0.676	2	23	glial cell development	BP	1	TLR4,EIF2B2	up_VCAV_EC
GO:0048666	0.607	0.669	2	258	neuron development	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:1901699	0.607	0.766	1	164	cellular response to nitrogen compound	BP	1	IGF1R	down_ACOR_EC
GO:0030521	0.607	0.77	1	19	androgen receptor signaling pathway	BP	1	PARK7	down_VCAV_EC
GO:0032272	0.607	0.77	1	18	negative regulation of protein polymerization	BP	1	CLIP3	down_VCAV_EC
GO:0035725	0.607	0.771	1	16	sodium ion transmembrane transport	BP	1	YWHAH	down_VSAP_EC
GO:0050982	0.607	0.78	1	9	detection of mechanical stimulus	BP	1	JUP	up_ACOR_VSMC
GO:0048813	0.607	0.765	1	39	dendrite morphogenesis	BP	1	CAMK2A	up_AFEM_EC
GO:0030029	0.607	0.767	1	239	actin filament-based process	BP	1	PDLIM3	up_APUL_EC
GO:0033043	0.607	0.773	1	446	regulation of organelle organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0032924	0.607	0.78	1	9	activin receptor signaling pathway	BP	1	CITED2	up_VSAP_EC
GO:0042752	0.607113004	0.76596	1	34	regulation of circadian rhythm	BP	1	PTGDS	up_ACOR_EC
GO:0016050	0.607336624	0.62095	3	119	vesicle organization	BP	1	AQP1,PREB,VPS16	up_ACOR_EC
GO:0060021	0.607353912	0.76574	1	34	roof of mouth development	BP	1	PYGO2	up_ACOR_EC
GO:0009792	0.608	0.514	11	231	embryo development ending in birth or egg	BP	1	SDC4,BMPR1A,LMO4,TBX15,SEMA3C,GLI3,ZFP36L1,IFT57,IRX5,PRKCSH,RDH10	down_VCAV_EC
GO:0051650	0.608	0.56	6	65	establishment of vesicle localization	BP	1	FBXL20,STX11,PSEN1,RAB11B,PREPL,DYNC1I1	up_ACOR_VSMC

GO:0060255	0.608	0.577	6	1782	regulation of macromolecule metabolic	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0009615	0.608	0.592	4	83	response to virus	BP	1	GPAM,RNF216,MAVS,GSDME	down_VCAV_EC
GO:0050680	0.608	0.597	4	44	negative regulation of epithelial cell proliferation	BP	1	BMP4,CDKN2B,LIMS2,SYNJ2BP	up_ACOR_VSMC
GO:1900180	0.608	0.596	4	50	regulation of protein localization to nucleus	BP	1	HCLS1,TMEM173,FERMT1,APOD	up_VCAV_EC
GO:0048856	0.608	0.645	3	1533	anatomical structure development	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0034622	0.608	0.672	2	421	cellular protein-containing complex assembly	BP	1	RPSA,STX4	down_ACOR_EC
GO:2000241	0.608	0.67	2	40	regulation of reproductive process	BP	1	SYDE1,B4GALT1	down_VCAV_EC
GO:0007154	0.608	0.703	2	1622	cell communication	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0048585	0.608	0.673	2	475	negative regulation of response to stimulus	BP	1	EYA1,CYP26B1	up_VFEM_EC
GO:0010718	0.608	0.676	2	21	positive regulation of epithelial to mesenchymal	BP	1	AXIN2,TGFBR2	up_VSAP_EC
GO:0042474	0.608	0.775	1	11	middle ear morphogenesis	BP	1	INSIG1	down_ACOR_VSMC
GO:1903115	0.608	0.774	1	12	regulation of actin filament-based movement	BP	1	CAV1	down_ACOR_VSMC
GO:1903432	0.608	0.769	1	18	regulation of TORC1 signaling	BP	1	CLEC16A	down_VCAV_EC
GO:0003401	0.608	0.771	1	15	axis elongation	BP	1	SIX4	down_VSAP_EC
GO:0045744	0.608	0.772	1	15	negative regulation of G protein-coupled receptor signaling pathway	BP	1	RGS2	down_VSAP_EC
GO:0060612	0.608	0.772	1	14	adipose tissue development	BP	1	NR1H4	down_VSAP_EC
GO:0009190	0.608	0.782	1	8	cyclic nucleotide biosynthetic process	BP	1	ADCY6	up_ACOR_VSMC
GO:0046676	0.608	0.779	1	9	negative regulation of insulin secretion	BP	1	PFKL	up_ACOR_VSMC
GO:0052652	0.608	0.782	1	8	cyclic purine nucleotide metabolic process	BP	1	ADCY6	up_ACOR_VSMC
GO:0008584	0.608	0.764	1	39	male gonad development	BP	1	HOXA9	up_AFEM_EC
GO:0043524	0.608	0.764	1	39	negative regulation of neuron apoptotic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0046546	0.608	0.764	1	39	development of primary male sexual	BP	1	HOXA9	up_AFEM_EC
GO:0051668	0.608	0.765	1	39	localization within membrane	BP	1	REEP2	up_AFEM_EC
GO:0021783	0.608	0.779	1	9	preganglionic parasympathetic fiber	BP	1	NAV2	up_VCAV_EC
GO:0033144	0.608	0.777	1	10	negative regulation of intracellular steroid hormone receptor	BP	1	SMARCA4	up_VCAV_EC
GO:0050650	0.608	0.775	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	CHST7	up_VCAV_EC
GO:1903793	0.608	0.775	1	11	positive regulation of anion transport	BP	1	ATP8A1	up_VCAV_EC
GO:0006144	0.608	0.779	1	9	purine nucleobase metabolic process	BP	1	GDA	up_VSAP_EC
GO:0034311	0.608	0.779	1	9	diol metabolic process	BP	1	PCBD1	up_VSAP_EC
GO:0038061	0.608048062	0.7651	1	34	NIK/NF-kappaB signaling	BP	1	NOD2	up_ACOR_EC
GO:0045778	0.608794233	0.76427	1	35	positive regulation of ossification	BP	1	CLSTN1	up_ACOR_EC
GO:0031326	0.609	0.474	27	1176	regulation of cellular biosynthetic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0070201	0.609	0.498	15	187	regulation of establishment of protein localization	BP	1	HCLS1,TMEM173,IWS1,FERMT1,TLR4,GATA3,ARG2,SH3GLB1,APOD,CD200,CTDSPL2,GCC2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0010608	0.609	0.527	9	154	posttranscriptional regulation of gene	BP	1	AARS,PUM3,SESN2,SMG7,EIF4EBP1,CNOT7,EIF5,CDC37,EIF2S1	down_VSAP_EC
GO:0051171	0.609	0.561	7	1697	regulation of nitrogen compound metabolic	BP	1	EYA1,HOXA9,MAP2K6,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0032535	0.609	0.555	6	128	regulation of cellular component size	BP	1	KIRREL1,TRPV2,ENSCAFG00000014978,AKT1S1,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0030595	0.609	0.574	5	57	leukocyte chemotaxis	BP	1	VEGFD,HRH1,F2RL1,CCL5,JAM3	up_ACOR_VSMC

GO:0001570	0.609	0.625	3	37	vasculogenesis	BP	1	CAV1,EMP2,SGPL1	down_ACOR_VSMC
GO:0045639	0.609	0.626	3	33	positive regulation of myeloid cell	BP	1	ISG15,FAM210B,CLSTN1	up_ACOR_VSMC
GO:0072028	0.609	0.624	3	37	nephron morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:0007165	0.609	0.644	3	1496	signal transduction	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0031047	0.609	0.627	3	33	gene silencing by RNA	BP	1	ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0010596	0.609	0.676	2	21	negative regulation of endothelial cell migration	BP	1	SYNJ2BP,JUP	up_ACOR_VSMC
GO:0010506	0.609	0.666	2	86	regulation of autophagy	BP	1	LEP,CLEC16A	up_AFEM_EC
GO:0051128	0.609	0.679	2	790	regulation of cellular component organization	BP	1	NKX2-5,BAMBI	up_VPOR_VSMC
GO:0009069	0.609	0.774	1	11	serine family amino acid metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0043299	0.609	0.769	1	18	leukocyte degranulation	BP	1	RAC2	down_VCAV_EC
GO:1902807	0.609	0.768	1	18	negative regulation of cell cycle G1/S phase	BP	1	KANK2	down_VCAV_EC
GO:2000134	0.609	0.768	1	18	negative regulation of G1/S transition of mitotic	BP	1	KANK2	down_VCAV_EC
GO:0031128	0.609	0.77	1	15	developmental induction	BP	1	CTNNB1	down_VSAP_EC
GO:0045191	0.609	0.771	1	14	regulation of isotype switching	BP	1	TFRC	down_VSAP_EC
GO:0045880	0.609	0.771	1	14	positive regulation of smoothened signaling	BP	1	CHSY1	down_VSAP_EC
GO:0010800	0.609	0.778	1	9	positive regulation of peptidyl-threonine	BP	1	APP	up_ACOR_VSMC
GO:0034614	0.609	0.763	1	39	cellular response to reactive oxygen species	BP	1	SOD1	up_AFEM_EC
GO:0071310	0.609	0.776	1	634	cellular response to organic substance	BP	1	TLR2	up_AFEM_VSMC
GO:0042398	0.609	0.773	1	12	cellular modified amino acid biosynthetic process	BP	1	GCH1	up_VCAV_EC
GO:0048485	0.609	0.778	1	9	sympathetic nervous system development	BP	1	GATA3	up_VCAV_EC
GO:0072079	0.609	0.773	1	12	nephron tubule formation	BP	1	GATA3	up_VCAV_EC
GO:0051253	0.609	0.769	1	359	negative regulation of RNA metabolic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002687	0.60907074	0.76388	1	36	positive regulation of leukocyte migration	BP	1	RARRES2	up_ACOR_EC
GO:0006754	0.609613373	0.76337	1	36	ATP biosynthetic process	BP	1	ALDOC	up_ACOR_EC
GO:0010604	0.61	0.44	76	919	positive regulation of macromolecule metabolic process	BP	1	HMGB1,SREBF1,IRAK1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,UBE2S,NEDD4,U2AF2,SLC29A1,PRELID1,RFC2,INSIG1,CAV1,RFC5,RFC3,FANCI,TIMELESS,THRAP3,TRUB2,FAM129B,AURKB,EZH2,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,SMARCC1,PLK3,PCNA,DHX33,SF3B4,CKS2,PDCD2,BRCA1,FASTKD3,EIF5A,E2F8,TFRC,PPARD,RAP2C,CYCS,NCL,RAC1,NUP62,EMP2,DTL,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,EZR,CLSPN,RBM14,RAD23A,CDC20,PSMC1,AIFM1,ARHGEF2,SUPT16H,TADA2A,HOXA9,GLI1,JMJD6,CCT4,ENSCAFG00000017103,AMER1,DCUN1D5,PIK3CD	down_ACOR_VSMC
GO:0006119	0.61	0.623	3	40	oxidative phosphorylation	BP	1	CDK1,CYCS,CYC1	down_ACOR_VSMC
GO:0007568	0.61	0.622	3	50	aging	BP	1	SERPINE1,NUAK1,CDKN1A	down_VSAP_EC
GO:0009145	0.61	0.669	2	40	purine nucleoside triphosphate biosynthetic	BP	1	ATP5MC1,ADK	down_VCAV_EC
GO:0009892	0.61	0.678	2	835	negative regulation of metabolic process	BP	1	HOXC10,LNPEP	up_AORT_EC
GO:0016079	0.61	0.672	2	27	synaptic vesicle exocytosis	BP	1	SNAP23,STX11	up_VCAV_EC
GO:1905268	0.61	0.676	2	20	negative regulation of chromatin organization	BP	1	KDM5A,KDM3A	up_VCAV_EC
GO:0046039	0.61	0.774	1	11	GTP metabolic process	BP	1	RAN	down_ACOR_VSMC
GO:0051181	0.61	0.774	1	11	cofactor transport	BP	1	SLC25A19	down_ACOR_VSMC
GO:1901068	0.61	0.774	1	11	guanosine-containing compound metabolic	BP	1	RAN	down_ACOR_VSMC

GO:0002444	0.61	0.767	1	18	myeloid leukocyte mediated immunity	BP	1	RAC2	down_VCAV_EC
GO:0048146	0.61	0.767	1	18	positive regulation of fibroblast proliferation	BP	1	DDR2	down_VCAV_EC
GO:0048662	0.61	0.767	1	18	negative regulation of smooth muscle cell	BP	1	CLSTN1	down_VCAV_EC
GO:1901576	0.61	0.822	1	1877	organic substance biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0006695	0.61	0.769	1	16	cholesterol biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:1902653	0.61	0.769	1	16	secondary alcohol biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:0080134	0.61	0.768	1	386	regulation of response to stress	BP	1	TAOK1	up_AORT_EC
GO:0032881	0.61	0.774	1	11	regulation of polysaccharide metabolic	BP	1	PDGFB	up_VCAV_EC
GO:0032885	0.61	0.774	1	11	regulation of polysaccharide	BP	1	PDGFB	up_VCAV_EC
GO:0030030	0.61	0.767	1	377	cell projection organization	BP	1	SHOX2	up_VFEM_VSMC
GO:0032880	0.61	0.765	1	266	regulation of protein localization	BP	1	NR1H4	up_VPUL_EC
GO:0044283	0.61	0.764	1	201	small molecule biosynthetic process	BP	1	GATM	up_VSAP_VSMC
GO:0022412	0.61071964	0.66496	2	76	cellular process involved in reproduction in multicellular organism	BP	1	FIGNL1,PYGO2	up_ACOR_EC
GO:0051128	0.611	0.458	38	790	regulation of cellular component organization	BP	1	SLC35F6,KIRREL1,LRP1,DCN,PRNP,SDC4,NABP2,LMO4,IGFBP6,TRPV2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,LCAT,SYDE1,CLSTN1,PRMT6,LRPAP1,THY1,TLX2,CLEC16A,CYBA,MAVS,CDH2,NCLN,MGARP,ACTR3B,UST,PRKCSH,DDR2,GREM1,PLEKHH2,EVI5L,RAC2,PACSIN3,RGMA,BRSK1	down_VCAV_EC
GO:0031323	0.611	0.574	6	1788	regulation of cellular metabolic process	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0006338	0.611	0.594	4	45	chromatin remodeling	BP	1	SMARCD2,MYC,CENPP,SMARCA2	up_VSAP_EC
GO:0010906	0.611	0.623	3	38	regulation of glucose metabolic process	BP	1	FAM3C,ENSCAFG00000010596,PMAIP1	up_VCAV_EC
GO:0007188	0.611	0.667	2	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	ADCY6,GNAZ	down_VCAV_EC
GO:0051291	0.611	0.674	2	21	protein heterooligomerization	BP	1	PCBD1,TRPS1	up_ACOR_VSMC
GO:0006164	0.611	0.664	2	86	purine nucleotide biosynthetic process	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0040008	0.611	0.763	1	179	regulation of growth	BP	1	ACVRL1	down_ACOR_EC
GO:0051347	0.611	0.763	1	182	positive regulation of transferase activity	BP	1	LYN	down_ACOR_EC
GO:0046164	0.611	0.772	1	11	alcohol catabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:1903393	0.611	0.773	1	11	positive regulation of adherens junction	BP	1	RAC1	down_ACOR_VSMC
GO:0009890	0.611	0.768	1	420	negative regulation of biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0007431	0.611	0.766	1	19	salivary gland development	BP	1	SEMA3C	down_VCAV_EC
GO:0048814	0.611	0.766	1	19	regulation of dendrite morphogenesis	BP	1	TLX2	down_VCAV_EC
GO:0035418	0.611	0.777	1	9	protein localization to synapse	BP	1	DAG1	up_ACOR_VSMC
GO:1905276	0.611	0.777	1	9	regulation of epithelial tube formation	BP	1	SEC24B	up_ACOR_VSMC
GO:0007143	0.611	0.775	1	10	female meiotic nuclear division	BP	1	FBXO5	up_VCAV_EC
GO:0046854	0.611	0.773	1	11	phosphatidylinositol phosphorylation	BP	1	IMPA1	up_VCAV_EC
GO:0051051	0.611	0.761	1	112	negative regulation of transport	BP	1	HOXA3	up_VPOR_EC
GO:0045859	0.611	0.762	1	219	regulation of protein kinase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0048514	0.611	0.763	1	214	blood vessel morphogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:0034968	0.61125974	0.76214	1	34	histone lysine methylation	BP	1	PYGO2	up_ACOR_EC

GO:0006629	0.612	0.463	31	382	lipid metabolic process	BP	1	FADS2,SCD,ACSL3,SQLE,FADS1,LSS,SREBF1,ACLY,HMGCR,SF1,MPDU1,CTDNEP1,INSIG1,CAV1,ENSCAFG00000018572,ABHD5,CDK4,DHCR24,BRCA1,MVD,ELOVL1,PPARD,VAC14,ELOVL6,FDFT1,SGPL1,LIPC,NUS1,GK5,PDSS1,ACADL	down_ACOR_VSMC
GO:0045934	0.612	0.472	24	407	negative regulation of nucleobase-containing compound metabolic process	BP	1	PRICKLE1,NR1H4,PLK3,ETV6,CBX5,FHL2,SMARCA4,PTPN2,MORF4L2,PEG3,MTDH,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,VLDLR,REST,ZMYND8,HIF1AN,SIX4	down_VSAP_EC
GO:0010467	0.612	0.509	14	1787	gene expression	BP	1	BARX1,HOXA3,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,RSL24D1,RPL10L,RRP15,PUM3,EIF5,CCAR1,RNF6	up_VPOR_EC
GO:0043408	0.612	0.516	10	211	regulation of MAPK cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,CSPG4,MYDGF,SASH1,CDH2,GSDME,SPRED1,SHC1	down_VCAV_EC
GO:0034641	0.612	0.545	9	2171	cellular nitrogen compound metabolic	BP	1	TBX15,EYA1,HOXA9,MME,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0032872	0.612	0.544	7	77	regulation of stress-activated MAPK cascade	BP	1	ARHGEF5,MAP3K5,F2RL1,MYC,SASH1,MYD88,QARS	up_VSAP_EC
GO:0007369	0.612	0.557	6	63	gastrulation	BP	1	MBP,BMP4,ENSCAFG00000006238,FRS2,DAG1,LAMA3	up_ACOR_VSMC
GO:0052547	0.612	0.589	4	82	regulation of peptidase activity	BP	1	CST3,RECK,PARK7,IFT57	down_VCAV_EC
GO:0048523	0.612	0.638	3	1399	negative regulation of cellular process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0045834	0.612	0.666	2	41	positive regulation of lipid metabolic process	BP	1	PDGFRB,AKT2	down_VCAV_EC
GO:0033209	0.612	0.671	2	24	tumor necrosis factor-mediated signaling	BP	1	ENSCAFG00000002015,TJP2	up_VCAV_EC
GO:2000736	0.612	0.673	2	21	regulation of stem cell differentiation	BP	1	ZFP36L2,LBH	up_VSAP_EC
GO:0010942	0.612	0.761	1	200	positive regulation of cell death	BP	1	LYN	down_ACOR_EC
GO:0003382	0.612	0.772	1	11	epithelial cell morphogenesis	BP	1	FLNB	down_ACOR_VSMC
GO:0032963	0.612	0.765	1	18	collagen metabolic process	BP	1	LARP6	down_VCAV_EC
GO:0048483	0.612	0.765	1	19	autonomic nervous system development	BP	1	TLX2	down_VCAV_EC
GO:0045912	0.612	0.768	1	15	negative regulation of carbohydrate metabolic	BP	1	ENPP1	down_VSAP_EC
GO:0006491	0.612	0.775	1	9	N-glycan processing	BP	1	FUT8	up_ACOR_VSMC
GO:0046040	0.612	0.776	1	9	IMP metabolic process	BP	1	NT5C2	up_ACOR_VSMC
GO:0009206	0.612	0.761	1	39	purine ribonucleoside triphosphate biosynthetic	BP	1	PPARGC1A	up_AFEM_EC
GO:0061178	0.612	0.771	1	12	regulation of insulin secretion involved in cellular response to	BP	1	HIF1A	up_VCAV_EC
GO:0048193	0.612	0.76	1	116	Golgi vesicle transport	BP	1	GCC2	up_VPOR_EC
GO:0006753	0.612	0.762	1	211	nucleoside phosphate metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:0050801	0.612004786	0.56681	5	200	ion homeostasis	BP	1	NR1H4,PTH1R,IFI6,SLC9A9,TMTC2	up_ACOR_EC
GO:0006820	0.613	0.517	10	109	anion transport	BP	1	GABRE,SLC16A12,OSR1,ABCB11,SLC25A12,RAB11B,SLC27A6,CTNS,SLC10A6,CLCN2	up_VSAP_EC
GO:0050803	0.613	0.571	5	55	regulation of synapse structure or activity	BP	1	FZD1,AMIGO1,LRRN3,ABL1,LRP4	up_VSAP_EC
GO:0050807	0.613	0.571	5	55	regulation of synapse organization	BP	1	FZD1,AMIGO1,LRRN3,ABL1,LRP4	up_VSAP_EC
GO:0072028	0.613	0.621	3	37	nephron morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0050679	0.613	0.617	3	62	positive regulation of epithelial cell proliferation	BP	1	BMPR1A,B4GALT1,MYDGF	down_VCAV_EC
GO:0051726	0.613	0.667	2	393	regulation of cell cycle	BP	1	USP28,ATRIP	down_ACOR_EC
GO:0009116	0.613	0.665	2	39	nucleoside metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:0071333	0.613	0.67	2	25	cellular response to glucose stimulus	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:1900542	0.613	0.669	2	26	regulation of purine nucleotide metabolic	BP	1	NOS2,HIF1A	up_VCAV_EC
GO:0044265	0.613	0.767	1	423	cellular macromolecule catabolic process	BP	1	USP33	down_AFEM_EC
GO:0006687	0.613	0.765	1	18	glycosphingolipid metabolic process	BP	1	ENSCAFG00000017708	down_VCAV_EC

GO:0070265	0.613	0.764	1	19	necrotic cell death	BP	1	GSDME	down_VCAV_EC
GO:0010647	0.613	0.767	1	460	positive regulation of cell communication	BP	1	CITED2	down_VPOR_EC
GO:0003416	0.613	0.775	1	9	endochondral bone growth	BP	1	DDR2	up_ACOR_VSMC
GO:0010165	0.613	0.775	1	9	response to X-ray	BP	1	XRRA1	up_ACOR_VSMC
GO:0045980	0.613	0.772	1	10	negative regulation of nucleotide metabolic	BP	1	DDIT4	up_ACOR_VSMC
GO:0016310	0.613	0.772	1	641	phosphorylation	BP	1	TLR2	up_AFEM_VSMC
GO:0002684	0.613	0.761	1	239	positive regulation of immune system process	BP	1	NR1H4	up_APUL_EC
GO:0031329	0.613	0.761	1	241	regulation of cellular catabolic process	BP	1	LZTS1	up_APUL_EC
GO:0018193	0.613	0.765	1	368	peptidyl-amino acid modification	BP	1	EYA1	up_VFEM_VSMC
GO:0120036	0.614	0.461	31	373	plasma membrane bounded cell projection organization	BP	1	EPHB1,KIT,IFRD1,PODXL,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,NECTIN2,MTOR,PREX2,NCKAP1,GDPD5,ENSCAFG00000010224,STMN1,SNX2,PAK2,APOD,NCK1,EXOC5,FES,RAPGEF2,CREB1,SPTBN4,ITGA6,ALS2,IQUB,SPATA6,FSCN1	up_VCAV_EC
GO:0006914	0.614	0.529	8	141	autophagy	BP	1	PLK3,SESN2,HIF1A,MTDH,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0061919	0.614	0.529	8	141	process utilizing autophagic mechanism	BP	1	PLK3,SESN2,HIF1A,MTDH,BNIP3,CDC37,SH3GLB1,HTT	down_VSAP_EC
GO:0006839	0.614	0.531	8	86	mitochondrial transport	BP	1	SLC8B1,SLC25A12,MFN2,SLC25A28,FBXO7,ZNF205,SLC25A40,BAG4	up_VSAP_EC
GO:0051480	0.614	0.589	4	50	regulation of cytosolic calcium ion concentration	BP	1	HMGB1,CAV1,GSTO1,CORO1A	down_ACOR_VSMC
GO:0048771	0.614	0.591	4	43	tissue remodeling	BP	1	LEP,RASSF2,GJA1,CHD7	up_ACOR_VSMC
GO:0090407	0.614	0.585	4	177	organophosphate biosynthetic process	BP	1	GPAM,ACACB,PPARGC1A,AGPAT2	up_AFEM_EC
GO:0048839	0.614	0.618	3	50	inner ear development	BP	1	PTPN11,SDC4,SIX4	down_VSAP_EC
GO:0006810	0.614	0.633	3	1244	transport	BP	1	HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:1903409	0.614	0.669	2	24	reactive oxygen species biosynthetic process	BP	1	CAV1,ARG2	down_ACOR_VSMC
GO:0032623	0.614	0.671	2	21	interleukin-2 production	BP	1	CD83,MAP3K7	up_ACOR_VSMC
GO:0090049	0.614	0.67	2	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	NRP1,PIK3C2A	up_ACOR_VSMC
GO:0006511	0.614	0.662	2	253	ubiquitin-dependent protein catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0051704	0.614	0.667	2	476	multi-organism process	BP	1	HOXA9,CYP26B1	up_VFEM_EC
GO:0009117	0.614	0.759	1	208	nucleotide metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0006359	0.614	0.772	1	10	regulation of transcription by RNA polymerase III	BP	1	NAB2	down_ACOR_VSMC
GO:0032008	0.614	0.764	1	19	positive regulation of TOR signaling	BP	1	CLEC16A	down_VCAV_EC
GO:0034605	0.614	0.763	1	18	cellular response to heat	BP	1	SCARA5	down_VCAV_EC
GO:0002886	0.614	0.772	1	10	regulation of myeloid leukocyte mediated	BP	1	F2RL1	up_ACOR_VSMC
GO:0061311	0.614	0.774	1	9	cell surface receptor signaling pathway involved in heart	BP	1	BMP4	up_ACOR_VSMC
GO:0032990	0.615	0.492	15	167	cell part morphogenesis	BP	1	ENPP2,SLIT2,ABL1,PLXNA4,SHOX2,POLDIP2,LRP4,DPYSL2,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:1903706	0.615	0.509	11	119	regulation of hemopoiesis	BP	1	TMEM176B,TMEM176A,CD83,RASSF2,BMP4,ISG15,FAM210B,P4HTM,CLSTN1,B2M,CNOT4	up_ACOR_VSMC
GO:0071704	0.615	0.571	9	3535	organic substance metabolic process	BP	1	EYA1,GATM,HOXA10,HOXA9,TBX15,FBP1,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0065007	0.615	0.594	7	3499	biological regulation	BP	1	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,IL22RA1,SLIT2	up_VPUL_VSMC
GO:0009896	0.615	0.549	6	127	positive regulation of catabolic process	BP	1	LRP1,DCN,AKT2,ZFP36L1,CLEC16A,PACSIN3	down_VCAV_EC
GO:0010639	0.615	0.55	6	128	negative regulation of organelle organization	BP	1	SLC35F6,CLIP3,PRMT6,CLEC16A,PLEKHH2,EVI5L	down_VCAV_EC
GO:0009636	0.615	0.552	6	66	response to toxic substance	BP	1	MBP,TP53INP1,PRKCE,SESN1,CAT,PARK7	up_ACOR_VSMC

GO:0009636	0.615	0.553	6	66	response to toxic substance	BP	1	SLC6A4,ABL1,SESN1,MAP3K5,ZNF580,HMOX1	up_VSAP_EC
GO:0032273	0.615	0.589	4	44	positive regulation of protein polymerization	BP	1	JMY,EVL,PRKCE,WASL	up_ACOR_VSMC
GO:0000086	0.615	0.616	3	52	G2/M transition of mitotic cell cycle	BP	1	BACH1,CALM1,CDKN1A	down_VSAP_EC
GO:0032755	0.615	0.668	2	24	positive regulation of interleukin-6 production	BP	1	HMGB1,ARHGEF2	down_ACOR_VSMC
GO:1903900	0.615	0.663	2	40	regulation of viral life cycle	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0022029	0.615	0.669	2	23	telencephalon cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0050850	0.615	0.769	1	11	positive regulation of calcium-mediated	BP	1	GSTO1	down_ACOR_VSMC
GO:0023056	0.615	0.766	1	462	positive regulation of signaling	BP	1	CITED2	down_VPOR_EC
GO:0008053	0.615	0.771	1	10	mitochondrial fusion	BP	1	BNIP3	up_ACOR_VSMC
GO:0045063	0.615	0.773	1	9	T-helper 1 cell differentiation	BP	1	IL18R1	up_ACOR_VSMC
GO:0097120	0.615	0.773	1	9	receptor localization to synapse	BP	1	DAG1	up_ACOR_VSMC
GO:1902745	0.615	0.773	1	9	positive regulation of lamellipodium	BP	1	RREB1	up_ACOR_VSMC
GO:1904031	0.615	0.771	1	10	positive regulation of cyclin-dependent protein	BP	1	CCNT1	up_ACOR_VSMC
GO:0001958	0.615	0.77	1	11	endochondral ossification	BP	1	MEF2C	up_VCAV_EC
GO:0036075	0.615	0.77	1	11	replacement ossification	BP	1	MEF2C	up_VCAV_EC
GO:0051129	0.615	0.759	1	221	negative regulation of cellular component	BP	1	TRIM9	up_VFEM_EC
GO:0031175	0.615	0.759	1	224	neuron projection development	BP	1	SHOX2	up_VSAP_VSMC
GO:0031109	0.615036933	0.75833	1	36	microtubule polymerization or	BP	1	TUBB4A	up_ACOR_EC
GO:0000226	0.615040673	0.56362	5	197	microtubule cytoskeleton organization	BP	1	BRSK1,DIXDC1,DCLK2,CHMP4B,TUBB4A	up_ACOR_EC
GO:0002706	0.615599433	0.75794	1	35	regulation of lymphocyte mediated immunity	BP	1	FZD5	up_ACOR_EC
GO:0034645	0.616	0.425	124	1546	cellular macromolecule biosynthetic process	BP	1	EDNRB,HCLS1,ST8SIA6,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,ST6GAL1,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,ZDHHC22,IRF8,SOX18,PELI1,PPP3CA,YES1,B3GNT5,TARSL2,MTOR,ELF4,HHAT,BMP2,HMG20A,HHEX,CHST7,CREM,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,GALNT18,PRKD2,THOC1,SMARCA4,TLR3,MFNG,NCK1,ESCO1,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,MRRF,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,BDP1,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,RAD17,SKIL,GPBP1,USP37,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,ZDHHC6,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC
GO:1903506	0.616	0.432	81	977	regulation of nucleic acid-templated transcription	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,HOXA10,ERF,TCERG1,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103	down_ACOR_VSMC

GO:0080090	0.616	0.455	40	1734	regulation of primary metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,RAB7A,AXIN2,YEATS2,ACACB,PPARGC1A,CCL5,CTIF,ADAM17,SAMD4B	up_AFEM_EC
GO:0000003	0.616	0.493	14	295	reproduction	BP	1	ADAMTS2,BMPR1A,RECK,SYDE1,MEA1,B4GALT1,MMP23,ZFP36L1,ENSCAFG00000017708,IRX5,RDH10,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0001822	0.616	0.528	8	98	kidney development	BP	1	GREM1,ARG2,HOXB7,IQGAP1,SGPL1,JMJD6,SIX4,AMER1	down_ACOR_VSMC
GO:0009161	0.616	0.563	5	103	ribonucleoside monophosphate	BP	1	NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2	down_VCAV_EC
GO:0042493	0.616	0.583	4	178	response to drug	BP	1	CRYAB,FIBIN,CHRM2,NR3C1	up_AFEM_EC
GO:0010628	0.616	0.587	4	527	positive regulation of gene expression	BP	1	ARHGEF2,ENSCAFG00000002015,ACVR2A,RNF6	up_VPOR_EC
GO:0032273	0.616	0.589	4	44	positive regulation of protein polymerization	BP	1	CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:0032680	0.616	0.618	3	36	regulation of tumor necrosis factor production	BP	1	ARG2,CACTIN,ARHGEF2	down_ACOR_VSMC
GO:0008637	0.616	0.618	3	35	apoptotic mitochondrial changes	BP	1	RHOT1,BNIP3,NAIF1	up_ACOR_VSMC
GO:0010717	0.616	0.619	3	32	regulation of epithelial to mesenchymal transition	BP	1	BMP4,DAG1,TGFBR1	up_ACOR_VSMC
GO:0019395	0.616	0.618	3	33	fatty acid oxidation	BP	1	LEP,PPARGC1A,ACAD11	up_ACOR_VSMC
GO:0008652	0.616	0.667	2	24	cellular amino acid biosynthetic process	BP	1	BCAT1,CTH	down_ACOR_VSMC
GO:0071347	0.616	0.666	2	25	cellular response to interleukin-1	BP	1	IRAK1,CACTIN	down_ACOR_VSMC
GO:1901607	0.616	0.667	2	24	alpha-amino acid biosynthetic process	BP	1	BCAT1,CTH	down_ACOR_VSMC
GO:0030518	0.616	0.662	2	42	intracellular steroid hormone receptor	BP	1	KANK2,PARK7	down_VCAV_EC
GO:0097479	0.616	0.662	2	41	synaptic vesicle localization	BP	1	TMEM230,CDH2	down_VCAV_EC
GO:0001892	0.616	0.663	2	35	embryonic placenta development	BP	1	TMED2,HIF1A	down_VSAP_EC
GO:0071156	0.616	0.668	2	21	regulation of cell cycle arrest	BP	1	CRADD,CDK9	up_VSAP_EC
GO:0051055	0.616	0.669	2	21	negative regulation of lipid biosynthetic process	BP	1	INSIG2,ENSCAFG00000000071	up_VSAP_EC
GO:0060561	0.616	0.768	1	11	apoptotic process involved in	BP	1	B4GALT1	down_ACOR_VSMC
GO:0016477	0.616	0.764	1	426	cell migration	BP	1	FSCN1	down_AFEM_EC
GO:0070169	0.616	0.762	1	18	positive regulation of biomineral tissue	BP	1	BMPR1A	down_VCAV_EC
GO:1905268	0.616	0.761	1	20	negative regulation of chromatin organization	BP	1	PRMT6	down_VCAV_EC
GO:0070988	0.616	0.765	1	14	demethylation	BP	1	KDM3A	down_VSAP_EC
GO:0006195	0.616	0.77	1	10	purine nucleotide catabolic process	BP	1	PDE5A	up_ACOR_VSMC
GO:0030890	0.616	0.772	1	9	positive regulation of B cell proliferation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0048820	0.616	0.772	1	9	hair follicle maturation	BP	1	FERMT1	up_ACOR_VSMC
GO:0032268	0.616	0.775	1	778	regulation of cellular protein metabolic process	BP	1	WNT7A	up_AORT_VSMC
GO:0006929	0.616	0.77	1	10	substrate-dependent cell migration	BP	1	NCK1	up_VCAV_EC
GO:2000144	0.616	0.767	1	12	positive regulation of DNA-templated transcription,	BP	1	IRF8	up_VCAV_EC
GO:0009101	0.616	0.756	1	113	glycoprotein biosynthetic process	BP	1	OSTC	up_VPOR_EC
GO:0010631	0.616	0.756	1	118	epithelial cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0090132	0.616	0.756	1	118	epithelium migration	BP	1	SEMA3A	up_VPOR_EC
GO:0097190	0.616	0.759	1	217	apoptotic signaling pathway	BP	1	EYA1	up_VFEM_EC
GO:1902533	0.616	0.759	1	271	positive regulation of intracellular signal	BP	1	CCL24	up_VPUL_EC
GO:0032147	0.616097675	0.65938	2	77	activation of protein kinase activity	BP	1	PAK3,PRKCD	up_ACOR_EC
GO:0032606	0.616954982	0.75666	1	35	type I interferon production	BP	1	MAVS	up_ACOR_EC

GO:0015833	0.617	0.466	25	521	peptide transport	BP	1	GPAM,SNX18,PRNP,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,GLI3,PARK7,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0048812	0.617	0.497	13	151	neuron projection morphogenesis	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,PPP3CA,PREX2,ENSCAFG00000010224,STMN1,RAPGEF2,CREB1,SPTBN4,ALS2	up_VCAV_EC
GO:0007276	0.617	0.502	12	130	gamete generation	BP	1	PRDX4,BMP4,ATRX,PDE5A,MARF1,AFF4,SPINK2,HPGD,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0098660	0.617	0.506	11	141	inorganic ion transmembrane transport	BP	1	NNT,NEDD4,CAV1,SLC30A1,GSTO1,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,ATP5F1D	down_ACOR_VSMC
GO:0050730	0.617	0.551	6	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	NRP1,PRKCE,PARP9,APP,PSEN1,DUSP22	up_ACOR_VSMC
GO:0048015	0.617	0.586	4	48	phosphatidylinositol-mediated signaling	BP	1	NEDD4,PPARD,EZR,PIK3CD	down_ACOR_VSMC
GO:0048017	0.617	0.586	4	48	inositol lipid-mediated signaling	BP	1	NEDD4,PPARD,EZR,PIK3CD	down_ACOR_VSMC
GO:0007411	0.617	0.587	4	45	axon guidance	BP	1	SLIT2,PLXNA4,DPYSL2,NFIB	up_VSAP_EC
GO:0097485	0.617	0.587	4	45	neuron projection guidance	BP	1	SLIT2,PLXNA4,DPYSL2,NFIB	up_VSAP_EC
GO:0002790	0.617	0.61	3	133	peptide secretion	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:1990542	0.617	0.619	3	32	mitochondrial transmembrane transport	BP	1	SLC8B1,SLC25A12,SLC25A28	up_VSAP_EC
GO:0006378	0.617	0.668	2	20	mRNA polyadenylation	BP	1	CCNT1,APP	up_ACOR_VSMC
GO:0006090	0.617	0.665	2	26	pyruvate metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0043066	0.617	0.659	2	253	negative regulation of apoptotic process	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0007420	0.617	0.757	1	169	brain development	BP	1	NRP2	down_ACOR_EC
GO:0045595	0.617	0.764	1	469	regulation of cell differentiation	BP	1	HDAC7	down_VPOR_EC
GO:0006139	0.617	0.816	1	1909	nucleobase-containing compound metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0009058	0.617	0.816	1	1910	biosynthetic process	BP	1	MOSPD1	down_VFEM_EC
GO:0050879	0.617	0.762	1	16	multicellular organismal movement	BP	1	HOMER1	down_VSAP_EC
GO:0050881	0.617	0.762	1	16	musculoskeletal movement	BP	1	HOMER1	down_VSAP_EC
GO:0030857	0.617	0.763	1	15	negative regulation of epithelial cell	BP	1	CTNNB1	down_VSAP_EC
GO:0031016	0.617	0.763	1	15	pancreas development	BP	1	CTNNB1	down_VSAP_EC
GO:0045995	0.617	0.756	1	40	regulation of embryonic development	BP	1	DLL1	up_AFEM_EC
GO:0051123	0.617	0.763	1	14	RNA polymerase II preinitiation complex	BP	1	HMGB1	up_VCAV_EC
GO:0035794	0.617	0.765	1	13	positive regulation of mitochondrial membrane permeability	BP	1	SH3GLB1	up_VCAV_EC
GO:1905710	0.617	0.765	1	13	positive regulation of membrane permeability	BP	1	SH3GLB1	up_VCAV_EC
GO:0006629	0.617	0.761	1	382	lipid metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0010647	0.617	0.764	1	460	positive regulation of cell communication	BP	1	GATA5	up_VPUL_VSMC
GO:0051252	0.617766578	0.46425	27	1051	regulation of RNA metabolic process	BP	1	NR1H4,GATA4,TRPS1,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0097191	0.617837099	0.65749	2	79	extrinsic apoptotic signaling pathway	BP	1	IFI6,NRP1	up_ACOR_EC
GO:0035150	0.617937359	0.7556	1	36	regulation of tube size	BP	1	FOXC2	up_ACOR_EC
GO:0050880	0.617937359	0.7556	1	36	regulation of blood vessel size	BP	1	FOXC2	up_ACOR_EC
GO:0006357	0.618	0.463	26	547	regulation of transcription by RNA polymerase II	BP	1	SMAD9,DCN,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TFE3,NR3C1,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,TSC22D3,GLIS2,GREM1,THRB,RGMA	down_VCAV_EC

GO:0060548	0.618	0.491	14	294	negative regulation of cell death	BP	1	GPAM,SLC35F6,PRNP,KANK2,AKT2,TMEM161A,LRPAP1,ARHGAP10,GLI3,PARK7,MYDGF,TSC22D3,SHC1,GREM1	down_VCAV_EC
GO:0043066	0.618	0.499	12	253	negative regulation of apoptotic process	BP	1	GPAM,SLC35F6,PRNP,AKT2,TMEM161A,ARHGAP10,GLI3,PARK7,MYDGF,TSC22D3,SHC1,GREM1	down_VCAV_EC
GO:0010035	0.618	0.547	6	107	response to inorganic substance	BP	1	HIF1A,CRYAB,KPNA4,BNIP3,CALM1,HOMER1	down_VSAP_EC
GO:0032268	0.618	0.551	6	778	regulation of cellular protein metabolic process	BP	1	ARHGEF2,ASPN,ACVR2A,PUM3,EIF5,ENSCAFG00000032731	up_VPOR_EC
GO:0043405	0.618	0.582	4	85	regulation of MAP kinase activity	BP	1	CSPG4,SASH1,SPRED1,SHC1	down_VCAV_EC
GO:0010977	0.618	0.617	3	33	negative regulation of neuron projection	BP	1	SLIT2,RTN4RL1,LRP4	up_VSAP_EC
GO:0032609	0.618	0.664	2	25	interferon-gamma production	BP	1	HMGB1,FAM49B	down_ACOR_VSMC
GO:0099504	0.618	0.66	2	42	synaptic vesicle cycle	BP	1	CDH2,BRSK1	down_VCAV_EC
GO:0048523	0.618	0.684	2	1399	negative regulation of cellular process	BP	1	EYA1,HOXA9	up_AFEM_VSMC
GO:0010941	0.618	0.664	2	524	regulation of cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0045736	0.618	0.767	1	11	negative regulation of cyclin-dependent protein serine/threonine kinase	BP	1	CDKN2C	down_ACOR_VSMC
GO:0003094	0.618	0.766	1	11	glomerular filtration	BP	1	EMP2	down_ACOR_VSMC
GO:1900026	0.618	0.767	1	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	RAC1	down_ACOR_VSMC
GO:1904030	0.618	0.767	1	11	negative regulation of cyclin-dependent protein	BP	1	CDKN2C	down_ACOR_VSMC
GO:1901264	0.618	0.76	1	18	carbohydrate derivative transport	BP	1	CYBA	down_VCAV_EC
GO:1901880	0.618	0.76	1	19	negative regulation of protein depolymerization	BP	1	PLEKHH2	down_VCAV_EC
GO:0007589	0.618	0.761	1	16	body fluid secretion	BP	1	HIF1A	down_VSAP_EC
GO:0015748	0.618	0.761	1	16	organophosphate ester transport	BP	1	APOE	down_VSAP_EC
GO:0032495	0.618	0.762	1	15	response to muramyl dipeptide	BP	1	ARHGEF2	down_VSAP_EC
GO:0035116	0.618	0.762	1	15	embryonic hindlimb morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0050885	0.618	0.763	1	14	neuromuscular process controlling balance	BP	1	AARS	down_VSAP_EC
GO:0009048	0.618	0.77	1	9	dosage compensation by inactivation of X	BP	1	PCGF5	up_ACOR_VSMC
GO:0017015	0.618	0.755	1	40	regulation of transforming growth factor beta receptor signaling	BP	1	ADAM17	up_AFEM_EC
GO:1903844	0.618	0.755	1	40	regulation of cellular response to transforming growth factor beta	BP	1	ADAM17	up_AFEM_EC
GO:0009968	0.618	0.761	1	392	negative regulation of signal transduction	BP	1	DKK2	up_AORT_EC
GO:0051726	0.618	0.761	1	393	regulation of cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0043931	0.618	0.77	1	9	ossification involved in bone maturation	BP	1	BMP2	up_VCAV_EC
GO:0051125	0.618	0.766	1	11	regulation of actin nucleation	BP	1	NCKAP1	up_VCAV_EC
GO:0070977	0.618	0.77	1	9	bone maturation	BP	1	BMP2	up_VCAV_EC
GO:0006536	0.618	0.768	1	10	glutamate metabolic process	BP	1	AADAT	up_VCAV_EC
GO:0035088	0.618	0.765	1	12	establishment or maintenance of	BP	1	FSCN1	up_VCAV_EC
GO:0061245	0.618	0.765	1	12	establishment or maintenance of bipolar	BP	1	FSCN1	up_VCAV_EC
GO:0070670	0.618	0.767	1	11	response to interleukin-4	BP	1	GATA3	up_VCAV_EC
GO:0071353	0.618	0.767	1	11	cellular response to interleukin-4	BP	1	GATA3	up_VCAV_EC
GO:1901700	0.618	0.761	1	364	response to oxygen-containing compound	BP	1	CYP26B1	up_VPOR_VSMC
GO:0023056	0.618	0.763	1	462	positive regulation of signaling	BP	1	GATA5	up_VPUL_VSMC
GO:0045859	0.618	0.756	1	219	regulation of protein kinase activity	BP	1	CAV1	up_VSAP_VSMC

GO:0010811	0.618740445	0.75484	1	36	positive regulation of cell-substrate adhesion	BP	1	NRP1	up_ACOR_EC
GO:0046631	0.618967048	0.75476	1	35	alpha-beta T cell activation	BP	1	PTGER4	up_ACOR_EC
GO:0008150	0.619	0.434	282	5646	biological_process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,GSTP1,NOTCH2,HSPB6,PDGFRB,SLC35F6,KIRREL1,CERCAM,SNX18,FBLN2,SMAD9,ITGB5,LRP1,DCN,MAOA,CFD,NAB2,NDN,ANGPT1,ARSA,PRNP,LUM,MT2A,SDC4,UBA52,FOLR2,VASN,ATP8B2,FBN1,ADCY6,GLIPR2,BGN,LARP6,SLC10A3,KANK2,THBS3,TMEM230,SH3BP1,COA1,BMPR1A,LOX,TLN2,KRTCAP2,VKORC1,NABP2,LMO4,EVC,RECK,FXYD1,IGFBP6,RPS10,TRPV2,ANPEP,COL6A1,CLIP3,NUMBL,FKBP10,CHID1,ARHGEF25,NAGLU,RHOD,OSMR,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,ERGIC1,AKT2,DOCK10,PSMF1,MICALL2,TTC8,LCAT,RHBDL1,ENSCAFG00000025332,SAMD4B,EEF2K,SNUPN,TFE3,ACAA1,CHCHD10,ME3,ENSCAFG00000018277,NR3C1,H6PD,SSR2,SYDE1,HSD3B7,HR,SCP2,HOXC4,PDIA4,RPL23,SLC39A6,LAMA3,RPL13,GLB1L,CLSTN1,PCSK7,PLCL1,DDOST,CACNB3,CSPG4,CYB5R3,TRIM8,PKD1,VDR,PRMT6,ENSCAFG00000013404,CABIN1,UROS,PRELP,NT5C2,EPHX1,ANXA11,ENTPD3,WIPF1,THNSL2,PGLS,POFUT1,TMEM161A,ATP5MC1,RASSF8,SCAMP4,CXXC5,GFPT2,UQCR10,SEMA3C,ASPN,POLDIP2,CRISPLD2,PIGS,ISOC2,HS3ST3B1,LRPAP1,GNAZ,EIF3K,THY1,FKBP5,GSTM4,NECAB3,RN	down_VCAV_EC
GO:0030182	0.619	0.456	31	327	neuron differentiation	BP	1	VEGFD,LEP,EPYC,FEZ1,ITM2C,BMP4,FGFR2,SEC24B,ZNF365,LMO4,TMEM108,NRP1,GPM6A,ULK2,UNC5B,SLITRK5,TBX20,FZD3,RND1,DAG1,APP,PSEN1,SIPA1L1,CLN8,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,WASL	up_ACOR_VSMC
GO:0006725	0.619	0.542	8	1956	cellular aromatic compound metabolic	BP	1	TBX15,EYA1,HOXA9,HOXA10,HOXA7,SIX1,YBX3,ADCY3	up_VFEM_EC
GO:0006650	0.619	0.547	6	78	glycerophospholipid metabolic process	BP	1	PDGFB,SERINC5,SH3GLB1,PLCG2,IMPA1,PIP5K1B	up_VCAV_EC
GO:0042592	0.619	0.583	4	522	homeostatic process	BP	1	C3AR1,HOXA3,ENSCAFG00000005494,ACVR2A	up_VPOR_EC
GO:0022408	0.619	0.585	4	44	negative regulation of cell-cell adhesion	BP	1	CD274,CDH1,ABL1,ASS1	up_VSAP_EC
GO:1901988	0.619	0.611	3	63	negative regulation of cell cycle phase transition	BP	1	KANK2,ZFP36L1,BRSK1	down_VCAV_EC
GO:0007040	0.619	0.616	3	33	lysosome organization	BP	1	TPCN2,HPS4,VPS11	up_VSAP_EC
GO:0080171	0.619	0.616	3	33	lytic vacuole organization	BP	1	TPCN2,HPS4,VPS11	up_VSAP_EC
GO:0046634	0.619	0.664	2	24	regulation of alpha-beta T cell activation	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:1901343	0.619	0.659	2	42	negative regulation of vasculature development	BP	1	DCN,SPRED1	down_VCAV_EC
GO:0042770	0.619	0.66	2	35	signal transduction in response to DNA damage	BP	1	SESN2,CDKN1A	down_VSAP_EC
GO:0006641	0.619	0.664	2	25	triglyceride metabolic process	BP	1	GK5,ENSCAFG00000010596	up_VCAV_EC
GO:0070059	0.619	0.663	2	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	1	NCK1,ATP2A1	up_VCAV_EC
GO:0006753	0.619	0.754	1	211	nucleoside phosphate metabolic process	BP	1	TNRC6B	down_ACOR_EC
GO:0070306	0.619	0.766	1	11	lens fiber cell differentiation	BP	1	NF2	down_ACOR_VSMC
GO:0097028	0.619	0.765	1	11	dendritic cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0014013	0.619	0.759	1	19	regulation of gliogenesis	BP	1	CDH2	down_VCAV_EC
GO:0055017	0.619	0.759	1	19	cardiac muscle tissue growth	BP	1	BMPR1A	down_VCAV_EC
GO:0002053	0.619	0.761	1	15	positive regulation of mesenchymal cell	BP	1	CTNNB1	down_VSAP_EC
GO:0055094	0.619	0.769	1	9	response to lipoprotein particle	BP	1	ABCA1	up_ACOR_VSMC
GO:0009743	0.619	0.754	1	40	response to carbohydrate	BP	1	GPAM	up_AFEM_EC
GO:0051262	0.619	0.754	1	40	protein tetramerization	BP	1	ACACB	up_AFEM_EC
GO:1903034	0.619	0.755	1	40	regulation of response to wounding	BP	1	KANK1	up_AFEM_EC

GO:0043603	0.619	0.76	1	372	cellular amide metabolic process	BP	1	LNPEP	up_AORT_EC
GO:0010676	0.619	0.763	1	13	positive regulation of cellular carbohydrate	BP	1	PMAIP1	up_VCAV_EC
GO:0031061	0.619	0.768	1	10	negative regulation of histone methylation	BP	1	KDM3A	up_VCAV_EC
GO:0071402	0.619	0.767	1	10	cellular response to lipoprotein particle	BP	1	MYD88	up_VSAP_EC
GO:0032647	0.619	0.767	1	10	regulation of interferon-alpha production	BP	1	MAVS	up_VSAP_EC
GO:0002757	0.619196694	0.65612	2	78	immune response-activating signal	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0051254	0.62	0.446	41	431	positive regulation of RNA metabolic process	BP	1	SMAD6,LBH,GATA5,GATA4,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0071705	0.62	0.458	28	582	nitrogen compound transport	BP	1	GPAM,SNX18,PRNP,FOLR2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,GLI3,PARK7,ZFP36L1,CYBA,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0055086	0.62	0.468	22	237	nucleobase-containing small molecule metabolic process	BP	1	ACSM3,ACACB,GDA,NADK,COQ9,ALDH6A1,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,ENTPD3,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,PNP,NDUFV1,DDIT4	up_VSAP_EC
GO:0051091	0.62	0.534	7	87	positive regulation of DNA-binding transcription factor activity	BP	1	IRAK1,PPRC1,MTDH,GREM1,DHX33,CTH,ARHGEF2	down_ACOR_VSMC
GO:0035305	0.62	0.614	3	37	negative regulation of dephosphorylation	BP	1	YWHAB,IQGAP1,KNL1	down_ACOR_VSMC
GO:0051100	0.62	0.61	3	53	negative regulation of binding	BP	1	DDIT3,GSK3B,DISC1	down_VSAP_EC
GO:1990845	0.62	0.61	3	51	adaptive thermogenesis	BP	1	PLCL1,DDIT3,KDM3A	down_VSAP_EC
GO:0071396	0.62	0.607	3	134	cellular response to lipid	BP	1	LBH,CRY2,NR3C1	up_AFEM_EC
GO:0106027	0.62	0.663	2	24	neuron projection organization	BP	1	EPHB1,RELN	up_VCAV_EC
GO:0035493	0.62	0.765	1	11	SNARE complex assembly	BP	1	STXBP6	down_ACOR_VSMC
GO:0072210	0.62	0.758	1	19	metanephric nephron development	BP	1	GREM1	down_VCAV_EC
GO:0010324	0.62	0.76	1	16	membrane invagination	BP	1	MYH9	down_VSAP_EC
GO:1901522	0.62	0.769	1	9	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical	BP	1	CHD6	up_ACOR_VSMC
GO:2000637	0.62	0.769	1	9	positive regulation of gene silencing by miRNA	BP	1	BMP4	up_ACOR_VSMC
GO:0002274	0.62	0.754	1	40	myeloid leukocyte activation	BP	1	BPI	up_AFEM_EC
GO:0045727	0.62	0.753	1	40	positive regulation of translation	BP	1	PRR16	up_AFEM_EC
GO:2000241	0.62	0.753	1	40	regulation of reproductive process	BP	1	OVOL1	up_AFEM_EC
GO:0019725	0.62	0.755	1	245	cellular homeostasis	BP	1	NR1H4	up_APUL_EC
GO:0060193	0.62	0.765	1	11	positive regulation of lipase activity	BP	1	SELE	up_VCAV_EC
GO:2001169	0.62	0.764	1	11	regulation of ATP biosynthetic process	BP	1	HIF1A	up_VCAV_EC
GO:0051301	0.62	0.753	1	117	cell division	BP	1	ARHGEF2	up_VPOR_EC
GO:1903706	0.62	0.752	1	119	regulation of hemopoiesis	BP	1	ACVR2A	up_VPOR_EC
GO:0051093	0.62	0.756	1	273	negative regulation of developmental process	BP	1	TBX5	up_VPUL_EC
GO:0042325	0.62	0.761	1	463	regulation of phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0061024	0.62	0.755	1	215	membrane organization	BP	1	CAV1	up_VSAP_VSMC
GO:0048515	0.620554107	0.75311	1	36	spermatid differentiation	BP	1	PYGO2	up_ACOR_EC

GO:0022414	0.621	0.478	17	294	reproductive process	BP	1	SULF1,CELF1,ETV6,PTPN11,TMED2,PTGS2,HIF1A,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SIX4,SPINK2,RTCB,SNRPA1,KDM3A	down_VSAP_EC
GO:0051128	0.621	0.548	6	790	regulation of cellular component organization	BP	1	ARHGEF2,ENSCAFG00000002015,SEMA3A,FBP1,TWF1,RNF6	up_VPOR_EC
GO:0046677	0.621	0.562	5	54	response to antibiotic	BP	1	TP53INP1,ADCY6,PRKCE,CAT,PARK7	up_ACOR_VSMC
GO:0090174	0.621	0.562	5	56	organelle membrane fusion	BP	1	USP6NL,SYT16,EVI5L,STX11,SGSM2	up_ACOR_VSMC
GO:0045444	0.621	0.578	4	84	fat cell differentiation	BP	1	CLIP3,ZFP36L1,NAPEPLD,ZBTB16	down_VCAV_EC
GO:0003158	0.621	0.612	3	38	endothelium development	BP	1	RAP2C,HOXB5,EZR	down_ACOR_VSMC
GO:0006342	0.621	0.662	2	24	chromatin silencing	BP	1	UHRF2,HIST2H2AC	up_VCAV_EC
GO:0032368	0.621	0.661	2	26	regulation of lipid transport	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0042307	0.621	0.662	2	23	positive regulation of protein import into	BP	1	HCLS1,TMEM173	up_VCAV_EC
GO:0042440	0.621	0.664	2	21	pigment metabolic process	BP	1	CPOX,HMOX1	up_VSAP_EC
GO:0048477	0.621	0.757	1	19	oogenesis	BP	1	FOXO3	down_VCAV_EC
GO:1902893	0.621	0.757	1	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	BMPR1A	down_VCAV_EC
GO:0050654	0.621	0.759	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	CHSY1	down_VSAP_EC
GO:0009145	0.621	0.752	1	40	purine nucleoside triphosphate biosynthetic	BP	1	PPARGC1A	up_AFEM_EC
GO:0022008	0.621	0.758	1	406	neurogenesis	BP	1	HOXC10	up_AORT_EC
GO:0046599	0.621	0.764	1	11	regulation of centriole replication	BP	1	PLK2	up_VCAV_EC
GO:0016050	0.621	0.752	1	119	vesicle organization	BP	1	HOOK3	up_VPOR_EC
GO:0048486	0.621	0.766	1	10	parasympathetic nervous system development	BP	1	PLXNA4	up_VSAP_EC
GO:0051253	0.621384024	0.51313	9	359	negative regulation of RNA metabolic process	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:0002761	0.621534168	0.75218	1	36	regulation of myeloid leukocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:1990138	0.621847833	0.75202	1	35	neuron projection extension	BP	1	NRP1	up_ACOR_EC
GO:0010033	0.622	0.428	72	772	response to organic substance	BP	1	FZD1,HNF4A,FAM107A,CD274,PTGFR,PPARGC1B,FOXRED2,SLIT2,CDH1,SLC6A4,FGF7,ABL1,GOT1,CHRM1,DLL1,EPN2,OSR1,PDGFD,TRAFD1,KLF15,CDC42EP2,RARG,CCBE1,MGST1,STAT5A,STAT6,F2RL1,RAB11B,LPL,PDK2,ZFP36L1,PIK3R1,GAS1,ZEB1,TBXA2R,SULF2,ABAT,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,STK16,CASTOR1,KCNB1,CDK9,CD83,PRMT2,OSBPL7,ZFP36L2,HPGD,RAF1,NCOA2,STX4,PQBP1,TIMP2,ACVRL1,UBQLN2,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,BGLAP,TGFBR2,CITED2,BAG4,LBH,KEAP1,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC
GO:0048585	0.622	0.441	44	475	negative regulation of response to stimulus	BP	1	FZD1,WNT11,ACKR3,AXIN2,C5AR2,TBC1D10C,SLIT2,ABL1,HDAC7,KLKB1,EPN2,SESN1,OSR1,TRAFD1,STAT6,F2RL1,GLIS2,MFN2,MYC,PIK3IP1,SULF2,HIC1,RTN4RL1,CREBRF,LRP4,GDPD5,CASTOR1,FBXO7,LIMD1,NLRX1,TKFC,FBLN1,RAF1,MAPKBP1,QARS,ARHGAP12,UBQLN2,PPP3CB,NCK1,HMOX1,NPRL3,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0010647	0.622	0.465	22	460	positive regulation of cell communication	BP	1	NOTCH2,PDGFRB,DCN,GLIPR2,BMPR1A,EVC,CSPG4,ATP6V0C,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,SPRED1,SHC1,FBH1,GREM1	down_VCAV_EC
GO:1990823	0.622	0.611	3	39	response to leukemia inhibitory factor	BP	1	LAPTM5,CREB1,KDM3A	up_VCAV_EC
GO:1990830	0.622	0.611	3	39	cellular response to leukemia inhibitory factor	BP	1	LAPTM5,CREB1,KDM3A	up_VCAV_EC
GO:0051289	0.622	0.66	2	25	protein homotetramerization	BP	1	TK1,CTH	down_ACOR_VSMC
GO:0002224	0.622	0.658	2	34	toll-like receptor signaling pathway	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0042107	0.622	0.662	2	22	cytokine metabolic process	BP	1	TLR1,TLR3	up_ACOR_VSMC

GO:0061383	0.622	0.663	2	20	trabecula morphogenesis	BP	1	EGLN1,CHD7	up_ACOR_VSMC
GO:0045184	0.622	0.659	2	532	establishment of protein localization	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0019218	0.622	0.66	2	25	regulation of steroid metabolic process	BP	1	BMP2,PROX1	up_VCAV_EC
GO:0019083	0.622	0.755	1	19	viral transcription	BP	1	TRIM8	down_VCAV_EC
GO:0002028	0.622	0.756	1	19	regulation of sodium ion transport	BP	1	FXYD1	down_VCAV_EC
GO:0048585	0.622	0.759	1	475	negative regulation of response to stimulus	BP	1	HDAC7	down_VPOR_EC
GO:0034308	0.622	0.757	1	16	primary alcohol metabolic process	BP	1	REST	down_VSAP_EC
GO:0043277	0.622	0.766	1	9	apoptotic cell clearance	BP	1	TXNDC5	up_ACOR_VSMC
GO:1900449	0.622	0.767	1	9	regulation of glutamate receptor signaling	BP	1	DAPK1	up_ACOR_VSMC
GO:0090199	0.622	0.759	1	15	regulation of release of cytochrome c from	BP	1	PMAIP1	up_VCAV_EC
GO:0090207	0.622	0.762	1	11	regulation of triglyceride metabolic process	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0006325	0.622	0.752	1	234	chromatin organization	BP	1	EYA1	up_VFEM_EC
GO:0097435	0.622	0.752	1	230	supramolecular fiber organization	BP	1	CDC42EP5	up_VFEM_EC
GO:0051129	0.622	0.752	1	221	negative regulation of cellular component	BP	1	CAV1	up_VSAP_VSMC
GO:0032204	0.622913725	0.751	1	35	regulation of telomere maintenance	BP	1	PKIB	up_ACOR_EC
GO:0034641	0.623	0.49	17	2171	cellular nitrogen compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,RRP15,PUM3,EIF5,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0051046	0.623	0.48	16	174	regulation of secretion	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,PASK,KCNB1,MAPKBP1,CYBA,STX4,KCNC4,PPP3CB,MAVS	up_VSAP_EC
GO:0009987	0.623	0.583	13	5086	cellular process	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,SPINK5,NETO1,TBX15,FBP1,EMX2,HOXA11,SHOX2,ATP8B4	up_VFEM_VSMC
GO:0048667	0.623	0.496	12	140	cell morphogenesis involved in neuron differentiation	BP	1	EPHB1,IFRD1,RELN,MEF2C,GATA3,RAB11A,PPP3CA,PREX2,STMN1,RAPGEF2,CREB1,SPTBN4	up_VCAV_EC
GO:1904951	0.623	0.556	5	108	positive regulation of establishment of protein localization	BP	1	PRNP,ENSCAFG00000014978,AKT2,GLI3,MAVS	down_VCAV_EC
GO:0050657	0.623	0.608	3	51	nucleic acid transport	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0050658	0.623	0.608	3	51	RNA transport	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0051236	0.623	0.608	3	51	establishment of RNA localization	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:1902806	0.623	0.611	3	33	regulation of cell cycle G1/S phase transition	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC
GO:0072666	0.623	0.662	2	21	establishment of protein localization to vacuole	BP	1	SCARB2,LAMP2	up_ACOR_VSMC
GO:0097061	0.623	0.662	2	21	dendritic spine organization	BP	1	ZNF365,WASL	up_ACOR_VSMC
GO:1903533	0.623	0.662	2	21	regulation of protein targeting	BP	1	TCAF1,INPP5K	up_ACOR_VSMC
GO:0060343	0.623	0.762	1	11	trabecula formation	BP	1	GREM1	down_ACOR_VSMC
GO:1901185	0.623	0.762	1	11	negative regulation of ERBB signaling pathway	BP	1	NUP62	down_ACOR_VSMC
GO:0010092	0.623	0.755	1	19	specification of animal organ identity	BP	1	GLI3	down_VCAV_EC
GO:1905954	0.623	0.755	1	19	positive regulation of lipid localization	BP	1	SCP2	down_VCAV_EC
GO:0046635	0.623	0.758	1	15	positive regulation of alpha-beta T cell	BP	1	SOCS5	down_VSAP_EC
GO:0042059	0.623	0.763	1	10	negative regulation of epidermal growth factor receptor signaling	BP	1	PSEN1	up_ACOR_VSMC
GO:0048532	0.623	0.766	1	9	anatomical structure arrangement	BP	1	NRP1	up_ACOR_VSMC
GO:0006810	0.623	0.783	1	1244	transport	BP	1	HOXA3	up_APUL_VSMC
GO:0007017	0.623	0.753	1	273	microtubule-based process	BP	1	ARHGEF2	up_VPUL_EC

GO:0009152	0.623032533	0.65203	2	80	purine ribonucleotide biosynthetic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0030004	0.623372897	0.75042	1	36	cellular monovalent inorganic cation	BP	1	SLC9A9	up_ACOR_EC
GO:0055088	0.623802167	0.74987	1	37	lipid homeostasis	BP	1	NR1H4	up_ACOR_EC
GO:2001141	0.624	0.424	81	979	regulation of RNA biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,HOXA10,ERF,TCERG1,SMARCAL1,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103	down_ACOR_VSMC
GO:0030522	0.624	0.543	6	67	intracellular receptor signaling pathway	BP	1	PPARGC1B,NLRX1,TKFC,PRMT2,NCOA2,LBH	up_VSAP_EC
GO:0042063	0.624	0.543	6	67	gliogenesis	BP	1	WASF3,ABL1,DLL1,KLF15,PLPP3,NFIB	up_VSAP_EC
GO:0021543	0.624	0.579	4	49	pallium development	BP	1	NF2,WDR62,ASPM,ENSCAFG00000010224	down_ACOR_VSMC
GO:0003006	0.624	0.574	4	180	developmental process involved in reproduction	BP	1	HOXA9,IRX5,LEP,TNC	up_AFEM_EC
GO:0048519	0.624	0.629	3	1554	negative regulation of biological process	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0035306	0.624	0.658	2	24	positive regulation of dephosphorylation	BP	1	SLC29A1,PPP2R5D	down_ACOR_VSMC
GO:0048008	0.624	0.659	2	24	platelet-derived growth factor receptor signaling	BP	1	IQGAP1,SGPL1	down_ACOR_VSMC
GO:1900182	0.624	0.656	2	33	positive regulation of protein localization to	BP	1	SESN2,ZPR1	down_VSAP_EC
GO:2001056	0.624	0.654	2	38	positive regulation of cysteine-type	BP	1	FAM162A,REST	down_VSAP_EC
GO:0021536	0.624	0.661	2	21	diencephalon development	BP	1	BMP4,NRP1	up_ACOR_VSMC
GO:0016236	0.624	0.651	2	88	macroautophagy	BP	1	CLEC16A,RAB7A	up_AFEM_EC
GO:0048523	0.624	0.678	2	1399	negative regulation of cellular process	BP	1	LIMK1,LRRC17	up_VCAV_VSMC
GO:0007032	0.624	0.66	2	22	endosome organization	BP	1	PLEKHF1,VPS11	up_VSAP_EC
GO:0014068	0.624	0.66	2	22	positive regulation of phosphatidylinositol 3-kinase signaling	BP	1	PDGFD,F2RL1	up_VSAP_EC
GO:0060711	0.624	0.66	2	21	labyrinthine layer development	BP	1	GJB5,ZFP36L1	up_VSAP_EC
GO:0021799	0.624	0.761	1	11	cerebral cortex radially oriented cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0032653	0.624	0.761	1	11	regulation of interleukin-10 production	BP	1	HMGB1	down_ACOR_VSMC
GO:0032663	0.624	0.754	1	19	regulation of interleukin-2 production	BP	1	PRNP	down_VCAV_EC
GO:0045010	0.624	0.754	1	19	actin nucleation	BP	1	ACTR3B	down_VCAV_EC
GO:0046902	0.624	0.755	1	18	regulation of mitochondrial membrane	BP	1	SLC35F6	down_VCAV_EC
GO:0030010	0.624	0.749	1	41	establishment of cell polarity	BP	1	KANK1	up_AFEM_EC
GO:0030878	0.624	0.759	1	13	thyroid gland development	BP	1	HHEX	up_VCAV_EC
GO:1900077	0.624	0.761	1	11	negative regulation of cellular response to	BP	1	NCK1	up_VCAV_EC
GO:0009611	0.624	0.748	1	122	response to wounding	BP	1	SLC7A11	up_VPOR_EC
GO:0031061	0.624	0.763	1	10	negative regulation of histone methylation	BP	1	PHF1	up_VSAP_EC
GO:0036294	0.62495292	0.74876	1	37	cellular response to decreased oxygen levels	BP	1	AQP1	up_ACOR_EC
GO:0071456	0.62495292	0.74876	1	37	cellular response to hypoxia	BP	1	AQP1	up_ACOR_EC

GO:0033554	0.625	0.427	67	708	cellular response to stress	BP	1	LEP,MAP3K8,MID1,CDC7,RASSF2,NACC2,PRKAA2,TM7SF3,TP53BP1,ATRX,TLR3,SH3RF2,PPARGC1A,TP53INP1,ZBTB40,ZNF365,SASH1,TMX3,ZBTB4,POLK,ITPR1,ANKRD1,F2RL1,FAM129A,GABARAPL1,DAPK1,BNIP3,CDKN1A,PTPN22,CHD2,OS9,STT3B,SESN3,SH3RF1,PRKCE,MARF1,FUT8,PARP9,CHD6,APP,PSEN1,SHPRH,PIK3C3,LAMP2,DUSP22,EDN1,SESN1,OXR1,NOD2,DMC1,DDIT4,SH3RF3,SERINC3,SCAMP5,HERPUD1,TXNDC5,MAP3K7,FAF2,BMT2,WFS1,RPAIN,WDR48,DZIP3,PARK7,STC2,ZFYVE1,FAN1	up_ACOR_VSMC
GO:0032870	0.625	0.489	13	162	cellular response to hormone stimulus	BP	1	KIT,PRCP,PPARG,BAIAP2L1,MEF2C,TFPI,ENSCAFG00000010596,SMARCA4,NCK1,ADIPOR2,UFSP2,KDM3A,NR4A1	up_VCAV_EC
GO:0016055	0.625	0.494	12	134	Wnt signaling pathway	BP	1	FZD1,WNT11,AXIN2,ABL1,RECK,PLPP3,FAM53B,SULF2,HIC1,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0198738	0.625	0.494	12	134	cell-cell signaling by wnt	BP	1	FZD1,WNT11,AXIN2,ABL1,RECK,PLPP3,FAM53B,SULF2,HIC1,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0032388	0.625	0.557	5	62	positive regulation of intracellular transport	BP	1	NEDD4,RAN,PLK3,DMAP1,EZR	down_ACOR_VSMC
GO:0009123	0.625	0.554	5	104	nucleoside monophosphate	BP	1	NT5C2,ATP5MC1,UQCR10,PARK7,AMPD2	down_VCAV_EC
GO:0044237	0.625	0.621	5	3491	cellular metabolic process	BP	1	CYP1A1,LIMK1,GATA5,C6,ENSCAFG00000028814	up_VCAV_VSMC
GO:0030098	0.625	0.574	4	87	lymphocyte differentiation	BP	1	GLI3,ZFP36L1,LOXL3,ZBTB16	down_VCAV_EC
GO:0051251	0.625	0.575	4	69	positive regulation of lymphocyte activation	BP	1	SOCS5,FAM49B,TFRC,CDKN1A	down_VSAP_EC
GO:0006796	0.625	0.666	2	938	phosphate-containing compound metabolic	BP	1	SUCLG2,NDUFA10	down_AFEM_EC
GO:0016575	0.625	0.659	2	23	histone deacetylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0060389	0.625	0.659	2	21	pathway-restricted SMAD protein phosphorylation	BP	1	ACVRL1,TGFBR2	up_VSAP_EC
GO:0006376	0.625	0.76	1	11	mRNA splice site selection	BP	1	SF3A1	down_ACOR_VSMC
GO:0070534	0.625	0.753	1	19	protein K63-linked ubiquitination	BP	1	SASH1	down_VCAV_EC
GO:0098586	0.625	0.753	1	19	cellular response to virus	BP	1	GSDME	down_VCAV_EC
GO:1901570	0.625	0.754	1	16	fatty acid derivative biosynthetic process	BP	1	PTGS2	down_VSAP_EC
GO:0007041	0.625	0.749	1	41	lysosomal transport	BP	1	RAB7A	up_AFEM_EC
GO:0014020	0.625	0.748	1	41	primary neural tube formation	BP	1	LUZP1	up_AFEM_EC
GO:0010524	0.625	0.759	1	12	positive regulation of calcium ion transport into	BP	1	APLNR	up_VCAV_EC
GO:0050891	0.625	0.758	1	12	multicellular organismal water homeostasis	BP	1	STMN1	up_VCAV_EC
GO:0071985	0.625	0.759	1	12	multivesicular body sorting pathway	BP	1	RAB27A	up_VCAV_EC
GO:0042981	0.625	0.757	1	471	regulation of apoptotic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0097190	0.625	0.75	1	217	apoptotic signaling pathway	BP	1	CAV1	up_VSAP_VSMC
GO:0051171	0.626	0.446	39	1697	regulation of nitrogen compound metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,RAB7A,AXIN2,YEATS2,PPARGC1A,CCL5,CTIF,ADAM17,SAMD4B	up_AFEM_EC
GO:0000003	0.626	0.472	17	295	reproduction	BP	1	SULF1,CELF1,ETV6,PTPN11,TMED2,PTGS2,HIF1A,PHC2,CTNNB1,CCNYL1,CDYL,INHBA,SIX4,SPINK2,RTCB,SNRPA1,KDM3A	down_VSAP_EC
GO:1902531	0.626	0.492	12	536	regulation of intracellular signal transduction	BP	1	CMKLR1,LEP,F3,LMCD1,TMEM100,PLAGL2,GREM1,CLEC16A,CYLD,LRRC15,CCL5,KANK1	up_AFEM_EC
GO:0043062	0.626	0.518	8	99	extracellular structure organization	BP	1	ACSL3,FSCN1,COLGALT1,SDC1,GREM1,B4GALT1,SERPINH1,LIPC	down_ACOR_VSMC
GO:0070302	0.626	0.528	7	78	regulation of stress-activated protein kinase	BP	1	ARHGEF5,MAP3K5,F2RL1,MYC,SASH1,MYD88,QARS	up_VSAP_EC
GO:0007254	0.626	0.541	6	67	JNK cascade	BP	1	ARHGEF5,MAP3K5,CDC42EP5,F2RL1,SASH1,MYD88	up_VSAP_EC
GO:0034333	0.626	0.656	2	25	adherens junction assembly	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0030154	0.626	0.666	2	1040	cell differentiation	BP	1	HDAC7,CITED2	down_VPOR_EC

GO:0015893	0.626	0.656	2	26	drug transport	BP	1	EDN1,RALBP1	up_VCAV_EC
GO:0061053	0.626	0.657	2	24	somite development	BP	1	NUP133,RBBP6	up_VCAV_EC
GO:0019941	0.626	0.65	2	258	modification-dependent protein catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0032446	0.626	0.65	2	255	protein modification by small protein conjugation	BP	1	KLHL28,RNF6	up_VPOR_EC
GO:0006508	0.626	0.655	2	483	proteolysis	BP	1	MME,TRIM9	up_VFEM_EC
GO:0021983	0.626	0.759	1	11	pituitary gland development	BP	1	GLI1	down_ACOR_VSMC
GO:0022617	0.626	0.759	1	11	extracellular matrix disassembly	BP	1	FSCN1	down_ACOR_VSMC
GO:1902305	0.626	0.758	1	12	regulation of sodium ion transmembrane transport	BP	1	NEDD4	down_ACOR_VSMC
GO:1903793	0.626	0.759	1	11	positive regulation of anion transport	BP	1	PRELID1	down_ACOR_VSMC
GO:0051704	0.626	0.755	1	476	multi-organism process	BP	1	CITED2	down_VPOR_EC
GO:0046483	0.626	0.81	1	1948	heterocycle metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0003338	0.626	0.755	1	15	metanephros morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0010669	0.626	0.761	1	10	epithelial structure maintenance	BP	1	NOD2	up_ACOR_VSMC
GO:0010738	0.626	0.763	1	9	regulation of protein kinase A signaling	BP	1	ENSCAFG00000029553	up_ACOR_VSMC
GO:0099054	0.626	0.763	1	9	presynapse assembly	BP	1	APP	up_ACOR_VSMC
GO:0030902	0.626	0.747	1	41	hindbrain development	BP	1	DLL1	up_AFEM_EC
GO:0000768	0.626	0.761	1	10	syncytium formation by plasma membrane fusion	BP	1	CDON	up_VCAV_EC
GO:0019432	0.626	0.761	1	10	triglyceride biosynthetic process	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0046460	0.626	0.761	1	10	neutral lipid biosynthetic process	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0046463	0.626	0.761	1	10	acylglycerol biosynthetic process	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:0006949	0.626	0.761	1	10	syncytium formation	BP	1	CDON	up_VCAV_EC
GO:0042491	0.626	0.761	1	10	inner ear auditory receptor cell	BP	1	JAG1	up_VCAV_EC
GO:0042789	0.626	0.761	1	10	mRNA transcription by RNA polymerase II	BP	1	SOX18	up_VCAV_EC
GO:0140253	0.626	0.761	1	10	cell-cell fusion	BP	1	CDON	up_VCAV_EC
GO:0090130	0.626	0.747	1	121	tissue migration	BP	1	SEMA3A	up_VPOR_EC
GO:0120036	0.626	0.754	1	373	plasma membrane bounded cell projection	BP	1	CHL1	up_VPOR_VSMC
GO:0051276	0.626	0.752	1	398	chromosome organization	BP	1	EYA1	up_VFEM_VSMC
GO:2000113	0.626	0.753	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	SHOX2	up_VFEM_VSMC
GO:0060148	0.626	0.761	1	10	positive regulation of posttranscriptional gene	BP	1	LIMD1	up_VSAP_EC
GO:0099601	0.626	0.761	1	10	regulation of neurotransmitter	BP	1	KLHL24	up_VSAP_EC
GO:0060627	0.626076607	0.57186	4	165	regulation of vesicle-mediated transport	BP	1	CALY,ACTN2,PREB,VPS16	up_ACOR_EC
GO:0060284	0.627	0.465	20	212	regulation of cell development	BP	1	ITM2C,BMP4,PDE5A,ZNF365,NRP1,ULK2,SMARCD3,FZD3,APP,PSEN1,CHD7,SIPA1L1,SSH3,EDN1,ASAP1,B2M,DISC1,DOCK5,RREB1,CRKL	up_ACOR_VSMC
GO:0051252	0.627	0.522	8	1051	regulation of RNA metabolic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0001763	0.627	0.528	7	78	morphogenesis of a branching structure	BP	1	HOXA11,SLIT2,FGF7,ABL1,SHOX2,NTN4,TGFBR2	up_VSAP_EC
GO:0016197	0.627	0.528	7	78	endosomal transport	BP	1	TBC1D10C,VPS36,AP5B1,RAB11B,DENND5A,AP5Z1,ZFYVE21	up_VSAP_EC
GO:0043542	0.627	0.572	4	86	endothelial cell migration	BP	1	DCN,SASH1,SPRED1,GREM1	down_VCAV_EC
GO:0006282	0.627	0.576	4	48	regulation of DNA repair	BP	1	FIGNL1,TIMELESS,HMGB1,CUL4A	up_VCAV_EC
GO:0043409	0.627	0.575	4	54	negative regulation of MAPK cascade	BP	1	TNIP1,ATF3,RAPGEF1,TLR4	up_VCAV_EC

GO:0003206	0.627	0.603	3	51	cardiac chamber morphogenesis	BP	1	FHL2,HIF1A,NRP1	down_VSAP_EC
GO:0051592	0.627	0.607	3	33	response to calcium ion	BP	1	TNNT2,PRKAA2,SLC25A12	up_ACOR_VSMC
GO:0034654	0.627	0.619	3	1236	nucleobase-containing compound biosynthetic	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0070613	0.627	0.655	2	25	regulation of protein processing	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:1903317	0.627	0.655	2	25	regulation of protein maturation	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0045844	0.627	0.656	2	24	positive regulation of striated muscle tissue	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0048636	0.627	0.656	2	24	positive regulation of muscle organ	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0006119	0.627	0.651	2	40	oxidative phosphorylation	BP	1	UQCR10,PARK7	down_VCAV_EC
GO:0043242	0.627	0.658	2	21	negative regulation of protein complex	BP	1	FGF13,MID1	up_ACOR_VSMC
GO:0060193	0.627	0.758	1	11	positive regulation of lipase activity	BP	1	ABHD5	down_ACOR_VSMC
GO:1900077	0.627	0.758	1	11	negative regulation of cellular response to	BP	1	NCOA5	down_ACOR_VSMC
GO:0031648	0.627	0.751	1	19	protein destabilization	BP	1	PRNP	down_VCAV_EC
GO:0042981	0.627	0.755	1	471	regulation of apoptotic process	BP	1	CITED2	down_VPOR_EC
GO:0006725	0.627	0.808	1	1956	cellular aromatic compound metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0070542	0.627	0.754	1	15	response to fatty acid	BP	1	NR1H4	down_VSAP_EC
GO:0090185	0.627	0.76	1	10	negative regulation of kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:0016125	0.627	0.746	1	41	sterol metabolic process	BP	1	LEP	up_AFEM_EC
GO:0016241	0.627	0.746	1	41	regulation of macroautophagy	BP	1	CLEC16A	up_AFEM_EC
GO:0034249	0.627	0.746	1	41	negative regulation of cellular amide metabolic	BP	1	SAMD4B	up_AFEM_EC
GO:0045834	0.627	0.747	1	41	positive regulation of lipid metabolic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0006721	0.627	0.754	1	14	terpenoid metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0021884	0.627	0.76	1	10	forebrain neuron development	BP	1	RAPGEF2	up_VCAV_EC
GO:0080134	0.627	0.752	1	386	regulation of response to stress	BP	1	EYA1	up_VFEM_VSMC
GO:0000186	0.627	0.76	1	10	activation of MAPKK activity	BP	1	MAP3K5	up_VSAP_EC
GO:0031062	0.627	0.76	1	10	positive regulation of histone methylation	BP	1	PHF1	up_VSAP_EC
GO:0051281	0.627	0.76	1	10	positive regulation of release of sequestered calcium ion into cytosol	BP	1	ABL1	up_VSAP_EC
GO:0030282	0.627196691	0.74659	1	37	bone mineralization	BP	1	PTH1R	up_ACOR_EC
GO:0012501	0.628	0.451	27	561	programmed cell death	BP	1	GPAM,SLC35F6,PRNP,KANK2,CLIP3,GABARAP,AKT2,ENSCAFG00000013404,TMEM161A,ARHGAP10,B4GALT1,GLI3,PARK7,ZMAT3,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0019222	0.628	0.489	15	1934	regulation of metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,ABHD5,PUM3,EIF5,CCAR1,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0042326	0.628	0.478	15	163	negative regulation of phosphorylation	BP	1	TBC1D10C,CEP85,SLIT2,ABL1,PLPP3,F2RL1,MYC,PIK3IP1,RTN4RL1,FBXO7,FBLN1,QARS,NCK1,DDIT4,LATS2	up_VSAP_EC
GO:0043410	0.628	0.486	13	144	positive regulation of MAPK cascade	BP	1	CDON,ACKR3,ARHGEF5,C5AR2,ABL1,MAP3K5,PDGFD,C1QTNF2,F2RL1,TRAF7,SASH1,MYD88,RAF1	up_VSAP_EC
GO:0010243	0.628	0.494	11	238	response to organonitrogen compound	BP	1	LRP1,PRNP,ADCY6,COL6A1,ENSCAFG00000014978,AKT2,ZFP36L1,SEC61B,RAB31,HM13,SHC1	down_VCAV_EC
GO:0009259	0.628	0.506	9	166	ribonucleotide metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC,PAPSS1,AK5	down_VSAP_EC
GO:0048193	0.628	0.508	9	116	Golgi vesicle transport	BP	1	ATP8A1,RAB6A,SNX2,EXOC5,GCC2,VPS54,CHIC2,ZW10,DOP1B	up_VCAV_EC
GO:0002366	0.628	0.539	6	65	leukocyte activation involved in immune	BP	1	PLCG2,TP53BP1,F2RL1,PRKCE,PSEN1,IL18R1	up_ACOR_VSMC

GO:0060538	0.628	0.574	4	51	skeletal muscle organ development	BP	1	FLNB,CAV1,MSC,SIX4	down_ACOR_VSMC
GO:0034612	0.628	0.601	3	63	response to tumor necrosis factor	BP	1	ZFP36L1,GSDME,FOXO3	down_VCAV_EC
GO:0098742	0.628	0.649	2	44	cell-cell adhesion via plasma-membrane	BP	1	CDH2,CD164	down_VCAV_EC
GO:0008088	0.628	0.656	2	21	axo-dendritic transport	BP	1	TMEM108,APP	up_ACOR_VSMC
GO:0046034	0.628	0.646	2	88	ATP metabolic process	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0008347	0.628	0.757	1	11	glial cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0008535	0.628	0.756	1	12	respiratory chain complex IV assembly	BP	1	FASTKD3	down_ACOR_VSMC
GO:0007260	0.628	0.75	1	19	tyrosine phosphorylation of STAT protein	BP	1	ARL2BP	down_VCAV_EC
GO:0048016	0.628	0.751	1	19	inositol phosphate-mediated signaling	BP	1	PRNP	down_VCAV_EC
GO:0045935	0.628	0.753	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	CITED2	down_VPOR_EC
GO:0051049	0.628	0.753	1	479	regulation of transport	BP	1	RAB11B	down_VPOR_EC
GO:2000107	0.628	0.752	1	16	negative regulation of leukocyte apoptotic	BP	1	HIF1A	down_VSAP_EC
GO:0003016	0.628	0.759	1	10	respiratory system process	BP	1	GAA	up_ACOR_VSMC
GO:0022402	0.628	0.751	1	407	cell cycle process	BP	1	TAOK1	up_AORT_EC
GO:0045893	0.628	0.751	1	413	positive regulation of transcription, DNA-	BP	1	HOXA9	up_AORT_EC
GO:0033146	0.628	0.756	1	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	UFSP2	up_VCAV_EC
GO:0033144	0.628	0.759	1	10	negative regulation of intracellular steroid hormone receptor	BP	1	LBH	up_VSAP_EC
GO:0021884	0.628	0.759	1	10	forebrain neuron development	BP	1	SLIT2	up_VSAP_EC
GO:0071702	0.629	0.444	33	687	organic substance transport	BP	1	GPAM,SNX18,PRNP,FOLR2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,LCAT,SNUPN,SSR2,SCP2,SCAMP4,CLTB,SSR3,PEX5,SCAMP2,OSBPL10,GLI3,PARK7,ZFP36L1,SLC2A10,CYBA,MAVS,TOM1,SEC61B,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SOAT1,SEC61A1	down_VCAV_EC
GO:0043254	0.629	0.477	15	164	regulation of protein complex assembly	BP	1	SMAD6,PRKAA2,LCAT,TUBB4A,SEC24B,ATXN2,LMO4,JMY,CLSTN1,EVL,TBX20,PRKCE,ASAP1,KIF9,WASL	up_ACOR_VSMC
GO:0010563	0.629	0.476	15	203	negative regulation of phosphorus metabolic process	BP	1	PPP2R5A,CDA,TNFAIP3,TNIP1,PDGFB,PDE4D,ATF3,RAPGEF1,TLR4,HHEX,PREX2,SH3BP5,SWAP70,NCK1,FKBP15	up_VCAV_EC
GO:0045936	0.629	0.476	15	203	negative regulation of phosphate metabolic process	BP	1	PPP2R5A,CDA,TNFAIP3,TNIP1,PDGFB,PDE4D,ATF3,RAPGEF1,TLR4,HHEX,PREX2,SH3BP5,SWAP70,NCK1,FKBP15	up_VCAV_EC
GO:0051222	0.629	0.536	6	103	positive regulation of protein transport	BP	1	NR1H4,PLK3,MYO1C,HIF1A,ZPR1,GSK3B	down_VSAP_EC
GO:0051650	0.629	0.552	5	65	establishment of vesicle localization	BP	1	RAB11A,RAB27A,SNAP23,STX11,SHROOM2	up_VCAV_EC
GO:0048583	0.629	0.582	4	1095	regulation of response to stimulus	BP	1	NR1H4,ARHGEF26,NPNT,NTRK2	up_APUL_EC
GO:0044264	0.629	0.606	3	32	cellular polysaccharide metabolic process	BP	1	PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0044272	0.629	0.65	2	35	sulfur compound biosynthetic process	BP	1	CHSY1,PAPSS1	down_VSAP_EC
GO:0045778	0.629	0.649	2	35	positive regulation of ossification	BP	1	ILK,CTNNB1	down_VSAP_EC
GO:0044262	0.629	0.645	2	89	cellular carbohydrate metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0021885	0.629	0.653	2	24	forebrain cell migration	BP	1	RELN,ENSCAFG00000010224	up_VCAV_EC
GO:0060419	0.629	0.654	2	22	heart growth	BP	1	ACACB,SAV1	up_VSAP_EC
GO:0032270	0.629	0.65	2	479	positive regulation of cellular protein metabolic	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0035176	0.629	0.757	1	11	social behavior	BP	1	ANXA7	down_ACOR_VSMC
GO:0051703	0.629	0.757	1	11	intraspecies interaction between organisms	BP	1	ANXA7	down_ACOR_VSMC
GO:1901565	0.629	0.751	1	442	organonitrogen compound catabolic	BP	1	USP33	down_AFEM_EC

GO:0050795	0.629	0.751	1	15	regulation of behavior	BP	1	APOE	down_VSAP_EC
GO:2000772	0.629	0.752	1	15	regulation of cellular senescence	BP	1	NUAK1	down_VSAP_EC
GO:0035176	0.629	0.756	1	11	social behavior	BP	1	PTCHD1	up_VCAV_EC
GO:0048806	0.629	0.758	1	10	genitalia development	BP	1	CHD7	up_VCAV_EC
GO:0051703	0.629	0.756	1	11	intraspecies interaction between organisms	BP	1	PTCHD1	up_VCAV_EC
GO:0060231	0.629	0.755	1	12	mesenchymal to epithelial transition	BP	1	GATA3	up_VCAV_EC
GO:0061099	0.629	0.754	1	13	negative regulation of protein tyrosine kinase	BP	1	SH3BP5	up_VCAV_EC
GO:0015850	0.629902291	0.74396	1	37	organic hydroxy compound transport	BP	1	AQP1	up_ACOR_EC
GO:0120039	0.63	0.479	14	158	plasma membrane bounded cell projection morphogenesis	BP	1	ENPP2,SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0045089	0.63	0.57	4	70	positive regulation of innate immune response	BP	1	NR1H4,PVR,LYN,GBP5	down_VSAP_EC
GO:1903555	0.63	0.603	3	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	ARG2,CACTIN,ARHGEF2	down_ACOR_VSMC
GO:1905952	0.63	0.604	3	33	regulation of lipid localization	BP	1	LEP,ABCA1,SCP2	up_ACOR_VSMC
GO:0071333	0.63	0.652	2	25	cellular response to glucose stimulus	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0000469	0.63	0.754	1	12	cleavage involved in rRNA processing	BP	1	NOB1	down_ACOR_VSMC
GO:0007549	0.63	0.755	1	11	dosage compensation	BP	1	BRCA1	down_ACOR_VSMC
GO:0045830	0.63	0.755	1	11	positive regulation of isotype switching	BP	1	TFRC	down_ACOR_VSMC
GO:0051973	0.63	0.749	1	19	positive regulation of telomerase activity	BP	1	GREM1	down_VCAV_EC
GO:0035136	0.63	0.75	1	16	forelimb morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0021783	0.63	0.759	1	9	preganglionic parasympathetic fiber	BP	1	NRP1	up_ACOR_VSMC
GO:0009201	0.63	0.743	1	41	ribonucleoside triphosphate biosynthetic	BP	1	PPARGC1A	up_AFEM_EC
GO:1902680	0.63	0.749	1	415	positive regulation of RNA biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:1903508	0.63	0.749	1	415	positive regulation of nucleic acid-templated	BP	1	HOXA9	up_AORT_EC
GO:1902914	0.63	0.755	1	11	regulation of protein polyubiquitination	BP	1	UBE2D1	up_VCAV_EC
GO:0030030	0.63	0.749	1	377	cell projection organization	BP	1	CHL1	up_VPOR_VSMC
GO:0019752	0.63	0.746	1	283	carboxylic acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0048585	0.63	0.751	1	475	negative regulation of response to stimulus	BP	1	SLIT2	up_VPUL_VSMC
GO:0051704	0.63	0.752	1	476	multi-organism process	BP	1	IL22RA1	up_VPUL_VSMC
GO:0001702	0.63	0.757	1	10	gastrulation with mouth forming second	BP	1	PLPP3	up_VSAP_EC
GO:0042491	0.63	0.757	1	10	inner ear auditory receptor cell	BP	1	DLL1	up_VSAP_EC
GO:0071158	0.63	0.757	1	10	positive regulation of cell cycle arrest	BP	1	CRADD	up_VSAP_EC
GO:2000757	0.63	0.757	1	10	negative regulation of peptidyl-lysine acetylation	BP	1	KLF15	up_VSAP_EC
GO:0051894	0.63	0.758	1	10	positive regulation of focal adhesion assembly	BP	1	ABL1	up_VSAP_EC
GO:0034620	0.630185269	0.74355	1	38	cellular response to unfolded protein	BP	1	EDEM2	up_ACOR_EC
GO:0051188	0.630330174	0.6443	2	81	cofactor biosynthetic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0050864	0.630498769	0.74351	1	36	regulation of B cell activation	BP	1	NOD2	up_ACOR_EC
GO:0018022	0.6306762	0.74334	1	36	peptidyl-lysine methylation	BP	1	PYGO2	up_ACOR_EC
GO:0023056	0.631	0.456	22	462	positive regulation of signaling	BP	1	NOTCH2,PDGFRB,DCN,GLIPR2,BMPR1A,EVC,CSPG4,ATP6V0C,PARK7,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,MAVS,CDH2,LOXL3,GSDME,SPRED1,SHC1,FBH1,GREM1	down_VCAV_EC
GO:0014070	0.631	0.511	8	172	response to organic cyclic compound	BP	1	SMAD9,ADCY6,KANK2,NR3C1,EPHX1,PARK7,ZFP36L1,MAVS	down_VCAV_EC

GO:0022412	0.631	0.524	7	76	cellular process involved in reproduction in multicellular organism	BP	1	BMP4,PDE5A,MARF1,AFF4,SPINK2,DMC1,JAM3	up_ACOR_VSMC
GO:0008544	0.631	0.535	6	75	epidermis development	BP	1	PRKCH,FERMT1,SOX18,FLNB,LDB2,JAG1	up_VCAV_EC
GO:0032409	0.631	0.57	4	52	regulation of transporter activity	BP	1	NEDD4,CAV1,GSTO1,REM1	down_ACOR_VSMC
GO:0044260	0.631	0.651	3	2593	cellular macromolecule metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0045639	0.631	0.603	3	33	positive regulation of myeloid cell	BP	1	PPARGC1B,ANKRD54,ZFP36L1	up_VSAP_EC
GO:0002690	0.631	0.65	2	26	positive regulation of leukocyte chemotaxis	BP	1	HMGB1,RAC1	down_ACOR_VSMC
GO:0050871	0.631	0.651	2	24	positive regulation of B cell activation	BP	1	MMP14,TFRC	down_ACOR_VSMC
GO:0071241	0.631	0.646	2	42	cellular response to inorganic substance	BP	1	PRNP,MT2A	down_VCAV_EC
GO:0009966	0.631	0.656	2	868	regulation of signal transduction	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0032411	0.631	0.652	2	24	positive regulation of transporter activity	BP	1	RELN,PLCG2	up_VCAV_EC
GO:0006613	0.631	0.753	1	12	cotranslational protein targeting to membrane	BP	1	TRAM1	down_ACOR_VSMC
GO:0014888	0.631	0.754	1	11	striated muscle adaptation	BP	1	EZH2	down_ACOR_VSMC
GO:0045824	0.631	0.754	1	11	negative regulation of innate immune response	BP	1	CACTIN	down_ACOR_VSMC
GO:0050650	0.631	0.754	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	XYLT1	down_ACOR_VSMC
GO:0050830	0.631	0.752	1	12	defense response to Gram-positive bacterium	BP	1	HMGB2	down_ACOR_VSMC
GO:0051125	0.631	0.754	1	11	regulation of actin nucleation	BP	1	CORO1A	down_ACOR_VSMC
GO:0016192	0.631	0.75	1	452	vesicle-mediated transport	BP	1	ANKRD50	down_AFEM_EC
GO:0010557	0.631	0.751	1	492	positive regulation of macromolecule biosynthetic process	BP	1	CITED2	down_VPOR_EC
GO:0042771	0.631	0.749	1	16	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	CDKN1A	down_VSAP_EC
GO:0010648	0.631	0.748	1	407	negative regulation of cell communication	BP	1	DKK2	up_AORT_EC
GO:0060341	0.631	0.745	1	255	regulation of cellular localization	BP	1	NR1H4	up_APUL_EC
GO:0051926	0.631	0.75	1	14	negative regulation of calcium ion transport	BP	1	STC1	up_VCAV_EC
GO:0051172	0.631	0.756	1	663	negative regulation of nitrogen compound	BP	1	LIMK1	up_VCAV_VSMC
GO:0010558	0.631	0.748	1	392	negative regulation of macromolecule biosynthetic process	BP	1	SHOX2	up_VFEM_VSMC
GO:0055085	0.631	0.746	1	284	transmembrane transport	BP	1	NR1H4	up_VPUL_EC
GO:0043067	0.631	0.75	1	479	regulation of programmed cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:0048821	0.631	0.756	1	10	erythrocyte development	BP	1	CITED2	up_VSAP_EC
GO:0007416	0.631580361	0.74245	1	36	synapse assembly	BP	1	LRP4	up_ACOR_EC

GO:0023052	0.632	0.405	150	1602	signaling	BP	1	GPR1,FZD1,ADGRD1,SEZ6L,CDON,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,INSIG2,PTGFR,SLC8B1,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,LRRC28,HOXD3,SLC6A4,FGF7,ABL1,GOT1,HDAC7,EMP2,KCNE3,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,DTX2,PDGFD,SAV1,RHPN1,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,CCBE1,STAT5A,STAT6,RECK,CISH,KLHL24,PLPP3,CAMKK2,RASD2,F2RL1,RAB11B,GLIS2,PDK2,MFN2,ZFP36L1,TRAF7,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,TBXA2R,SULF2,SHOX2,SLC12A6,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,GABBR2,LRP4,PASK,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,NCEH1,NTN4,ASB8,TMEM17,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CD83,PRMT2,FBLN1,ZFP36L2,HPGD,IGFBP6,RAF1,MAPKBP1,PPP2R5B,CYBA,ZNF205,NCOA2,STX4,ZFAND5,PSD4,KCNC4,QARS,ARHGAP12,ACVRL1,UBQLN2,ARHGAP10,UNC93B1,RAPGEF3,HTRA2,FLOT1,PLPP5,PPP3CB,NCK1,MAVS,IRAK1BP1,KRCC1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC
GO:0006928	0.632	0.427	51	557	movement of cell or subcellular component	BP	1	EMX2,HOXA7,PEX7,TWIST2,WNT11,FAM107A,ARHGEF5,C5AR2,ENPP2,SLC8B1,SLIT2,CDH1,FGF7,ABL1,HDAC7,EMP2,KCNE3,IL17RC,FUZ,PDGFD,PLXNA4,HSD3B7,CCBE1,STAT5A,RECK,F2RL1,DDR2,PIK3R1,TIAM1,TBXA2R,CFAP69,SASH1,MYD88,DPYSL2,FRMD6,WIPF1,KIF27,LIMD1,FBLN1,MYO1B,NFIB,ZNF580,STX4,ZFAND5,ACVRL1,NCK1,HMOX1,MAP2K2,TGFBR2,SAA1,BAG4	up_VSAP_EC
GO:0006875	0.632	0.531	6	129	cellular metal ion homeostasis	BP	1	PRNP,SLC39A6,THY1,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0051347	0.632	0.565	4	182	positive regulation of transferase activity	BP	1	LEP,GREM1,DCUN1D3,ADAM17	up_AFEM_EC
GO:0046661	0.632	0.571	4	45	male sex differentiation	BP	1	HOXA11,HOXA9,PATZ1,CITED2	up_VSAP_EC
GO:0007498	0.632	0.6	3	38	mesoderm development	BP	1	CTDNEP1,NF2,ITGA2	down_ACOR_VSMC
GO:1902850	0.632	0.598	3	52	microtubule cytoskeleton organization involved in	BP	1	MZT1,KPNB1,HTT	down_VSAP_EC
GO:0072078	0.632	0.602	3	33	nephron tubule morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0051606	0.632	0.602	3	33	detection of stimulus	BP	1	CHRM1,NR2F6,DENND5A	up_VSAP_EC
GO:0003018	0.632	0.645	2	42	vascular process in circulatory system	BP	1	ADCY6,CLSTN1	down_VCAV_EC
GO:0044282	0.632	0.642	2	89	small molecule catabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0009410	0.632	0.649	2	27	response to xenobiotic stimulus	BP	1	PDGFB,AHR	up_VCAV_EC
GO:0044706	0.632	0.649	2	27	multi-multicellular organism process	BP	1	PTGS2,ARHGDIB	up_VCAV_EC
GO:0048255	0.632	0.753	1	11	mRNA stabilization	BP	1	THRAP3	down_ACOR_VSMC
GO:0034766	0.632	0.747	1	19	negative regulation of ion transmembrane transport	BP	1	AKT2	down_VCAV_EC
GO:0044088	0.632	0.748	1	17	regulation of vacuole organization	BP	1	SH3GLB1	down_VSAP_EC
GO:0050701	0.632	0.748	1	16	interleukin-1 secretion	BP	1	GBP5	down_VSAP_EC
GO:1902743	0.632	0.748	1	16	regulation of lamellipodium	BP	1	FSCN1	down_VSAP_EC
GO:2001258	0.632	0.753	1	11	negative regulation of cation channel activity	BP	1	KCNE3	up_ACOR_VSMC
GO:0008299	0.632	0.749	1	14	isoprenoid biosynthetic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0051049	0.632	0.75	1	479	regulation of transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0043555	0.632	0.755	1	10	regulation of translation in response to stress	BP	1	NCK1	up_VSAP_EC
GO:0060765	0.632	0.755	1	10	regulation of androgen receptor signaling	BP	1	PRMT2	up_VSAP_EC
GO:0090278	0.632	0.755	1	10	negative regulation of peptide hormone	BP	1	KCNB1	up_VSAP_EC

GO:0019725	0.632518093	0.52986	6	245	cellular homeostasis	BP	1	NR1H4,PTH1R,AQP1,KCNB1,SLC9A9,PRKACA	up_ACOR_EC
GO:0044257	0.633	0.443	30	327	cellular protein catabolic process	BP	1	ZRANB1,SKP2,SH3RF2,ISG15,ZNRF3,CTSS,KLHL20,CTSB,BNIP3,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,LAMP2,CLN8,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0043632	0.633	0.451	24	262	modification-dependent macromolecule catabolic process	BP	1	ZRANB1,SKP2,SH3RF2,ISG15,ZNRF3,KLHL20,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,SIAH1,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0010950	0.633	0.571	4	44	positive regulation of endopeptidase activity	BP	1	CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0033500	0.633	0.596	3	64	carbohydrate homeostasis	BP	1	ENSCAFG00000014978,PARK7,FOXO3	down_VCAV_EC
GO:0042593	0.633	0.596	3	64	glucose homeostasis	BP	1	ENSCAFG00000014978,PARK7,FOXO3	down_VCAV_EC
GO:0031324	0.633	0.601	3	735	negative regulation of cellular metabolic process	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0045185	0.633	0.648	2	25	maintenance of protein location	BP	1	INSIG1,YWHAB	down_ACOR_VSMC
GO:0048525	0.633	0.649	2	25	negative regulation of viral process	BP	1	ILF3,TRIM35	down_ACOR_VSMC
GO:0051235	0.633	0.641	2	90	maintenance of location	BP	1	CRY2,ACACB	up_AFEM_EC
GO:0071326	0.633	0.649	2	26	cellular response to monosaccharide stimulus	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0071331	0.633	0.649	2	26	cellular response to hexose stimulus	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0042092	0.633	0.753	1	11	type 2 immune response	BP	1	ARG2	down_ACOR_VSMC
GO:0042102	0.633	0.746	1	19	positive regulation of T cell proliferation	BP	1	GPAM	down_VCAV_EC
GO:0043067	0.633	0.749	1	479	regulation of programmed cell death	BP	1	CITED2	down_VPOR_EC
GO:0006508	0.633	0.749	1	483	proteolysis	BP	1	CST3	down_VPOR_EC
GO:0002712	0.633	0.748	1	15	regulation of B cell mediated immunity	BP	1	TFRC	down_VSAP_EC
GO:0002889	0.633	0.748	1	15	regulation of immunoglobulin	BP	1	TFRC	down_VSAP_EC
GO:0050853	0.633	0.754	1	10	B cell receptor signaling pathway	BP	1	PLCG2	up_ACOR_VSMC
GO:0023057	0.633	0.746	1	409	negative regulation of signaling	BP	1	DKK2	up_AORT_EC
GO:0035305	0.633555576	0.74037	1	37	negative regulation of dephosphorylation	BP	1	PPP1R26	up_ACOR_EC
GO:0002764	0.633621337	0.64084	2	80	immune response-regulating signaling	BP	1	NR1H4,NOD2	up_ACOR_EC
GO:0010628	0.634	0.44	31	527	positive regulation of gene expression	BP	1	ARHGEF2,VEGFA,MYH9,TMED2,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,MSN,HIF1A,ACTG2,ZPR1,YES1,PEG3,DDX39B,ACTA2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0006366	0.634	0.479	13	583	transcription by RNA polymerase II	BP	1	HOXA9,LEP,HOXA7,DLL1,LMCD1,THRB,TMEM100,GREM1,NFE2L1,GREM2,MYBL1,NR3C1,PPARGC1A	up_AFEM_EC
GO:0034504	0.634	0.495	10	111	protein localization to nucleus	BP	1	CDH1,GLIS2,MORC3,PIK3R1,CIZ1,FBXO4,NUP98,SNUPN,TAF8,MAVS	up_VSAP_EC
GO:0080090	0.634	0.534	7	1734	regulation of primary metabolic process	BP	1	EYA1,HOXA9,MAP2K6,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0050663	0.634	0.595	3	52	cytokine secretion	BP	1	NR1H4,LYN,GBP5	down_VSAP_EC
GO:0006694	0.634	0.597	3	42	steroid biosynthetic process	BP	1	BMP2,PROX1,LBR	up_VCAV_EC
GO:0006413	0.634	0.643	2	42	translational initiation	BP	1	EIF3K,EIF4EBP1	down_VCAV_EC
GO:0006909	0.634	0.643	2	42	phagocytosis	BP	1	ANXA11,CYBA	down_VCAV_EC
GO:0014812	0.634	0.65	2	21	muscle cell migration	BP	1	SEMA6D,DOCK5	up_ACOR_VSMC
GO:1901606	0.634	0.649	2	22	alpha-amino acid catabolic process	BP	1	ENSCAFG00000002977,SARDH	up_ACOR_VSMC
GO:0051173	0.634	0.654	2	874	positive regulation of nitrogen compound	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:2000117	0.634	0.647	2	27	negative regulation of cysteine-type	BP	1	PAK2,PTGS2	up_VCAV_EC
GO:0043632	0.634	0.641	2	262	modification-dependent macromolecule catabolic	BP	1	USP33,RNF6	up_VPOR_EC

GO:2000780	0.634	0.752	1	11	negative regulation of double-strand break	BP	1	PARPBP	down_ACOR_VSMC
GO:0010823	0.634	0.746	1	17	negative regulation of mitochondrion	BP	1	BNIP3	down_VSAP_EC
GO:0015909	0.634	0.746	1	16	long-chain fatty acid transport	BP	1	APOE	down_VSAP_EC
GO:0046427	0.634	0.746	1	16	positive regulation of JAK-STAT cascade	BP	1	LYN	down_VSAP_EC
GO:0060840	0.634	0.739	1	42	artery development	BP	1	LUZP1	up_AFEM_EC
GO:1903047	0.634	0.742	1	257	mitotic cell cycle process	BP	1	LZTS1	up_APUL_EC
GO:0007140	0.634	0.754	1	10	male meiotic nuclear division	BP	1	FIGNL1	up_VCAV_EC
GO:0010243	0.634	0.741	1	238	response to organonitrogen	BP	1	AVPR1A	up_VFEM_EC
GO:0038179	0.634	0.754	1	10	neurotrophin signaling pathway	BP	1	RAF1	up_VSAP_EC
GO:2000278	0.634297771	0.73963	1	37	regulation of DNA biosynthetic process	BP	1	PKIB	up_ACOR_EC
GO:0046649	0.634957394	0.56231	4	162	lymphocyte activation	BP	1	FZD5,NOD2,PTGER4,PRKCD	up_ACOR_EC
GO:0031323	0.635	0.435	41	1788	regulation of cellular metabolic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,MYO1D,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,BVES,AXIN2,YEATS2,ACACB,PPARGC1A,CCL5,CTIF,ADAM17,SAMD4B	up_AFEM_EC
GO:0009892	0.635	0.431	40	835	negative regulation of metabolic process	BP	1	CST3,NOTCH2,KIRREL1,DCN,NAB2,PRNP,BGN,KANK2,RECK,AKT1S1,TIMP2,PSMF1,SAMD4B,NR3C1,HR,CLSTN1,PLCL1,PRMT6,CXXC5,ASPN,POLDIP2,LRPAP1,THY1,CC2D1A,GLI3,PARK7,ZFP36L1,CLEC16A,LOXL3,ORMDL3,SPRED1,A2M,TSC22D3,GLIS2,SHC1,PYM1,FBH1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0009889	0.635	0.446	27	1190	regulation of biosynthetic process	BP	1	HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0045321	0.635	0.487	11	191	leukocyte activation	BP	1	SOCS5,FAM49B,MSN,CX3CL1,PTPN2,CTNNB1,TFRC,LYN,SDC4,BTK,CDKN1A	down_VSAP_EC
GO:0045934	0.635	0.498	9	407	negative regulation of nucleobase-containing compound metabolic	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,TENT5C,NR3C1,AXIN2	up_AFEM_EC
GO:0046777	0.635	0.519	7	86	protein autophosphorylation	BP	1	IRAK1,CAV1,GREM1,NEK2,RAP2C,TTK,MELK	down_ACOR_VSMC
GO:0019953	0.635	0.516	7	152	sexual reproduction	BP	1	ADAMTS2,MEA1,B4GALT1,ENSCAFG00000017708,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0006650	0.635	0.519	7	78	glycerophospholipid metabolic process	BP	1	NAPEPLD,ENPP2,INPP5E,PIK3R1,PLA2G6,LCAT,ZFYVE21	up_VSAP_EC
GO:0051172	0.635	0.547	5	663	negative regulation of nitrogen compound	BP	1	CXHXorf57,ENSCAFG00000002015,ASPN,FBP1,MTDH	up_VPOR_EC
GO:0044237	0.635	0.639	4	3491	cellular metabolic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0044344	0.635	0.599	3	33	cellular response to fibroblast growth factor	BP	1	FGFR2,FGF18,FRS2	up_ACOR_VSMC
GO:0071774	0.635	0.599	3	33	response to fibroblast growth factor	BP	1	FGFR2,FGF18,FRS2	up_ACOR_VSMC
GO:0010604	0.635	0.603	3	919	positive regulation of macromolecule metabolic	BP	1	CCL24,PTGER2,ARHGEF2	up_VPUL_EC
GO:0032835	0.635	0.649	2	21	glomerulus development	BP	1	BMP4,NID1	up_ACOR_VSMC
GO:0034763	0.635	0.646	2	27	negative regulation of transmembrane transport	BP	1	CTTNBP2NL,RSC1A1	up_VCAV_EC
GO:0043069	0.635	0.64	2	262	negative regulation of programmed cell death	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0010629	0.635	0.645	2	502	negative regulation of gene expression	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0032355	0.635	0.752	1	10	response to estradiol	BP	1	FAM210B	up_ACOR_VSMC
GO:1903671	0.635	0.752	1	10	negative regulation of sprouting angiogenesis	BP	1	SYNJ2BP	up_ACOR_VSMC
GO:0002833	0.635	0.749	1	12	positive regulation of response to biotic	BP	1	NECTIN2	up_VCAV_EC
GO:0007549	0.635	0.751	1	11	dosage compensation	BP	1	CDYL	up_VCAV_EC
GO:0010517	0.635	0.75	1	11	regulation of phospholipase activity	BP	1	SELE	up_VCAV_EC

GO:0022617	0.635	0.751	1	11	extracellular matrix disassembly	BP	1	FSCN1	up_VCAV_EC
GO:0042634	0.635	0.75	1	11	regulation of hair cycle	BP	1	FERMT1	up_VCAV_EC
GO:0048488	0.635	0.753	1	10	synaptic vesicle endocytosis	BP	1	PPP3CB	up_VSAP_EC
GO:0050931	0.635	0.752	1	10	pigment cell differentiation	BP	1	HPS4	up_VSAP_EC
GO:0140238	0.635	0.753	1	10	presynaptic endocytosis	BP	1	PPP3CB	up_VSAP_EC
GO:0002683	0.636	0.492	10	126	negative regulation of immune system process	BP	1	HMGB1,MNDA,HSPA9,PRMT1,HMGB3,HOXA7,ARG2,CACTIN,EZR,HOXA9	down_ACOR_VSMC
GO:0044262	0.636	0.508	8	89	cellular carbohydrate metabolic process	BP	1	LEP,ENOSF1,PPIP5K1,PYGM,PRKCE,DDIT4,GAA,INPP5K	up_ACOR_VSMC
GO:0005996	0.636	0.563	4	85	monosaccharide metabolic process	BP	1	AKT2,H6PD,POFUT1,B4GALT1	down_VCAV_EC
GO:0043535	0.636	0.567	4	45	regulation of blood vessel endothelial cell migration	BP	1	FGF18,NRP1,JUP,PIK3C2A	up_ACOR_VSMC
GO:0051234	0.636	0.61	3	1283	establishment of localization	BP	1	HOXA3,NKX2-5,TRPC4	up_VPOR_VSMC
GO:0048588	0.636	0.641	2	44	developmental cell growth	BP	1	NDN,TRPV2	down_VCAV_EC
GO:0051252	0.636	0.656	2	1051	regulation of RNA metabolic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0019915	0.636	0.647	2	22	lipid storage	BP	1	ACACB,SOAT1	up_VSAP_EC
GO:0042790	0.636	0.75	1	11	nucleolar large rRNA transcription by RNA	BP	1	NCL	down_ACOR_VSMC
GO:1901836	0.636	0.75	1	11	regulation of transcription of nucleolar large rRNA by RNA polymerase I	BP	1	NCL	down_ACOR_VSMC
GO:0042127	0.636	0.745	1	452	regulation of cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:1903201	0.636	0.742	1	20	regulation of oxidative stress-induced cell death	BP	1	PARK7	down_VCAV_EC
GO:0021955	0.636	0.745	1	15	central nervous system neuron axonogenesis	BP	1	CDH11	down_VSAP_EC
GO:0051781	0.636	0.743	1	18	positive regulation of cell division	BP	1	VEGFA	down_VSAP_EC
GO:0007566	0.636	0.751	1	10	embryo implantation	BP	1	RECK	up_ACOR_VSMC
GO:0043370	0.636	0.751	1	10	regulation of CD4-positive, alpha-beta T cell	BP	1	CD83	up_ACOR_VSMC
GO:0001657	0.636	0.737	1	42	ureteric bud development	BP	1	GREM1	up_AFEM_EC
GO:0072163	0.636	0.737	1	42	mesonephric epithelium development	BP	1	GREM1	up_AFEM_EC
GO:0072164	0.636	0.737	1	42	mesonephric tubule development	BP	1	GREM1	up_AFEM_EC
GO:0097237	0.636	0.737	1	42	cellular response to toxic substance	BP	1	SOD1	up_AFEM_EC
GO:0051234	0.636	0.772	1	1283	establishment of localization	BP	1	HOXA3	up_APUL_VSMC
GO:0060914	0.636	0.75	1	11	heart formation	BP	1	MEF2C	up_VCAV_EC
GO:0006518	0.636	0.741	1	290	peptide metabolic process	BP	1	ENSCAFG00000028814	up_VPUL_EC
GO:0015800	0.636	0.751	1	10	acidic amino acid transport	BP	1	SLC25A12	up_VSAP_EC
GO:0043279	0.636	0.751	1	10	response to alkaloid	BP	1	ABAT	up_VSAP_EC
GO:0060135	0.636	0.751	1	10	maternal process involved in female pregnancy	BP	1	CITED2	up_VSAP_EC
GO:0050820	0.636	0.751	1	10	positive regulation of coagulation	BP	1	HPSE	up_VSAP_EC
GO:0050853	0.636	0.752	1	10	B cell receptor signaling pathway	BP	1	ABL1	up_VSAP_EC
GO:0010556	0.636391243	0.44229	29	1137	regulation of macromolecule biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,PKIB,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0031326	0.636801993	0.44078	30	1176	regulation of cellular biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,PKIB,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC

GO:0031325	0.637	0.409	86	914	positive regulation of cellular metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MBP,LIPT2,SKP2,PRKAA2,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,SH3RF2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,AR,SASH1,LMO4,FGF18,PLAC8B,F2RL1,FAM129A,DAPK1,BNIP3,EGLN1,CDKN1A,CRLF3,NRP1,PTPN22,NPNT,SMARCD3,SMPD1,PRKCE,CCNT1,FRS2,RNF19A,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,ZKSCAN1,SH3BP4,ENSCAFG00000029553,PARK7,TEAD1,NGRN,HMBOX1,SSBP2,BVES,CRKL	up_ACOR_VSMC
GO:0015833	0.637	0.423	48	521	peptide transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,STX11,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,CHD7,LAMP2,JUP,CCL5,RAB11B,EDN1,NOD2,LMTK2,AP2B1,SCAMP5,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0031331	0.637	0.492	10	110	positive regulation of cellular catabolic process	BP	1	PRKAA2,SH3RF2,TP53INP1,DAPK1,BNIP3,RNF19A,PSEN1,DISC1,HERPUD1,SH3BP4	up_ACOR_VSMC
GO:0051188	0.637	0.516	7	81	cofactor biosynthetic process	BP	1	MAT2B,PCBD1,ALDOC,DDIT4,PTS,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0045860	0.637	0.526	6	132	positive regulation of protein kinase activity	BP	1	PRNP,CSPG4,SASH1,MAPRE3,DDR2,SHC1	down_VCAV_EC
GO:0010605	0.637	0.597	3	745	negative regulation of macromolecule metabolic	BP	1	PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0001656	0.637	0.641	2	35	metanephros development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:1901701	0.637	0.638	2	271	cellular response to oxygen-containing	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0009880	0.637	0.646	2	22	embryonic pattern specification	BP	1	DLL1,ZBTB16	up_VSAP_EC
GO:0048870	0.637	0.744	1	451	cell motility	BP	1	FSCN1	down_AFEM_EC
GO:0051674	0.637	0.744	1	451	localization of cell	BP	1	FSCN1	down_AFEM_EC
GO:0048708	0.637	0.741	1	20	astrocyte differentiation	BP	1	LRP1	down_VCAV_EC
GO:0051716	0.637	0.801	1	2001	cellular response to stimulus	BP	1	PLCL1	down_VFEM_EC
GO:0002763	0.637	0.742	1	17	positive regulation of myeloid leukocyte	BP	1	EVI2B	down_VSAP_EC
GO:0014909	0.637	0.744	1	15	smooth muscle cell migration	BP	1	SERPINE1	down_VSAP_EC
GO:0032212	0.637	0.744	1	16	positive regulation of telomere maintenance via	BP	1	CTNNB1	down_VSAP_EC
GO:1904358	0.637	0.744	1	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	CTNNB1	down_VSAP_EC
GO:0043616	0.637	0.751	1	10	keratinocyte proliferation	BP	1	FERMT1	up_ACOR_VSMC
GO:0046636	0.637	0.75	1	10	negative regulation of alpha-beta T cell	BP	1	CD274	up_ACOR_VSMC
GO:0048821	0.637	0.75	1	10	erythrocyte development	BP	1	CITED2	up_ACOR_VSMC
GO:0003337	0.637	0.75	1	10	mesenchymal to epithelial transition involved in metanephros	BP	1	BMP4	up_ACOR_VSMC
GO:0006997	0.637	0.736	1	42	nucleus organization	BP	1	DMPK	up_AFEM_EC
GO:0019748	0.637	0.746	1	13	secondary metabolic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0033598	0.637	0.748	1	11	mammary gland epithelial cell proliferation	BP	1	GATA3	up_VCAV_EC
GO:0048486	0.637	0.75	1	10	parasympathetic nervous system development	BP	1	NAV2	up_VCAV_EC
GO:0030511	0.637	0.751	1	10	positive regulation of transforming growth factor beta receptor	BP	1	CITED2	up_VSAP_EC
GO:0045428	0.637	0.751	1	10	regulation of nitric oxide biosynthetic process	BP	1	ASS1	up_VSAP_EC
GO:0046636	0.637	0.75	1	10	negative regulation of alpha-beta T cell	BP	1	CD274	up_VSAP_EC

GO:0090181	0.637	0.75	1	10	regulation of cholesterol metabolic process	BP	1	LMF1	up_VSAP_EC
GO:1903846	0.637	0.751	1	10	positive regulation of cellular response to transforming growth	BP	1	CITED2	up_VSAP_EC
GO:0050918	0.637	0.75	1	10	positive chemotaxis	BP	1	F2RL1	up_VSAP_EC
GO:0010243	0.637	0.738	1	238	response to organonitrogen	BP	1	CAV1	up_VSAP_VSMC
GO:0030030	0.638	0.436	31	377	cell projection organization	BP	1	EPHB1,KIT,IFRD1,PODXL,RELN,MEF2C,RAPGEF1,GATA3,RAB11A,PPP3CA,NECTIN2,MTOR,PREX2,NCKAP1,GDPD5,ENSCAFG00000010224,STMN1,SNX2,PAK2,APOD,NCK1,EXOC5,FES,RAPGEF2,CREB1,SPTBN4,ITGA6,ALS2,IQUB,SPATA6,FSCN1	up_VCAV_EC
GO:0006955	0.638	0.437	30	327	immune response	BP	1	CD274,MAP3K14,ENPP2,ABL1,EMP2,DLL1,CTSS,TRAFD1,TNFSF13,CDC42EP2,STAT6,F2RL1,RBCK1,PLA2G6,MYD88,TFE3,CFD,NLRX1,TKFC,CD83,PNP,CYBA,STX4,PQBP1,UNC93B1,FLOT1,PPP3CB,MAVS,IRAK1BP1,JCHAIN	up_VSAP_EC
GO:1903530	0.638	0.467	15	165	regulation of secretion by cell	BP	1	HNF4A,CD274,C5AR2,SLC8B1,ABL1,IL17RC,ANXA4,F2RL1,PASK,KCNB1,MAPKBP1,STX4,KCNC4,PPP3CB,MAVS	up_VSAP_EC
GO:0120031	0.638	0.47	14	154	plasma membrane bounded cell projection assembly	BP	1	ACTN2,EVI5L,WASF3,ARHGEF26,IFT43,F2RL1,NRP1,EVL,SSH3,ASAP1,DISC1,ATXN10,INPP5K,ENSCAFG00000013536	up_ACOR_VSMC
GO:0044772	0.638	0.504	8	144	mitotic cell cycle phase transition	BP	1	PLK3,ZPR1,EIF4EBP1,BACH1,RBBP8,CALM1,INHBA,CDKN1A	down_VSAP_EC
GO:0010508	0.638	0.593	3	38	positive regulation of autophagy	BP	1	MTDH,PLK3,RNF152	down_ACOR_VSMC
GO:0070059	0.638	0.643	2	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	1	TXNDC12,AIFM1	down_ACOR_VSMC
GO:0006928	0.638	0.642	2	557	movement of cell or subcellular component	BP	1	TBX5,NTRK2	up_APUL_EC
GO:0008283	0.638	0.643	2	545	cell proliferation	BP	1	TBX5,HOXA3	up_APUL_EC
GO:0098781	0.638	0.645	2	22	ncRNA transcription	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0065003	0.638	0.644	2	616	protein-containing complex assembly	BP	1	MYBPC2,CCL24	up_VPUL_EC
GO:0006622	0.638	0.748	1	11	protein targeting to lysosome	BP	1	NEDD4	down_ACOR_VSMC
GO:0009299	0.638	0.748	1	11	mRNA transcription	BP	1	SREBF1	down_ACOR_VSMC
GO:0040018	0.638	0.747	1	11	positive regulation of multicellular organism	BP	1	EZR	down_ACOR_VSMC
GO:0060045	0.638	0.748	1	11	positive regulation of cardiac muscle cell	BP	1	GLI1	down_ACOR_VSMC
GO:2000008	0.638	0.746	1	12	regulation of protein localization to cell surface	BP	1	SLC29A1	down_ACOR_VSMC
GO:0021695	0.638	0.74	1	20	cerebellar cortex development	BP	1	NAGLU	down_VCAV_EC
GO:0043407	0.638	0.74	1	19	negative regulation of MAP kinase activity	BP	1	SPRED1	down_VCAV_EC
GO:0042246	0.638	0.741	1	17	tissue regeneration	BP	1	IFRD1	down_VSAP_EC
GO:0098751	0.638	0.743	1	15	bone cell development	BP	1	PTPN11	down_VSAP_EC
GO:0033198	0.638	0.75	1	10	response to ATP	BP	1	P2RX7	up_ACOR_VSMC
GO:1901099	0.638	0.749	1	10	negative regulation of signal transduction in	BP	1	UNC5B	up_ACOR_VSMC
GO:1901223	0.638	0.75	1	10	negative regulation of NIK/NF-kappaB signaling	BP	1	RASSF2	up_ACOR_VSMC
GO:2001240	0.638	0.749	1	10	negative regulation of extrinsic apoptotic signaling pathway in	BP	1	UNC5B	up_ACOR_VSMC
GO:0006413	0.638	0.736	1	42	translational initiation	BP	1	CTIF	up_AFEM_EC
GO:0030218	0.638	0.735	1	42	erythrocyte differentiation	BP	1	NFE2L1	up_AFEM_EC
GO:1904036	0.638	0.749	1	10	negative regulation of epithelial cell apoptotic	BP	1	ABL1	up_VSAP_EC

GO:0044271	0.638419554	0.43226	38	1501	cellular nitrogen compound biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,AZIN2,PRKCD,PM20D1,EFEMP1,TLE2	up_ACOR_EC
GO:0002520	0.639	0.472	13	279	immune system development	BP	1	NOTCH2,FBN1,LMO4,TFE3,CLSTN1,GLI3,EEF2,ZFP36L1,LOXL3,RAB7B,FOXO3,ZBTB16,ANKRD54	down_VCAV_EC
GO:0001654	0.639	0.49	10	110	eye development	BP	1	BMP4,GJA1,CITED2,NRP1,GPM6A,SMARCD3,FRS2,CPAMD8,CHD7,CLN8	up_ACOR_VSMC
GO:0048880	0.639	0.49	10	110	sensory system development	BP	1	BMP4,GJA1,CITED2,NRP1,GPM6A,SMARCD3,FRS2,CPAMD8,CHD7,CLN8	up_ACOR_VSMC
GO:0150063	0.639	0.49	10	110	visual system development	BP	1	BMP4,GJA1,CITED2,NRP1,GPM6A,SMARCD3,FRS2,CPAMD8,CHD7,CLN8	up_ACOR_VSMC
GO:0008217	0.639	0.593	3	38	regulation of blood pressure	BP	1	NAV2,PRCP,EMP2	down_ACOR_VSMC
GO:0019438	0.639	0.606	3	1258	aromatic compound biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0005976	0.639	0.594	3	34	polysaccharide metabolic process	BP	1	C1QTNF2,PHKA2,PASK	up_VSAP_EC
GO:0014902	0.639	0.594	3	34	myotube differentiation	BP	1	CDON,SHOX2,FLOT1	up_VSAP_EC
GO:0044265	0.639	0.639	2	423	cellular macromolecule catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0007187	0.639	0.637	2	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	ADCY6,GNAZ	down_VCAV_EC
GO:0033077	0.639	0.644	2	22	T cell differentiation in thymus	BP	1	BMP4,B2M	up_ACOR_VSMC
GO:0035690	0.639	0.634	2	91	cellular response to drug	BP	1	CHRM2,NR3C1	up_AFEM_EC
GO:0033344	0.639	0.745	1	12	cholesterol efflux	BP	1	SREBF2	down_ACOR_VSMC
GO:0030593	0.639	0.74	1	19	neutrophil chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0010501	0.639	0.742	1	15	RNA secondary structure unwinding	BP	1	DDX39B	down_VSAP_EC
GO:0043392	0.639	0.742	1	16	negative regulation of DNA binding	BP	1	DDIT3	down_VSAP_EC
GO:0043921	0.639	0.748	1	10	modulation by host of viral transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0045601	0.639	0.749	1	10	regulation of endothelial cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0052312	0.639	0.748	1	10	modulation of transcription in other organism involved in	BP	1	INPP5K	up_ACOR_VSMC
GO:0052472	0.639	0.748	1	10	modulation by host of symbiont transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0046165	0.639	0.735	1	42	alcohol biosynthetic process	BP	1	MOXD1	up_AFEM_EC
GO:0006312	0.639	0.746	1	11	mitotic recombination	BP	1	SMC5	up_VCAV_EC
GO:0045684	0.639	0.745	1	12	positive regulation of epidermis development	BP	1	PRKCH	up_VCAV_EC
GO:0046718	0.639	0.744	1	13	viral entry into host cell	BP	1	NECTIN2	up_VCAV_EC
GO:0051338	0.639	0.737	1	288	regulation of transferase activity	BP	1	FLRT3	up_VPUL_EC
GO:0046627	0.639	0.748	1	10	negative regulation of insulin receptor signaling	BP	1	NCK1	up_VSAP_EC
GO:0009206	0.639774825	0.73391	1	39	purine ribonucleoside triphosphate biosynthetic	BP	1	ALDOC	up_ACOR_EC
GO:0080135	0.64	0.468	14	240	regulation of cellular response to stress	BP	1	ARHGEF2,P4HB,HYOU1,NUAK1,PTGS2,HIF1A,TNIK,PTPN2,DDX39B,CTNNB1,LYN,SH3RF3,USP14,MID1	down_VSAP_EC
GO:0048858	0.64	0.468	14	159	cell projection morphogenesis	BP	1	ENPP2,SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0072594	0.64	0.469	14	155	establishment of protein localization to organelle	BP	1	PEX7,CDH1,PEX2,VPS36,MFN2,PIK3R1,NUP98,FBXO7,LONP2,SNUPN,PEX6,MAVS,BAG4,NCOA4	up_VSAP_EC
GO:0000165	0.64	0.48	11	236	MAPK cascade	BP	1	NOTCH2,PDGFRB,GLIPR2,CSPG4,ZFP36L1,MYDGF,SASH1,CDH2,GSDME,SPRED1,SHC1	down_VCAV_EC
GO:0018108	0.64	0.513	7	79	peptidyl-tyrosine phosphorylation	BP	1	ENPP2,IL6R,FGF7,ABL1,PDGFD,PLPP3,LRP4	up_VSAP_EC
GO:1903532	0.64	0.513	7	78	positive regulation of secretion by cell	BP	1	CD274,ABL1,IL17RC,F2RL1,STX4,PPP3CB,MAVS	up_VSAP_EC

GO:0002250	0.64	0.525	6	68	adaptive immune response	BP	1	CD274,EMP2,STAT6,MYD88,PPP3CB,JCHAIN	up_VSAP_EC
GO:0033500	0.64	0.54	5	64	carbohydrate homeostasis	BP	1	BIRC5,ADIPOR2,PRCP,ENSCAFG00000005299,NCOA5	down_ACOR_VSMC
GO:0042593	0.64	0.54	5	64	glucose homeostasis	BP	1	BIRC5,ADIPOR2,PRCP,ENSCAFG00000005299,NCOA5	down_ACOR_VSMC
GO:0097435	0.64	0.536	5	230	supramolecular fiber organization	BP	1	CRYAB,MFAP4,GREM1,CDC42EP5,KANK1	up_AFEM_EC
GO:0030326	0.64	0.561	4	51	embryonic limb morphogenesis	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0035113	0.64	0.561	4	51	embryonic appendage morphogenesis	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0071482	0.64	0.593	3	34	cellular response to light stimulus	BP	1	MFAP4,TP53INP1,CDKN1A	up_ACOR_VSMC
GO:2001243	0.64	0.594	3	33	negative regulation of intrinsic apoptotic	BP	1	HERPUD1,WFS1,PARK7	up_ACOR_VSMC
GO:0018130	0.64	0.605	3	1261	heterocycle biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0072655	0.64	0.593	3	33	establishment of protein localization to	BP	1	MFN2,FBXO7,BAG4	up_VSAP_EC
GO:0006672	0.64	0.593	3	33	ceramide metabolic process	BP	1	CERS4,ENSCAFG00000000071,B3GALT4	up_VSAP_EC
GO:0046165	0.64	0.637	2	42	alcohol biosynthetic process	BP	1	CYB5R3,PARK7	down_VCAV_EC
GO:1903829	0.64	0.634	2	91	positive regulation of cellular protein	BP	1	LEP,CYLD	up_AFEM_EC
GO:0033143	0.64	0.641	2	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	SMARCA4,UFSP2	up_VCAV_EC
GO:0000271	0.64	0.643	2	22	polysaccharide biosynthetic process	BP	1	C1QTNF2,PASK	up_VSAP_EC
GO:2000378	0.64	0.744	1	12	negative regulation of reactive oxygen species	BP	1	CAV1	down_ACOR_VSMC
GO:0021545	0.64	0.738	1	21	cranial nerve development	BP	1	GLI3	down_VCAV_EC
GO:0046513	0.64	0.739	1	19	ceramide biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:1905332	0.64	0.738	1	20	positive regulation of morphogenesis of an	BP	1	GREM1	down_VCAV_EC
GO:0010629	0.64	0.742	1	502	negative regulation of gene expression	BP	1	HDAC7	down_VPOR_EC
GO:1901360	0.64	0.798	1	2016	organic cyclic compound metabolic process	BP	1	MOSPD1	down_VFEM_EC
GO:0046627	0.64	0.748	1	10	negative regulation of insulin receptor signaling	BP	1	INPP5K	up_ACOR_VSMC
GO:0032508	0.64	0.746	1	11	DNA duplex unwinding	BP	1	GINS4	up_VCAV_EC
GO:0080134	0.64	0.739	1	386	regulation of response to stress	BP	1	ANKRD6	up_VPOR_VSMC
GO:2000113	0.64	0.74	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0021696	0.64	0.748	1	10	cerebellar cortex morphogenesis	BP	1	DLL1	up_VSAP_EC
GO:0032355	0.64	0.748	1	10	response to estradiol	BP	1	PTGFR	up_VSAP_EC
GO:1901223	0.64	0.747	1	10	negative regulation of NIK/NF-kappaB signaling	BP	1	HDAC7	up_VSAP_EC
GO:2000725	0.64	0.747	1	10	regulation of cardiac muscle cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0030195	0.64	0.748	1	10	negative regulation of blood coagulation	BP	1	KLKB1	up_VSAP_EC
GO:0090102	0.64	0.747	1	10	cochlea development	BP	1	ZEB1	up_VSAP_EC
GO:1900047	0.64	0.748	1	10	negative regulation of hemostasis	BP	1	KLKB1	up_VSAP_EC
GO:0018205	0.640309341	0.5857	3	122	peptidyl-lysine modification	BP	1	PHF20,PIAS1,PYGO2	up_ACOR_EC
GO:0030433	0.64051194	0.7333	1	38	ubiquitin-dependent ERAD pathway	BP	1	EDEM2	up_ACOR_EC
GO:0060349	0.640524178	0.73328	1	38	bone morphogenesis	BP	1	SOX9	up_ACOR_EC
GO:0007498	0.640870635	0.73294	1	38	mesoderm development	BP	1	FOXC2	up_ACOR_EC

GO:0120036	0.641	0.428	35	373	plasma membrane bounded cell projection organization	BP	1	ACTN2,EPYC,FEZ1,ITM2C,EVI5L,FGFR2,SEC24B,WASF3,ZNF365,TMEM108,ARHGEF26,IFT43,F2RL1,NRP1,GPM6A,ULK2,UNC5B,EVL,SLITRK5,FZD3,TTC17,DAG1,APP,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,INPP5K,WASL,ENSCAFG00000013536,RREB1	up_ACOR_VSMC
GO:0051051	0.641	0.501	8	112	negative regulation of transport	BP	1	FERMT1,STC1,CTTNBP2NL,ARG2,RSC1A1,APOD,CD200,HMGB1	up_VCAV_EC
GO:0034765	0.641	0.511	7	91	regulation of ion transmembrane transport	BP	1	NEDD4,CAV1,SLC30A1,CLIC1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:2000058	0.641	0.524	6	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	SH3RF2,RNF19A,PSEN1,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0022409	0.641	0.541	5	56	positive regulation of cell-cell adhesion	BP	1	LEP,CD83,CITED2,CD274,PTPN22	up_ACOR_VSMC
GO:0071704	0.641	0.605	5	3535	organic substance metabolic process	BP	1	CYP1A1,LIMK1,GATA5,C6,ENSCAFG00000028814	up_VCAV_VSMC
GO:0043414	0.641	0.557	4	70	macromolecule methylation	BP	1	NR1H4,IWS1,PRMT1,KDM3A	down_VSAP_EC
GO:0045184	0.641	0.559	4	532	establishment of protein localization	BP	1	XPOT,ENSCAFG00000002015,GCC2,SRP54	up_VPOR_EC
GO:0061041	0.641	0.592	3	34	regulation of wound healing	BP	1	KLKB1,HPSE,F2RL1	up_VSAP_EC
GO:0070301	0.641	0.64	2	25	cellular response to hydrogen peroxide	BP	1	EZH2,SIGMAR1	down_ACOR_VSMC
GO:0034637	0.641	0.641	2	25	cellular carbohydrate biosynthetic process	BP	1	B3GNT2,B4GALT1	down_ACOR_VSMC
GO:0065008	0.641	0.65	2	1056	regulation of biological quality	BP	1	CITED2,RAB11B	down_VPOR_EC
GO:0072376	0.641	0.745	1	11	protein activation cascade	BP	1	PRCP	down_ACOR_VSMC
GO:0098868	0.641	0.744	1	11	bone growth	BP	1	POC1A	down_ACOR_VSMC
GO:0021766	0.641	0.737	1	20	hippocampus development	BP	1	GLI3	down_VCAV_EC
GO:0045005	0.641	0.736	1	21	DNA-dependent DNA replication maintenance	BP	1	FBH1	down_VCAV_EC
GO:0061614	0.641	0.737	1	20	pri-miRNA transcription by RNA polymerase II	BP	1	BMPR1A	down_VCAV_EC
GO:1903313	0.641	0.74	1	16	positive regulation of mRNA metabolic process	BP	1	CNOT7	down_VSAP_EC
GO:0008045	0.641	0.749	1	9	motor neuron axon guidance	BP	1	NRP1	up_ACOR_VSMC
GO:0046320	0.641	0.747	1	10	regulation of fatty acid oxidation	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0051797	0.641	0.746	1	10	regulation of hair follicle development	BP	1	FERMT1	up_ACOR_VSMC
GO:0090181	0.641	0.747	1	10	regulation of cholesterol metabolic process	BP	1	LMF1	up_ACOR_VSMC
GO:1902622	0.641	0.745	1	11	regulation of neutrophil migration	BP	1	JAM3	up_ACOR_VSMC
GO:0051246	0.641	0.752	1	832	regulation of protein metabolic process	BP	1	WNT7A	up_AORT_VSMC
GO:0080135	0.641	0.734	1	240	regulation of cellular response to stress	BP	1	EYA1	up_VFEM_EC
GO:0044255	0.641	0.735	1	293	cellular lipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0034113	0.641	0.747	1	10	heterotypic cell-cell adhesion	BP	1	FLOT1	up_VSAP_EC
GO:0045879	0.641	0.747	1	10	negative regulation of smoothened signaling	BP	1	GLIS2	up_VSAP_EC
GO:0090140	0.641	0.746	1	10	regulation of mitochondrial fission	BP	1	DDHD1	up_VSAP_EC
GO:0090185	0.641	0.747	1	10	negative regulation of kidney development	BP	1	OSR1	up_VSAP_EC
GO:0060338	0.641	0.746	1	10	regulation of type I interferon-mediated	BP	1	MAVS	up_VSAP_EC
GO:0120031	0.642	0.475	12	154	plasma membrane bounded cell projection assembly	BP	1	KIT,PODXL,MTOR,NCKAP1,ENSCAFG00000010224,NCK1,EXOC5,RAPGEF2,ITGA6,IQUB,SPATA6,FSCN1	up_VCAV_EC
GO:0030098	0.642	0.501	8	87	lymphocyte differentiation	BP	1	PLCG2,LEP,CD83,BMP4,PTPN22,CHD7,B2M,IL18R1	up_ACOR_VSMC
GO:0015672	0.642	0.501	8	89	monovalent inorganic cation transport	BP	1	AMIGO1,KCNE3,OSR1,KLHL24,KCNB1,ENSCAFG00000013366,FXYD1,KCNC4	up_VSAP_EC
GO:0071900	0.642	0.52	6	131	regulation of protein serine/threonine kinase	BP	1	CSPG4,THY1,SASH1,SPRED1,MAPRE3,SHC1	down_VCAV_EC
GO:0031396	0.642	0.536	5	90	regulation of protein ubiquitination	BP	1	PRICKLE1,HSPA5,TRIB3,NXN,SPOPL	down_VSAP_EC

GO:0070371	0.642	0.536	5	91	ERK1 and ERK2 cascade	BP	1	PTPN11,PTPN2,LYN,ATF3,NRP1	down_VSAP_EC
GO:0017157	0.642	0.539	5	58	regulation of exocytosis	BP	1	EXPH5,FBXL20,F2RL1,SCAMP5,PREPL	up_ACOR_VSMC
GO:0021987	0.642	0.59	3	37	cerebral cortex development	BP	1	WDR62,ASPM,ENSCAFG00000010224	down_ACOR_VSMC
GO:0023052	0.642	0.609	3	1602	signaling	BP	1	HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0045893	0.642	0.586	3	413	positive regulation of transcription, DNA-	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0000726	0.642	0.641	2	21	non-recombinational repair	BP	1	TP53BP1,PARP9	up_ACOR_VSMC
GO:0072132	0.642	0.64	2	23	mesenchyme morphogenesis	BP	1	GATA5,TBX20	up_ACOR_VSMC
GO:0033692	0.642	0.736	1	20	cellular polysaccharide biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0051897	0.642	0.736	1	20	positive regulation of protein kinase B signaling	BP	1	MYDGF	down_VCAV_EC
GO:0051894	0.642	0.745	1	10	positive regulation of focal adhesion assembly	BP	1	NRP1	up_ACOR_VSMC
GO:0060438	0.642	0.745	1	10	trachea development	BP	1	BMP4	up_ACOR_VSMC
GO:2001026	0.642	0.746	1	10	regulation of endothelial cell chemotaxis	BP	1	FGF18	up_ACOR_VSMC
GO:0001932	0.642	0.737	1	416	regulation of protein phosphorylation	BP	1	TAOK1	up_AORT_EC
GO:0008206	0.642	0.744	1	11	bile acid metabolic process	BP	1	PROX1	up_VCAV_EC
GO:0032768	0.642	0.743	1	12	regulation of monooxygenase activity	BP	1	GCH1	up_VCAV_EC
GO:0045071	0.642	0.742	1	12	negative regulation of viral genome replication	BP	1	PROX1	up_VCAV_EC
GO:0000165	0.642	0.733	1	236	MAPK cascade	BP	1	CDC42EP5	up_VFEM_EC
GO:0045944	0.642	0.735	1	287	positive regulation of transcription by RNA polymerase II	BP	1	ARHGEF2	up_VPUL_EC
GO:0000291	0.642	0.745	1	10	nuclear-transcribed mRNA catabolic process,	BP	1	EXOSC7	up_VSAP_EC
GO:0008053	0.642	0.745	1	10	mitochondrial fusion	BP	1	MFN2	up_VSAP_EC
GO:0045980	0.642	0.745	1	10	negative regulation of nucleotide metabolic	BP	1	DDIT4	up_VSAP_EC
GO:0010803	0.642	0.745	1	10	regulation of tumor necrosis factor-mediated signaling pathway	BP	1	F2RL1	up_VSAP_EC
GO:0045197	0.642	0.745	1	10	establishment or maintenance of epithelial cell apical/basal polarity	BP	1	WNT11	up_VSAP_EC
GO:0061437	0.642	0.745	1	10	renal system vasculature development	BP	1	OSR1	up_VSAP_EC
GO:0061440	0.642	0.745	1	10	kidney vasculature development	BP	1	OSR1	up_VSAP_EC
GO:0016049	0.642933119	0.58277	3	124	cell growth	BP	1	SOX9,ESM1,NRP1	up_ACOR_EC
GO:0010628	0.643	0.42	43	527	positive regulation of gene expression	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,EIF4A3,HNRNPD,SREBF2,HINFP,U2AF2,INSIG1,CAV1,THRAP3,TRUB2,FAM129B,GREM1,SMARCC1,DHX33,SF3B4,CKS2,BRCA1,FASTKD3,EIF5A,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,EZR,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,ENSCAFG00000017103,PIK3CD	down_ACOR_VSMC
GO:0097193	0.643	0.534	5	109	intrinsic apoptotic signaling pathway	BP	1	TMEM161A,PARK7,ZMAT3,GSDME,FBH1	down_VCAV_EC
GO:0034654	0.643	0.569	4	1236	nucleobase-containing compound biosynthetic	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0051668	0.643	0.588	3	39	localization within membrane	BP	1	NDC1,INSIG1,RAC1	down_ACOR_VSMC
GO:0051304	0.643	0.588	3	38	chromosome separation	BP	1	RAD21,ZW10,FBXO5	up_VCAV_EC
GO:0007411	0.643	0.633	2	45	axon guidance	BP	1	SEMA3C,GLI3	down_VCAV_EC
GO:0097485	0.643	0.633	2	45	neuron projection guidance	BP	1	SEMA3C,GLI3	down_VCAV_EC
GO:0043631	0.643	0.641	2	21	RNA polyadenylation	BP	1	CCNT1,APP	up_ACOR_VSMC
GO:1901992	0.643	0.639	2	23	positive regulation of mitotic cell cycle phase	BP	1	CDC7,APP	up_ACOR_VSMC

GO:1990266	0.643	0.638	2	24	neutrophil migration	BP	1	CCL5,JAM3	up_ACOR_VSMC
GO:0072522	0.643	0.631	2	91	purine-containing compound biosynthetic	BP	1	ACACB,PPARGC1A	up_AFEM_EC
GO:0045445	0.643	0.637	2	27	myoblast differentiation	BP	1	MEF2C,CDON	up_VCAV_EC
GO:0060674	0.643	0.741	1	12	placenta blood vessel development	BP	1	FOSL1	down_ACOR_VSMC
GO:0001676	0.643	0.744	1	10	long-chain fatty acid metabolic process	BP	1	CYP2J2	up_ACOR_VSMC
GO:0032801	0.643	0.745	1	10	receptor catabolic process	BP	1	ZNRF3	up_ACOR_VSMC
GO:1900101	0.643	0.743	1	11	regulation of endoplasmic reticulum unfolded protein response	BP	1	WFS1	up_ACOR_VSMC
GO:0072089	0.643	0.73	1	43	stem cell proliferation	BP	1	OVOL1	up_AFEM_EC
GO:0045648	0.643	0.74	1	13	positive regulation of erythrocyte	BP	1	HIF1A	up_VCAV_EC
GO:0007166	0.643	0.744	1	686	cell surface receptor signaling pathway	BP	1	GATA5	up_VCAV_VSMC
GO:0015936	0.643	0.745	1	10	coenzyme A metabolic process	BP	1	DCAKD	up_VSAP_EC
GO:0043370	0.643	0.745	1	10	regulation of CD4-positive, alpha-beta T cell	BP	1	CD83	up_VSAP_EC
GO:0045745	0.643	0.744	1	10	positive regulation of G protein-coupled receptor signaling pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0046685	0.643	0.745	1	10	response to arsenic-containing substance	BP	1	HMOX1	up_VSAP_EC
GO:0046686	0.643	0.745	1	10	response to cadmium ion	BP	1	HMOX1	up_VSAP_EC
GO:0034381	0.643	0.745	1	10	plasma lipoprotein particle clearance	BP	1	LMF1	up_VSAP_EC
GO:0071604	0.643	0.744	1	10	transforming growth factor beta production	BP	1	WNT11	up_VSAP_EC
GO:0071634	0.643	0.744	1	10	regulation of transforming growth factor beta	BP	1	WNT11	up_VSAP_EC
GO:0008217	0.643317872	0.73046	1	38	regulation of blood pressure	BP	1	RNLS	up_ACOR_EC
GO:0018193	0.644	0.426	34	368	peptidyl-amino acid modification	BP	1	GALNT3,LEP,PLCL1,ST3GAL5,CDC7,RASSF2,TPST2,LIPT2,PRKAA2,ATRX,LATS2,TMX3,CAMK2D,MAGT1,EGLN1,NRP1,DMPK,STT3B,P4HA1,PRKCE,FUT8,PARP9,APP,PSEN1,PSKH1,DUSP22,OXR1,PHF20,LMTK2,MAP3K7,INPP5K,ENSCAFG00000029553,PARK7,ZDHHC21	up_ACOR_VSMC
GO:0030036	0.644	0.447	20	223	actin cytoskeleton organization	BP	1	WNT11,FAM107A,ARHGEF5,WASF3,PPARGC1B,SLIT2,FGF7,ABL1,EMP2,CDC42EP5,CORO2B,CDC42EP2,F2RL1,PIK3R1,FRMD6,WIPF1,MYO1B,ARHGAP12,NCK1,BAG4	up_VSAP_EC
GO:0051056	0.644	0.509	7	87	regulation of small GTPase mediated signal	BP	1	ENSCAFG00000030005,PSD4,STMN1,NUP62,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0061351	0.644	0.557	4	50	neural precursor cell proliferation	BP	1	NF2,ASPM,MELK,ARHGEF2	down_ACOR_VSMC
GO:0045598	0.644	0.558	4	47	regulation of fat cell differentiation	BP	1	LEP,FNDC5,CCDC3,DKKL1	up_ACOR_VSMC
GO:0034101	0.644	0.558	4	45	erythrocyte homeostasis	BP	1	ANKRD54,ZFP36L1,HMOX1,CITED2	up_VSAP_EC
GO:0006475	0.644	0.584	3	54	internal protein amino acid acetylation	BP	1	IWS1,NAA10,MORF4L2	down_VSAP_EC
GO:0035850	0.644	0.637	2	25	epithelial cell differentiation involved in	BP	1	GREM1,IQGAP1	down_ACOR_VSMC
GO:0008037	0.644	0.639	2	22	cell recognition	BP	1	NRP1,APP	up_ACOR_VSMC
GO:0055024	0.644	0.639	2	22	regulation of cardiac muscle tissue	BP	1	DLL1,SAV1	up_VSAP_EC
GO:0030514	0.644	0.74	1	12	negative regulation of BMP signaling pathway	BP	1	GREM1	down_ACOR_VSMC
GO:0071108	0.644	0.741	1	11	protein K48-linked deubiquitination	BP	1	BAP1	down_ACOR_VSMC
GO:0051452	0.644	0.734	1	20	intracellular pH reduction	BP	1	ATP6V0C	down_VCAV_EC
GO:0006690	0.644	0.737	1	16	icosanoid metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0044106	0.644	0.735	1	17	cellular amine metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0048583	0.644	0.758	1	1095	regulation of response to stimulus	BP	1	GATA5	down_VSAP_VSMC

GO:0021696	0.644	0.744	1	10	cerebellar cortex morphogenesis	BP	1	ZNF365	up_ACOR_VSMC
GO:0048534	0.644	0.731	1	262	hematopoietic or lymphoid organ	BP	1	HOXA3	up_APUL_EC
GO:0010558	0.644	0.735	1	392	negative regulation of macromolecule biosynthetic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0010557	0.644	0.738	1	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0045935	0.644	0.738	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA5	up_VPUL_VSMC
GO:0009268	0.644	0.744	1	10	response to pH	BP	1	RAB11B	up_VSAP_EC
GO:0010907	0.644	0.743	1	10	positive regulation of glucose metabolic process	BP	1	C1QTNF2	up_VSAP_EC
GO:0035994	0.644	0.744	1	10	response to muscle stretch	BP	1	RAF1	up_VSAP_EC
GO:0086003	0.644	0.744	1	10	cardiac muscle cell contraction	BP	1	KCNE3	up_VSAP_EC
GO:0086004	0.644	0.744	1	10	regulation of cardiac muscle cell contraction	BP	1	KCNE3	up_VSAP_EC
GO:0009260	0.644062104	0.62944	2	83	ribonucleotide biosynthetic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0046390	0.644062104	0.62944	2	83	ribose phosphate biosynthetic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0032092	0.644264804	0.7295	1	38	positive regulation of protein binding	BP	1	PLCL1	up_ACOR_EC
GO:0006869	0.644635251	0.62891	2	81	lipid transport	BP	1	CFI,PRKCD	up_ACOR_EC
GO:0010508	0.64492953	0.72882	1	38	positive regulation of autophagy	BP	1	TP53INP2	up_ACOR_EC
GO:0009117	0.645	0.449	19	208	nucleotide metabolic process	BP	1	ACSM3,ACACB,NADK,COQ9,NDUFS1,ENSCAFG00000004260,PDK2,FXN,GALK1,CTNS,NDUFS2,NT5C2,ACSS2,MVK,DCAKD,ENSCAFG00000013366,PNP,NDUFV1,DDIT4	up_VSAP_EC
GO:0019216	0.645	0.49	9	101	regulation of lipid metabolic process	BP	1	LEP,HTR2B,PPARGC1A,ORMDL3,CCDC3,PRKCE,DKKL1,ENSCAFG00000029553,LMF1	up_ACOR_VSMC
GO:0070085	0.645	0.532	5	95	glycosylation	BP	1	GALNT1,PLOD3,STT3A,EXT1,RPN1	down_VSAP_EC
GO:0032874	0.645	0.535	5	57	positive regulation of stress-activated MAPK	BP	1	ARHGEF5,MAP3K5,F2RL1,SASH1,MYD88	up_VSAP_EC
GO:0038061	0.645	0.588	3	34	NIK/NF-kappaB signaling	BP	1	HDAC7,RBCK1,SASH1	up_VSAP_EC
GO:0001707	0.645	0.636	2	25	mesoderm formation	BP	1	NF2,ITGA2	down_ACOR_VSMC
GO:0006915	0.645	0.635	2	550	apoptotic process	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0001910	0.645	0.739	1	12	regulation of leukocyte mediated cytotoxicity	BP	1	FAM49B	down_ACOR_VSMC
GO:0060231	0.645	0.739	1	12	mesenchymal to epithelial transition	BP	1	GREM1	down_ACOR_VSMC
GO:1901661	0.645	0.739	1	12	quinone metabolic process	BP	1	PDSS1	down_ACOR_VSMC
GO:0045604	0.645	0.734	1	17	regulation of epidermal cell differentiation	BP	1	ERRFI1	down_VSAP_EC
GO:2000142	0.645	0.735	1	17	regulation of DNA-templated transcription,	BP	1	CTNNB1	down_VSAP_EC
GO:0051254	0.645	0.735	1	431	positive regulation of RNA metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0071702	0.645	0.742	1	687	organic substance transport	BP	1	CA2	up_VCAV_VSMC
GO:0031343	0.645	0.743	1	10	positive regulation of cell killing	BP	1	F2RL1	up_VSAP_EC
GO:0033137	0.645	0.743	1	10	negative regulation of peptidyl-serine	BP	1	NCK1	up_VSAP_EC
GO:0016567	0.645	0.73	1	232	protein ubiquitination	BP	1	CAV1	up_VSAP_VSMC
GO:0051054	0.645071856	0.62843	2	81	positive regulation of DNA metabolic process	BP	1	PKIB,PRKCD	up_ACOR_EC
GO:0006351	0.646	0.501	8	1069	transcription, DNA-templated	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0007159	0.646	0.507	7	79	leukocyte cell-cell adhesion	BP	1	CD274,ZBTB16,CD83,PNP,ASS1,NCK1,TGFBR2	up_VSAP_EC
GO:0000302	0.646	0.554	4	52	response to reactive oxygen species	BP	1	PPP1R15B,EZH2,PLK3,SIGMAR1	down_ACOR_VSMC
GO:1990845	0.646	0.554	4	51	adaptive thermogenesis	BP	1	CAV1,ADIPOR2,HOXC10,ELOVL6	down_ACOR_VSMC

GO:0010921	0.646	0.555	4	46	regulation of phosphatase activity	BP	1	PPARGC1B,SH2D4A,TMEM225B,BAG4	up_VSAP_EC
GO:0043401	0.646	0.555	4	46	steroid hormone mediated signaling	BP	1	PPARGC1B,CREBRF,PRMT2,LBH	up_VSAP_EC
GO:0019362	0.646	0.586	3	35	pyridine nucleotide metabolic process	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0046496	0.646	0.586	3	35	nicotinamide nucleotide metabolic process	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0071248	0.646	0.586	3	35	cellular response to metal ion	BP	1	PRKAA2,BNIP3,B2M	up_ACOR_VSMC
GO:0048667	0.646	0.579	3	140	cell morphogenesis involved in neuron	BP	1	PLXNA4,CAMK2A,LRRN2	up_AFEM_EC
GO:1902680	0.646	0.582	3	415	positive regulation of RNA biosynthetic process	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:1903508	0.646	0.582	3	415	positive regulation of nucleic acid-templated	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:1901565	0.646	0.632	2	442	organonitrogen compound catabolic	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0001889	0.646	0.637	2	22	liver development	BP	1	CITED2,LIMS2	up_ACOR_VSMC
GO:0045682	0.646	0.634	2	27	regulation of epidermis development	BP	1	PRKCH,FERMT1	up_VCAV_EC
GO:0045739	0.646	0.635	2	26	positive regulation of DNA repair	BP	1	TIMELESS,HMGB1	up_VCAV_EC
GO:0009135	0.646	0.637	2	22	purine nucleoside diphosphate metabolic	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0009179	0.646	0.637	2	22	purine ribonucleoside diphosphate metabolic	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0046031	0.646	0.637	2	22	ADP metabolic process	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0050767	0.646	0.728	1	184	regulation of neurogenesis	BP	1	LYN	down_ACOR_EC
GO:0071480	0.646	0.739	1	12	cellular response to gamma radiation	BP	1	MAP3K20	down_ACOR_VSMC
GO:0035115	0.646	0.738	1	12	embryonic forelimb morphogenesis	BP	1	HOXA9	down_ACOR_VSMC
GO:0002027	0.646	0.732	1	20	regulation of heart rate	BP	1	IRX5	down_VCAV_EC
GO:0042035	0.646	0.731	1	20	regulation of cytokine biosynthetic process	BP	1	MAST2	down_VCAV_EC
GO:0031328	0.646	0.736	1	512	positive regulation of cellular biosynthetic	BP	1	CITED2	down_VPOR_EC
GO:0034314	0.646	0.735	1	16	Arp2/3 complex-mediated actin nucleation	BP	1	ACTR3	down_VSAP_EC
GO:0042181	0.646	0.733	1	17	ketone biosynthetic process	BP	1	REST	down_VSAP_EC
GO:0043279	0.646	0.742	1	10	response to alkaloid	BP	1	PRKCE	up_ACOR_VSMC
GO:0070198	0.646	0.742	1	10	protein localization to chromosome, telomeric	BP	1	ATRX	up_ACOR_VSMC
GO:0008542	0.646	0.738	1	13	visual learning	BP	1	HIF1A	up_VCAV_EC
GO:0071675	0.646	0.737	1	13	regulation of mononuclear cell	BP	1	HMGB1	up_VCAV_EC
GO:0070925	0.646	0.73	1	293	organelle assembly	BP	1	MYBPC2	up_VPUL_EC
GO:0006743	0.646	0.742	1	10	ubiquinone metabolic process	BP	1	COQ9	up_VSAP_EC
GO:0006744	0.646	0.742	1	10	ubiquinone biosynthetic process	BP	1	COQ9	up_VSAP_EC
GO:0003171	0.646	0.742	1	10	atrioventricular valve development	BP	1	TGFBR2	up_VSAP_EC
GO:0071157	0.646	0.742	1	10	negative regulation of cell cycle arrest	BP	1	CDK9	up_VSAP_EC
GO:0097345	0.646	0.742	1	10	mitochondrial outer membrane	BP	1	ZNF205	up_VSAP_EC
GO:1901663	0.646	0.742	1	10	quinone biosynthetic process	BP	1	COQ9	up_VSAP_EC
GO:0044249	0.646296968	0.4189	47	1851	cellular biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PORCN,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PTGDS,GUCY1B1,PIAS1,CHPT1,MAVS,FOXC2,PIGS,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,AZIN2,AGPAT2,PRKCD,PM20D1,EFEMP1,TLE2	up_ACOR_EC
GO:0009891	0.64662308	0.46475	13	521	positive regulation of biosynthetic process	BP	1	CDH3,NR1H4,GATA4,PKIB,SOX9,FZD5,CCDC3,RASL11A,NOD2,SMAD6,MAVS,TP53INP2,PRKCD	up_ACOR_EC

GO:0034248	0.646911955	0.57836	3	125	regulation of cellular amide metabolic process	BP	1	NR1H4,KLHL25,PRKCD	up_ACOR_EC
GO:1903829	0.647	0.496	8	91	positive regulation of cellular protein	BP	1	CDH1,GLIS2,ICE1,PIK3R1,LRP4,KCNB1,STX4,MAVS	up_VSAP_EC
GO:0006402	0.647	0.517	6	77	mRNA catabolic process	BP	1	TENT2,CNOT6,PAN3,CNOT7,SMG7,DCP2	up_VCAV_EC
GO:0006357	0.647	0.553	4	547	regulation of transcription by RNA polymerase II	BP	1	BARX1,ARHGEF2,ACVR2A,MTDH	up_VPOR_EC
GO:0048592	0.647	0.581	3	53	eye morphogenesis	BP	1	BCAR3,HIF1A,CTNNB1	down_VSAP_EC
GO:0050856	0.647	0.738	1	12	regulation of T cell receptor signaling	BP	1	EZR	down_ACOR_VSMC
GO:0035272	0.647	0.73	1	21	exocrine system development	BP	1	SEMA3C	down_VCAV_EC
GO:0043331	0.647	0.73	1	20	response to dsRNA	BP	1	MAVS	down_VCAV_EC
GO:1901019	0.647	0.731	1	20	regulation of calcium ion transmembrane transporter activity	BP	1	CACNB3	down_VCAV_EC
GO:0033363	0.647	0.741	1	10	secretory granule organization	BP	1	ABCA1	up_ACOR_VSMC
GO:0036003	0.647	0.741	1	10	positive regulation of transcription from RNA polymerase II promoter in response to stress	BP	1	CHD6	up_ACOR_VSMC
GO:0038179	0.647	0.741	1	10	neurotrophin signaling pathway	BP	1	TMEM108	up_ACOR_VSMC
GO:0046164	0.647	0.739	1	11	alcohol catabolic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0002052	0.647	0.743	1	9	positive regulation of neuroblast proliferation	BP	1	HIF1A	up_VCAV_EC
GO:0060045	0.647	0.739	1	11	positive regulation of cardiac muscle cell	BP	1	MEF2C	up_VCAV_EC
GO:0032940	0.647	0.728	1	231	secretion by cell	BP	1	TLR2	up_VSAP_VSMC
GO:2000112	0.648	0.394	104	1119	regulation of cellular macromolecule biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,PYM1,F2RL1,RBL2,GLIS2,DDR2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,ANKHD1,TRERF1,E2F4,NPAS2,LIMD1,RPUSD4,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772,SOAT1	up_VSAP_EC
GO:0043549	0.648	0.439	22	244	regulation of kinase activity	BP	1	MAP3K14,ARHGEF5,CEP85,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,CAMKK2,AMBRA1,RBL2,DDR2,TRAF7,PIK3R1,PIK3IP1,RTN4RL1,SASH1,FBXO7,MAP2K2,TGFBR2,LATS2	up_VSAP_EC
GO:0090407	0.648	0.453	16	177	organophosphate biosynthetic process	BP	1	ACACB,NADK,PPIP5K1,PDK2,GALK1,PLA2G6,MOCOS,LCAT,ACSS2,MVK,PNPO,DCAKD,ENSCAFG00000013366,PNP,IDH1,DDIT4	up_VSAP_EC
GO:0009314	0.648	0.492	8	143	response to radiation	BP	1	PLK3,BHLHE40,HIF1A,GNAQ,CRYAB,EIF2S1,RDH11,CDKN1A	down_VSAP_EC
GO:0031349	0.648	0.504	7	90	positive regulation of defense response	BP	1	HMGB1,IRAK1,CAV1,CACTIN,HMGB2,RBM14,POLR3F	down_ACOR_VSMC
GO:0060271	0.648	0.53	5	89	cilium assembly	BP	1	EXOC5,RPGR,DYNLL1,HTT,DISC1	down_VSAP_EC
GO:0031056	0.648	0.553	4	50	regulation of histone modification	BP	1	SREBF1,BRCA1,NOC2L,TADA2A	down_ACOR_VSMC
GO:0032271	0.648	0.551	4	73	regulation of protein polymerization	BP	1	ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0071704	0.648	0.625	4	3535	organic substance metabolic process	BP	1	HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0006468	0.648	0.552	4	544	protein phosphorylation	BP	1	ARHGEF2,ASPN,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0051171	0.648	0.573	4	1697	regulation of nitrogen compound metabolic	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0032479	0.648	0.584	3	33	regulation of type I interferon production	BP	1	PLCG2,TLR3,PTPN22	up_ACOR_VSMC

GO:0045807	0.648	0.584	3	35	positive regulation of endocytosis	BP	1	PLCG2,F2RL1,B2M	up_ACOR_VSMC
GO:0016052	0.648	0.584	3	34	carbohydrate catabolic process	BP	1	DHDH,GALK1,DDIT4	up_VSAP_EC
GO:0051494	0.648	0.628	2	44	negative regulation of cytoskeleton organization	BP	1	CLIP3,PLEKHH2	down_VCAV_EC
GO:0043207	0.648	0.726	1	216	response to external biotic stimulus	BP	1	LYN	down_ACOR_EC
GO:0051707	0.648	0.726	1	216	response to other organism	BP	1	LYN	down_ACOR_EC
GO:0019229	0.648	0.736	1	12	regulation of vasoconstriction	BP	1	CAV1	down_ACOR_VSMC
GO:1902692	0.648	0.738	1	11	regulation of neuroblast proliferation	BP	1	ASPM	down_ACOR_VSMC
GO:0008088	0.648	0.729	1	21	axo-dendritic transport	BP	1	MGARP	down_VCAV_EC
GO:0033554	0.648	0.739	1	708	cellular response to stress	BP	1	EYA1	up_AFEM_VSMC
GO:0030334	0.648	0.727	1	267	regulation of cell migration	BP	1	TBX5	up_APUL_EC
GO:0048663	0.648	0.735	1	13	neuron fate commitment	BP	1	DLL4	up_VCAV_EC
GO:0071407	0.648	0.725	1	129	cellular response to organic cyclic compound	BP	1	RNF6	up_VPOR_EC
GO:0000165	0.648	0.727	1	236	MAPK cascade	BP	1	CAV1	up_VSAP_VSMC
GO:0012501	0.649	0.409	52	561	programmed cell death	BP	1	THRB,WNT11,CD274,ACKR3,MAP3K14,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,DFFB,PDK2,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,HIC1,PTPMT1,ENSCAFG00000011993,PRMT2,KDM2B,RAF1,ZNF205,XKR8,STX4,QARS,ARHGAP10,HTRA2,NCK1,KRCC1,HMOX1,MAP2K2,TGFBR2,CITED2,CASP12,TRADD,DEDD2,DDIT4,LATS2	up_VSAP_EC
GO:0006915	0.649	0.409	51	550	apoptotic process	BP	1	THRB,WNT11,CD274,ACKR3,MAP3K14,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,DFFB,PDK2,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,HIC1,PTPMT1,PRMT2,KDM2B,RAF1,ZNF205,XKR8,STX4,QARS,ARHGAP10,HTRA2,NCK1,KRCC1,HMOX1,MAP2K2,TGFBR2,CITED2,CASP12,TRADD,DEDD2,DDIT4,LATS2	up_VSAP_EC
GO:0030031	0.649	0.459	14	155	cell projection assembly	BP	1	ACTN2,EVI5L,WASF3,ARHGEF26,IFT43,F2RL1,NRP1,EVL,SSH3,ASAP1,DISC1,ATXN10,INPP5K,ENSCAFG00000013536	up_ACOR_VSMC
GO:0044238	0.649	0.493	14	3383	primary metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CYP26B1,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0042060	0.649	0.485	9	103	wound healing	BP	1	HNF4A,KLKB1,PDGFD,HPSE,F2RL1,HPS4,FBLN1,ACVRL1,HMOX1	up_VSAP_EC
GO:0097659	0.649	0.497	8	1072	nucleic acid-templated transcription	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0009127	0.649	0.552	4	47	purine nucleoside monophosphate biosynthetic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0009168	0.649	0.552	4	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0008360	0.649	0.552	4	46	regulation of cell shape	BP	1	WASF3,CDC42EP5,CDC42EP2,LIMD1	up_VSAP_EC
GO:0032412	0.649	0.552	4	46	regulation of ion transmembrane	BP	1	KCNE3,OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0001818	0.649	0.578	3	65	negative regulation of cytokine production	BP	1	PRNP,CHID1,BPI	down_VCAV_EC
GO:0044267	0.649	0.601	3	1583	cellular protein metabolic process	BP	1	CST3,MGAT4B,GBGT1	down_VPOR_EC
GO:0032006	0.649	0.579	3	52	regulation of TOR signaling	BP	1	SESN2,HIF1A,SEC13	down_VSAP_EC
GO:0009266	0.649	0.626	2	43	response to temperature stimulus	BP	1	TRPV2,SCARA5	down_VCAV_EC
GO:0050707	0.649	0.627	2	44	regulation of cytokine secretion	BP	1	GPAM,MAVS	down_VCAV_EC
GO:0031047	0.649	0.629	2	33	gene silencing by RNA	BP	1	CNOT7,SND1	down_VSAP_EC
GO:0033627	0.649	0.633	2	22	cell adhesion mediated by integrin	BP	1	FERMT1,NPNT	up_ACOR_VSMC

GO:0035914	0.649	0.633	2	22	skeletal muscle cell differentiation	BP	1	CITED2,ANKRD1	up_ACOR_VSMC
GO:0060968	0.649	0.633	2	23	regulation of gene silencing	BP	1	PPP3CA,UHRF2	up_VCAV_EC
GO:0050891	0.649	0.736	1	12	multicellular organismal water homeostasis	BP	1	STMN1	down_ACOR_VSMC
GO:2001222	0.649	0.737	1	11	regulation of neuron migration	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0006893	0.649	0.729	1	20	Golgi to plasma membrane transport	BP	1	RAB31	down_VCAV_EC
GO:0051972	0.649	0.729	1	20	regulation of telomerase activity	BP	1	GREM1	down_VCAV_EC
GO:0000281	0.649	0.73	1	18	mitotic cytokinesis	BP	1	ANLN	down_VSAP_EC
GO:0021602	0.649	0.731	1	16	cranial nerve morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0060428	0.649	0.731	1	17	lung epithelium development	BP	1	ERRFI1	down_VSAP_EC
GO:1904036	0.649	0.739	1	10	negative regulation of epithelial cell apoptotic	BP	1	WFS1	up_ACOR_VSMC
GO:0098742	0.649	0.724	1	44	cell-cell adhesion via plasma-membrane	BP	1	CDH18	up_AFEM_EC
GO:0032880	0.649	0.726	1	266	regulation of protein localization	BP	1	NR1H4	up_APUL_EC
GO:0001759	0.649	0.734	1	13	organ induction	BP	1	BMP2	up_VCAV_EC
GO:0071825	0.649	0.735	1	12	protein-lipid complex subunit organization	BP	1	ABCA1	up_VCAV_EC
GO:0071827	0.649	0.735	1	12	plasma lipoprotein particle organization	BP	1	ABCA1	up_VCAV_EC
GO:0034097	0.649	0.725	1	238	response to cytokine	BP	1	MME	up_VFEM_EC
GO:0002684	0.649	0.726	1	239	positive regulation of immune system process	BP	1	TOX	up_VFEM_EC
GO:0030029	0.649	0.726	1	239	actin filament-based process	BP	1	CAV1	up_VSAP_VSMC
GO:0009145	0.649488229	0.72389	1	40	purine nucleoside triphosphate biosynthetic	BP	1	ALDOC	up_ACOR_EC
GO:0045893	0.65	0.483	9	413	positive regulation of transcription, DNA-	BP	1	HOXA9,LBH,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0072507	0.65	0.492	8	103	divalent inorganic cation homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0006732	0.65	0.526	5	107	coenzyme metabolic process	BP	1	GPAM,H6PD,PGLS,ACSS2,ACAT1	down_VCAV_EC
GO:0007249	0.65	0.548	4	71	I-kappaB kinase/NF-kappaB signaling	BP	1	NR1H4,MTDH,CTNNB1,BTK	down_VSAP_EC
GO:0046916	0.65	0.581	3	35	cellular transition metal ion homeostasis	BP	1	EGLN1,ATP7A,APP	up_ACOR_VSMC
GO:1901863	0.65	0.631	2	25	positive regulation of muscle tissue	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0051851	0.65	0.632	2	23	modification by host of symbiont morphology or	BP	1	F2RL1,INPP5K	up_ACOR_VSMC
GO:0001824	0.65	0.63	2	27	blastocyst development	BP	1	SKIL,GINS4	up_VCAV_EC
GO:0051148	0.65	0.734	1	12	negative regulation of muscle cell differentiation	BP	1	EZH2	down_ACOR_VSMC
GO:0006929	0.65	0.738	1	10	substrate-dependent cell migration	BP	1	NRP1	up_ACOR_VSMC
GO:0007143	0.65	0.737	1	10	female meiotic nuclear division	BP	1	MARF1	up_ACOR_VSMC
GO:0001702	0.65	0.737	1	10	gastrulation with mouth forming second	BP	1	FRS2	up_ACOR_VSMC
GO:0033144	0.65	0.738	1	10	negative regulation of intracellular steroid hormone receptor	BP	1	LBH	up_ACOR_VSMC
GO:1902108	0.65	0.732	1	14	regulation of mitochondrial membrane permeability involved in	BP	1	SH3GLB1	up_VCAV_EC
GO:0043549	0.65	0.725	1	244	regulation of kinase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0051336	0.650424177	0.51024	6	251	regulation of hydrolase activity	BP	1	PCSK1N,IFI6,DYNC1I1,CST3,PRKCD,PPP1R26	up_ACOR_EC
GO:0042127	0.651	0.417	36	452	regulation of cell proliferation	BP	1	HMGB1,HMGA1,MNDA,HOXA3,SLC25A5,CDCA7L,BIRC5,PRMT1,CAV1,FAM129B,NF2,CDKN2C,EZH2,GREM1,CDK4,RNASEH2B,ARG2,PDCD2,MVD,B4GALT1,TFRC,NRAS,PPARD,NUP62,EMP2,HMGB2,CDK2,SMARCB1,ENSCAFG00000005299,CORO1A,ASPM,GLI1,TINF2,HMGN1,SIX4,MTBP	down_ACOR_VSMC

GO:0040008	0.651	0.456	14	179	regulation of growth	BP	1	IFRD1,CDA,MEF2C,CHD7,EDN1,RAB11A,IRF8,MTOR,PROX1,SMARCA4,CREB1,VPS54,SPTBN4,HIF1A	up_VCAV_EC
GO:0032774	0.651	0.496	8	1073	RNA biosynthetic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,CCAR1,RNF6	up_VPOR_EC
GO:0032259	0.651	0.547	4	71	methylation	BP	1	NR1H4,IWS1,PRMT1,KDM3A	down_VSAP_EC
GO:1901800	0.651	0.55	4	46	positive regulation of proteasomal protein catabolic process	BP	1	SH3RF2,RNF19A,PSEN1,HERPUD1	up_ACOR_VSMC
GO:0072521	0.651	0.545	4	185	purine-containing compound metabolic	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0022904	0.651	0.578	3	43	respiratory electron transport chain	BP	1	CDK1,CYCS,CYC1	down_ACOR_VSMC
GO:0007154	0.651	0.599	3	1622	cell communication	BP	1	HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0050808	0.651	0.622	2	93	synapse organization	BP	1	DMPK,TNC	up_AFEM_EC
GO:0065008	0.651	0.64	2	1056	regulation of biological quality	BP	1	HOXA3,SLIT2	up_VPUL_VSMC
GO:0042981	0.651	0.729	1	471	regulation of apoptotic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0048538	0.651	0.727	1	20	thymus development	BP	1	LMO4	down_VCAV_EC
GO:1903573	0.651	0.727	1	20	negative regulation of response to endoplasmic	BP	1	PARK7	down_VCAV_EC
GO:0042474	0.651	0.734	1	11	middle ear morphogenesis	BP	1	EDN1	up_ACOR_VSMC
GO:0060765	0.651	0.737	1	10	regulation of androgen receptor signaling	BP	1	PARK7	up_ACOR_VSMC
GO:0022904	0.651	0.722	1	43	respiratory electron transport chain	BP	1	PPARGC1A	up_AFEM_EC
GO:0048588	0.651	0.722	1	44	developmental cell growth	BP	1	PLXNA4	up_AFEM_EC
GO:0009649	0.651	0.732	1	13	entrainment of circadian clock	BP	1	ENSCAFG00000010596	up_VCAV_EC
GO:1900006	0.651	0.735	1	11	positive regulation of dendrite development	BP	1	RELN	up_VCAV_EC
GO:0000122	0.652	0.473	10	218	negative regulation of transcription by RNA polymerase II	BP	1	KANK2,NR3C1,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,TSC22D3,GLIS2,THRB	down_VCAV_EC
GO:0061025	0.652	0.513	6	69	membrane fusion	BP	1	USP6NL,SYT16,EVI5L,MX1,STX11,SGSM2	up_ACOR_VSMC
GO:0007165	0.652	0.524	6	1496	signal transduction	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0002263	0.652	0.574	3	68	cell activation involved in immune response	BP	1	LRP1,LOXL3,RAC2	down_VCAV_EC
GO:0031327	0.652	0.575	3	412	negative regulation of cellular biosynthetic	BP	1	ENSCAFG00000002015,FBP1,MTDH	up_VPOR_EC
GO:0071326	0.652	0.628	2	26	cellular response to monosaccharide stimulus	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0071331	0.652	0.628	2	26	cellular response to hexose stimulus	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0097581	0.652	0.628	2	26	lamellipodium organization	BP	1	FSCN1,RAC1	down_ACOR_VSMC
GO:0040011	0.652	0.626	2	505	locomotion	BP	1	EMX2,CAV1	up_VSAP_VSMC
GO:0042088	0.652	0.732	1	12	T-helper 1 type immune response	BP	1	HMGB1	down_ACOR_VSMC
GO:0002686	0.652	0.733	1	12	negative regulation of leukocyte migration	BP	1	HOXA7	down_ACOR_VSMC
GO:0050764	0.652	0.731	1	13	regulation of phagocytosis	BP	1	HMGB1	down_ACOR_VSMC
GO:0071622	0.652	0.73	1	13	regulation of granulocyte chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:1902110	0.652	0.732	1	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	SLC25A5	down_ACOR_VSMC
GO:1902686	0.652	0.732	1	12	mitochondrial outer membrane permeabilization involved	BP	1	SLC25A5	down_ACOR_VSMC
GO:0001756	0.652	0.728	1	17	somitogenesis	BP	1	TMED2	down_VSAP_EC
GO:0043299	0.652	0.727	1	18	leukocyte degranulation	BP	1	LYN	down_VSAP_EC
GO:0001841	0.652	0.721	1	44	neural tube formation	BP	1	LUZP1	up_AFEM_EC
GO:0022612	0.652	0.721	1	44	gland morphogenesis	BP	1	TNC	up_AFEM_EC

GO:0051494	0.652	0.72	1	44	negative regulation of cytoskeleton organization	BP	1	KANK1	up_AFEM_EC
GO:0007010	0.652	0.727	1	441	cytoskeleton organization	BP	1	TAOK1	up_AORT_EC
GO:0007017	0.652	0.724	1	273	microtubule-based process	BP	1	TUBB4A	up_APUL_EC
GO:0014002	0.652	0.734	1	11	astrocyte development	BP	1	TLR4	up_VCAV_EC
GO:0022411	0.652	0.72	1	130	cellular component disassembly	BP	1	ARHGEF2	up_VPOR_EC
GO:0032970	0.652	0.721	1	130	regulation of actin filament-based process	BP	1	TWF1	up_VPOR_EC
GO:0010629	0.652	0.73	1	502	negative regulation of gene expression	BP	1	GATA5	up_VPUL_VSMC
GO:0030031	0.653	0.463	12	155	cell projection assembly	BP	1	KIT,PODXL,MTOR,NCKAP1,ENSCAFG00000010224,NCK1,EXOC5,RAPGEF2,ITGA6,IQUB,SPATA6,FSCN1	up_VCAV_EC
GO:0043085	0.653	0.496	7	323	positive regulation of catalytic activity	BP	1	LEP,F3,GREM1,RASGEF1B,DCUN1D3,CCL5,ADAM17	up_AFEM_EC
GO:0060070	0.653	0.509	6	105	canonical Wnt signaling pathway	BP	1	PRICKLE1,ILK,CTNNB1,APOE,DDIT3,DISC1	down_VSAP_EC
GO:0007179	0.653	0.527	5	57	transforming growth factor beta receptor	BP	1	ZEB1,HPGD,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0010675	0.653	0.548	4	46	regulation of cellular carbohydrate metabolic	BP	1	LEP,PRKCE,DDIT4,INPP5K	up_ACOR_VSMC
GO:0010565	0.653	0.577	3	40	regulation of cellular ketone metabolic process	BP	1	BMP2,PROX1,PTGS2	up_VCAV_EC
GO:0001764	0.653	0.622	2	45	neuron migration	BP	1	NDN,PEX5	down_VCAV_EC
GO:0043154	0.653	0.628	2	23	negative regulation of cysteine-type endopeptidase activity	BP	1	SH3RF1,PARK7	up_ACOR_VSMC
GO:0060968	0.653	0.629	2	23	regulation of gene silencing	BP	1	ZC3H10,LIMD1	up_VSAP_EC
GO:0021782	0.653	0.628	2	23	glial cell development	BP	1	WASF3,DLL1	up_VSAP_EC
GO:0097306	0.653	0.724	1	22	cellular response to alcohol	BP	1	ADCY6	down_VCAV_EC
GO:0015031	0.653	0.729	1	510	protein transport	BP	1	RAB11B	down_VPOR_EC
GO:1904035	0.653	0.727	1	16	regulation of epithelial cell apoptotic process	BP	1	SERPINE1	down_VSAP_EC
GO:0002097	0.653	0.733	1	11	tRNA wobble base modification	BP	1	TRMT9B	up_ACOR_VSMC
GO:0022408	0.653	0.72	1	44	negative regulation of cell-cell adhesion	BP	1	CYLD	up_AFEM_EC
GO:0045619	0.653	0.72	1	44	regulation of lymphocyte differentiation	BP	1	CYLD	up_AFEM_EC
GO:0030104	0.653	0.73	1	13	water homeostasis	BP	1	STMN1	up_VCAV_EC
GO:0034661	0.653	0.731	1	12	ncRNA catabolic process	BP	1	TENT2	up_VCAV_EC
GO:0051656	0.653	0.719	1	129	establishment of organelle localization	BP	1	HOOK3	up_VPOR_EC
GO:0022402	0.653	0.726	1	407	cell cycle process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0006885	0.653216699	0.72014	1	39	regulation of pH	BP	1	SLC9A9	up_ACOR_EC
GO:0043524	0.653273831	0.72008	1	39	negative regulation of neuron apoptotic process	BP	1	NRP1	up_ACOR_EC
GO:0010468	0.654	0.395	75	1270	regulation of gene expression	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,MYH9,NR1H4,PLK3,SERPINE1,ETV6,MEIS2,PRKACB,CBX5,AARS,TMED2,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,MSN,HIF1A,IWS1,ACTG2,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,APOE,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,CDC37,GTF2H1,ARMCX3,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,GLO1,CDYL,A2M,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0010608	0.654	0.462	12	154	posttranscriptional regulation of gene	BP	1	MOV10,QKI,PPP3CA,MTOR,TENT2,TUT7,ENC1,SECISBP2L,NCK1,DPH5,CNOT7,SMG7	up_VCAV_EC
GO:0009636	0.654	0.524	5	66	response to toxic substance	BP	1	PPP1R15B,TIMELESS,EZH2,GSTO1,SIGMAR1	down_ACOR_VSMC
GO:0031929	0.654	0.525	5	62	TOR signaling	BP	1	RELN,GATA3,MTOR,PREX2,HIF1A	up_VCAV_EC

GO:0030178	0.654	0.546	4	52	negative regulation of Wnt signaling pathway	BP	1	CAV1,GREM1,GLI1,AMER1	down_ACOR_VSMC
GO:0045017	0.654	0.546	4	52	glycerolipid biosynthetic process	BP	1	ACSL3,SREBF1,CTDNEP1,VAC14	down_ACOR_VSMC
GO:0048522	0.654	0.594	3	1484	positive regulation of cellular process	BP	1	GPSM2,SRSF6,FSCN1	down_AFEM_EC
GO:0034440	0.654	0.577	3	35	lipid oxidation	BP	1	LEP,PPARGC1A,ACAD11	up_ACOR_VSMC
GO:0010033	0.654	0.579	3	772	response to organic substance	BP	1	MME,AVPR1A,CYP26B1	up_VFEM_EC
GO:0060402	0.654	0.578	3	35	calcium ion transport into cytosol	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0045005	0.654	0.628	2	21	DNA-dependent DNA replication maintenance	BP	1	ATRX,ZNF365	up_ACOR_VSMC
GO:0071214	0.654	0.618	2	93	cellular response to abiotic stimulus	BP	1	CRYAB,MFAP4	up_AFEM_EC
GO:0104004	0.654	0.618	2	93	cellular response to environmental stimulus	BP	1	CRYAB,MFAP4	up_AFEM_EC
GO:0007165	0.654	0.648	2	1496	signal transduction	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0051588	0.654	0.625	2	28	regulation of neurotransmitter	BP	1	MEF2C,SNCAIP	up_VCAV_EC
GO:0097205	0.654	0.73	1	12	renal filtration	BP	1	EMP2	down_ACOR_VSMC
GO:0016126	0.654	0.723	1	20	sterol biosynthetic process	BP	1	CYB5R3	down_VCAV_EC
GO:0009891	0.654	0.728	1	521	positive regulation of biosynthetic process	BP	1	CITED2	down_VPOR_EC
GO:0032273	0.654	0.718	1	44	positive regulation of protein polymerization	BP	1	CDC42EP5	up_AFEM_EC
GO:0050707	0.654	0.719	1	44	regulation of cytokine secretion	BP	1	GPAM	up_AFEM_EC
GO:0000132	0.654	0.732	1	11	establishment of mitotic spindle orientation	BP	1	ZW10	up_VCAV_EC
GO:0051294	0.654	0.732	1	11	establishment of spindle orientation	BP	1	ZW10	up_VCAV_EC
GO:0021772	0.654	0.731	1	11	olfactory bulb development	BP	1	SLIT2	up_VSAP_EC
GO:0021988	0.654	0.731	1	11	olfactory lobe development	BP	1	SLIT2	up_VSAP_EC
GO:0030097	0.654	0.72	1	244	hemopoiesis	BP	1	HOXA9	up_VSAP_VSMC
GO:0009893	0.654373339	0.42816	25	995	positive regulation of metabolic process	BP	1	CDH3,NR1H4,GATA4,PKIB,SOX9,ENSCAFG00000004331,EDEM2,FZD5,CCDC3,DUSP26,RASL11A,NOD2,SMAD6,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,TP53INP2,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0032268	0.655	0.394	72	778	regulation of cellular protein metabolic process	BP	1	ADRA1B,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,MBP,RECK,SKP2,PRKAA2,BMP4,FGFR2,ATRX,TLR3,SH3RF2,LATS2,PDE5A,ISG15,SASH1,PTPN3,FGF18,NDRG2,CDKN2B,CST3,F2RL1,FAM129A,DAPK1,RBM4B,CDKN1A,NRP1,PTPN22,NPNT,OS9,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,RNF19A,DAG1,PARP9,APP,PSEN1,SYNJ2BP,SPINK2,CCL5,DDR2,PERP,DUSP22,EDN1,OXR1,AKTIP,DUSP26,NOD2,LRRC4,FAM107A,PRKAG3,DISC1,SH3RF3,DCUN1D4,HERPUD1,MAP3K7,INPP5K,WFS1,WDR48,CTIF,ENSCAFG00000029553,PARK7,NGRN,CRKL	up_ACOR_VSMC
GO:1902680	0.655	0.476	9	415	positive regulation of RNA biosynthetic process	BP	1	HOXA9,LBH,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:1903508	0.655	0.476	9	415	positive regulation of nucleic acid-templated	BP	1	HOXA9,LBH,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0006874	0.655	0.496	7	91	cellular calcium ion homeostasis	BP	1	HMGB1,CAV1,SLC30A1,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0051100	0.655	0.544	4	53	negative regulation of binding	BP	1	CAV1,AURKB,STMN1,NEK2	down_ACOR_VSMC
GO:1903531	0.655	0.575	3	41	negative regulation of secretion by cell	BP	1	ARG2,RSC1A1,CD200	up_VCAV_EC
GO:1901292	0.655	0.576	3	34	nucleoside phosphate catabolic process	BP	1	GALK1,ENTPD3,DDIT4	up_VSAP_EC
GO:0008150	0.655	1	2	5646	biological_process	BP	1	SCAMP4,CST3	down_AORT_EC
GO:0051147	0.655	0.62	2	44	regulation of muscle cell differentiation	BP	1	RBM38,GREM1	down_VCAV_EC
GO:0090307	0.655	0.625	2	26	mitotic spindle assembly	BP	1	RAB11A,MZT1	up_VCAV_EC
GO:0045071	0.655	0.729	1	12	negative regulation of viral genome replication	BP	1	ILF3	down_ACOR_VSMC

GO:0061045	0.655	0.73	1	12	negative regulation of wound healing	BP	1	TFPI	down_ACOR_VSMC
GO:0021536	0.655	0.722	1	21	diencephalon development	BP	1	BMPR1A	down_VCAV_EC
GO:0090559	0.655	0.723	1	20	regulation of membrane permeability	BP	1	SLC35F6	down_VCAV_EC
GO:2000736	0.655	0.722	1	21	regulation of stem cell differentiation	BP	1	SEMA3C	down_VCAV_EC
GO:0043300	0.655	0.731	1	11	regulation of leukocyte degranulation	BP	1	F2RL1	up_ACOR_VSMC
GO:0051098	0.655	0.717	1	129	regulation of binding	BP	1	HOXA3	up_VPOR_EC
GO:0045830	0.655	0.731	1	11	positive regulation of isotype switching	BP	1	STAT6	up_VSAP_EC
GO:0043552	0.655	0.73	1	11	positive regulation of phosphatidylinositol 3-kinase activity	BP	1	AMBRA1	up_VSAP_EC
GO:0090218	0.655	0.73	1	11	positive regulation of lipid kinase activity	BP	1	AMBRA1	up_VSAP_EC
GO:0008630	0.655491556	0.71776	1	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	CLU	up_ACOR_EC
GO:0051246	0.656	0.392	77	832	regulation of protein metabolic process	BP	1	ADRA1B,TLR1,SMAD6,LEP,PLCL1,MAP3K8,MID1,HTR2B,RASSF2,MBP,FBXL20,RECK,SKP2,PRKAA2,ITM2C,BMP4,FGFR2,ATRX,TLR3,SH3RF2,LATS2,PDE5A,ISG15,SASH1,PTPN3,FGF18,NDRG2,CDKN2B,CST3,F2RL1,FAM129A,DAPK1,RBM4B,EGLN1,CDKN1A,NRP1,PTPN22,NPNT,OS9,SMPD1,SH3RF1,PRKCE,CCNT1,FRS2,RNF19A,DAG1,PARP9,APP,PSEN1,SYNJ2BP,SPINK2,CCL5,DDR2,PERP,DUSP22,EDN1,OXR1,AKTIP,DUSP26,NOD2,LRRC4,FAM107A,PRKAG3,DISC1,SH3RF3,DCUN1D4,HERPUD1,MAP3K7,INPP5K,WFS1,AZIN2,WDR48,CTIF,ENSCAFG00000029553,PARK7,NGRN,CRKL	up_ACOR_VSMC
GO:0007423	0.656	0.451	14	155	sensory organ development	BP	1	BMP4,FGFR2,GJA1,SEC24B,CITED2,NRP1,GPM6A,SMARCD3,FZD3,FRS2,CPAMD8,CHD7,CLN8,EDN1	up_ACOR_VSMC
GO:0050778	0.656	0.465	11	141	positive regulation of immune response	BP	1	HMGB1,IRAK1,MNDA,CAV1,TFRC,FAM49B,CACTIN,HMGB2,EZR,RBM14,POLR3F	down_ACOR_VSMC
GO:0001822	0.656	0.479	9	98	kidney development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NRP1,NPNT,NID1,ARID5B,WFS1	up_ACOR_VSMC
GO:0002757	0.656	0.507	6	78	immune response-activating signal	BP	1	HMGB1,IRAK1,MNDA,CAV1,CACTIN,EZR	down_ACOR_VSMC
GO:0046467	0.656	0.545	4	45	membrane lipid biosynthetic process	BP	1	CERS4,ENSCAFG00000000071,HACD4,B3GALT4	up_VSAP_EC
GO:0042770	0.656	0.575	3	35	signal transduction in response to DNA damage	BP	1	ATRX,ANKRD1,CDKN1A	up_ACOR_VSMC
GO:0070887	0.656	0.577	3	775	cellular response to chemical stimulus	BP	1	MME,AVPR1A,CYP26B1	up_VFEM_EC
GO:1901568	0.656	0.623	2	26	fatty acid derivative metabolic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0012501	0.656	0.624	2	561	programmed cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0097306	0.656	0.626	2	22	cellular response to alcohol	BP	1	CTNNA1,BLM	up_VCAV_EC
GO:0007167	0.656	0.618	2	274	enzyme linked receptor protein signaling pathway	BP	1	ASPN,ACVR2A	up_VPOR_EC
GO:0051247	0.656	0.622	2	502	positive regulation of protein metabolic process	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0006221	0.656	0.728	1	12	pyrimidine nucleotide biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0009057	0.656	0.725	1	473	macromolecule catabolic process	BP	1	USP33	down_AFEM_EC
GO:0090049	0.656	0.721	1	21	regulation of cell migration involved in sprouting angiogenesis	BP	1	SPRED1	down_VCAV_EC
GO:1902017	0.656	0.721	1	21	regulation of cilium assembly	BP	1	EVI5L	down_VCAV_EC
GO:0009303	0.656	0.725	1	16	rRNA transcription	BP	1	SMARCA4	down_VSAP_EC
GO:0007200	0.656	0.723	1	18	phospholipase C-activating G protein-coupled receptor signaling	BP	1	GNAQ	down_VSAP_EC
GO:1900015	0.656	0.723	1	17	regulation of cytokine production involved in inflammatory response	BP	1	GBP5	down_VSAP_EC
GO:1904894	0.656	0.723	1	17	positive regulation of STAT cascade	BP	1	LYN	down_VSAP_EC

GO:0046039	0.656	0.729	1	11	GTP metabolic process	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:1901068	0.656	0.729	1	11	guanosine-containing compound metabolic	BP	1	ENSCAFG00000018611	up_ACOR_VSMC
GO:0097164	0.656	0.717	1	44	ammonium ion metabolic process	BP	1	MOXD1	up_AFEM_EC
GO:0045992	0.656	0.728	1	12	negative regulation of embryonic development	BP	1	GATA3	up_VCAV_EC
GO:0055086	0.656	0.719	1	237	nucleobase-containing small molecule metabolic	BP	1	ADCY3	up_VFEM_EC
GO:0043436	0.656	0.72	1	303	oxoacid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0043543	0.656073028	0.61617	2	84	protein acylation	BP	1	PHF20,PORCN	up_ACOR_EC
GO:0010565	0.656776927	0.71628	1	40	regulation of cellular ketone metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0043170	0.657	0.382	175	2980	macromolecule metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,ENSCAFG00000032470,TRIB3,PGAM1,TMED2,PUM3,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,HIF1A,FOXP4,USP12,MRPL1,IWS1,DNAJC10,ACTG2,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,UCHL5,MORF4L2,SPOPL,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,GTF2H1,ARMCX3,CUL2,HTT,REST,RBBP8,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,NR4A2,EXT1,SPOP,CALM1,GLO1,DISC1,ENSCAFG00000015065,RAD23A,CDYL,PAK2,LRRTM2,A2M,INHBA,LRRFIP2,CAMK2D,BCAS2,NR4A	down_VSAP_EC
GO:0044267	0.657	0.382	123	1583	cellular protein metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,ST8SIA6,KIT,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,CTSC,PDE4D,IWS1,MEF2C,ATF3,TIPARP,RAPGEF1,WWP1,TLR4,QKI,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,ZDHHC22,PSME4,NEDD9,PELI1,YES1,ENSCAFG00000010893,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,ENSCAFG00000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,TLR3,MFNG,NCK1,ESCO1,DPH5,VHL,OTUD4,WSB1,PARP4,FES,NSD1,MRRF,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,HMGB1,NOS2,PMAIP1,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,KDM3A,LMTK2,ATRX,RBBP6,ZDHHC6,TNFAIP1,IVNS1ABP,JCAD,PSMB9,PSMD12,TET2,ARHGEF2,ITCH,CDON	up_VCAV_EC
GO:0007283	0.657	0.484	8	91	spermatogenesis	BP	1	PRDX4,ATRX,AFF4,SPINK2,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0072522	0.657	0.485	8	91	purine-containing compound biosynthetic	BP	1	ACACB,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,PNP,DDIT4	up_VSAP_EC
GO:1901361	0.657	0.492	7	154	organic cyclic compound catabolic process	BP	1	MAOA,SAMD4B,ENTPD3,ZFP36L1,PYM1,FBH1,ACAT1	down_VCAV_EC
GO:0009152	0.657	0.495	7	80	purine ribonucleotide biosynthetic process	BP	1	ACACB,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0060541	0.657	0.54	4	73	respiratory system development	BP	1	ERRFI1,CTNNB1,PLOD3,SIX4	down_VSAP_EC
GO:0019438	0.657	0.553	4	1258	aromatic compound biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0006914	0.657	0.567	3	141	autophagy	BP	1	LEP,CLEC16A,RAB7A	up_AFEM_EC
GO:0061919	0.657	0.567	3	141	process utilizing autophagic mechanism	BP	1	LEP,CLEC16A,RAB7A	up_AFEM_EC

GO:1905897	0.657	0.574	3	34	regulation of response to endoplasmic reticulum	BP	1	PIK3R1,UBQLN2,NCK1	up_VSAP_EC
GO:0045580	0.657	0.62	2	35	regulation of T cell differentiation	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:0010628	0.657	0.724	1	527	positive regulation of gene expression	BP	1	CITED2	down_VPOR_EC
GO:0035329	0.657	0.723	1	16	hippo signaling	BP	1	WWC3	down_VSAP_EC
GO:0001895	0.657	0.73	1	10	retina homeostasis	BP	1	CLN8	up_ACOR_VSMC
GO:0051181	0.657	0.728	1	11	cofactor transport	BP	1	TCN2	up_ACOR_VSMC
GO:0099601	0.657	0.731	1	10	regulation of neurotransmitter	BP	1	DAPK1	up_ACOR_VSMC
GO:0008631	0.657	0.725	1	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	HIF1A	up_VCAV_EC
GO:0016055	0.657	0.714	1	134	Wnt signaling pathway	BP	1	BARX1	up_VPOR_EC
GO:0198738	0.657	0.714	1	134	cell-cell signaling by wnt	BP	1	BARX1	up_VPOR_EC
GO:0032607	0.657	0.729	1	11	interferon-alpha production	BP	1	MAVS	up_VSAP_EC
GO:0043549	0.657	0.717	1	244	regulation of kinase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0016202	0.657011101	0.71616	1	39	regulation of striated muscle tissue	BP	1	TBX5	up_ACOR_EC
GO:0051262	0.657402067	0.71562	1	40	protein tetramerization	BP	1	ACTN2	up_ACOR_EC
GO:0002683	0.65755957	0.56647	3	126	negative regulation of immune system process	BP	1	SOX9,MMP28,PTGER4	up_ACOR_EC
GO:0010604	0.657649677	0.42765	23	919	positive regulation of macromolecule metabolic process	BP	1	CDH3,GATA4,PKIB,SOX9,ENSCAFG00000004331,EDEM2,FZD5,DUSP26,RASL11A,NOD2,SMAD6,PAK3,TNFRSF19,PIAS1,MAVS,LRP4,SH3RF3,CLU,TP53INP2,RARRES2,RNF114,NRP1,PRKCD	up_ACOR_EC
GO:0007166	0.658	0.394	63	686	cell surface receptor signaling pathway	BP	1	FZD1,ADGRD1,CDON,WNT11,HNF4A,CD274,AXIN2,LIMS2,SLIT2,HOXD3,FGF7,ABL1,GOT1,EMP2,DLL1,EPN2,DTX2,PDGFD,ANXA4,PLXNA4,CCBE1,STAT5A,STAT6,RECK,KLHL24,PLPP3,F2RL1,GLIS2,PDK2,PIK3R1,RBCK1,FAM53B,GAS1,ZEB1,SULF2,SHOX2,HIC1,RTN4RL1,SASH1,CREBRF,MYD88,LRP4,GDPD5,TSPAN5,NCEH1,TMEM17,LIMD1,ENSCAFG00000011993,HPGD,IGFBP6,RAF1,STX4,ZFAND5,ACVRL1,HTRA2,NCK1,MAVS,HMOX1,TGFBR2,CITED2,TRADD,DEDD2,LATS2	up_VSAP_EC
GO:0006928	0.658	0.402	45	557	movement of cell or subcellular component	BP	1	FSCN1,HMGB1,ANLN,FMNL3,RACGAP1,KIF2A,SDC1,FBXO5,B3GNT2,CFAP298,CAV1,CENPE,MMP14,STMN1,GREM1,HOXA7,KIF22,B4GALT1,PRCP,PPARD,RAP2C,RAC1,EMP2,NUP188,HMGB2,TRAK1,KIF4A,KIF15,CORO1A,SGPL1,PHACTR4,ASPM,ENSCAFG00000010224,ITGA2,ARHGEF2,TWIST2,KIF11,NUS1,AMOTL1,SIX4,DEPDC1B,TTLL1,KIF21B,KIF24,PIK3CD	down_ACOR_VSMC
GO:0051254	0.658	0.41	35	431	positive regulation of RNA metabolic process	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,U2AF2,INSIG1,THRAP3,FAM129B,GREM1,SMARCC1,DHX33,SF3B4,CKS2,BRCA1,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,ENSCAFG00000017103	down_ACOR_VSMC
GO:0051051	0.658	0.469	10	112	negative regulation of transport	BP	1	C5AR2,GABRE,KCNE3,OSR1,ANXA4,F2RL1,KCNB1,MAPKBP1,UBQLN2,BAG4	up_VSAP_EC
GO:0071396	0.658	0.502	6	134	cellular response to lipid	BP	1	ADCY6,KANK2,NR3C1,PARK7,ZFP36L1,SASH1	down_VCAV_EC
GO:0002040	0.658	0.542	4	46	sprouting angiogenesis	BP	1	BMP4,NRP1,SYNJ2BP,PIK3C2A	up_ACOR_VSMC
GO:0090090	0.658	0.542	4	44	negative regulation of canonical Wnt signaling	BP	1	MLLT3,FERMT1,LATS2,ZNRF3	up_ACOR_VSMC
GO:1901362	0.658	0.586	3	1293	organic cyclic compound biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0110110	0.658	0.573	3	34	positive regulation of animal organ	BP	1	HOXA11,FGF7,TGFBR2	up_VSAP_EC
GO:0008150	0.658	1	2	5646	biological_process	BP	1	JUP,GATA5	down_VFEM_VSMC
GO:0050896	0.658	0.671	2	2346	response to stimulus	BP	1	GATA5,TGFBR1	down_VSAP_VSMC

GO:0043067	0.658	0.723	1	479	regulation of programmed cell death	BP	1	IVNS1ABP	down_AFEM_EC
GO:0051704	0.658	0.723	1	476	multi-organism process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0097061	0.658	0.72	1	21	dendritic spine organization	BP	1	PRNP	down_VCAV_EC
GO:0002275	0.658	0.72	1	18	myeloid cell activation involved in immune	BP	1	LYN	down_VSAP_EC
GO:1902807	0.658	0.721	1	18	negative regulation of cell cycle G1/S phase	BP	1	CDKN1A	down_VSAP_EC
GO:1903825	0.658	0.721	1	17	organic acid transmembrane transport	BP	1	SLC38A1	down_VSAP_EC
GO:1905039	0.658	0.721	1	17	carboxylic acid transmembrane transport	BP	1	SLC38A1	down_VSAP_EC
GO:2000134	0.658	0.721	1	18	negative regulation of G1/S transition of mitotic	BP	1	CDKN1A	down_VSAP_EC
GO:0006120	0.658	0.726	1	12	mitochondrial electron transport, NADH to	BP	1	PARK7	up_ACOR_VSMC
GO:0060317	0.658	0.728	1	11	cardiac epithelial to mesenchymal transition	BP	1	TGFBR1	up_ACOR_VSMC
GO:0010950	0.658	0.715	1	44	positive regulation of endopeptidase activity	BP	1	F3	up_AFEM_EC
GO:0040007	0.658	0.717	1	276	growth	BP	1	TBX5	up_APUL_EC
GO:1902533	0.658	0.717	1	271	positive regulation of intracellular signal	BP	1	NPNT	up_APUL_EC
GO:0009299	0.658	0.728	1	11	mRNA transcription	BP	1	SOX18	up_VCAV_EC
GO:0080182	0.658	0.728	1	11	histone H3-K4 trimethylation	BP	1	TET2	up_VCAV_EC
GO:0006082	0.658	0.718	1	305	organic acid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0006336	0.658	0.727	1	11	DNA replication-independent nucleosome	BP	1	CENPP	up_VSAP_EC
GO:0014002	0.658	0.728	1	11	astrocyte development	BP	1	DLL1	up_VSAP_EC
GO:1902749	0.658401185	0.7147	1	39	regulation of cell cycle G2/M phase transition	BP	1	BRSK1	up_ACOR_EC
GO:0016192	0.659	0.404	41	452	vesicle-mediated transport	BP	1	EXPH5,DNAJC6,ACTN2,PLCG2,LEP,CDC7,HTR2B,USP6NL,FBXL20,SYT16,EVI5L,ABCA1,SEC24B,ATXN2,STX11,TMEM108,KLHL20,F2RL1,LRPAP1,MYO1B,APP,PSEN1,SGSM2,SYNJ2BP,PIK3C3,RAB11B,GTF2A1L,AKTIP,LMTK2,B2M,AP2B1,SCAMP5,SCRN2,SAR1B,TXNDC5,VPS26A,RAB5C,PREPL,BVES,LMF1,PIK3C2A	up_ACOR_VSMC
GO:0010564	0.659	0.438	17	217	regulation of cell cycle process	BP	1	PLK2,PDGFB,EDN1,RAB11A,UHRF2,SENP6,TAOK1,BLM,SMC5,RAD21,RAD17,CUL4A,ZW10,ATRX,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0009117	0.659	0.46	11	208	nucleotide metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ENTPD4,ALDOC,PAPSS1,AK5,CMPK1	down_VSAP_EC
GO:0018130	0.659	0.551	4	1261	heterocycle biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0044093	0.659	0.617	2	437	positive regulation of molecular function	BP	1	LYN,HOXA3	down_ACOR_EC
GO:0062013	0.659	0.62	2	27	positive regulation of small molecule metabolic	BP	1	SREBF1,CDK1	down_ACOR_VSMC
GO:0032273	0.659	0.616	2	44	positive regulation of protein polymerization	BP	1	KIRREL1,ACTR3B	down_VCAV_EC
GO:0051258	0.659	0.613	2	94	protein polymerization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0051963	0.659	0.62	2	26	regulation of synapse assembly	BP	1	EPHB1,MEF2C	up_VCAV_EC
GO:0042491	0.659	0.729	1	10	inner ear auditory receptor cell	BP	1	SEC24B	up_ACOR_VSMC
GO:0048488	0.659	0.729	1	10	synaptic vesicle endocytosis	BP	1	DNAJC6	up_ACOR_VSMC
GO:0071402	0.659	0.729	1	10	cellular response to lipoprotein particle	BP	1	ABCA1	up_ACOR_VSMC
GO:0140238	0.659	0.729	1	10	presynaptic endocytosis	BP	1	DNAJC6	up_ACOR_VSMC
GO:1901185	0.659	0.727	1	11	negative regulation of ERBB signaling pathway	BP	1	PSEN1	up_ACOR_VSMC
GO:0007411	0.659	0.714	1	45	axon guidance	BP	1	PLXNA4	up_AFEM_EC
GO:0097485	0.659	0.714	1	45	neuron projection guidance	BP	1	PLXNA4	up_AFEM_EC
GO:0051093	0.659	0.716	1	273	negative regulation of developmental process	BP	1	TBX5	up_APUL_EC

GO:0033344	0.659	0.725	1	12	cholesterol efflux	BP	1	ABCA1	up_VCAV_EC
GO:0048339	0.659	0.724	1	13	paraxial mesoderm development	BP	1	NUP133	up_VCAV_EC
GO:0045934	0.659	0.72	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	NKX2-5	up_VPOR_VSMC
GO:0031328	0.659	0.722	1	512	positive regulation of cellular biosynthetic	BP	1	GATA5	up_VPUL_VSMC
GO:0080182	0.659	0.727	1	11	histone H3-K4 trimethylation	BP	1	WDR82	up_VSAP_EC
GO:1900026	0.659	0.727	1	11	positive regulation of substrate adhesion-dependent cell spreading	BP	1	ABL1	up_VSAP_EC
GO:1901137	0.659	0.715	1	232	carbohydrate derivative biosynthetic process	BP	1	GALNT17	up_VSAP_VSMC
GO:0009201	0.659415995	0.71337	1	41	ribonucleoside triphosphate biosynthetic	BP	1	ALDOC	up_ACOR_EC
GO:0002274	0.659689817	0.7132	1	40	myeloid leukocyte activation	BP	1	PRKCD	up_ACOR_EC
GO:0048468	0.66	0.398	50	553	cell development	BP	1	HOXA11,THRB,CDON,HNF4A,AXIN2,WASF3,AMIGO1,RADIL,IRX5,SLIT2,HOXD3,ABL1,DLL1,OSR1,ADAMTSL4,PLXNA4,RILPL2,ZBTB16,RARG,F2RL1,IRX3,ZEB1,SULF2,SHOX2,RTN4RL1,MYD88,LRP4,DPYSL2,GDPD5,FRMD6,E2F4,FBXO7,NTN4,LIMD1,NR2F6,FBLN1,NFIB,CYB5D2,CDNF,PQBP1,TTL,HTRA2,FLOT1,NCK1,ULK1,MAP2K2,TGFBR2,CITED2,OGN,LATS2	up_VSAP_EC
GO:0018108	0.66	0.491	7	79	peptidyl-tyrosine phosphorylation	BP	1	LEP,NRP1,PRKCE,PARP9,APP,PSEN1,DUSP22	up_ACOR_VSMC
GO:0035690	0.66	0.536	4	91	cellular response to drug	BP	1	PRNP,ADCY6,NR3C1,PARK7	down_VCAV_EC
GO:0071236	0.66	0.569	3	39	cellular response to antibiotic	BP	1	TIMELESS,EZH2,SIGMAR1	down_ACOR_VSMC
GO:0044271	0.66	0.587	3	1501	cellular nitrogen compound biosynthetic	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC
GO:0070585	0.66	0.57	3	34	protein localization to mitochondrion	BP	1	MFN2,FBXO7,BAG4	up_VSAP_EC
GO:0048583	0.66	0.63	2	1095	regulation of response to stimulus	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0001570	0.66	0.615	2	37	vasculogenesis	BP	1	CTNNB1,MYO1E	down_VSAP_EC
GO:1901136	0.66	0.615	2	38	carbohydrate derivative catabolic process	BP	1	CEMIP2,ENTPD4	down_VSAP_EC
GO:0009119	0.66	0.617	2	32	ribonucleoside metabolic process	BP	1	CDA,ACPP	up_VCAV_EC
GO:0072283	0.66	0.725	1	12	metanephric renal vesicle morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:0048585	0.66	0.72	1	475	negative regulation of response to stimulus	BP	1	IVNS1ABP	down_AFEM_EC
GO:0051291	0.66	0.716	1	21	protein heterooligomerization	BP	1	COL6A1	down_VCAV_EC
GO:0015833	0.66	0.722	1	521	peptide transport	BP	1	RAB11B	down_VPOR_EC
GO:0007080	0.66	0.719	1	18	mitotic metaphase plate congression	BP	1	KPNB1	down_VSAP_EC
GO:0045670	0.66	0.72	1	16	regulation of osteoclast differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0001764	0.66	0.713	1	45	neuron migration	BP	1	CAMK2A	up_AFEM_EC
GO:0035556	0.66	0.733	1	845	intracellular signal transduction	BP	1	ESR1	up_AORT_VSMC
GO:0034103	0.66	0.724	1	12	regulation of tissue remodeling	BP	1	PPP3CA	up_VCAV_EC
GO:1901135	0.66	0.719	1	390	carbohydrate derivative metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0016601	0.66	0.726	1	11	Rac protein signal transduction	BP	1	TIAM1	up_VSAP_EC
GO:0006622	0.66	0.725	1	11	protein targeting to lysosome	BP	1	NCOA4	up_VSAP_EC

GO:0048518	0.661	0.387	81	1676	positive regulation of biological process	BP	1	GPAM,NOTCH2,HSPB6,PDGFRB,SLC35F6,KIRREL1,FBLN2,LRP1,DCN,CFD,PRNP,LUM,SDC4,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,EVC,FXYD1,TRPV2,CLIP3,NUMBL,RHOD,OSMR,ENSCAFG00000014978,SSBP2,AKT2,TFE3,SYDE1,SCP2,CLSTN1,CSPG4,TRIM8,TMEM161A,SEMA3C,POLDIP2,THY1,TEAD1,PEX5,ATP6V0C,B4GALT1,GLI3,PARK7,ADAMTSL4,EEF2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,IFT57,MAVS,CDH2,EDIL3,LOXL3,GSDME,LSM10,SPRED1,ACTR3B,RAB7B,A2M,MAPRE3,GLIS2,TWIST2,DDR2,SHC1,PYM1,FBH1,GREM1,RAC2,NAPEPLD,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,ANKRD54,ECM2	down_VCAV_EC
GO:0006952	0.661	0.414	29	319	defense response	BP	1	NAPEPLD,MAP3K14,C5AR2,ACKR2,ABL1,IL17RC,TRAFD1,CDC42EP2,F2RL1,BATF2,PLA2G6,TBXA2R,MYD88,CFD,NLRX1,TKFC,CD83,RNF216,MAPKBP1,CYBA,STX4,PQBP1,UNC93B1,FLOT1,MAVS,HMOX1,SAA1,JCHAIN,DDIT4	up_VSAP_EC
GO:0044255	0.661	0.423	23	293	cellular lipid metabolic process	BP	1	SCD,ACSL3,SREBF1,HMGCR,MPDU1,CTDNEP1,INSIG1,CAV1,ENSCAFG00000018572,ABHD5,BRCA1,MVD,ELOVL1,PPARD,VAC14,ELOVL6,FDFT1,SGPL1,LIPC,NUS1,GK5,PDSS1,ACADL	down_ACOR_VSMC
GO:0050730	0.661	0.517	5	66	regulation of peptidyl-tyrosine phosphorylation	BP	1	CAV1,NF2,GREM1,RAP2C,ARHGEF2	down_ACOR_VSMC
GO:0051258	0.661	0.515	5	94	protein polymerization	BP	1	MZT1,ACTR3,TWF1,PLEKHG2,CAPG	down_VSAP_EC
GO:0070304	0.661	0.517	5	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	ARHGEF5,MAP3K5,F2RL1,SASH1,MYD88	up_VSAP_EC
GO:0071346	0.661	0.567	3	41	cellular response to interferon-gamma	BP	1	FLNB,SLC29A1,CDC42EP4	down_ACOR_VSMC
GO:0006754	0.661	0.57	3	36	ATP biosynthetic process	BP	1	PPARGC1A,ALDOC,DDIT4	up_ACOR_VSMC
GO:0033865	0.661	0.567	3	43	nucleoside bisphosphate metabolic process	BP	1	PANK3,PIPOX,ELOVL7	up_VCAV_EC
GO:0033875	0.661	0.567	3	43	ribonucleoside bisphosphate metabolic	BP	1	PANK3,PIPOX,ELOVL7	up_VCAV_EC
GO:0034032	0.661	0.567	3	43	purine nucleoside bisphosphate metabolic	BP	1	PANK3,PIPOX,ELOVL7	up_VCAV_EC
GO:0002708	0.661	0.618	2	26	positive regulation of lymphocyte mediated	BP	1	TFRC,FAM49B	down_ACOR_VSMC
GO:0046785	0.661	0.62	2	23	microtubule polymerization	BP	1	FGF13,TUBB4A	up_ACOR_VSMC
GO:0016032	0.661	0.611	2	94	viral process	BP	1	LRRC15,RAB7A	up_AFEM_EC
GO:0031325	0.661	0.625	2	914	positive regulation of cellular metabolic process	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0002708	0.661	0.618	2	26	positive regulation of lymphocyte mediated	BP	1	GATA3,NECTIN2	up_VCAV_EC
GO:0045738	0.661	0.723	1	12	negative regulation of DNA repair	BP	1	PARPBP	down_ACOR_VSMC
GO:0060602	0.661	0.723	1	12	branch elongation of an epithelium	BP	1	SIX4	down_ACOR_VSMC
GO:0072604	0.661	0.723	1	12	interleukin-6 secretion	BP	1	HMGB1	down_ACOR_VSMC
GO:0051496	0.661	0.718	1	17	positive regulation of stress fiber assembly	BP	1	NRP1	down_VSAP_EC
GO:0070231	0.661	0.718	1	18	T cell apoptotic process	BP	1	HIF1A	down_VSAP_EC
GO:1900181	0.661	0.724	1	11	negative regulation of protein localization to	BP	1	FERMT1	up_ACOR_VSMC
GO:0018107	0.661	0.711	1	45	peptidyl-threonine phosphorylation	BP	1	CAMK2A	up_AFEM_EC
GO:0046661	0.661	0.711	1	45	male sex differentiation	BP	1	HOXA9	up_AFEM_EC
GO:0051196	0.661	0.722	1	13	regulation of coenzyme metabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0001932	0.661	0.718	1	416	regulation of protein phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0031327	0.661	0.718	1	412	negative regulation of cellular biosynthetic	BP	1	NKX2-5	up_VPOR_VSMC
GO:0051336	0.661	0.713	1	251	regulation of hydrolase activity	BP	1	TIAM1	up_VFEM_EC
GO:0001881	0.661	0.724	1	11	receptor recycling	BP	1	RAB11B	up_VSAP_EC

GO:0010883	0.661	0.725	1	11	regulation of lipid storage	BP	1	ACACB	up_VSAP_EC
GO:0034405	0.661	0.725	1	11	response to fluid shear stress	BP	1	ASS1	up_VSAP_EC
GO:0006473	0.662	0.516	5	66	protein acetylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:1903034	0.662	0.567	3	40	regulation of response to wounding	BP	1	TFPI,CAV1,PPARD	down_ACOR_VSMC
GO:0035601	0.662	0.613	2	36	protein deacylation	BP	1	MORF4L2,REST	down_VSAP_EC
GO:0098732	0.662	0.613	2	36	macromolecule deacylation	BP	1	MORF4L2,REST	down_VSAP_EC
GO:0030149	0.662	0.722	1	12	sphingolipid catabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0002714	0.662	0.723	1	12	positive regulation of B cell mediated immunity	BP	1	TFRC	down_ACOR_VSMC
GO:0046466	0.662	0.722	1	12	membrane lipid catabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0002891	0.662	0.723	1	12	positive regulation of immunoglobulin mediated immune	BP	1	TFRC	down_ACOR_VSMC
GO:0006508	0.662	0.719	1	483	proteolysis	BP	1	USP33	down_AFEM_EC
GO:0042089	0.662	0.715	1	21	cytokine biosynthetic process	BP	1	MAST2	down_VCAV_EC
GO:1905207	0.662	0.717	1	17	regulation of cardiocyte differentiation	BP	1	PRICKLE1	down_VSAP_EC
GO:0048806	0.662	0.725	1	10	genitalia development	BP	1	CHD7	up_ACOR_VSMC
GO:0001823	0.662	0.71	1	45	mesonephros development	BP	1	GREM1	up_AFEM_EC
GO:0055002	0.662	0.711	1	45	striated muscle cell development	BP	1	BVES	up_AFEM_EC
GO:0033043	0.662	0.717	1	446	regulation of organelle organization	BP	1	TAOK1	up_AORT_EC
GO:0035561	0.662	0.723	1	12	regulation of chromatin binding	BP	1	PPP3CA	up_VCAV_EC
GO:0030856	0.662948	0.7096	1	41	regulation of epithelial cell differentiation	BP	1	SOX9	up_ACOR_EC
GO:0032535	0.663	0.462	10	128	regulation of cellular component size	BP	1	CAPG,LIMA1,RAC1,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,ARPC1B,ANXA7	down_ACOR_VSMC
GO:0006839	0.663	0.488	7	86	mitochondrial transport	BP	1	RHOT1,MICU2,BNIP3,PSEN1,SLC25A20,SLC25A12,NAIF1	up_ACOR_VSMC
GO:0001763	0.663	0.499	6	78	morphogenesis of a branching structure	BP	1	TIMELESS,MMP14,GREM1,HOXB7,B4GALT1,SIX4	down_ACOR_VSMC
GO:0006810	0.663	0.524	5	1244	transport	BP	1	NETO1,SLC16A12,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0070507	0.663	0.534	4	73	regulation of microtubule cytoskeleton organization	BP	1	ARHGEF2,CTNNB1,GSK3B,MID1	down_VSAP_EC
GO:0055082	0.663	0.531	4	189	cellular chemical homeostasis	BP	1	RAB20,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0042221	0.663	0.542	4	1012	response to chemical	BP	1	EMX2,TLR2,CAV1,FGF5	up_VSAP_VSMC
GO:0016202	0.663	0.566	3	39	regulation of striated muscle tissue	BP	1	GREM1,GLI1,SIX4	down_ACOR_VSMC
GO:0051101	0.663	0.567	3	35	regulation of DNA binding	BP	1	CLSTN1,PSEN1,PARK7	up_ACOR_VSMC
GO:0051128	0.663	0.569	3	790	regulation of cellular component organization	BP	1	TRIM9,SIX1,CDC42EP5	up_VFEM_EC
GO:0062014	0.663	0.567	3	35	negative regulation of small molecule metabolic	BP	1	INSIG2,ACACB,DDIT4	up_VSAP_EC
GO:0018107	0.663	0.611	2	45	peptidyl-threonine phosphorylation	BP	1	CAMK2D,SPRED1	down_VCAV_EC
GO:0060350	0.663	0.617	2	23	endochondral bone morphogenesis	BP	1	BMP4,FGF18	up_ACOR_VSMC
GO:0010604	0.663	0.622	2	919	positive regulation of macromolecule metabolic	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0033059	0.663	0.721	1	12	cellular pigmentation	BP	1	TRAPPC6A	down_ACOR_VSMC
GO:1902373	0.663	0.721	1	12	negative regulation of mRNA catabolic process	BP	1	THRAP3	down_ACOR_VSMC
GO:0045851	0.663	0.714	1	21	pH reduction	BP	1	ATP6V0C	down_VCAV_EC
GO:0007189	0.663	0.714	1	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	ADCY6	down_VCAV_EC
GO:0010718	0.663	0.714	1	21	positive regulation of epithelial to mesenchymal	BP	1	GLIPR2	down_VCAV_EC
GO:0060148	0.663	0.724	1	10	positive regulation of posttranscriptional gene	BP	1	BMP4	up_ACOR_VSMC

GO:0008643	0.663	0.709	1	45	carbohydrate transport	BP	1	LEP	up_AFEM_EC
GO:0034101	0.663	0.709	1	45	erythrocyte homeostasis	BP	1	NFE2L1	up_AFEM_EC
GO:0034250	0.663	0.709	1	45	positive regulation of cellular amide metabolic	BP	1	PRR16	up_AFEM_EC
GO:0043902	0.663	0.709	1	45	positive regulation of multi-organism process	BP	1	RAB7A	up_AFEM_EC
GO:0051701	0.663	0.71	1	45	interaction with host	BP	1	RAB7A	up_AFEM_EC
GO:0006622	0.663	0.723	1	11	protein targeting to lysosome	BP	1	GCC2	up_VCAV_EC
GO:0014888	0.663	0.722	1	11	striated muscle adaptation	BP	1	KLF15	up_VSAP_EC
GO:0002700	0.663612365	0.70901	1	40	regulation of production of molecular mediator of immune response	BP	1	FZD5	up_ACOR_EC
GO:0006164	0.663687867	0.60753	2	86	purine nucleotide biosynthetic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0008219	0.664	0.411	29	611	cell death	BP	1	GPAM,SLC35F6,LRP1,PRNP,KANK2,CLIP3,GABARAP,AKT2,ENSCAFG00000013404,TMEM161A,LRPAP1,ARHGAP10,B4GALT1,GLI3,PARK7,ZMAT3,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0043161	0.664	0.439	15	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	SH3RF2,KLHL20,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,RNF181,HERPUD1,FAF2,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0016071	0.664	0.442	14	248	mRNA metabolic process	BP	1	CELF1,IWS1,SNRPB2,SMG7,PRPF3,DDX39B,CNOT7,PDCD11,STRAP,DDIT3,REST,ENSCAFG00000015065,BCAS2,SNRPA1	down_VSAP_EC
GO:0009755	0.664	0.534	4	52	hormone-mediated signaling pathway	BP	1	NEDD4,THRAP3,ADIPOR2,PRCP	down_ACOR_VSMC
GO:0031348	0.664	0.536	4	46	negative regulation of defense response	BP	1	TRAFD1,NLRX1,TKFC,MAPKBP1	up_VSAP_EC
GO:0065007	0.664	0.649	3	3499	biological regulation	BP	1	GATA5,TGFBR1,MEIS2	down_VSAP_VSMC
GO:0005976	0.664	0.566	3	34	polysaccharide metabolic process	BP	1	PYGM,GAA,INPP5K	up_ACOR_VSMC
GO:0045893	0.664	0.612	2	413	positive regulation of transcription, DNA-	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0042255	0.664	0.613	2	29	ribosome assembly	BP	1	DDX28,ENSCAFG00000015189	down_ACOR_VSMC
GO:0034968	0.664	0.612	2	34	histone lysine methylation	BP	1	IWS1,KDM3A	down_VSAP_EC
GO:0042147	0.664	0.611	2	38	retrograde transport, endosome to Golgi	BP	1	TMEM87B,RAB6A	down_VSAP_EC
GO:0032206	0.664	0.616	2	23	positive regulation of telomere maintenance	BP	1	ATRX,HMBOX1	up_ACOR_VSMC
GO:1902041	0.664	0.616	2	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	DAPK1,PARK7	up_ACOR_VSMC
GO:0060322	0.664	0.71	1	193	head development	BP	1	NRP2	down_ACOR_EC
GO:0035561	0.664	0.72	1	12	regulation of chromatin binding	BP	1	GMNN	down_ACOR_VSMC
GO:0045911	0.664	0.72	1	12	positive regulation of DNA recombination	BP	1	TFRC	down_ACOR_VSMC
GO:0001947	0.664	0.713	1	21	heart looping	BP	1	IFT57	down_VCAV_EC
GO:0051055	0.664	0.713	1	21	negative regulation of lipid biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:0061371	0.664	0.713	1	21	determination of heart left/right asymmetry	BP	1	IFT57	down_VCAV_EC
GO:1902531	0.664	0.718	1	536	regulation of intracellular signal transduction	BP	1	HDAC7	down_VPOR_EC
GO:0032611	0.664	0.714	1	17	interleukin-1 beta production	BP	1	GBP5	down_VSAP_EC
GO:1903078	0.664	0.714	1	19	positive regulation of protein localization to	BP	1	KIF5B	down_VSAP_EC
GO:0007140	0.664	0.723	1	10	male meiotic nuclear division	BP	1	DMC1	up_ACOR_VSMC
GO:0060119	0.664	0.724	1	10	inner ear receptor cell development	BP	1	SEC24B	up_ACOR_VSMC
GO:0051187	0.664	0.719	1	13	cofactor catabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0016477	0.664	0.715	1	426	cell migration	BP	1	EMX2	up_VFEM_VSMC
GO:0040036	0.664	0.721	1	11	regulation of fibroblast growth factor receptor	BP	1	SULF2	up_VSAP_EC

GO:0090314	0.664	0.721	1	11	positive regulation of protein targeting to	BP	1	KCNB1	up_VSAP_EC
GO:0035967	0.664462686	0.70785	1	42	cellular response to topologically incorrect	BP	1	EDEM2	up_ACOR_EC
GO:1901135	0.665	0.41	28	390	carbohydrate derivative metabolic process	BP	1	NPR1,ST8SIA6,KIT,PANK3,CDA,TNIP1,PDGFB,ST6GAL1,LYVE1,GK5,PIPOX,ADSS,GUCY1A1,B3GNT5,ACPP,BMP2,CHST7,CREM,ST3GAL6,GALNT18,CHST1,ELOVL7,MFNG,ENSCAFG00000024323,SLC25A25,GUCY1B1,HIF1A,TET2	up_VCAV_EC
GO:0032880	0.665	0.421	21	266	regulation of protein localization	BP	1	ACSL3,HMGB1,SREBF1,SLC29A1,RAN,BIRC5,INSIG1,CDK1,NF2,MMP14,PLK3,ARG2,NDC80,ARHGDIA,NUP62,RSL1D1,DMAP1,ENSCAFG00000005299,EZR,CCT4,SIX4	down_ACOR_VSMC
GO:0044089	0.665	0.438	15	170	positive regulation of cellular component biogenesis	BP	1	WNT11,ARHGEF5,AMIGO1,LRRN3,ABL1,CDC42EP5,FUZ,CDC42EP2,F2RL1,ICE1,PIP4K2B,FLOT1,NCK1,BAG4,JCHAIN	up_VSAP_EC
GO:1901698	0.665	0.449	12	266	response to nitrogen compound	BP	1	LRP1,PRNP,ADCY6,COL6A1,ENSCAFG00000014978,AKT2,ZFP36L1,MAVS,SEC61B,RAB31,HM13,SHC1	down_VCAV_EC
GO:0022411	0.665	0.461	10	130	cellular component disassembly	BP	1	TMOD1,STMN1,SWAP70,SMARCA4,MRRF,TAOK1,HIF1A,TMOD3,ARHGEF2,FSCN1	up_VCAV_EC
GO:0044085	0.665	0.48	8	1076	cellular component biogenesis	BP	1	MZT1,ENSCAFG00000002015,FBP1,RSL24D1,RPL10L,TWF1,RRP15,SRP54	up_VPOR_EC
GO:0035148	0.665	0.512	5	66	tube formation	BP	1	PODXL,GATA3,BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0006996	0.665	0.522	5	1301	organelle organization	BP	1	EYA1,TRIM9,CYP26B1,CDC42EP5,MTSS1	up_VFEM_EC
GO:0032102	0.665	0.56	3	67	negative regulation of response to external	BP	1	KANK2,CHID1,RGMA	down_VCAV_EC
GO:0071897	0.665	0.562	3	54	DNA biosynthetic process	BP	1	SMG7,CTNNB1,CDKN1A	down_VSAP_EC
GO:0015850	0.665	0.61	2	37	organic hydroxy compound transport	BP	1	PTPN11,APOE	down_VSAP_EC
GO:2000278	0.665	0.61	2	37	regulation of DNA biosynthetic process	BP	1	CTNNB1,CDKN1A	down_VSAP_EC
GO:0040019	0.665	0.718	1	12	positive regulation of embryonic development	BP	1	SIX4	down_ACOR_VSMC
GO:2000677	0.665	0.719	1	12	regulation of transcription regulatory region DNA	BP	1	FAM129B	down_ACOR_VSMC
GO:0008306	0.665	0.712	1	21	associative learning	BP	1	BRSK1	down_VCAV_EC
GO:0090183	0.665	0.712	1	21	regulation of kidney development	BP	1	GREM1	down_VCAV_EC
GO:0042886	0.665	0.717	1	527	amide transport	BP	1	RAB11B	down_VPOR_EC
GO:0043403	0.665	0.721	1	11	skeletal muscle tissue regeneration	BP	1	GJA1	up_ACOR_VSMC
GO:0048486	0.665	0.722	1	10	parasympathetic nervous system development	BP	1	NRP1	up_ACOR_VSMC
GO:0070306	0.665	0.721	1	11	lens fiber cell differentiation	BP	1	FRS2	up_ACOR_VSMC
GO:0035023	0.665	0.707	1	46	regulation of Rho protein signal transduction	BP	1	KANK1	up_AFEM_EC
GO:2000145	0.665	0.71	1	279	regulation of cell motility	BP	1	TBX5	up_APUL_EC
GO:0030099	0.665	0.706	1	133	myeloid cell differentiation	BP	1	ACVR2A	up_VPOR_EC
GO:0042592	0.665	0.716	1	522	homeostatic process	BP	1	HOXA3	up_VPUL_VSMC
GO:0035315	0.665	0.721	1	11	hair cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:2000377	0.665099917	0.70729	1	41	regulation of reactive oxygen species metabolic	BP	1	PRKCD	up_ACOR_EC

GO:0031326	0.666	0.375	109	1176	regulation of cellular biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,ANKHD1,TRERF1,E2F4,NPAS2,LIMD1,RPUSD4,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,ZNF517,ASS1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772,SOAT1	up_VSAP_EC
GO:0006915	0.666	0.412	26	550	apoptotic process	BP	1	GPAM,SLC35F6,PRNP,CLIP3,GABARAP,AKT2,ENSCAFG00000013404,TMEM161A,ARHGAP10,B4GALT1,GLI3,PARK7,ZMAT3,ADAMTSL4,ZFP36L1,MYDGF,IFT57,GSDME,TSC22D3,SHC1,FBH1,GREM1,GLS2,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0044270	0.666	0.453	11	147	cellular nitrogen compound catabolic process	BP	1	CDA,TENT2,CNOT6,ENSCAFG00000024323,PAN3,CNOT7,SMG7,BLVRA,HIF1A,DCP2,TET2	up_VCAV_EC
GO:0080090	0.666	0.553	4	1734	regulation of primary metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0051302	0.666	0.533	4	47	regulation of cell division	BP	1	FGF7,DLL1,MYC,LBH	up_VSAP_EC
GO:0022409	0.666	0.559	3	56	positive regulation of cell-cell adhesion	BP	1	SOCS5,FAM49B,TFRC	down_VSAP_EC
GO:0009890	0.666	0.56	3	420	negative regulation of biosynthetic process	BP	1	ENSCAFG00000002015,FBP1,MTDH	up_VPOR_EC
GO:1902680	0.666	0.61	2	415	positive regulation of RNA biosynthetic process	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:1903508	0.666	0.61	2	415	positive regulation of nucleic acid-templated	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0072384	0.666	0.613	2	24	organelle transport along microtubule	BP	1	KIF3C,HIF1A	up_VCAV_EC
GO:0008631	0.666	0.716	1	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	MELK	down_ACOR_VSMC
GO:0048333	0.666	0.718	1	12	mesodermal cell differentiation	BP	1	ITGA2	down_ACOR_VSMC
GO:0090199	0.666	0.714	1	15	regulation of release of cytochrome c from	BP	1	PRELID1	down_ACOR_VSMC
GO:0050790	0.666	0.715	1	532	regulation of catalytic activity	BP	1	CST3	down_VPOR_EC
GO:0051965	0.666	0.713	1	17	positive regulation of synapse assembly	BP	1	LRRTM2	down_VSAP_EC
GO:0045840	0.666	0.718	1	12	positive regulation of mitotic nuclear division	BP	1	EDN1	up_ACOR_VSMC
GO:0009894	0.666	0.708	1	277	regulation of catabolic process	BP	1	LZTS1	up_APUL_EC
GO:0006891	0.666	0.718	1	12	intra-Golgi vesicle-mediated transport	BP	1	RAB6A	up_VCAV_EC
GO:0021591	0.666	0.718	1	12	ventricular system development	BP	1	RAPGEF2	up_VCAV_EC
GO:0035315	0.666	0.72	1	11	hair cell differentiation	BP	1	JAG1	up_VCAV_EC
GO:0098868	0.666	0.72	1	11	bone growth	BP	1	STC1	up_VCAV_EC
GO:0009891	0.666	0.715	1	521	positive regulation of biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0010941	0.666	0.716	1	524	regulation of cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:1901984	0.666	0.719	1	11	negative regulation of protein acetylation	BP	1	KLF15	up_VSAP_EC
GO:1903393	0.666	0.719	1	11	positive regulation of adherens junction	BP	1	ABL1	up_VSAP_EC
GO:0023014	0.666	0.708	1	248	signal transduction by protein phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0044248	0.66618881	0.43063	17	691	cellular catabolic process	BP	1	THNSL2,ATG16L2,SARDH,EDEM2,KLHL25,PIAS1,CLU,ALDOC,CHMP4B,TP53INP2,VPS16,RNF114,UBE2H,HM13,PRKCD,PM20D1,ENSCAFG00000010493	up_ACOR_EC

GO:0002697	0.666265006	0.60465	2	85	regulation of immune effector process	BP	1	FZD5,MAVS	up_ACOR_EC
GO:0048634	0.666742514	0.70563	1	40	regulation of muscle organ development	BP	1	TBX5	up_ACOR_EC
GO:0042886	0.667	0.392	48	527	amide transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,STX11,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,CHD7,LAMP2,JUP,CCL5,RAB11B,EDN1,NOD2,LMTK2,AP2B1,SCAMP5,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0030030	0.667	0.401	35	377	cell projection organization	BP	1	ACTN2,EPYC,FEZ1,ITM2C,EVI5L,FGFR2,SEC24B,WASF3,ZNF365,TMEM108,ARHGEF26,IFT43,F2RL1,NRP1,GPM6A,ULK2,UNC5B,EVL,SLITRK5,FZD3,TTC17,DAG1,APP,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,ATXN10,FEZ2,INPP5K,WASL,ENSCAFG00000013536,RREB1	up_ACOR_VSMC
GO:1901362	0.667	0.41	29	1293	organic cyclic compound biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,SDR42E1,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A	up_AFEM_EC
GO:0032269	0.667	0.414	24	306	negative regulation of cellular protein metabolic process	BP	1	ILF3,USP4,EIF4A3,HMGCR,U2AF2,SLC29A1,PPP1R15B,BIRC5,CAV1,NF2,CDKN2C,GREM1,SMARCC1,DHCR24,BRCA1,NOC2L,YWHAB,NCL,NUP62,CACTIN,ENSCAFG00000005299,EZR,RBM14,TINF2	down_ACOR_VSMC
GO:0051223	0.667	0.439	14	181	regulation of protein transport	BP	1	HCLS1,TMEM173,IWS1,FERMT1,TLR4,GATA3,ARG2,APOD,CD200,CTDSPL2,GCC2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0016043	0.667	0.501	7	1973	cellular component organization	BP	1	NR1H4,TUBB4A,ARHGEF26,SLITRK5,NPNT,NTRK2,PDLIM3	up_APUL_EC
GO:0035303	0.667	0.51	5	65	regulation of dephosphorylation	BP	1	SLC29A1,PPP2R5D,YWHAB,IQGAP1,KNL1	down_ACOR_VSMC
GO:0032088	0.667	0.611	2	26	negative regulation of NF-kappaB transcription	BP	1	IRAK1,CACTIN	down_ACOR_VSMC
GO:0022904	0.667	0.607	2	43	respiratory electron transport chain	BP	1	UQCR10,PARK7	down_VCAV_EC
GO:0043901	0.667	0.607	2	44	negative regulation of multi-organism process	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:1901657	0.667	0.607	2	43	glycosyl compound metabolic process	BP	1	NT5C2,ADK	down_VCAV_EC
GO:1904591	0.667	0.612	2	25	positive regulation of protein import	BP	1	HCLS1,TMEM173	up_VCAV_EC
GO:0007063	0.667	0.717	1	12	regulation of sister chromatid cohesion	BP	1	FEN1	down_ACOR_VSMC
GO:0038034	0.667	0.709	1	21	signal transduction in absence of ligand	BP	1	FOXO3	down_VCAV_EC
GO:0097192	0.667	0.709	1	21	extrinsic apoptotic signaling pathway in	BP	1	FOXO3	down_VCAV_EC
GO:0010941	0.667	0.714	1	524	regulation of cell death	BP	1	CITED2	down_VPOR_EC
GO:0060706	0.667	0.719	1	11	cell differentiation involved in embryonic	BP	1	SPINT2	up_ACOR_VSMC
GO:0002520	0.667	0.707	1	279	immune system development	BP	1	HOXA3	up_APUL_EC
GO:0007632	0.667	0.714	1	14	visual behavior	BP	1	HIF1A	up_VCAV_EC
GO:0006511	0.667	0.706	1	253	ubiquitin-dependent protein catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:0010517	0.667	0.718	1	11	regulation of phospholipase activity	BP	1	ABL1	up_VSAP_EC
GO:0008206	0.667	0.718	1	11	bile acid metabolic process	BP	1	ACAA1	up_VSAP_EC
GO:0033598	0.667	0.718	1	11	mammary gland epithelial cell proliferation	BP	1	STAT6	up_VSAP_EC
GO:1902230	0.667	0.719	1	11	negative regulation of intrinsic apoptotic signaling pathway in	BP	1	ACKR3	up_VSAP_EC
GO:0033135	0.667495686	0.70482	1	40	regulation of peptidyl-serine phosphorylation	BP	1	PLCL1	up_ACOR_EC
GO:0006979	0.667735652	0.55485	3	130	response to oxidative stress	BP	1	AQP1,GUCY1B1,PRKCD	up_ACOR_EC

GO:0007165	0.668	0.369	139	1496	signal transduction	BP	1	GPR1,FZD1,ADGRD1,SEZ6L,CDON,WNT11,HNF4A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,INSIG2,PTGFR,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,LRRC28,HOXD3,FGF7,ABL1,GOT1,HDAC7,EMP2,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,DTX2,PDGFD,SAV1,RHPN1,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,CCBE1,STAT5A,STAT6,RECK,CISH,KLHL24,PLPP3,CAMKK2,RASD2,F2RL1,GLIS2,PDK2,MFN2,ZFP36L1,TRAF7,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,TBXA2R,SULF2,SHOX2,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,GABBR2,LRP4,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,NCEH1,ASB8,TMEM17,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CD83,PRMT2,FBLN1,ZFP36L2,HPGD,IGFBP6,RAF1,MAPKBP1,PPP2R5B,CYBA,ZNF205,NCOA2,STX4,ZFAND5,PSD4,QARS,ARHGAP12,ACVRL1,UBQLN2,ARHGAP10,UNC93B1,RAPGEF3,HTRA2,FLOT1,PLPP5,PPP3CB,NCK1,MAVS,IRAK1BP1,KRCC1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,LATS2	up_VSAP_EC
GO:0045892	0.668	0.479	7	328	negative regulation of transcription, DNA-	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1	up_AFEM_EC
GO:0002703	0.668	0.53	4	47	regulation of leukocyte mediated immunity	BP	1	STAT6,F2RL1,STX4,PPP3CB	up_VSAP_EC
GO:0010952	0.668	0.531	4	46	positive regulation of peptidase activity	BP	1	CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0007259	0.668	0.559	3	42	JAK-STAT cascade	BP	1	HCLS1,KIT,CNOT7	up_VCAV_EC
GO:0043401	0.668	0.605	2	46	steroid hormone mediated signaling	BP	1	KANK2,PARK7	down_VCAV_EC
GO:0045944	0.668	0.604	2	287	positive regulation of transcription by RNA polymerase II	BP	1	ARHGEF2,ACVR2A	up_VPOR_EC
GO:0021517	0.668	0.715	1	12	ventral spinal cord development	BP	1	HOXC10	down_ACOR_VSMC
GO:0033962	0.668	0.716	1	12	cytoplasmic mRNA processing body assembly	BP	1	EDC3	down_ACOR_VSMC
GO:0051240	0.668	0.712	1	489	positive regulation of multicellular organismal	BP	1	SRSF6	down_AFEM_EC
GO:0097300	0.668	0.71	1	17	programmed necrotic cell death	BP	1	ARHGEF2	down_VSAP_EC
GO:0065009	0.668	0.72	1	735	regulation of molecular function	BP	1	TLR2	up_AFEM_VSMC
GO:0048523	0.668	0.742	1	1399	negative regulation of cellular process	BP	1	TBX5	up_APUL_VSMC
GO:0021772	0.668	0.718	1	11	olfactory bulb development	BP	1	CHD7	up_VCAV_EC
GO:0021988	0.668	0.718	1	11	olfactory lobe development	BP	1	CHD7	up_VCAV_EC
GO:0033013	0.668	0.712	1	15	tetrapyrrole metabolic process	BP	1	BLVRA	up_VCAV_EC
GO:0050710	0.668	0.715	1	13	negative regulation of cytokine secretion	BP	1	ARG2	up_VCAV_EC
GO:0009890	0.668	0.711	1	420	negative regulation of biosynthetic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0019220	0.668	0.713	1	525	regulation of phosphate metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0051174	0.668	0.713	1	525	regulation of phosphorus metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0006986	0.66859959	0.70337	1	42	response to unfolded protein	BP	1	EDEM2	up_ACOR_EC
GO:0016192	0.669	0.417	21	452	vesicle-mediated transport	BP	1	SNX18,LRP1,SDC4,TMEM230,CLIP3,ERGIC1,AKT2,MICALL2,ANXA11,LRPAP1,CLTB,MYO1B,YIF1A,CYBA,RAB7B,RAB31,ARHGAP1,GREM1,EVI5L,RAC2,PACSIN3	down_VCAV_EC
GO:0045321	0.669	0.433	15	191	leukocyte activation	BP	1	HMGB1,MNDA,PRELID1,CAV1,TXLNA,MMP14,HMGB3,ARG2,TFRC,FAM49B,TOX,CORO1A,ELF4,JMJD6,CTPS1	down_ACOR_VSMC
GO:0046903	0.669	0.436	14	255	secretion	BP	1	NR1H4,PTPN11,EXOC5,SEL1L,HIF1A,LYN,GSK3B,GBP5,SDC4,REST,SCAMP1,RAB11FIP1,INHBA,RHBDF2	down_VSAP_EC
GO:0046700	0.669	0.449	11	147	heterocycle catabolic process	BP	1	CDA,TENT2,CNOT6,ENSCAFG00000024323,PAN3,CNOT7,SMG7,BLVRA,HIF1A,DCP2,TET2	up_VCAV_EC

GO:0006793	0.669	0.484	7	948	phosphorus metabolic process	BP	1	ARHGEF2,AK5,ASPN,ACVR2A,FBP1,ENSCAFG00000032731,GNPNAT1	up_VPOR_EC
GO:0030100	0.669	0.507	5	70	regulation of endocytosis	BP	1	HMGB1,ARFGAP1,CAV1,GREM1,HIST1H1A	down_ACOR_VSMC
GO:0007219	0.669	0.509	5	59	Notch signaling pathway	BP	1	GATA5,PSEN2,PSEN1,SYNJ2BP,PERP	up_ACOR_VSMC
GO:0032502	0.669	0.58	3	1661	developmental process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0048332	0.669	0.609	2	26	mesoderm morphogenesis	BP	1	NF2,ITGA2	down_ACOR_VSMC
GO:0048869	0.669	0.62	2	1119	cellular developmental process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0001776	0.669	0.611	2	23	leukocyte homeostasis	BP	1	ABL1,PPP3CB	up_VSAP_EC
GO:0045453	0.669	0.714	1	12	bone resorption	BP	1	TFRC	down_ACOR_VSMC
GO:0032387	0.669	0.708	1	20	negative regulation of intracellular transport	BP	1	CRYAB	down_VSAP_EC
GO:0050704	0.669	0.717	1	11	regulation of interleukin-1 secretion	BP	1	NOD2	up_ACOR_VSMC
GO:1903393	0.669	0.716	1	11	positive regulation of adherens junction	BP	1	NRP1	up_ACOR_VSMC
GO:0010921	0.669	0.703	1	46	regulation of phosphatase activity	BP	1	MYO1D	up_AFEM_EC
GO:0006835	0.669	0.714	1	13	dicarboxylic acid transport	BP	1	LRRC8D	up_VCAV_EC
GO:1901616	0.669	0.711	1	15	organic hydroxy compound catabolic	BP	1	IMPA1	up_VCAV_EC
GO:0032386	0.669	0.702	1	137	regulation of intracellular transport	BP	1	GCC2	up_VPOR_EC
GO:0060343	0.669	0.717	1	11	trabecula formation	BP	1	PPARGC1B	up_VSAP_EC
GO:0030001	0.669124452	0.52411	4	172	metal ion transport	BP	1	KCNB1,ACTN2,SLC9A9,ATP7B	up_ACOR_EC
GO:0045892	0.67	0.431	15	328	negative regulation of transcription, DNA-templated	BP	1	NAB2,KANK2,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,LOXL3,TSC22D3,GLIS2,SHC1,GREM1,THRB	down_VCAV_EC
GO:0048812	0.67	0.44	13	151	neuron projection morphogenesis	BP	1	SLIT2,ABL1,PLXNA4,SHOX2,LRP4,DPYSL2,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0019693	0.67	0.461	9	172	ribose phosphate metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ENTPD4,ALDOC,PAPSS1,AK5	down_VSAP_EC
GO:0031323	0.67	0.495	7	1788	regulation of cellular metabolic process	BP	1	EYA1,HOXA9,MAP2K6,HOXA10,HOXA7,SIX1,YBX3	up_VFEM_EC
GO:0045732	0.67	0.491	6	78	positive regulation of protein catabolic process	BP	1	NEDD4,PLK3,DTL,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0051648	0.67	0.493	6	69	vesicle localization	BP	1	FBXL20,STX11,PSEN1,RAB11B,PREPL,DYNC1I1	up_ACOR_VSMC
GO:1901214	0.67	0.491	6	81	regulation of neuron death	BP	1	EPHB1,CD34,MEF2C,TLR4,GATA3,HIF1A	up_VCAV_EC
GO:0032434	0.67	0.508	5	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	SH3RF2,RNF19A,PSEN1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0010243	0.67	0.504	5	238	response to organonitrogen	BP	1	LEP,CRY2,AVPR1A,CAMK2A,KANK1	up_AFEM_EC
GO:0006352	0.67	0.527	4	56	DNA-templated transcription, initiation	BP	1	HMGB1,THRAP3,FOSL1,PSMC1	down_ACOR_VSMC
GO:0050821	0.67	0.528	4	48	protein stabilization	BP	1	RASSF2,LAMP2,WFS1,PARK7	up_ACOR_VSMC
GO:0051052	0.67	0.552	3	145	regulation of DNA metabolic process	BP	1	GREM1,AXIN2,PPARGC1A	up_AFEM_EC
GO:0051668	0.67	0.558	3	39	localization within membrane	BP	1	MALL,RELN,NUP133	up_VCAV_EC
GO:0048660	0.67	0.56	3	35	regulation of smooth muscle cell proliferation	BP	1	IL6R,MFN2,HMOX1	up_VSAP_EC
GO:0010033	0.67	0.561	3	772	response to organic substance	BP	1	TLR2,CAV1,FGF5	up_VSAP_VSMC
GO:0061097	0.67	0.607	2	27	regulation of protein tyrosine kinase activity	BP	1	CAV1,RAP2C	down_ACOR_VSMC
GO:0061008	0.67	0.609	2	23	hepaticobiliary system development	BP	1	CITED2,LIMS2	up_ACOR_VSMC
GO:0010948	0.67	0.6	2	96	negative regulation of cell cycle process	BP	1	OVOL1,DCUN1D3	up_AFEM_EC
GO:0002456	0.67	0.609	2	23	T cell mediated immunity	BP	1	EMP2,PPP3CB	up_VSAP_EC
GO:0009185	0.67	0.609	2	23	ribonucleoside diphosphate metabolic	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0055023	0.67	0.714	1	12	positive regulation of cardiac muscle tissue	BP	1	GLI1	down_ACOR_VSMC
GO:0001889	0.67	0.706	1	22	liver development	BP	1	PRKCSH	down_VCAV_EC

GO:0031060	0.67	0.705	1	23	regulation of histone methylation	BP	1	PRMT6	down_VCAV_EC
GO:0042440	0.67	0.706	1	21	pigment metabolic process	BP	1	UROS	down_VCAV_EC
GO:0045184	0.67	0.711	1	532	establishment of protein localization	BP	1	RAB11B	down_VPOR_EC
GO:0048146	0.67	0.708	1	18	positive regulation of fibroblast proliferation	BP	1	CDKN1A	down_VSAP_EC
GO:0090342	0.67	0.709	1	17	regulation of cell aging	BP	1	NUAK1	down_VSAP_EC
GO:0009648	0.67	0.715	1	11	photoperiodism	BP	1	RBM4B	up_ACOR_VSMC
GO:0032881	0.67	0.715	1	11	regulation of polysaccharide metabolic	BP	1	INPP5K	up_ACOR_VSMC
GO:0032885	0.67	0.715	1	11	regulation of polysaccharide	BP	1	INPP5K	up_ACOR_VSMC
GO:0043153	0.67	0.715	1	11	entrainment of circadian clock by photoperiod	BP	1	RBM4B	up_ACOR_VSMC
GO:0031345	0.67	0.701	1	46	negative regulation of cell projection organization	BP	1	KANK1	up_AFEM_EC
GO:0032412	0.67	0.701	1	46	regulation of ion transmembrane	BP	1	FXYD1	up_AFEM_EC
GO:0072606	0.67	0.713	1	12	interleukin-8 secretion	BP	1	NOS2	up_VCAV_EC
GO:0034655	0.67	0.701	1	135	nucleobase-containing compound catabolic	BP	1	FBP1	up_VPOR_EC
GO:0010628	0.67	0.711	1	527	positive regulation of gene expression	BP	1	GATA5	up_VPUL_VSMC
GO:0060193	0.67	0.716	1	11	positive regulation of lipase activity	BP	1	LMF1	up_VSAP_EC
GO:0072577	0.67	0.715	1	11	endothelial cell apoptotic process	BP	1	ABL1	up_VSAP_EC
GO:2000351	0.67	0.715	1	11	regulation of endothelial cell apoptotic process	BP	1	ABL1	up_VSAP_EC
GO:0043405	0.670466011	0.59986	2	85	regulation of MAP kinase activity	BP	1	FZD5,PRKCD	up_ACOR_EC
GO:0071705	0.671	0.385	53	582	nitrogen compound transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,STX11,ANKRD1,F2RL1,CDKN1A,PTPN22,TCN2,OS9,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,CHD7,LAMP2,JUP,CCL5,CLN8,RAB11B,EDN1,SLC25A20,NOD2,LMTK2,AP2B1,SCAMP5,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,AZIN2,RPAIN,SLC25A12,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:1902679	0.671	0.476	7	329	negative regulation of RNA biosynthetic process	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1	up_AFEM_EC
GO:1903507	0.671	0.476	7	329	negative regulation of nucleic acid-templated	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1	up_AFEM_EC
GO:0009108	0.671	0.505	5	68	coenzyme biosynthetic process	BP	1	ACLY,ELOVL1,ELOVL6,PDHA1,PDSS1	down_ACOR_VSMC
GO:0048639	0.671	0.557	3	39	positive regulation of developmental growth	BP	1	PPARD,EZR,GLI1	down_ACOR_VSMC
GO:0009743	0.671	0.557	3	40	response to carbohydrate	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0030856	0.671	0.556	3	41	regulation of epithelial cell differentiation	BP	1	CAV1,EZH2,HOXA7	down_ACOR_VSMC
GO:0001892	0.671	0.557	3	35	embryonic placenta development	BP	1	GJB5,ZFP36L1,CITED2	up_VSAP_EC
GO:0043467	0.671	0.558	3	35	regulation of generation of precursor metabolites	BP	1	C1QTNF2,PASK,DDIT4	up_VSAP_EC
GO:0014066	0.671	0.607	2	26	regulation of phosphatidylinositol 3-	BP	1	NEDD4,PPARD	down_ACOR_VSMC
GO:0017038	0.671	0.599	2	96	protein import	BP	1	LEP,CRY2	up_AFEM_EC
GO:0070838	0.671	0.6	2	96	divalent metal ion transport	BP	1	CAMK2A,NIPAL1	up_AFEM_EC
GO:0030510	0.671	0.606	2	27	regulation of BMP signaling pathway	BP	1	CTDSPL2,SKIL	up_VCAV_EC
GO:0072332	0.671	0.606	2	29	intrinsic apoptotic signaling pathway by p53	BP	1	USP28,PMAIP1	up_VCAV_EC
GO:0051353	0.671	0.711	1	13	positive regulation of oxidoreductase activity	BP	1	NUS1	down_ACOR_VSMC
GO:0060419	0.671	0.704	1	22	heart growth	BP	1	BMPR1A	down_VCAV_EC
GO:0009605	0.671	0.71	1	538	response to external stimulus	BP	1	HSD3B7	down_VPOR_EC
GO:0035065	0.671	0.708	1	17	regulation of histone acetylation	BP	1	IWS1	down_VSAP_EC

GO:0050850	0.671	0.714	1	11	positive regulation of calcium-mediated	BP	1	C28H10orf71	up_ACOR_VSMC
GO:1901984	0.671	0.715	1	11	negative regulation of protein acetylation	BP	1	PARK7	up_ACOR_VSMC
GO:1901565	0.671	0.708	1	442	organonitrogen compound catabolic	BP	1	LNPEP	up_AORT_EC
GO:0007029	0.671	0.708	1	16	endoplasmic reticulum organization	BP	1	CAV2	up_VCAV_EC
GO:0031324	0.671	0.716	1	735	negative regulation of cellular metabolic process	BP	1	LIMK1	up_VCAV_VSMC
GO:0065009	0.671	0.716	1	735	regulation of molecular function	BP	1	LIMK1	up_VCAV_VSMC
GO:2001169	0.671	0.714	1	11	regulation of ATP biosynthetic process	BP	1	DDIT4	up_VSAP_EC
GO:0030513	0.671	0.714	1	11	positive regulation of BMP signaling pathway	BP	1	ACVRL1	up_VSAP_EC
GO:2001022	0.671976855	0.69967	1	42	positive regulation of response to DNA damage	BP	1	PRKCD	up_ACOR_EC
GO:0046907	0.672	0.385	49	536	intracellular transport	BP	1	EXPH5,SH3TC2,RHOT1,ACTN2,LEP,TCAF1,USP6NL,FBXL20,FERMT1,BMP4,EVI5L,ABCA1,SCARB2,SEC24B,STX11,TMEM108,IFT43,KLHL20,CDKN1A,PTPN22,OS9,SCP2,SCG5,APP,PSEN1,SGSM2,SYNJ2BP,PIK3C3,LAMP2,JUP,RAB11B,DYNC1I2,AKTIP,LMTK2,AP2B1,SAR1B,HERPUD1,SUN1,VPS26A,INPP5K,FAF2,PREPL,RPAIN,DYNC1I1,PARK7,ENSCAFG00000013536,BVES,LMF1,PTPN14	up_ACOR_VSMC
GO:0006812	0.672	0.424	17	222	cation transport	BP	1	NNT,NEDD4,HOXA3,CAV1,SLC30A1,NKAIN1,TFRC,GSTO1,CDK2,NIPA2,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0007507	0.672	0.424	17	194	heart development	BP	1	FZD1,WNT11,AXIN2,ACACB,DLL1,OSR1,SAV1,ZFP36L1,SHOX2,LOX,SMG9,ACVRL1,PPP3CB,MAP2K2,TGFBR2,NPRL3,CITED2	up_VSAP_EC
GO:0001933	0.672	0.438	13	146	negative regulation of protein phosphorylation	BP	1	TBC1D10C,CEP85,SLIT2,ABL1,PLPP3,F2RL1,MYC,RTN4RL1,FBXO7,FBLN1,QARS,NCK1,LATS2	up_VSAP_EC
GO:0034655	0.672	0.486	6	135	nucleobase-containing compound catabolic	BP	1	SAMD4B,ENTPD3,ZFP36L1,PYM1,FBH1,ACAT1	down_VCAV_EC
GO:0051171	0.672	0.505	6	1697	regulation of nitrogen compound metabolic	BP	1	NR1H4,PLCL1,PCSK1N,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0050900	0.672	0.522	4	89	leukocyte migration	BP	1	HSD3B7,THY1,B4GALT1,RAC2	down_VCAV_EC
GO:0014065	0.672	0.556	3	39	phosphatidylinositol 3-kinase signaling	BP	1	NEDD4,PPARD,PIK3CD	down_ACOR_VSMC
GO:0051254	0.672	0.553	3	431	positive regulation of RNA metabolic process	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0070887	0.672	0.558	3	775	cellular response to chemical stimulus	BP	1	TLR2,CAV1,FGF5	up_VSAP_VSMC
GO:0010921	0.672	0.601	2	46	regulation of phosphatase activity	BP	1	PDGFRB,SPRED1	down_VCAV_EC
GO:2000112	0.672	0.617	2	1119	regulation of cellular macromolecule biosynthetic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0007368	0.672	0.603	2	37	determination of left/right symmetry	BP	1	TMED2,HIF1A	down_VSAP_EC
GO:0071705	0.672	0.605	2	582	nitrogen compound transport	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0043170	0.672	0.817	1	2980	macromolecule metabolic process	BP	1	CST3	down_AORT_EC
GO:0014855	0.672	0.703	1	22	striated muscle cell proliferation	BP	1	BMPR1A	down_VCAV_EC
GO:0048468	0.672	0.708	1	553	cell development	BP	1	CITED2	down_VPOR_EC
GO:0001709	0.672	0.713	1	11	cell fate determination	BP	1	BMP4	up_ACOR_VSMC
GO:0021983	0.672	0.713	1	11	pituitary gland development	BP	1	BMP4	up_ACOR_VSMC
GO:0045668	0.672	0.714	1	11	negative regulation of osteoblast differentiation	BP	1	SMAD6	up_ACOR_VSMC
GO:0071453	0.672	0.699	1	46	cellular response to oxygen levels	BP	1	ANGPT4	up_AFEM_EC
GO:0045806	0.672	0.708	1	15	negative regulation of endocytosis	BP	1	HMGB1	up_VCAV_EC
GO:0050772	0.672	0.71	1	13	positive regulation of axonogenesis	BP	1	RAB11A	up_VCAV_EC
GO:0001709	0.672	0.713	1	11	cell fate determination	BP	1	EBF2	up_VSAP_EC

GO:0033554	0.673	0.38	57	708	cellular response to stress	BP	1	EPHB1,PLK2,CXCL8,TNFAIP3,MAP3K11,LRRC8D,STK10,SH2D3C,CD34,MEF2C,ATF3,TLR4,EDN1,RALB,PSME4,FIGNL1,MTSS1,ARG2,MTOR,MAP3K3,BMP2,SLK,MAPK13,PAK2,THOC1,TLR3,APOD,NCK1,TIMELESS,PDIA5,GUCY1B1,PTGS2,ETAA1,USP28,TAOK1,GCH1,ENSCAFG00000002897,ASF1A,HMGB1,PMAIP1,BLM,RIPK1,SMC5,USP13,RAD21,RAD17,SKIL,CUL4A,HIF1A,ATRX,HP1BP3,TOPBP1,RBBP6,VASH1,ATP2A1,ARHGEF2,GINS4	up_VCAV_EC
GO:0015931	0.673	0.504	5	59	nucleobase-containing compound transport	BP	1	ZFP36L1,NUP98,SNUPN,FLOT1,TGFBR2	up_VSAP_EC
GO:0030833	0.673	0.504	5	59	regulation of actin filament polymerization	BP	1	SLIT2,CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:2000116	0.673	0.55	3	67	regulation of cysteine-type endopeptidase	BP	1	CST3,PARK7,IFT57	down_VCAV_EC
GO:0017015	0.673	0.554	3	40	regulation of transforming growth factor beta receptor signaling	BP	1	FERMT1,SKIL,ZEB1	up_VCAV_EC
GO:1903844	0.673	0.554	3	40	regulation of cellular response to transforming growth factor beta	BP	1	FERMT1,SKIL,ZEB1	up_VCAV_EC
GO:0006446	0.673	0.604	2	27	regulation of translational initiation	BP	1	PPP1R15B,RBM14	down_ACOR_VSMC
GO:0002040	0.673	0.599	2	46	sprouting angiogenesis	BP	1	SPRED1,GREM1	down_VCAV_EC
GO:0050790	0.673	0.603	2	532	regulation of catalytic activity	BP	1	MAP2K6,TIAM1	up_VFEM_EC
GO:0048583	0.673	0.616	2	1095	regulation of response to stimulus	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0032649	0.673	0.606	2	23	regulation of interferon-gamma production	BP	1	CD274,ABL1	up_VSAP_EC
GO:0046718	0.673	0.709	1	13	viral entry into host cell	BP	1	CAV1	down_ACOR_VSMC
GO:0097734	0.673	0.709	1	13	extracellular exosome biogenesis	BP	1	SDC1	down_ACOR_VSMC
GO:1990182	0.673	0.709	1	13	exosomal secretion	BP	1	SDC1	down_ACOR_VSMC
GO:0033627	0.673	0.702	1	22	cell adhesion mediated by integrin	BP	1	FBN1	down_VCAV_EC
GO:0051341	0.673	0.702	1	22	regulation of oxidoreductase activity	BP	1	PARK7	down_VCAV_EC
GO:0009888	0.673	0.708	1	545	tissue development	BP	1	CITED2	down_VPOR_EC
GO:0034641	0.673	0.77	1	2171	cellular nitrogen compound metabolic	BP	1	MOSPD1	down_VFEM_EC
GO:0006687	0.673	0.704	1	18	glycosphingolipid metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0000038	0.673	0.71	1	12	very long-chain fatty acid metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0000045	0.673	0.698	1	46	autophagosome assembly	BP	1	RAB7A	up_AFEM_EC
GO:0009142	0.673	0.699	1	46	nucleoside triphosphate biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0001958	0.673	0.712	1	11	endochondral ossification	BP	1	PEX7	up_VSAP_EC
GO:0090207	0.673	0.712	1	11	regulation of triglyceride metabolic process	BP	1	LMF1	up_VSAP_EC
GO:0021846	0.673	0.712	1	11	cell proliferation in forebrain	BP	1	EMX2	up_VSAP_EC
GO:0036075	0.673	0.712	1	11	replacement ossification	BP	1	PEX7	up_VSAP_EC
GO:0060914	0.673	0.712	1	11	heart formation	BP	1	AXIN2	up_VSAP_EC
GO:0016241	0.67328766	0.69835	1	41	regulation of macroautophagy	BP	1	CHMP4B	up_ACOR_EC
GO:0016567	0.674	0.419	18	232	protein ubiquitination	BP	1	USP4,UBE2S,U2AF2,SLC29A1,UBE2T,CAV1,FANCI,UHRF1,RNF152,BRCA1,UBE2J2,DTL,UBE2K,CDC20,UBE2C,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0051716	0.674	0.44	15	2001	cellular response to stimulus	BP	1	C3AR1,BARX1,CXHXorf57,ARHGEF2,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,PDE1C,STK17B,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0050877	0.674	0.456	9	164	nervous system process	BP	1	SLC1A4,AARS,RPGR,HIF1A,UBA6,APOE,UBA5,HTT,ARF4	down_VSAP_EC
GO:0017038	0.674	0.475	7	96	protein import	BP	1	HCLS1,TMEM173,FERMT1,PPP3CA,APOD,NUP133,IPO11	up_VCAV_EC
GO:0048863	0.674	0.487	6	70	stem cell differentiation	BP	1	FZD1,HOXA7,OSR1,ZFP36L2,CITED2,LBH	up_VSAP_EC

GO:0009141	0.674	0.499	5	110	nucleoside triphosphate metabolic process	BP	1	ENTPD3,ATP5MC1,UQCR10,ADK,PARK7	down_VCAV_EC
GO:0051048	0.674	0.552	3	42	negative regulation of secretion	BP	1	ARG2,RSC1A1,CD200	up_VCAV_EC
GO:0014074	0.674	0.604	2	26	response to purine-containing compound	BP	1	PDXP,EZR	down_ACOR_VSMC
GO:0051963	0.674	0.603	2	26	regulation of synapse assembly	BP	1	SIX4,TPBG	down_ACOR_VSMC
GO:0046128	0.674	0.605	2	23	purine ribonucleoside metabolic process	BP	1	NT5C2,PNP	up_VSAP_EC
GO:0072091	0.674	0.604	2	24	regulation of stem cell proliferation	BP	1	ZFP36L1,FBLN1	up_VSAP_EC
GO:0034660	0.674	0.699	1	211	ncRNA metabolic process	BP	1	WDR12	down_ACOR_EC
GO:0035794	0.674	0.708	1	13	positive regulation of mitochondrial membrane permeability	BP	1	SLC25A5	down_ACOR_VSMC
GO:0042130	0.674	0.708	1	13	negative regulation of T cell proliferation	BP	1	ARG2	down_ACOR_VSMC
GO:1905710	0.674	0.708	1	13	positive regulation of membrane permeability	BP	1	SLC25A5	down_ACOR_VSMC
GO:0048661	0.674	0.704	1	17	positive regulation of smooth muscle cell	BP	1	SULF1	down_VSAP_EC
GO:0072395	0.674	0.711	1	11	signal transduction involved in cell cycle	BP	1	CDKN1A	up_ACOR_VSMC
GO:0072401	0.674	0.711	1	11	signal transduction involved in DNA integrity	BP	1	CDKN1A	up_ACOR_VSMC
GO:0072422	0.674	0.711	1	11	signal transduction involved in DNA damage	BP	1	CDKN1A	up_ACOR_VSMC
GO:0010952	0.674	0.697	1	46	positive regulation of peptidase activity	BP	1	F3	up_AFEM_EC
GO:0070897	0.674	0.705	1	16	transcription preinitiation complex assembly	BP	1	HMGB1	up_VCAV_EC
GO:0043269	0.674	0.697	1	135	regulation of ion transport	BP	1	HOXA3	up_VPOR_EC
GO:0071417	0.674	0.696	1	142	cellular response to organonitrogen	BP	1	ARHGEF2	up_VPOR_EC
GO:1900077	0.674	0.711	1	11	negative regulation of cellular response to	BP	1	NCK1	up_VSAP_EC
GO:1900181	0.674	0.711	1	11	negative regulation of protein localization to	BP	1	FBXO4	up_VSAP_EC
GO:0001568	0.674	0.699	1	252	blood vessel development	BP	1	CAV1	up_VSAP_VSMC
GO:0043066	0.674	0.698	1	253	negative regulation of apoptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:0006413	0.674046324	0.69739	1	42	translational initiation	BP	1	KLHL25	up_ACOR_EC
GO:0006694	0.674526456	0.69686	1	42	steroid biosynthetic process	BP	1	NR1H4	up_ACOR_EC
GO:0010506	0.674864804	0.59475	2	86	regulation of autophagy	BP	1	CHMP4B,TP53INP2	up_ACOR_EC
GO:0051254	0.675	0.404	25	431	positive regulation of RNA metabolic process	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:1902679	0.675	0.426	15	329	negative regulation of RNA biosynthetic process	BP	1	NAB2,KANK2,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,LOXL3,TSC22D3,GLIS2,SHC1,GREM1,THRB	down_VCAV_EC
GO:1903507	0.675	0.426	15	329	negative regulation of nucleic acid-templated transcription	BP	1	NAB2,KANK2,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,LOXL3,TSC22D3,GLIS2,SHC1,GREM1,THRB	down_VCAV_EC
GO:0019538	0.675	0.444	13	1713	protein metabolic process	BP	1	OSTC,OGA,ARHGEF2,ASPN,ACVR2A,RSL24D1,RPL10L,KLHL28,PUM3,EIF5,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0019932	0.675	0.474	7	82	second-messenger-mediated signaling	BP	1	ADGRD1,PTGFR,TBC1D10C,CAMKK2,PDK2,TBXA2R,PPP3CB	up_VSAP_EC
GO:0044248	0.675	0.503	5	691	cellular catabolic process	BP	1	FBP1,MTDH,ABHD5,USP33,RNF6	up_VPOR_EC
GO:2000377	0.675	0.552	3	41	regulation of reactive oxygen species metabolic	BP	1	CAV1,ARG2,PRCP	down_ACOR_VSMC
GO:0061333	0.675	0.553	3	35	renal tubule morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0022406	0.675	0.553	3	35	membrane docking	BP	1	SCFD2,STX4,VPS11	up_VSAP_EC
GO:0007044	0.675	0.601	2	27	cell-substrate junction assembly	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:1901799	0.675	0.603	2	24	negative regulation of proteasomal protein catabolic process	BP	1	OS9,PARK7	up_ACOR_VSMC

GO:0071496	0.675	0.594	2	97	cellular response to external stimulus	BP	1	CLEC16A,POSTN	up_AFEM_EC
GO:0031341	0.675	0.707	1	13	regulation of cell killing	BP	1	FAM49B	down_ACOR_VSMC
GO:0051646	0.675	0.708	1	12	mitochondrion localization	BP	1	TRAK1	down_ACOR_VSMC
GO:0030513	0.675	0.71	1	11	positive regulation of BMP signaling pathway	BP	1	BMP4	up_ACOR_VSMC
GO:0042092	0.675	0.71	1	11	type 2 immune response	BP	1	NOD2	up_ACOR_VSMC
GO:0060343	0.675	0.71	1	11	trabecula formation	BP	1	EGLN1	up_ACOR_VSMC
GO:0090314	0.675	0.71	1	11	positive regulation of protein targeting to	BP	1	TCAF1	up_ACOR_VSMC
GO:0019941	0.675	0.698	1	258	modification-dependent protein catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:0032446	0.675	0.698	1	255	protein modification by small protein conjugation	BP	1	EYA1	up_VFEM_EC
GO:0009648	0.675	0.71	1	11	photoperiodism	BP	1	NR2F6	up_VSAP_EC
GO:0043153	0.675	0.71	1	11	entrainment of circadian clock by photoperiod	BP	1	NR2F6	up_VSAP_EC
GO:0072395	0.675	0.71	1	11	signal transduction involved in cell cycle	BP	1	CRADD	up_VSAP_EC
GO:0072401	0.675	0.71	1	11	signal transduction involved in DNA integrity	BP	1	CRADD	up_VSAP_EC
GO:0072422	0.675	0.71	1	11	signal transduction involved in DNA damage	BP	1	CRADD	up_VSAP_EC
GO:0030317	0.675	0.71	1	11	flagellated sperm motility	BP	1	CFAP69	up_VSAP_EC
GO:0097722	0.675	0.71	1	11	sperm motility	BP	1	CFAP69	up_VSAP_EC
GO:0060341	0.675	0.697	1	255	regulation of cellular localization	BP	1	CAV1	up_VSAP_VSMC
GO:0030010	0.675463434	0.69594	1	41	establishment of cell polarity	BP	1	BRSK1	up_ACOR_EC
GO:1901861	0.675917244	0.69544	1	41	regulation of muscle tissue development	BP	1	TBX5	up_ACOR_EC
GO:0009893	0.676	0.41	22	995	positive regulation of metabolic process	BP	1	HOXA9,CMKLR1,LEP,LBH,PRR16,DLL1,F3,MLLT11,THRB,GREM1,NFE2L1,TENT5C,CLEC16A,MYBL1,DCUN1D3,BVES,RAB7A,AXIN2,PPARGC1A,CCL5,ADAM17,TNC	up_AFEM_EC
GO:0051222	0.676	0.463	8	103	positive regulation of protein transport	BP	1	HCLS1,TMEM173,FERMT1,GATA3,CTDSPL2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0002253	0.676	0.473	7	92	activation of immune response	BP	1	HMGB1,IRAK1,MNDA,CAV1,CACTIN,EZR,RBM14	down_ACOR_VSMC
GO:0031589	0.676	0.473	7	93	cell-substrate adhesion	BP	1	GREM1,HOXA7,PPARD,RAC1,EMP2,CORO1A,RADIL	down_ACOR_VSMC
GO:0030003	0.676	0.47	7	157	cellular cation homeostasis	BP	1	PRNP,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0015711	0.676	0.474	7	81	organic anion transport	BP	1	SLC16A12,OSR1,ABCB11,SLC25A12,SLC27A6,CTNS,SLC10A6	up_VSAP_EC
GO:0002685	0.676	0.52	4	55	regulation of leukocyte migration	BP	1	HMGB1,MMP14,HOXA7,RAC1	down_ACOR_VSMC
GO:0010811	0.676	0.551	3	36	positive regulation of cell-substrate adhesion	BP	1	ABL1,EMP2,ECM2	up_VSAP_EC
GO:0009410	0.676	0.601	2	27	response to xenobiotic stimulus	BP	1	MCM7,GSTO1	down_ACOR_VSMC
GO:0036473	0.676	0.601	2	27	cell death in response to oxidative stress	BP	1	SIGMAR1,MELK	down_ACOR_VSMC
GO:0060349	0.676	0.597	2	38	bone morphogenesis	BP	1	SERPINH1,CHSY1	down_VSAP_EC
GO:0072511	0.676	0.593	2	97	divalent inorganic cation transport	BP	1	CAMK2A,NIPAL1	up_AFEM_EC
GO:0006412	0.676	0.696	1	245	translation	BP	1	RPSA	down_ACOR_EC
GO:0008542	0.676	0.706	1	13	visual learning	BP	1	HMGCR	down_ACOR_VSMC
GO:0030201	0.676	0.708	1	12	heparan sulfate proteoglycan metabolic	BP	1	XYLT1	down_ACOR_VSMC
GO:0060711	0.676	0.7	1	21	labyrinthine layer development	BP	1	ZFP36L1	down_VCAV_EC
GO:0071230	0.676	0.699	1	23	cellular response to amino acid stimulus	BP	1	COL6A1	down_VCAV_EC
GO:1904019	0.676	0.699	1	22	epithelial cell apoptotic process	BP	1	ZFP36L1	down_VCAV_EC
GO:0051567	0.676	0.71	1	10	histone H3-K9 methylation	BP	1	ATRX	up_ACOR_VSMC
GO:1900077	0.676	0.709	1	11	negative regulation of cellular response to	BP	1	INPP5K	up_ACOR_VSMC

GO:0022900	0.676	0.695	1	46	electron transport chain	BP	1	PPARGC1A	up_AFEM_EC
GO:0046903	0.676	0.697	1	255	secretion	BP	1	CA9	up_VFEM_EC
GO:0006584	0.676	0.709	1	11	catecholamine metabolic process	BP	1	SULT1A1	up_VSAP_EC
GO:0009712	0.676	0.709	1	11	catechol-containing compound metabolic	BP	1	SULT1A1	up_VSAP_EC
GO:0042092	0.676	0.709	1	11	type 2 immune response	BP	1	STAT6	up_VSAP_EC
GO:0050650	0.676	0.709	1	11	chondroitin sulfate proteoglycan biosynthetic	BP	1	CHST7	up_VSAP_EC
GO:0060706	0.676	0.709	1	11	cell differentiation involved in embryonic	BP	1	GJB5	up_VSAP_EC
GO:0010556	0.677	0.363	105	1137	regulation of macromolecule biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,GLIS2,DDR2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,ANKHD1,TRERF1,E2F4,NPAS2,LIMD1,RPUSD4,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772,SOAT1	up_VSAP_EC
GO:0044255	0.677	0.409	21	293	cellular lipid metabolic process	BP	1	TEK,ADGRF5,KIT,PDGFB,GK5,EDN1,PTGS1,SERINC5,SPTLC2,SAMD8,CREM,ST3GAL6,ENSCAFG00000010596,SH3GLB1,ELOVL7,APOD,PTGS2,PLCG2,IMPA1,PIP5K1B,ALDH1A3	up_VCAV_EC
GO:0006753	0.677	0.44	11	211	nucleoside phosphate metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ENTPD4,ALDOC,PAPSS1,AK5,CMPK1	down_VSAP_EC
GO:0071407	0.677	0.447	10	129	cellular response to organic cyclic compound	BP	1	TFPI,NEDD4,INSIG1,CAV1,RAD51,THRAP3,EZH2,CDK4,PDXP,EZR	down_ACOR_VSMC
GO:0000278	0.677	0.47	7	331	mitotic cell cycle	BP	1	GAS1,OVOL1,CAMK2A,CYLD,MYBL1,DCUN1D3,FAP	up_AFEM_EC
GO:0016571	0.677	0.55	3	39	histone methylation	BP	1	PRMT1,EZH2,FBL	down_ACOR_VSMC
GO:0006355	0.677	0.557	3	974	regulation of transcription, DNA-	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0008543	0.677	0.599	2	27	fibroblast growth factor receptor signaling	BP	1	IQGAP1,FGF5	down_ACOR_VSMC
GO:0030148	0.677	0.599	2	28	sphingolipid biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0032648	0.677	0.602	2	23	regulation of interferon-beta production	BP	1	TLR3,PTPN22	up_ACOR_VSMC
GO:0050709	0.677	0.599	2	28	negative regulation of protein secretion	BP	1	ARG2,CD200	up_VCAV_EC
GO:0009607	0.677	0.695	1	232	response to biotic stimulus	BP	1	LYN	down_ACOR_EC
GO:0046470	0.677	0.705	1	13	phosphatidylcholine metabolic process	BP	1	ACSL3	down_ACOR_VSMC
GO:0072202	0.677	0.705	1	13	cell differentiation involved in metanephros	BP	1	GREM1	down_ACOR_VSMC
GO:0002287	0.677	0.701	1	17	alpha-beta T cell activation involved in	BP	1	SOCS5	down_VSAP_EC
GO:0002292	0.677	0.701	1	17	T cell differentiation involved in immune	BP	1	SOCS5	down_VSAP_EC
GO:0002293	0.677	0.701	1	17	alpha-beta T cell differentiation involved in	BP	1	SOCS5	down_VSAP_EC
GO:0002294	0.677	0.701	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	SOCS5	down_VSAP_EC
GO:0002534	0.677	0.7	1	18	cytokine production involved in inflammatory	BP	1	GBP5	down_VSAP_EC
GO:0032652	0.677	0.7	1	18	regulation of interleukin-1 production	BP	1	NR1H4	down_VSAP_EC
GO:0042093	0.677	0.701	1	17	T-helper cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0071260	0.677	0.699	1	19	cellular response to mechanical stimulus	BP	1	BNIP3	down_VSAP_EC
GO:0051125	0.677	0.708	1	11	regulation of actin nucleation	BP	1	WASL	up_ACOR_VSMC

GO:0002703	0.677	0.693	1	47	regulation of leukocyte mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0051983	0.677	0.694	1	47	regulation of chromosome segregation	BP	1	AXIN2	up_AFEM_EC
GO:0035384	0.677	0.703	1	14	thioester biosynthetic process	BP	1	ELOVL7	up_VCAV_EC
GO:0071616	0.677	0.703	1	14	acyl-CoA biosynthetic process	BP	1	ELOVL7	up_VCAV_EC
GO:1902808	0.677	0.706	1	12	positive regulation of cell cycle G1/S phase	BP	1	CUL4A	up_VCAV_EC
GO:1901698	0.677	0.696	1	266	response to nitrogen compound	BP	1	AVPR1A	up_VFEM_EC
GO:1902531	0.677	0.704	1	536	regulation of intracellular signal transduction	BP	1	SLIT2	up_VPUL_VSMC
GO:0048013	0.677	0.708	1	11	ephrin receptor signaling pathway	BP	1	NCK1	up_VSAP_EC
GO:0043243	0.677	0.708	1	11	positive regulation of protein complex	BP	1	F2RL1	up_VSAP_EC
GO:0051640	0.6770946	0.51496	4	174	organelle localization	BP	1	CDH3,DYNC1I1,PREB,CHMP4B	up_ACOR_EC
GO:0099504	0.677367384	0.6937	1	42	synaptic vesicle cycle	BP	1	BRSK1	up_ACOR_EC
GO:2000112	0.677393177	0.39959	28	1119	regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,PKIB,SOX9,PKNOX2,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:1903047	0.678	0.41	20	257	mitotic cell cycle process	BP	1	PLK2,PDGFB,EDN1,RAB11A,PPP3CA,MZT1,STMN1,CENPC,TAOK1,BLM,SMC5,RAD21,RAD17,USP37,CUL4A,ZW10,ATRX,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0010631	0.678	0.453	9	118	epithelial cell migration	BP	1	HMGB1,ANLN,GREM1,PRCP,PPARD,EMP2,NUP188,NUS1,AMOTL1	down_ACOR_VSMC
GO:0090132	0.678	0.453	9	118	epithelium migration	BP	1	HMGB1,ANLN,GREM1,PRCP,PPARD,EMP2,NUP188,NUS1,AMOTL1	down_ACOR_VSMC
GO:0071214	0.678	0.461	8	93	cellular response to abiotic stimulus	BP	1	MFAP4,GJA1,TLR3,TP53INP1,ANKRD1,BNIP3,CDKN1A,RAB11B	up_ACOR_VSMC
GO:0104004	0.678	0.461	8	93	cellular response to environmental stimulus	BP	1	MFAP4,GJA1,TLR3,TP53INP1,ANKRD1,BNIP3,CDKN1A,RAB11B	up_ACOR_VSMC
GO:0034976	0.678	0.495	5	112	response to endoplasmic reticulum stress	BP	1	ENSCAFG00000014978,PDIA4,PARK7,SEC61B,HM13	down_VCAV_EC
GO:0001649	0.678	0.518	4	54	osteoblast differentiation	BP	1	FBXO5,GREM1,TWIST2,GLI1	down_ACOR_VSMC
GO:0030509	0.678	0.52	4	47	BMP signaling pathway	BP	1	FZD1,ABL1,LRP4,ACVRL1	up_VSAP_EC
GO:0055076	0.678	0.547	3	44	transition metal ion homeostasis	BP	1	CP,SLC39A8,HIF1A	up_VCAV_EC
GO:0010522	0.678	0.6	2	24	regulation of calcium ion transport into cytosol	BP	1	PRKCE,CHD7	up_ACOR_VSMC
GO:0051702	0.678	0.6	2	24	interaction with symbiont	BP	1	F2RL1,INPP5K	up_ACOR_VSMC
GO:0090329	0.678	0.6	2	25	regulation of DNA-dependent DNA	BP	1	BLM,ATRX	up_VCAV_EC
GO:1900407	0.678	0.599	2	24	regulation of cellular response to oxidative	BP	1	FZD1,FBXO7	up_VSAP_EC
GO:0030865	0.678	0.704	1	13	cortical cytoskeleton organization	BP	1	EZR	down_ACOR_VSMC
GO:0035710	0.678	0.698	1	22	CD4-positive, alpha-beta T cell activation	BP	1	LOXL3	down_VCAV_EC
GO:0043507	0.678	0.697	1	23	positive regulation of JUN kinase activity	BP	1	SASH1	down_VCAV_EC
GO:0006336	0.678	0.706	1	11	DNA replication-independent nucleosome	BP	1	ATRX	up_ACOR_VSMC
GO:0090207	0.678	0.707	1	11	regulation of triglyceride metabolic process	BP	1	LMF1	up_ACOR_VSMC
GO:0055001	0.678	0.693	1	47	muscle cell development	BP	1	BVES	up_AFEM_EC
GO:1903008	0.678	0.693	1	47	organelle disassembly	BP	1	CLEC16A	up_AFEM_EC
GO:0019752	0.678	0.695	1	283	carboxylic acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0006220	0.678	0.702	1	14	pyrimidine nucleotide metabolic process	BP	1	DCK	up_VCAV_EC
GO:0009395	0.678	0.705	1	12	phospholipid catabolic process	BP	1	PLCG2	up_VCAV_EC
GO:0051489	0.678	0.702	1	14	regulation of filopodium assembly	BP	1	FSCN1	up_VCAV_EC
GO:0060317	0.678	0.706	1	11	cardiac epithelial to mesenchymal transition	BP	1	TGFBR2	up_VSAP_EC

GO:0009058	0.678013763	0.38482	48	1910	biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PORCN,FZD5,CCDC3,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PTGDS,GUCY1B1,PIAS1,CHPT1,MAVS,FOXC2,PIGS,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,AZIN2,AGPAT2,PRKCD,PM20D1,EFEMP1,TLE2	up_ACOR_EC
GO:0071407	0.678886392	0.54203	3	129	cellular response to organic cyclic compound	BP	1	AQP1,PAK3,MAVS	up_ACOR_EC
GO:0007041	0.678999766	0.692	1	41	lysosomal transport	BP	1	VPS16	up_ACOR_EC
GO:0001816	0.679	0.423	15	194	cytokine production	BP	1	HMGB1,IRAK1,SLC29A1,DHX33,ARG2,FAM49B,RAC1,IQGAP1,CACTIN,HMGB2,EZR,POLR3F,BAP1,MAST2,ARHGEF2	down_ACOR_VSMC
GO:0030258	0.679	0.482	6	71	lipid modification	BP	1	LEP,LCAT,PPARGC1A,PLPP2,ACAD11,INPP5K	up_ACOR_VSMC
GO:1901362	0.679	0.528	4	1293	organic cyclic compound biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0009266	0.679	0.546	3	43	response to temperature stimulus	BP	1	EPHB1,CD34,MMP24	up_VCAV_EC
GO:1903506	0.679	0.554	3	977	regulation of nucleic acid-templated transcription	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0007416	0.679	0.594	2	36	synapse assembly	BP	1	LRRTM2,SIX4	down_VSAP_EC
GO:0110053	0.679	0.589	2	98	regulation of actin filament organization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:1902531	0.679	0.595	2	536	regulation of intracellular signal transduction	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0045047	0.679	0.701	1	14	protein targeting to ER	BP	1	TRAM1	down_ACOR_VSMC
GO:0051187	0.679	0.703	1	13	cofactor catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0061099	0.679	0.702	1	13	negative regulation of protein tyrosine kinase	BP	1	CAV1	down_ACOR_VSMC
GO:0072599	0.679	0.701	1	14	establishment of protein localization to endoplasmic reticulum	BP	1	TRAM1	down_ACOR_VSMC
GO:0000271	0.679	0.696	1	22	polysaccharide biosynthetic process	BP	1	AKT2	down_VCAV_EC
GO:0043124	0.679	0.698	1	17	negative regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4	down_VSAP_EC
GO:0046513	0.679	0.698	1	19	ceramide biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0060760	0.679	0.699	1	17	positive regulation of response to cytokine	BP	1	ADAM17	down_VSAP_EC
GO:0035176	0.679	0.706	1	11	social behavior	BP	1	CLN8	up_ACOR_VSMC
GO:0051057	0.679	0.706	1	11	positive regulation of small GTPase mediated signal transduction	BP	1	F2RL1	up_ACOR_VSMC
GO:0051703	0.679	0.706	1	11	intraspecies interaction between organisms	BP	1	CLN8	up_ACOR_VSMC
GO:0055085	0.679	0.695	1	284	transmembrane transport	BP	1	NR1H4	up_APUL_EC
GO:0043113	0.679	0.704	1	12	receptor clustering	BP	1	RELN	up_VCAV_EC
GO:0050673	0.679	0.691	1	135	epithelial cell proliferation	BP	1	ACVR2A	up_VPOR_EC
GO:0071242	0.679	0.706	1	11	cellular response to ammonium ion	BP	1	CHRM1	up_VSAP_EC
GO:0000902	0.679	0.694	1	266	cell morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0002831	0.679565455	0.69124	1	42	regulation of response to biotic stimulus	BP	1	MAVS	up_ACOR_EC

GO:0009889	0.68	0.36	110	1190	regulation of biosynthetic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,ANKHD1,TRERF1,E2F4,NPAS2,LIMD1,RPUSD4,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,CYBA,ZNF205,NCOA2,EIF3K,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,ZNF517,ASS1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772,SOAT1	up_VSAP_EC
GO:0044085	0.68	0.372	61	1076	cellular component biogenesis	BP	1	VEGFA,CELF1,NR1H4,C1QTNF6,ACTN1,VASP,SEC24D,PTPN11,EXOC5,FSCN1,MZT1,DPYSL3,FBLIM1,ANKRA2,SRP54,WDR1,MYO1C,MSN,RPGR,DYNLL1,TUBB,MRPL1,TNIK,PRPF3,DDX39B,BRD2,CNOT7,ACTR3,CTNNB1,KPNB1,ANLN,CRYAB,ENSCAFG00000002015,APOE,PLOD3,PDCD11,KLF5,STRAP,DDIT3,TWF1,PLEKHG2,TLN1,PLS3,GSK3B,GBP5,SH3GLB1,SDC4,HTT,REST,EIF2S1,PRMT1,DISC1,CLTC,LRRTM2,CAPG,SIX4,RSL24D1,NRP1,TNFAIP1,SEC13,MYBPC2	down_VSAP_EC
GO:0032880	0.68	0.432	12	266	regulation of protein localization	BP	1	GPAM,LRP1,PRNP,CLIP3,ENSCAFG00000014978,AKT2,TRIM8,GLI3,PARK7,MAVS,CDH2,GLIS2	down_VCAV_EC
GO:0002221	0.68	0.592	2	46	pattern recognition receptor signaling	BP	1	CYBA,RAB7B	down_VCAV_EC
GO:0002758	0.68	0.592	2	46	innate immune response-activating signal	BP	1	CYBA,RAB7B	down_VCAV_EC
GO:0032680	0.68	0.593	2	36	regulation of tumor necrosis factor production	BP	1	ARHGEF2,NR1H4	down_VSAP_EC
GO:0010522	0.68	0.598	2	24	regulation of calcium ion transport into cytosol	BP	1	ABL1,CYBA	up_VSAP_EC
GO:0043043	0.68	0.692	1	247	peptide biosynthetic process	BP	1	RPSA	down_ACOR_EC
GO:0051129	0.68	0.692	1	221	negative regulation of cellular component	BP	1	ACVRL1	down_ACOR_EC
GO:0033687	0.68	0.701	1	13	osteoblast proliferation	BP	1	GREM1	down_ACOR_VSMC
GO:0038084	0.68	0.702	1	13	vascular endothelial growth factor signaling	BP	1	NUS1	down_ACOR_VSMC
GO:0001736	0.68	0.694	1	23	establishment of planar polarity	BP	1	BRSK1	down_VCAV_EC
GO:0007164	0.68	0.694	1	23	establishment of tissue polarity	BP	1	BRSK1	down_VCAV_EC
GO:0009311	0.68	0.695	1	21	oligosaccharide metabolic process	BP	1	B4GALT1	down_VCAV_EC
GO:0016233	0.68	0.695	1	22	telomere capping	BP	1	NABP2	down_VCAV_EC
GO:0042107	0.68	0.695	1	22	cytokine metabolic process	BP	1	MAST2	down_VCAV_EC
GO:0007049	0.68	0.7	1	560	cell cycle	BP	1	CITED2	down_VPOR_EC
GO:0042102	0.68	0.696	1	19	positive regulation of T cell proliferation	BP	1	TFRC	down_VSAP_EC
GO:0050919	0.68	0.707	1	10	negative chemotaxis	BP	1	SEMA5A	up_ACOR_VSMC
GO:0032715	0.68	0.705	1	11	negative regulation of interleukin-6 production	BP	1	PTPN22	up_ACOR_VSMC
GO:0009127	0.68	0.69	1	47	purine nucleoside monophosphate biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0009168	0.68	0.69	1	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0042177	0.68	0.69	1	47	negative regulation of protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0008104	0.68	0.707	1	763	protein localization	BP	1	TLR2	up_AFEM_VSMC
GO:0001836	0.68	0.697	1	18	release of cytochrome c from mitochondria	BP	1	PMAIP1	up_VCAV_EC

GO:0051052	0.68	0.69	1	145	regulation of DNA metabolic process	BP	1	CXHXorf57	up_VPOR_EC
GO:1901698	0.68	0.692	1	266	response to nitrogen compound	BP	1	CAV1	up_VSAP_VSMC
GO:0055067	0.680940692	0.68969	1	42	monovalent inorganic cation homeostasis	BP	1	SLC9A9	up_ACOR_EC
GO:0019438	0.681	0.397	28	1258	aromatic compound biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A	up_AFEM_EC
GO:0009165	0.681	0.45	9	104	nucleotide biosynthetic process	BP	1	ACACB,NADK,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,PNP,DDIT4	up_VSAP_EC
GO:0060485	0.681	0.458	8	93	mesenchyme development	BP	1	WNT11,AXIN2,OSR1,ZFP36L1,TIAM1,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0048634	0.681	0.545	3	40	regulation of muscle organ development	BP	1	GREM1,GLI1,SIX4	down_ACOR_VSMC
GO:0048856	0.681	0.563	3	1533	anatomical structure development	BP	1	SRSF6,GABPA,FSCN1	down_AFEM_EC
GO:0032984	0.681	0.541	3	70	protein-containing complex disassembly	BP	1	CLEC16A,PYM1,PLEKHH2	down_VCAV_EC
GO:0072524	0.681	0.545	3	37	pyridine-containing compound metabolic	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:2001141	0.681	0.553	3	979	regulation of RNA biosynthetic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0033045	0.681	0.591	2	38	regulation of sister chromatid segregation	BP	1	NAA10,CTNNB1	down_VSAP_EC
GO:0098781	0.681	0.597	2	22	ncRNA transcription	BP	1	ELL2,GTF3C1	up_ACOR_VSMC
GO:0010646	0.681	0.602	2	945	regulation of cell communication	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0010463	0.681	0.594	2	28	mesenchymal cell proliferation	BP	1	BMP2,ZEB1	up_VCAV_EC
GO:0030878	0.681	0.701	1	13	thyroid gland development	BP	1	HOXA3	down_ACOR_VSMC
GO:0048663	0.681	0.7	1	13	neuron fate commitment	BP	1	HOXC10	down_ACOR_VSMC
GO:0071675	0.681	0.701	1	13	regulation of mononuclear cell	BP	1	HMGB1	down_ACOR_VSMC
GO:0099024	0.681	0.701	1	13	plasma membrane invagination	BP	1	AURKB	down_ACOR_VSMC
GO:0040011	0.681	0.699	1	505	locomotion	BP	1	FSCN1	down_AFEM_EC
GO:0000462	0.681	0.694	1	22	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	MRPS11	down_VCAV_EC
GO:0032642	0.681	0.693	1	22	regulation of chemokine production	BP	1	MAVS	down_VCAV_EC
GO:0007399	0.681	0.699	1	564	nervous system development	BP	1	CITED2	down_VPOR_EC
GO:0007528	0.681	0.697	1	17	neuromuscular junction development	BP	1	SIX4	down_VSAP_EC
GO:0050922	0.681	0.704	1	11	negative regulation of chemotaxis	BP	1	NRP1	up_ACOR_VSMC
GO:0060674	0.681	0.702	1	12	placenta blood vessel development	BP	1	SPINT1	up_ACOR_VSMC
GO:0070129	0.681	0.701	1	12	regulation of mitochondrial translation	BP	1	NGRN	up_ACOR_VSMC
GO:1901985	0.681	0.703	1	11	positive regulation of protein acetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:1905037	0.681	0.689	1	47	autophagosome organization	BP	1	RAB7A	up_AFEM_EC
GO:0032879	0.681	0.705	1	767	regulation of localization	BP	1	TLR2	up_AFEM_VSMC
GO:0043489	0.681	0.7	1	13	RNA stabilization	BP	1	TENT2	up_VCAV_EC
GO:0043632	0.681	0.691	1	262	modification-dependent macromolecule catabolic	BP	1	TRIM9	up_VFEM_EC
GO:0001522	0.681	0.704	1	11	pseudouridine synthesis	BP	1	RPUSD4	up_VSAP_EC
GO:0046164	0.681	0.703	1	11	alcohol catabolic process	BP	1	INPP5E	up_VSAP_EC
GO:2001258	0.681	0.703	1	11	negative regulation of cation channel activity	BP	1	KCNE3	up_VSAP_EC
GO:0044319	0.681	0.701	1	12	wound healing, spreading of cells	BP	1	ACVRL1	up_VSAP_EC
GO:0071526	0.681	0.702	1	12	semaphorin-plexin signaling pathway	BP	1	PLXNA4	up_VSAP_EC
GO:0090504	0.681	0.701	1	12	epiboly	BP	1	ACVRL1	up_VSAP_EC

GO:0090505	0.681	0.701	1	12	epiboly involved in wound healing	BP	1	ACVRL1	up_VSAP_EC
GO:0002822	0.681293414	0.68929	1	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	FZD5	up_ACOR_EC
GO:0009605	0.682	0.396	25	538	response to external stimulus	BP	1	GPAM,PDGFRB,CFD,KANK2,CHID1,GABARAP,HSD3B7,ENSCAFG00000013404,WIPF1,SEMA3C,FKBP5,RNF216,GLI3,PARK7,SASH1,CLEC16A,BPI,CYBA,MAVS,GSDME,A2M,SHC1,RAC2,NAPEPLD,RGMA	down_VCAV_EC
GO:0000165	0.682	0.404	21	236	MAPK cascade	BP	1	CDON,ACKR3,ARHGEF5,C5AR2,TBC1D10C,ABL1,MAP3K5,CDC42EP5,PDGFD,C1QTNF2,F2RL1,ZFP36L1,TRAF7,MYC,SASH1,MYD88,FBLN1,ZFP36L2,RAF1,QARS,MAP2K2	up_VSAP_EC
GO:0016055	0.682	0.432	12	134	Wnt signaling pathway	BP	1	LGR6,ZRANB1,RECK,MLLT3,FERMT1,FGFR2,LATS2,ZNRF3,CLSTN1,FZD3,PSEN1,DISC1	up_ACOR_VSMC
GO:0198738	0.682	0.432	12	134	cell-cell signaling by wnt	BP	1	LGR6,ZRANB1,RECK,MLLT3,FERMT1,FGFR2,LATS2,ZNRF3,CLSTN1,FZD3,PSEN1,DISC1	up_ACOR_VSMC
GO:0055114	0.682	0.454	8	157	oxidation-reduction process	BP	1	ENPP1,ENSCAFG00000007260,SESN2,HIF1A,NDUFA4L2,PPP1R3C,BNIP3,GSK3B	down_VSAP_EC
GO:1903829	0.682	0.457	8	91	positive regulation of cellular protein	BP	1	LEP,TCAF1,PRKAA2,PTPN22,PARP9,PSEN1,JUP,PARK7	up_ACOR_VSMC
GO:0098813	0.682	0.456	8	102	nuclear chromosome segregation	BP	1	RAB11A,CENPC,ESCO1,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0002764	0.682	0.478	6	80	immune response-regulating signaling	BP	1	HMGB1,IRAK1,MNDA,CAV1,CACTIN,EZR	down_ACOR_VSMC
GO:0006836	0.682	0.515	4	47	neurotransmitter transport	BP	1	SLC6A4,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0072330	0.682	0.54	3	68	monocarboxylic acid biosynthetic process	BP	1	THNSL2,PARK7,RDH10	down_VCAV_EC
GO:0001933	0.682	0.538	3	146	negative regulation of protein phosphorylation	BP	1	GREM1,CYLD,LRRC15	up_AFEM_EC
GO:0010556	0.682	0.606	2	1137	regulation of macromolecule	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0006892	0.682	0.59	2	39	post-Golgi vesicle-mediated transport	BP	1	EXOC5,BLZF1	down_VSAP_EC
GO:0048584	0.682	0.594	2	592	positive regulation of response to stimulus	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0007127	0.682	0.594	2	28	meiosis I	BP	1	CENPC,FBXO5	up_VCAV_EC
GO:0061982	0.682	0.594	2	28	meiosis I cell cycle process	BP	1	CENPC,FBXO5	up_VCAV_EC
GO:0006468	0.682	0.593	2	544	protein phosphorylation	BP	1	MAP2K6,CDC42EP5	up_VFEM_EC
GO:0021885	0.682	0.595	2	24	forebrain cell migration	BP	1	EMX2,SLIT2	up_VSAP_EC
GO:0051150	0.682	0.699	1	13	regulation of smooth muscle cell differentiation	BP	1	CTH	down_ACOR_VSMC
GO:0003143	0.682	0.693	1	22	embryonic heart tube morphogenesis	BP	1	IFT57	down_VCAV_EC
GO:1903510	0.682	0.693	1	22	mucopolysaccharide metabolic process	BP	1	DCN	down_VCAV_EC
GO:0006312	0.682	0.702	1	11	mitotic recombination	BP	1	DMC1	up_ACOR_VSMC
GO:0048015	0.682	0.688	1	48	phosphatidylinositol-mediated signaling	BP	1	LEP	up_AFEM_EC
GO:0048017	0.682	0.688	1	48	inositol lipid-mediated signaling	BP	1	LEP	up_AFEM_EC
GO:0042325	0.682	0.696	1	463	regulation of phosphorylation	BP	1	TAOK1	up_AORT_EC
GO:0048566	0.682	0.699	1	13	embryonic digestive tract development	BP	1	CXCL8	up_VCAV_EC
GO:1901701	0.682	0.69	1	271	cellular response to oxygen-containing	BP	1	CYP26B1	up_VFEM_EC
GO:0043085	0.682	0.692	1	323	positive regulation of catalytic activity	BP	1	CCL24	up_VPUL_EC
GO:0006468	0.682	0.698	1	544	protein phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0045740	0.682	0.701	1	12	positive regulation of DNA replication	BP	1	CIZ1	up_VSAP_EC
GO:0007052	0.682923569	0.68745	1	42	mitotic spindle organization	BP	1	CHMP4B	up_ACOR_EC

GO:0009891	0.683	0.389	30	521	positive regulation of biosynthetic process	BP	1	ARHGEF2,VEGFA,NR1H4,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,HIF1A,SLC45A3,ZPR1,PTPN2,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,APOE,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0072001	0.683	0.455	8	104	renal system development	BP	1	GREM1,ARG2,HOXB7,IQGAP1,SGPL1,JMJD6,SIX4,AMER1	down_ACOR_VSMC
GO:0060348	0.683	0.476	6	78	bone development	BP	1	KIT,FLI1,MEF2C,STC1,BMP2,TJP2	up_VCAV_EC
GO:0001837	0.683	0.513	4	48	epithelial to mesenchymal transition	BP	1	WNT11,AXIN2,TIAM1,TGFBR2	up_VSAP_EC
GO:0030073	0.683	0.542	3	42	insulin secretion	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0014032	0.683	0.592	2	27	neural crest cell development	BP	1	NOLC1,PHACTR4	down_ACOR_VSMC
GO:0090501	0.683	0.592	2	29	RNA phosphodiester bond hydrolysis	BP	1	WDR33,NOB1	down_ACOR_VSMC
GO:0014031	0.683	0.592	2	27	mesenchymal cell development	BP	1	NOLC1,PHACTR4	down_ACOR_VSMC
GO:0006733	0.683	0.588	2	45	oxidoreduction coenzyme metabolic process	BP	1	H6PD,PGLS	down_VCAV_EC
GO:0006796	0.683	0.6	2	938	phosphate-containing compound metabolic	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0098659	0.683	0.698	1	13	inorganic cation import across plasma membrane	BP	1	SLC30A1	down_ACOR_VSMC
GO:0099587	0.683	0.698	1	13	inorganic ion import across plasma membrane	BP	1	SLC30A1	down_ACOR_VSMC
GO:0045069	0.683	0.691	1	22	regulation of viral genome replication	BP	1	MAVS	down_VCAV_EC
GO:1903578	0.683	0.691	1	22	regulation of ATP metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0007549	0.683	0.701	1	11	dosage compensation	BP	1	PCGF5	up_ACOR_VSMC
GO:0042634	0.683	0.702	1	11	regulation of hair cycle	BP	1	FERMT1	up_ACOR_VSMC
GO:0072202	0.683	0.698	1	13	cell differentiation involved in metanephros	BP	1	PDGFB	up_VCAV_EC
GO:0032880	0.683	0.689	1	266	regulation of protein localization	BP	1	SIX1	up_VFEM_EC
GO:0032446	0.683	0.689	1	255	protein modification by small protein conjugation	BP	1	CAV1	up_VSAP_VSMC
GO:0051716	0.684	0.361	96	2001	cellular response to stimulus	BP	1	PCOLCE,NOTCH2,PDGFRB,SLC35F6,SMAD9,ITGB5,LRP1,DCN,NDN,ANGPT1,PRNP,MT2A,VASN,FBN1,ADCY6,GLIPR2,BGN,KANK2,SH3BP1,BMPR1A,NABP2,EVC,RECK,IGFBP6,COL6A1,NUMBL,ARHGEF25,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,AKT2,DOCK10,NR3C1,SYDE1,HSD3B7,PDIA4,CLSTN1,PLCL1,CSPG4,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,GFPT2,SEMA3C,ASPN,GNAZ,THY1,TEAD1,CYP1B1,ARHGAP10,ATP6V0C,GLI3,PARK7,ZMAT3,MAST2,SCARA5,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ENSCAFG00000018194,ARL2BP,IFT57,MAVS,CDH2,LOXL3,MPV17,GSDME,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,RAB7B,SPNS1,SEC61B,GLIS2,RAB31,HM13,ARHGAP1,SHC1,CRCP,FBH1,GREM1,NPHP4,RAC2,FOXO3,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:0010639	0.684	0.462	7	128	negative regulation of organelle organization	BP	1	ARHGEF2,NAA10,BNIP3,TWF1,CAPG,KDM3A,MID1	down_VSAP_EC
GO:0000082	0.684	0.511	4	57	G1/S transition of mitotic cell cycle	BP	1	PLK2,PPP3CA,USP37,CUL4A	up_VCAV_EC
GO:0022898	0.684	0.512	4	48	regulation of transmembrane	BP	1	KCNE3,OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0034645	0.684	0.561	3	1546	cellular macromolecule biosynthetic process	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC
GO:0090304	0.684	0.563	3	1694	nucleic acid metabolic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0032606	0.684	0.543	3	35	type I interferon production	BP	1	PLCG2,TLR3,PTPN22	up_ACOR_VSMC
GO:0051254	0.684	0.589	2	431	positive regulation of RNA metabolic process	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0042475	0.684	0.592	2	26	odontogenesis of dentin-containing tooth	BP	1	BMP2,ITGA6	up_VCAV_EC
GO:1905209	0.684	0.697	1	13	positive regulation of cardiocyte differentiation	BP	1	GREM1	down_ACOR_VSMC

GO:0007422	0.684	0.693	1	18	peripheral nervous system development	BP	1	ILK	down_VSAP_EC
GO:0018345	0.684	0.698	1	12	protein palmitoylation	BP	1	ZDHHC21	up_ACOR_VSMC
GO:0006282	0.684	0.686	1	48	regulation of DNA repair	BP	1	AXIN2	up_AFEM_EC
GO:0090316	0.684	0.686	1	48	positive regulation of intracellular protein	BP	1	LEP	up_AFEM_EC
GO:0006915	0.684	0.696	1	550	apoptotic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0010591	0.684	0.699	1	12	regulation of lamellipodium assembly	BP	1	SLIT2	up_VSAP_EC
GO:0048534	0.684	0.688	1	262	hematopoietic or lymphoid organ	BP	1	HOXA9	up_VSAP_VSMC
GO:0008104	0.685	0.366	61	763	protein localization	BP	1	ACSL3,HMGB1,SREBF1,RPA1,DDX39A,STXBP6,USP4,HINFP,NEDD4,ZW10,CENPA,SLC29A1,NDC1,RRBP1,TIMM44,POLA2,CTDNEP1,HSPA9,RAN,HM13,BIRC5,INSIG1,CAV1,CDK1,NF2,AURKB,MMP14,EZH2,PLK3,ARG2,DHCR24,ENSCAFG00000011598,PREB,TFRC,TRAM1,NDC80,IPO4,ARHGDIA,YWHAB,NUP62,EMP2,NUP188,HASPIN,RSL1D1,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,MIOS,TTK,KNL1,PMPCA,TINF2,CCT4,SIX4,MTBP	down_ACOR_VSMC
GO:0033036	0.685	0.378	40	852	macromolecule localization	BP	1	GPAM,SNX18,LRP1,PRNP,FBN1,TLN2,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,LCAT,SNUPN,SSR2,SCP2,TRIM8,SCAMP4,CLTB,SSR3,WDR45,PEX5,SCAMP2,OSBPL10,GLI3,PARK7,ZFP36L1,ARL2BP,MAVS,CDH2,TOM1,ENSCAFG00000017708,SEC61B,GLIS2,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SOAT1,SEC61A1	down_VCAV_EC
GO:0009205	0.685	0.462	7	98	purine ribonucleoside triphosphate metabolic	BP	1	RAN,CDK1,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0030100	0.685	0.475	6	70	regulation of endocytosis	BP	1	DLL1,F2RL1,CYBA,UBQLN2,FLOT1,PPP3CB	up_VSAP_EC
GO:0043547	0.685	0.491	5	61	positive regulation of GTPase activity	BP	1	ARHGEF5,TBC1D10C,TBC1D2B,F2RL1,TIAM1	up_VSAP_EC
GO:0046677	0.685	0.51	4	54	response to antibiotic	BP	1	PPP1R15B,TIMELESS,EZH2,SIGMAR1	down_ACOR_VSMC
GO:0001659	0.685	0.51	4	54	temperature homeostasis	BP	1	TLR4,PTGS2,ADIPOR2,KDM3A	up_VCAV_EC
GO:0021543	0.685	0.51	4	49	pallium development	BP	1	EMX2,CDON,SLIT2,MCPH1	up_VSAP_EC
GO:0022900	0.685	0.539	3	46	electron transport chain	BP	1	CDK1,CYCS,CYC1	down_ACOR_VSMC
GO:0061326	0.685	0.54	3	41	renal tubule development	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0072080	0.685	0.54	3	41	nephron tubule development	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0008286	0.685	0.542	3	36	insulin receptor signaling pathway	BP	1	PDK2,PIK3R1,NCK1	up_VSAP_EC
GO:0031348	0.685	0.586	2	46	negative regulation of defense response	BP	1	CHID1,A2M	down_VCAV_EC
GO:0045132	0.685	0.592	2	23	meiotic chromosome segregation	BP	1	DMC1,SUN1	up_ACOR_VSMC
GO:0002286	0.685	0.592	2	24	T cell activation involved in immune response	BP	1	STAT6,F2RL1	up_VSAP_EC
GO:0015698	0.685	0.592	2	24	inorganic anion transport	BP	1	GABRE,CLCN2	up_VSAP_EC
GO:0032370	0.685	0.696	1	13	positive regulation of lipid transport	BP	1	PRELID1	down_ACOR_VSMC
GO:0000184	0.685	0.692	1	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	SMG7	down_VSAP_EC
GO:0006040	0.685	0.698	1	12	amino sugar metabolic process	BP	1	EXTL2	up_ACOR_VSMC
GO:0033598	0.685	0.699	1	11	mammary gland epithelial cell proliferation	BP	1	RREB1	up_ACOR_VSMC
GO:0018210	0.685	0.685	1	48	peptidyl-threonine modification	BP	1	CAMK2A	up_AFEM_EC
GO:0003231	0.685	0.684	1	48	cardiac ventricle development	BP	1	LUZP1	up_AFEM_EC
GO:0003279	0.685	0.685	1	48	cardiac septum development	BP	1	LUZP1	up_AFEM_EC
GO:1905330	0.685	0.685	1	48	regulation of morphogenesis of an	BP	1	GREM1	up_AFEM_EC
GO:0072698	0.685	0.696	1	13	protein localization to microtubule cytoskeleton	BP	1	HOOK3	up_VCAV_EC

GO:0006357	0.685	0.695	1	547	regulation of transcription by RNA polymerase II	BP	1	GATA5	up_VPUL_VSMC
GO:0031326	0.686	0.353	110	1176	regulation of cellular biosynthetic process	BP	1	TLR1,SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,HTR2B,MEIS2,NACC2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,ORMDL3,SMARCD3,TBX20,CCNT1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,STC2,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0030029	0.686	0.4	21	239	actin filament-based process	BP	1	WNT11,FAM107A,ARHGEF5,WASF3,PPARGC1B,SLIT2,FGF7,ABL1,EMP2,KCNE3,CDC42EP5,CORO2B,CDC42EP2,F2RL1,PIK3R1,FRMD6,WIPF1,MYO1B,ARHGAP12,NCK1,BAG4	up_VSAP_EC
GO:0051246	0.686	0.476	6	832	regulation of protein metabolic process	BP	1	ARHGEF2,ASPN,ACVR2A,PUM3,EIF5,ENSCAFG00000032731	up_VPOR_EC
GO:0032956	0.686	0.486	5	116	regulation of actin cytoskeleton organization	BP	1	KIRREL1,RHOD,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0046822	0.686	0.509	4	53	regulation of nucleocytoplasmic	BP	1	NEDD4,RAN,DMAP1,RBM14	down_ACOR_VSMC
GO:0030178	0.686	0.509	4	52	negative regulation of Wnt signaling pathway	BP	1	FERMT1,RAPGEF1,BMP2,MCC	up_VCAV_EC
GO:0006996	0.686	0.52	4	1301	organelle organization	BP	1	NR1H4,MYBPC2,CCL24,ARHGEF2	up_VPUL_EC
GO:0006909	0.686	0.539	3	42	phagocytosis	BP	1	HMGB1,CORO1A,JMJD6	down_ACOR_VSMC
GO:0006814	0.686	0.589	2	28	sodium ion transport	BP	1	NEDD4,NKAIN1	down_ACOR_VSMC
GO:0009142	0.686	0.584	2	46	nucleoside triphosphate biosynthetic process	BP	1	ATP5MC1,ADK	down_VCAV_EC
GO:0046467	0.686	0.584	2	45	membrane lipid biosynthetic process	BP	1	PIGS,ORMDL3	down_VCAV_EC
GO:0009205	0.686	0.581	2	98	purine ribonucleoside triphosphate metabolic	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0023051	0.686	0.596	2	954	regulation of signaling	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0045669	0.686	0.59	2	24	positive regulation of osteoblast differentiation	BP	1	ZHX3,DDR2	up_VSAP_EC
GO:0007193	0.686	0.694	1	13	adenylate cyclase-inhibiting G protein-coupled receptor signaling	BP	1	PRMT5	down_ACOR_VSMC
GO:0032469	0.686	0.694	1	13	endoplasmic reticulum calcium ion homeostasis	BP	1	THADA	down_ACOR_VSMC
GO:0032651	0.686	0.695	1	13	regulation of interleukin-1 beta production	BP	1	ARG2	down_ACOR_VSMC
GO:1901021	0.686	0.695	1	13	positive regulation of calcium ion transmembrane	BP	1	GSTO1	down_ACOR_VSMC
GO:0006915	0.686	0.694	1	550	apoptotic process	BP	1	CITED2	down_VPOR_EC
GO:0008206	0.686	0.697	1	11	bile acid metabolic process	BP	1	LEP	up_ACOR_VSMC
GO:0048536	0.686	0.696	1	12	spleen development	BP	1	CITED2	up_ACOR_VSMC
GO:0090189	0.686	0.696	1	12	regulation of branching involved in ureteric bud	BP	1	BMP4	up_ACOR_VSMC
GO:0022898	0.686	0.684	1	48	regulation of transmembrane	BP	1	FXYD1	up_AFEM_EC
GO:0045595	0.686	0.69	1	469	regulation of cell differentiation	BP	1	HOXA9	up_AORT_EC
GO:0032469	0.686	0.695	1	13	endoplasmic reticulum calcium ion homeostasis	BP	1	ATP2A1	up_VCAV_EC
GO:0045143	0.686	0.695	1	13	homologous chromosome segregation	BP	1	CENPC	up_VCAV_EC
GO:0019068	0.686	0.693	1	15	virion assembly	BP	1	USP6NL	up_VCAV_EC

GO:2001023	0.686	0.694	1	14	regulation of response to drug	BP	1	RIPK1	up_VCAV_EC
GO:0032879	0.686	0.7	1	767	regulation of localization	BP	1	CA2	up_VCAV_VSMC
GO:0006914	0.686	0.683	1	141	autophagy	BP	1	MTDH	up_VPOR_EC
GO:0051259	0.686	0.683	1	140	protein complex oligomerization	BP	1	FBP1	up_VPOR_EC
GO:0061919	0.686	0.683	1	141	process utilizing autophagic mechanism	BP	1	MTDH	up_VPOR_EC
GO:0033962	0.686	0.696	1	12	cytoplasmic mRNA processing body assembly	BP	1	LIMD1	up_VSAP_EC
GO:0043069	0.686	0.685	1	262	negative regulation of programmed cell death	BP	1	CAV1	up_VSAP_VSMC
GO:1901576	0.686490763	0.37617	47	1877	organic substance biosynthetic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PORCN,FZD5,CCDC3,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PTGDS,GUCY1B1,PIAS1,CHPT1,MAVS,FOXC2,PIGS,LRP4,CLSTN1,AK7,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,AZIN2,AGPAT2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0071705	0.687	0.368	53	582	nitrogen compound transport	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,TBC1D10C,TBC1D2B,CDH1,SLC6A4,ABL1,PEX2,OSR1,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,SLC25A12,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,ZFP36L1,PIK3R1,CTNS,PASK,NUP98,AZIN2,HPS4,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,CYBA,STX4,VPS11,FLOT1,PPP3CB,PEX6,MAVS,TGFBR2,BAG4,NCOA4,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0006807	0.687	0.452	13	3221	nitrogen compound metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0098771	0.687	0.448	8	180	inorganic ion homeostasis	BP	1	PRNP,ENSCAFG00000018277,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0045786	0.687	0.504	4	195	negative regulation of cell cycle	BP	1	GAS1,OVOL1,DCUN1D3,FAP	up_AFEM_EC
GO:0015849	0.687	0.507	4	56	organic acid transport	BP	1	LRRC8D,SLC38A1,SLCO3A1,NOS2	up_VCAV_EC
GO:0046942	0.687	0.507	4	56	carboxylic acid transport	BP	1	LRRC8D,SLC38A1,SLCO3A1,NOS2	up_VCAV_EC
GO:0030203	0.687	0.588	2	27	glycosaminoglycan metabolic process	BP	1	XYLT1,UGDH	down_ACOR_VSMC
GO:0030154	0.687	0.599	2	1040	cell differentiation	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0051092	0.687	0.583	2	47	positive regulation of NF-kappaB transcription	BP	1	RAB7B,GREM1	down_VCAV_EC
GO:0045814	0.687	0.588	2	27	negative regulation of gene expression,	BP	1	UHRF2,HIST2H2AC	up_VCAV_EC
GO:0050794	0.687	0.806	1	3075	regulation of cellular process	BP	1	CST3	down_AORT_EC
GO:0009247	0.687	0.687	1	22	glycolipid biosynthetic process	BP	1	PIGS	down_VCAV_EC
GO:0061008	0.687	0.687	1	23	hepaticobiliary system development	BP	1	PRKCSH	down_VCAV_EC
GO:0061178	0.687	0.695	1	12	regulation of insulin secretion involved in cellular response to	BP	1	PRKCE	up_ACOR_VSMC
GO:0010033	0.687	0.699	1	772	response to organic substance	BP	1	TLR2	up_AFEM_VSMC
GO:0051270	0.687	0.685	1	296	regulation of cellular component movement	BP	1	TBX5	up_APUL_EC
GO:0048870	0.687	0.689	1	451	cell motility	BP	1	EMX2	up_VFEM_VSMC
GO:0051674	0.687	0.689	1	451	localization of cell	BP	1	EMX2	up_VFEM_VSMC
GO:0045911	0.687	0.695	1	12	positive regulation of DNA recombination	BP	1	STAT6	up_VSAP_EC
GO:0097755	0.687	0.695	1	12	positive regulation of blood vessel diameter	BP	1	F2RL1	up_VSAP_EC
GO:0006412	0.687	0.684	1	245	translation	BP	1	PRR16	up_VSAP_VSMC
GO:0043484	0.687509887	0.6821	1	43	regulation of RNA splicing	BP	1	RBM38	up_ACOR_EC
GO:0030098	0.687539318	0.57988	2	87	lymphocyte differentiation	BP	1	FZD5,PTGER4	up_ACOR_EC

GO:0015031	0.688	0.37	46	510	protein transport	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,STX11,ANKRD1,F2RL1,CDKN1A,PTPN22,OS9,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,LAMP2,JUP,CCL5,RAB11B,NOD2,LMTK2,AP2B1,SCAMP5,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0019439	0.688	0.428	11	150	aromatic compound catabolic process	BP	1	CDA,TENT2,CNOT6,ENSCAFG00000024323,PAN3,CNOT7,SMG7,BLVRA,HIF1A,DCP2,TET2	up_VCAV_EC
GO:0009896	0.688	0.429	11	127	positive regulation of catabolic process	BP	1	PLEKHF1,MFN2,ZFP36L1,FBXO7,RNF166,PIP4K2B,OSBPL7,ZFP36L2,UBQLN2,TNRC6C,HMOX1	up_VSAP_EC
GO:0022607	0.688	0.462	7	969	cellular component assembly	BP	1	MZT1,ENSCAFG00000002015,FBP1,RSL24D1,RPL10L,TWF1,SRP54	up_VPOR_EC
GO:0018105	0.688	0.483	5	116	peptidyl-serine phosphorylation	BP	1	AKT2,PLCL1,PARK7,MAST2,CAMK2D	down_VCAV_EC
GO:0010970	0.688	0.581	2	48	transport along microtubule	BP	1	IFT57,MGARP	down_VCAV_EC
GO:0071453	0.688	0.582	2	46	cellular response to oxygen levels	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0099111	0.688	0.581	2	48	microtubule-based transport	BP	1	IFT57,MGARP	down_VCAV_EC
GO:0019219	0.688	0.599	2	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:1903555	0.688	0.583	2	37	regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2,NR1H4	down_VSAP_EC
GO:0006094	0.688	0.588	2	24	gluconeogenesis	BP	1	PDK2,PC	up_VSAP_EC
GO:0090398	0.688	0.588	2	24	cellular senescence	BP	1	ABL1,YPEL3	up_VSAP_EC
GO:0010737	0.688	0.692	1	13	protein kinase A signaling	BP	1	EZR	down_ACOR_VSMC
GO:0032873	0.688	0.693	1	13	negative regulation of stress-activated MAPK	BP	1	EZR	down_ACOR_VSMC
GO:0070303	0.688	0.693	1	13	negative regulation of stress-activated protein kinase signaling cascade	BP	1	EZR	down_ACOR_VSMC
GO:0010812	0.688	0.687	1	19	negative regulation of cell-substrate adhesion	BP	1	SERPINE1	down_VSAP_EC
GO:0030032	0.688	0.687	1	19	lamellipodium assembly	BP	1	FSCN1	down_VSAP_EC
GO:0050821	0.688	0.681	1	48	protein stabilization	BP	1	CRYAB	up_AFEM_EC
GO:0070887	0.688	0.697	1	775	cellular response to chemical stimulus	BP	1	TLR2	up_AFEM_VSMC
GO:0006826	0.688	0.69	1	15	iron ion transport	BP	1	LMTK2	up_VCAV_EC
GO:0016242	0.688	0.692	1	13	negative regulation of macroautophagy	BP	1	MTOR	up_VCAV_EC
GO:0017145	0.688	0.693	1	13	stem cell division	BP	1	ARHGEF2	up_VCAV_EC
GO:0030865	0.688	0.692	1	13	cortical cytoskeleton organization	BP	1	EPB41	up_VCAV_EC
GO:0043687	0.688	0.692	1	14	post-translational protein modification	BP	1	ESCO1	up_VCAV_EC
GO:0000280	0.688	0.68	1	145	nuclear division	BP	1	MZT1	up_VPOR_EC
GO:0006811	0.688	0.685	1	330	ion transport	BP	1	HOXA3	up_VPUL_EC
GO:0007155	0.688	0.685	1	324	cell adhesion	BP	1	FLRT3	up_VPUL_EC
GO:0032880	0.688	0.683	1	266	regulation of protein localization	BP	1	TLR2	up_VSAP_VSMC
GO:0050680	0.688375731	0.68099	1	44	negative regulation of epithelial cell proliferation	BP	1	SOX9	up_ACOR_EC
GO:0032101	0.689	0.412	15	173	regulation of response to external stimulus	BP	1	VEGFD,LEP,TLR3,SASH1,FGF18,F2RL1,ENPP4,NRP1,PTPN22,PARP9,APP,CCL5,NOD2,JAM3,PARK7	up_ACOR_VSMC
GO:0019725	0.689	0.426	11	245	cellular homeostasis	BP	1	PRNP,ENSCAFG00000014978,ENSCAFG00000018277,PDIA4,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ORMDL3,ATOX1	down_VCAV_EC
GO:0098662	0.689	0.44	9	131	inorganic cation transmembrane transport	BP	1	PDE4D,CHD7,APLNR,SLC39A8,KCNJ3,KCNJ2,SLC25A25,PLCG2,MCU	up_VCAV_EC
GO:0031669	0.689	0.47	6	72	cellular response to nutrient levels	BP	1	FAM107A,SESN1,MAP3K5,PDK2,CASTOR1,NPRL3	up_VSAP_EC

GO:0002443	0.689	0.47	6	71	leukocyte mediated immunity	BP	1	EMP2,STAT6,F2RL1,MYD88,STX4,PPP3CB	up_VSAP_EC
GO:0008064	0.689	0.47	6	72	regulation of actin polymerization or	BP	1	SLIT2,CDC42EP5,CDC42EP2,F2RL1,NCK1,BAG4	up_VSAP_EC
GO:0030832	0.689	0.47	6	72	regulation of actin filament length	BP	1	SLIT2,CDC42EP5,CDC42EP2,F2RL1,NCK1,BAG4	up_VSAP_EC
GO:0051648	0.689	0.485	5	69	vesicle localization	BP	1	RAB11A,RAB27A,SNAP23,STX11,SHROOM2	up_VCAV_EC
GO:1903531	0.689	0.536	3	41	negative regulation of secretion by cell	BP	1	SREBF1,ARG2,EZR	down_ACOR_VSMC
GO:0045089	0.689	0.531	3	70	positive regulation of innate immune response	BP	1	CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0008406	0.689	0.533	3	57	gonad development	BP	1	INHBA,SIX4,SPINK2	down_VSAP_EC
GO:0045137	0.689	0.533	3	57	development of primary sexual characteristics	BP	1	INHBA,SIX4,SPINK2	down_VSAP_EC
GO:0048659	0.689	0.537	3	36	smooth muscle cell proliferation	BP	1	IL6R,MFN2,HMOX1	up_VSAP_EC
GO:0018022	0.689	0.583	2	36	peptidyl-lysine methylation	BP	1	IWS1,KDM3A	down_VSAP_EC
GO:0006793	0.689	0.593	2	948	phosphorus metabolic process	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0072077	0.689	0.692	1	13	renal vesicle morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:0072273	0.689	0.692	1	13	metanephric nephron morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:0045943	0.689	0.688	1	17	positive regulation of transcription by RNA	BP	1	SMARCA4	down_VSAP_EC
GO:0010862	0.689	0.693	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	BMP4	up_ACOR_VSMC
GO:0042398	0.689	0.692	1	12	cellular modified amino acid biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1900006	0.689	0.695	1	11	positive regulation of dendrite development	BP	1	PSEN1	up_ACOR_VSMC
GO:0044319	0.689	0.692	1	12	wound healing, spreading of cells	BP	1	MTOR	up_VCAV_EC
GO:0048854	0.689	0.692	1	13	brain morphogenesis	BP	1	HHEX	up_VCAV_EC
GO:0090504	0.689	0.692	1	12	epiboly	BP	1	MTOR	up_VCAV_EC
GO:0090505	0.689	0.692	1	12	epiboly involved in wound healing	BP	1	MTOR	up_VCAV_EC
GO:0045892	0.689	0.684	1	328	negative regulation of transcription, DNA-	BP	1	NR1H4	up_VPUL_EC
GO:0048468	0.689	0.69	1	553	cell development	BP	1	SLIT2	up_VPUL_VSMC
GO:0002714	0.689	0.693	1	12	positive regulation of B cell mediated immunity	BP	1	STAT6	up_VSAP_EC
GO:0002891	0.689	0.693	1	12	positive regulation of immunoglobulin mediated immune	BP	1	STAT6	up_VSAP_EC
GO:0034724	0.689	0.693	1	12	DNA replication-independent nucleosome	BP	1	CENPP	up_VSAP_EC
GO:0001944	0.689	0.682	1	263	vasculature development	BP	1	CAV1	up_VSAP_VSMC
GO:0043043	0.689	0.682	1	247	peptide biosynthetic process	BP	1	PRR16	up_VSAP_VSMC
GO:0044282	0.689086367	0.57797	2	89	small molecule catabolic process	BP	1	THNSL2,SARDH	up_ACOR_EC
GO:0019637	0.69	0.381	30	342	organophosphate metabolic process	BP	1	PIP5K1B,PLCG2,HTR2B,LCAT,CHPT1,PPARGC1A,PIGN,PDE5A,PIGS,PLPP2,PFKM,ADCY6,PIP5K1,PIGG,SMPD1,CRLS1,ENSCAFG00000018611,CLN8,ALDOC,ENTPD3,DDIT4,SERINC3,SERINC1,CFI,INPP5K,PFKL,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0010563	0.69	0.401	18	203	negative regulation of phosphorus metabolic process	BP	1	SH2D4A,TBC1D10C,CEP85,SLIT2,ABL1,PLPP3,F2RL1,MYC,PIK3IP1,TMEM225B,RTN4RL1,FBXO7,FBLN1,QARS,NCK1,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0045936	0.69	0.401	18	203	negative regulation of phosphate metabolic process	BP	1	SH2D4A,TBC1D10C,CEP85,SLIT2,ABL1,PLPP3,F2RL1,MYC,PIK3IP1,TMEM225B,RTN4RL1,FBXO7,FBLN1,QARS,NCK1,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:1902105	0.69	0.468	6	80	regulation of leukocyte differentiation	BP	1	HMGB1,PRELID1,MMP14,HMGB3,HOXA7,TOX	down_ACOR_VSMC
GO:0034404	0.69	0.505	4	50	nucleobase-containing small molecule	BP	1	PDE5A,ALDOC,ENTPD3,DDIT4	up_ACOR_VSMC
GO:0034341	0.69	0.534	3	43	response to interferon-gamma	BP	1	FLNB,SLC29A1,CDC42EP4	down_ACOR_VSMC

GO:2001022	0.69	0.534	3	42	positive regulation of response to DNA damage	BP	1	HMGB1,TIMELESS,PCNA	down_ACOR_VSMC
GO:0048519	0.69	0.553	3	1554	negative regulation of biological process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0034198	0.69	0.584	2	27	cellular response to amino acid starvation	BP	1	RNF152,MIOS	down_ACOR_VSMC
GO:1990928	0.69	0.584	2	27	response to amino acid starvation	BP	1	RNF152,MIOS	down_ACOR_VSMC
GO:0071347	0.69	0.585	2	25	cellular response to interleukin-1	BP	1	ANKRD1,CCL5	up_ACOR_VSMC
GO:0048259	0.69	0.586	2	24	regulation of receptor-mediated endocytosis	BP	1	UBQLN2,FLOT1	up_VSAP_EC
GO:0045921	0.69	0.586	2	24	positive regulation of exocytosis	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0072665	0.69	0.585	2	25	protein localization to vacuole	BP	1	VPS36,NCOA4	up_VSAP_EC
GO:0006468	0.69	0.583	2	544	protein phosphorylation	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0045843	0.69	0.691	1	13	negative regulation of striated muscle tissue	BP	1	SIX4	down_ACOR_VSMC
GO:1902041	0.69	0.683	1	23	regulation of extrinsic apoptotic signaling pathway via death	BP	1	PARK7	down_VCAV_EC
GO:0010171	0.69	0.685	1	18	body morphogenesis	BP	1	PTPN11	down_VSAP_EC
GO:0002714	0.69	0.692	1	12	positive regulation of B cell mediated immunity	BP	1	NECTIN2	up_VCAV_EC
GO:0002891	0.69	0.692	1	12	positive regulation of immunoglobulin mediated immune	BP	1	NECTIN2	up_VCAV_EC
GO:0043410	0.69	0.679	1	144	positive regulation of MAPK cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0040007	0.69	0.681	1	276	growth	BP	1	SIX1	up_VFEM_EC
GO:1902679	0.69	0.683	1	329	negative regulation of RNA biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:1903507	0.69	0.683	1	329	negative regulation of nucleic acid-templated	BP	1	NR1H4	up_VPUL_EC
GO:0045058	0.69	0.691	1	12	T cell selection	BP	1	STAT6	up_VSAP_EC
GO:0045860	0.690990757	0.52775	3	132	positive regulation of protein kinase activity	BP	1	FZD5,PAK3,PRKCD	up_ACOR_EC
GO:0097435	0.691	0.395	20	230	supramolecular fiber organization	BP	1	WNT11,FAM107A,ARHGEF5,PPARGC1B,SLIT2,ABL1,EMP2,CDC42EP5,CDC42EP2,KLHL24,F2RL1,DDR2,PIK3R1,LOX,WIPF1,MYO1B,ARHGAP12,NCK1,BAG4,DPT	up_VSAP_EC
GO:0060537	0.691	0.432	10	117	muscle tissue development	BP	1	CDON,DLL1,OSR1,SAV1,GTF3C5,SHOX2,ZFAND5,FLOT1,NPRL3,CITED2	up_VSAP_EC
GO:1901990	0.691	0.447	8	94	regulation of mitotic cell cycle phase transition	BP	1	FAM107A,CRADD,ZFP36L1,FBXO7,ZFP36L2,TPRA1,CDC26,LSM10	up_VSAP_EC
GO:0016042	0.691	0.467	6	80	lipid catabolic process	BP	1	ABHD5,CDK4,PPARD,SGPL1,LIPC,ACADL	down_ACOR_VSMC
GO:0043434	0.691	0.467	6	80	response to peptide hormone	BP	1	PPARG,BAIAP2L1,MTOR,NCK1,CREB1,NR4A1	up_VCAV_EC
GO:0048193	0.691	0.48	5	116	Golgi vesicle transport	BP	1	ERGIC1,MYO1B,YIF1A,RAB7B,RAB31	down_VCAV_EC
GO:0001659	0.691	0.503	4	54	temperature homeostasis	BP	1	CAV1,ADIPOR2,HOXC10,ELOVL6	down_ACOR_VSMC
GO:0006643	0.691	0.53	3	68	membrane lipid metabolic process	BP	1	PIGS,ORMDL3,ENSCAFG00000017708	down_VCAV_EC
GO:0030004	0.691	0.534	3	36	cellular monovalent inorganic cation	BP	1	SLC26A7,DMXL1,SLC8A1	up_ACOR_VSMC
GO:0031109	0.691	0.535	3	36	microtubule polymerization or	BP	1	FGF13,MID1,TUBB4A	up_ACOR_VSMC
GO:0042472	0.691	0.583	2	27	inner ear morphogenesis	BP	1	INSIG1,SIX4	down_ACOR_VSMC
GO:0006282	0.691	0.578	2	48	regulation of DNA repair	BP	1	TMEM161A,FBH1	down_VCAV_EC
GO:0008089	0.691	0.688	1	14	anterograde axonal transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0001974	0.691	0.689	1	13	blood vessel remodeling	BP	1	HOXA3	down_ACOR_VSMC
GO:2001259	0.691	0.689	1	13	positive regulation of cation channel activity	BP	1	GSTO1	down_ACOR_VSMC
GO:0035137	0.691	0.685	1	18	hindlimb morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0060563	0.691	0.684	1	18	neuroepithelial cell differentiation	BP	1	SERPINE1	down_VSAP_EC

GO:0060260	0.691	0.69	1	12	regulation of transcription initiation from RNA polymerase II promoter	BP	1	CLSTN1	up_ACOR_VSMC
GO:0048585	0.691	0.686	1	475	negative regulation of response to stimulus	BP	1	DKK2	up_AORT_EC
GO:0044255	0.691	0.68	1	293	cellular lipid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0006359	0.691	0.695	1	10	regulation of transcription by RNA polymerase III	BP	1	MTOR	up_VCAV_EC
GO:0060412	0.691	0.687	1	15	ventricular septum morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0007010	0.691	0.685	1	441	cytoskeleton organization	BP	1	NKX2-5	up_VPOR_VSMC
GO:0022610	0.691	0.682	1	326	biological adhesion	BP	1	FLRT3	up_VPUL_EC
GO:0033344	0.691	0.691	1	12	cholesterol efflux	BP	1	SOAT1	up_VSAP_EC
GO:0043113	0.691	0.69	1	12	receptor clustering	BP	1	LRP4	up_VSAP_EC
GO:0030334	0.691	0.68	1	267	regulation of cell migration	BP	1	CAV1	up_VSAP_VSMC
GO:0050673	0.691508335	0.52707	3	135	epithelial cell proliferation	BP	1	CDH3,SOX9,PYGO2	up_ACOR_EC
GO:0006334	0.6916304	0.67711	1	45	nucleosome assembly	BP	1	SOX9	up_ACOR_EC
GO:0072522	0.691958105	0.57447	2	91	purine-containing compound biosynthetic	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0044237	0.691963124	0.36255	89	3491	cellular metabolic process	BP	1	CDH3,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,CALY,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PCSK1N,PHF20,ATG16L2,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,ENSCAFG00000028814,SMAD6,B3GNT7,KLHL25,ZMYND8,NIT2,PTGDS,PAK3,CFI,GUCY1B1,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,CHPT1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,RBM38,CLU,SFMBT2,ALDOC,ZNF229,CHMP4B,TP53INP2,RARRES2,VPS16,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,PRKCD,PPP1R26,PM20D1,PYGO2,DBNDD2,EFEMP1,ENSCAFG00000010493,CCNYL1,TLE2	up_ACOR_EC
GO:0009987	0.692	0.48	17	5086	cellular process	BP	1	TBX5,HOXA3,NR1H4,EVI2B,RGS1,MRC1,MYBPC2,STK32B,ENSCAFG00000028814,NR4A2,WIF1,CCL24,HTR7,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0048545	0.692	0.481	5	68	response to steroid hormone	BP	1	TFPI,NEDD4,CAV1,THRAP3,HMGB2	down_ACOR_VSMC
GO:0003007	0.692	0.499	4	94	heart morphogenesis	BP	1	NOTCH2,BMPR1A,SEMA3C,IFT57	down_VCAV_EC
GO:0031323	0.692	0.524	4	1788	regulation of cellular metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0060401	0.692	0.532	3	42	cytosolic calcium ion transport	BP	1	CAV1,GSTO1,CORO1A	down_ACOR_VSMC
GO:0071241	0.692	0.531	3	42	cellular response to inorganic substance	BP	1	RAD51,TIMELESS,IQGAP1	down_ACOR_VSMC
GO:0009059	0.692	0.552	3	1563	macromolecule biosynthetic process	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC
GO:0051171	0.692	0.553	3	1697	regulation of nitrogen compound metabolic	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0006406	0.692	0.582	2	27	mRNA export from nucleus	BP	1	DDX39A,DDX39B	down_ACOR_VSMC
GO:0071427	0.692	0.582	2	27	mRNA-containing ribonucleoprotein complex export from	BP	1	DDX39A,DDX39B	down_ACOR_VSMC
GO:0036503	0.692	0.577	2	47	ERAD pathway	BP	1	SEC61B,HM13	down_VCAV_EC
GO:0051896	0.692	0.579	2	39	regulation of protein kinase B signaling	BP	1	MTDH,DDIT3	down_VSAP_EC
GO:0044786	0.692	0.584	2	23	cell cycle DNA replication	BP	1	CDC7,ATRX	up_ACOR_VSMC
GO:0048524	0.692	0.581	2	30	positive regulation of viral process	BP	1	SMARCA4,CNOT7	up_VCAV_EC
GO:0097530	0.692	0.579	2	33	granulocyte migration	BP	1	CXCL8,PDE4D	up_VCAV_EC
GO:0051438	0.692	0.584	2	24	regulation of ubiquitin-protein transferase	BP	1	ABL1,ZER1	up_VSAP_EC

GO:0022602	0.692	0.688	1	13	ovulation cycle process	BP	1	SGPL1	down_ACOR_VSMC
GO:0048048	0.692	0.688	1	13	embryonic eye morphogenesis	BP	1	PHACTR4	down_ACOR_VSMC
GO:0043489	0.692	0.688	1	13	RNA stabilization	BP	1	THRAP3	down_ACOR_VSMC
GO:0009064	0.692	0.68	1	23	glutamine family amino acid metabolic process	BP	1	GLS2	down_VCAV_EC
GO:0012501	0.692	0.686	1	561	programmed cell death	BP	1	CITED2	down_VPOR_EC
GO:0006821	0.692	0.683	1	18	chloride transport	BP	1	CLCN3	down_VSAP_EC
GO:0001541	0.692	0.689	1	12	ovarian follicle development	BP	1	DMC1	up_ACOR_VSMC
GO:0071480	0.692	0.689	1	12	cellular response to gamma radiation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0009057	0.692	0.684	1	473	macromolecule catabolic process	BP	1	LNPEP	up_AORT_EC
GO:0050771	0.692	0.691	1	11	negative regulation of axonogenesis	BP	1	IFRD1	up_VCAV_EC
GO:0006091	0.692	0.677	1	139	generation of precursor metabolites and energy	BP	1	FBP1	up_VPOR_EC
GO:0012501	0.692	0.687	1	561	programmed cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:0031399	0.692	0.687	1	559	regulation of protein modification process	BP	1	SLIT2	up_VPUL_VSMC
GO:0006486	0.692104157	0.57429	2	91	protein glycosylation	BP	1	GALNT5,B3GNT7	up_ACOR_EC
GO:0043413	0.692104157	0.57429	2	91	macromolecule glycosylation	BP	1	GALNT5,B3GNT7	up_ACOR_EC
GO:1902533	0.693	0.386	24	271	positive regulation of intracellular signal transduction	BP	1	CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,C5AR2,PLEKHF1,IL6R,ABL1,MAP3K5,PDGFD,C1QTNF2,HPSE,F2RL1,TRAF7,RBCK1,SASH1,MYD88,S100A4,ENSCAFG00000011993,RAF1,NCK1,BAG4,TRADD	up_VSAP_EC
GO:0006790	0.693	0.478	5	99	sulfur compound metabolic process	BP	1	ENPP1,ENSCAFG00000032470,ENSCAFG00000028814,CHSY1,PAPSS1	down_VSAP_EC
GO:0051234	0.693	0.49	5	1283	establishment of localization	BP	1	NETO1,SLC16A12,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0032270	0.693	0.578	2	479	positive regulation of cellular protein metabolic	BP	1	ACVRL1,LYN	down_ACOR_EC
GO:0007173	0.693	0.581	2	27	epidermal growth factor receptor signaling	BP	1	NUP62,IQGAP1	down_ACOR_VSMC
GO:0046889	0.693	0.582	2	24	positive regulation of lipid biosynthetic process	BP	1	HTR2B,CCDC3	up_ACOR_VSMC
GO:1901566	0.693	0.581	2	598	organonitrogen compound biosynthetic	BP	1	GALNT17,ZDHHC16	up_APUL_EC
GO:0008543	0.693	0.58	2	27	fibroblast growth factor receptor signaling	BP	1	GATA3,PRKD2	up_VCAV_EC
GO:0007049	0.693	0.58	2	560	cell cycle	BP	1	MAP2K6,CYP26B1	up_VFEM_EC
GO:0009605	0.693	0.579	2	538	response to external stimulus	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0071470	0.693	0.687	1	13	cellular response to osmotic stress	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0006661	0.693	0.68	1	23	phosphatidylinositol biosynthetic process	BP	1	PIGS	down_VCAV_EC
GO:0046785	0.693	0.68	1	23	microtubule polymerization	BP	1	CLIP3	down_VCAV_EC
GO:2000379	0.693	0.681	1	20	positive regulation of reactive oxygen species	BP	1	CDKN1A	down_VSAP_EC
GO:0006359	0.693	0.692	1	10	regulation of transcription by RNA polymerase III	BP	1	GTF3C1	up_ACOR_VSMC
GO:0045830	0.693	0.69	1	11	positive regulation of isotype switching	BP	1	TP53BP1	up_ACOR_VSMC
GO:0050764	0.693	0.687	1	13	regulation of phagocytosis	BP	1	F2RL1	up_ACOR_VSMC
GO:0040001	0.693	0.688	1	12	establishment of mitotic spindle localization	BP	1	ZW10	up_VCAV_EC
GO:1901021	0.693	0.687	1	13	positive regulation of calcium ion transmembrane	BP	1	PLCG2	up_VCAV_EC
GO:0007063	0.693	0.688	1	12	regulation of sister chromatid cohesion	BP	1	AXIN2	up_VSAP_EC

GO:0009889	0.694	0.345	111	1190	regulation of biosynthetic process	BP	1	TLR1,SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,HTR2B,MEIS2,NACC2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,ORMDL3,SMARCD3,TBX20,CCDC3,CCNT1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,STC2,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0051649	0.694	0.362	49	630	establishment of localization in cell	BP	1	HCLS1,KIT,MX2,TMEM173,PDE4D,IWS1,MEF2C,FERMT1,CHD7,RAB11A,KIF3C,APLNR,RAB27A,SNCAIP,PPP3CA,NECTIN2,HOOK3,SNAP23,HHEX,RAB6A,ANKRD50,ABCA1,SNX2,THOC1,SH3GLB1,AKAP12,APOD,CENPC,FES,EHD4,PLCG2,CTDSPL2,PAN3,GCC2,STX11,SMG7,VPS54,TBC1D1,NUP133,DNAJC13,ZW10,HIF1A,IPO11,ALS2,LMTK2,DOP1B,SHROOM2,RABGAP1,USP6NL	up_VCAV_EC
GO:0045893	0.694	0.373	33	413	positive regulation of transcription, DNA-templated	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,INSIG1,THRAP3,FAM129B,GREM1,SMARCC1,DHX33,CKS2,BRCA1,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,ENSCAFG00000017103	down_ACOR_VSMC
GO:0006807	0.694	0.512	6	3221	nitrogen compound metabolic process	BP	1	CST3,HDAC7,CITED2,MGAT4B,TBX15,GBGT1	down_VPOR_EC
GO:0031098	0.694	0.463	6	109	stress-activated protein kinase signaling cascade	BP	1	TNIK,LYN,MAPK10,PAK2,SH3RF3,MID1	down_VSAP_EC
GO:0051301	0.694	0.462	6	117	cell division	BP	1	ARHGEF2,VEGFA,MYH9,PLK3,ANLN,CALM1	down_VSAP_EC
GO:0080090	0.694	0.479	6	1734	regulation of primary metabolic process	BP	1	NR1H4,PLCL1,PCSK1N,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:2001233	0.694	0.524	3	149	regulation of apoptotic signaling pathway	BP	1	MLLT11,PLAGL2,CYLD	up_AFEM_EC
GO:0051928	0.694	0.579	2	28	positive regulation of calcium ion transport	BP	1	CAV1,GSTO1	down_ACOR_VSMC
GO:0051252	0.694	0.59	2	1051	regulation of RNA metabolic process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0033209	0.694	0.581	2	24	tumor necrosis factor-mediated signaling	BP	1	F2RL1,CCDC3	up_ACOR_VSMC
GO:0048278	0.694	0.58	2	25	vesicle docking	BP	1	STX11,BVES	up_ACOR_VSMC
GO:1901983	0.694	0.581	2	24	regulation of protein acetylation	BP	1	PRKAA2,PARK7	up_ACOR_VSMC
GO:0023052	0.694	0.602	2	1602	signaling	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0055072	0.694	0.578	2	30	iron ion homeostasis	BP	1	CP,HIF1A	up_VCAV_EC
GO:0007156	0.694	0.58	2	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	PCDH19,CDH1	up_VSAP_EC
GO:0035850	0.694	0.58	2	25	epithelial cell differentiation involved in	BP	1	OSR1,KLF15	up_VSAP_EC
GO:0035082	0.694	0.685	1	13	axoneme assembly	BP	1	TTLL1	down_ACOR_VSMC
GO:0050702	0.694	0.686	1	13	interleukin-1 beta secretion	BP	1	ARG2	down_ACOR_VSMC
GO:0015908	0.694	0.679	1	23	fatty acid transport	BP	1	AKT2	down_VCAV_EC
GO:0061640	0.694	0.679	1	23	cytoskeleton-dependent cytokinesis	BP	1	SNX18	down_VCAV_EC
GO:0046637	0.694	0.681	1	18	regulation of alpha-beta T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0090303	0.694	0.681	1	18	positive regulation of wound healing	BP	1	SERPINE1	down_VSAP_EC
GO:0099172	0.694	0.689	1	11	presynapse organization	BP	1	APP	up_ACOR_VSMC

GO:0030308	0.694	0.674	1	49	negative regulation of cell growth	BP	1	DCUN1D3	up_AFEM_EC
GO:0022603	0.694	0.677	1	301	regulation of anatomical structure morphogenesis	BP	1	TBX5	up_APUL_EC
GO:1901031	0.694	0.687	1	12	regulation of response to reactive oxygen species	BP	1	SESN1	up_VSAP_EC
GO:0048333	0.694	0.687	1	12	mesodermal cell differentiation	BP	1	HOXA11	up_VSAP_EC
GO:0071417	0.695	0.422	11	142	cellular response to organonitrogen	BP	1	SREBF1,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,PDXP,EZR,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0045787	0.695	0.427	10	117	positive regulation of cell cycle	BP	1	CRADD,SLC6A4,ABL1,CDC25B,POLDIP2,GDPD5,CDK9,TTL,LSM10,CITED2	up_VSAP_EC
GO:0044403	0.695	0.427	10	116	symbiont process	BP	1	NAPEPLD,F2RL1,MYD88,MON1B,PC,EIF3G,EIF3L,EIF3D,MAVS,ULK1	up_VSAP_EC
GO:0009260	0.695	0.451	7	83	ribonucleotide biosynthetic process	BP	1	ACACB,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0046390	0.695	0.451	7	83	ribose phosphate biosynthetic process	BP	1	ACACB,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:1901990	0.695	0.495	4	94	regulation of mitotic cell cycle phase transition	BP	1	KANK2,ZFP36L1,LSM10,BRSK1	down_VCAV_EC
GO:0010594	0.695	0.524	3	71	regulation of endothelial cell migration	BP	1	DCN,SASH1,SPRED1	down_VCAV_EC
GO:2001235	0.695	0.525	3	69	positive regulation of apoptotic signaling	BP	1	PARK7,GSDME,FBH1	down_VCAV_EC
GO:1903322	0.695	0.526	3	59	positive regulation of protein modification by small protein conjugation	BP	1	PRICKLE1,HSPA5,TRIB3	down_VSAP_EC
GO:0072088	0.695	0.529	3	36	nephron epithelium morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0006754	0.695	0.53	3	36	ATP biosynthetic process	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:1904659	0.695	0.53	3	36	glucose transmembrane transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0009127	0.695	0.573	2	47	purine nucleoside monophosphate biosynthetic process	BP	1	ATP5MC1,AMPD2	down_VCAV_EC
GO:0009168	0.695	0.573	2	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	ATP5MC1,AMPD2	down_VCAV_EC
GO:0002532	0.695	0.579	2	25	production of molecular mediator involved in inflammatory response	BP	1	LEP,NOD2	up_ACOR_VSMC
GO:0070227	0.695	0.579	2	25	lymphocyte apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0060325	0.695	0.685	1	13	face morphogenesis	BP	1	SGPL1	down_ACOR_VSMC
GO:1901992	0.695	0.677	1	23	positive regulation of mitotic cell cycle phase	BP	1	LSM10	down_VCAV_EC
GO:0034613	0.695	0.684	1	576	cellular protein localization	BP	1	RAB11B	down_VPOR_EC
GO:0072210	0.695	0.679	1	19	metanephric nephron development	BP	1	CTNNB1	down_VSAP_EC
GO:0035315	0.695	0.687	1	11	hair cell differentiation	BP	1	SEC24B	up_ACOR_VSMC
GO:0006888	0.695	0.673	1	49	ER to Golgi vesicle-mediated transport	BP	1	GAS1	up_AFEM_EC
GO:0098900	0.695	0.682	1	15	regulation of action potential	BP	1	KCNJ2	up_VCAV_EC
GO:1905898	0.695	0.682	1	16	positive regulation of response to endoplasmic	BP	1	NCK1	up_VCAV_EC
GO:0001934	0.695	0.675	1	274	positive regulation of protein phosphorylation	BP	1	MAP2K6	up_VFEM_EC
GO:0030947	0.695	0.686	1	12	regulation of vascular endothelial growth factor receptor signaling	BP	1	EPN2	up_VSAP_EC
GO:0072358	0.695	0.675	1	268	cardiovascular system development	BP	1	CAV1	up_VSAP_VSMC
GO:0009057	0.696	0.425	10	473	macromolecule catabolic process	BP	1	CTSS,TENT5C,CLEC16A,CYLD,RAB7A,AXIN2,CTIF,FAP,SAMD4B,RNF181	up_AFEM_EC
GO:0006366	0.696	0.496	4	583	transcription by RNA polymerase II	BP	1	BARX1,ARHGEF2,ACVR2A,MTDH	up_VPOR_EC
GO:0048812	0.696	0.521	3	151	neuron projection morphogenesis	BP	1	PLXNA4,CAMK2A,LRRN2	up_AFEM_EC
GO:0009126	0.696	0.569	2	100	purine nucleoside monophosphate metabolic process	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0009167	0.696	0.569	2	100	purine ribonucleoside monophosphate metabolic process	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC

GO:0045581	0.696	0.683	1	13	negative regulation of T cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0043154	0.696	0.676	1	23	negative regulation of cysteine-type endopeptidase activity	BP	1	PARK7	down_VCAV_EC
GO:0002027	0.696	0.678	1	20	regulation of heart rate	BP	1	CALM1	down_VSAP_EC
GO:0051973	0.696	0.678	1	19	positive regulation of telomerase activity	BP	1	CTNNB1	down_VSAP_EC
GO:0040036	0.696	0.687	1	11	regulation of fibroblast growth factor receptor	BP	1	FGFR2	up_ACOR_VSMC
GO:0051148	0.696	0.685	1	12	negative regulation of muscle cell differentiation	BP	1	FRS2	up_ACOR_VSMC
GO:0060231	0.696	0.685	1	12	mesenchymal to epithelial transition	BP	1	BMP4	up_ACOR_VSMC
GO:0071985	0.696	0.685	1	12	multivesicular body sorting pathway	BP	1	EXPH5	up_ACOR_VSMC
GO:0045935	0.696	0.679	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	HOXA9	up_AORT_EC
GO:0040012	0.696	0.675	1	303	regulation of locomotion	BP	1	TBX5	up_APUL_EC
GO:0046638	0.696	0.684	1	13	positive regulation of alpha-beta T cell	BP	1	ITPKB	up_VCAV_EC
GO:0043269	0.697	0.425	10	135	regulation of ion transport	BP	1	NEDD4,HOXA3,PRELID1,CAV1,SLC30A1,CLIC1,NKAIN1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0001503	0.697	0.439	8	109	ossification	BP	1	MEF2C,FIGNL1,BMP2,BMP2K,JAG1,ASF1A,HIF1A,FBXO5	up_VCAV_EC
GO:0043170	0.697	0.486	7	2980	macromolecule metabolic process	BP	1	EYA1,HOXA10,HOXA9,TBX15,EMX2,HOXA11,SHOX2	up_VFEM_VSMC
GO:0007249	0.697	0.461	6	71	I-kappaB kinase/NF-kappaB signaling	BP	1	HTR2B,TLR3,F2RL1,PRKCE,NOD2,MAP3K7	up_ACOR_VSMC
GO:0019222	0.697	0.48	6	1934	regulation of metabolic process	BP	1	NR1H4,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0009156	0.697	0.497	4	50	ribonucleoside monophosphate	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:1901861	0.697	0.526	3	41	regulation of muscle tissue development	BP	1	GREM1,GLI1,SIX4	down_ACOR_VSMC
GO:0055088	0.697	0.527	3	37	lipid homeostasis	BP	1	LCAT,ABCA1,ORMDL3	up_ACOR_VSMC
GO:2000278	0.697	0.528	3	37	regulation of DNA biosynthetic process	BP	1	ANKRD1,CDKN1A,HMBOX1	up_ACOR_VSMC
GO:0035305	0.697	0.527	3	37	negative regulation of dephosphorylation	BP	1	SH2D4A,TMEM225B,BAG4	up_VSAP_EC
GO:0106106	0.697	0.57	2	48	cold-induced thermogenesis	BP	1	TRPV2,PLCL1	down_VCAV_EC
GO:0120161	0.697	0.57	2	48	regulation of cold-induced thermogenesis	BP	1	TRPV2,PLCL1	down_VCAV_EC
GO:0032608	0.697	0.577	2	24	interferon-beta production	BP	1	TLR3,PTPN22	up_ACOR_VSMC
GO:0009199	0.697	0.569	2	100	ribonucleoside triphosphate metabolic	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0005977	0.697	0.577	2	26	glycogen metabolic process	BP	1	PCDH12,PPP1CB	up_VCAV_EC
GO:0006073	0.697	0.577	2	26	cellular glucan metabolic process	BP	1	PCDH12,PPP1CB	up_VCAV_EC
GO:0009166	0.697	0.574	2	31	nucleotide catabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0016999	0.697	0.575	2	30	antibiotic metabolic process	BP	1	ST6GAL1,KDM3A	up_VCAV_EC
GO:0044042	0.697	0.577	2	26	glucan metabolic process	BP	1	PCDH12,PPP1CB	up_VCAV_EC
GO:0045214	0.697	0.683	1	13	sarcomere organization	BP	1	SIX4	down_ACOR_VSMC
GO:0006879	0.697	0.675	1	23	cellular iron ion homeostasis	BP	1	SCARA5	down_VCAV_EC
GO:0032602	0.697	0.675	1	23	chemokine production	BP	1	MAVS	down_VCAV_EC
GO:0070727	0.697	0.681	1	579	cellular macromolecule localization	BP	1	RAB11B	down_VPOR_EC
GO:0043367	0.697	0.678	1	18	CD4-positive, alpha-beta T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0060113	0.697	0.678	1	18	inner ear receptor cell differentiation	BP	1	SDC4	down_VSAP_EC
GO:2000826	0.697	0.681	1	14	regulation of heart morphogenesis	BP	1	BMP2	up_VCAV_EC
GO:1905114	0.697	0.67	1	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	BARX1	up_VPOR_EC

GO:0010524	0.697	0.684	1	12	positive regulation of calcium ion transport into	BP	1	ABL1	up_VSAP_EC
GO:0040019	0.697	0.684	1	12	positive regulation of embryonic development	BP	1	OSR1	up_VSAP_EC
GO:0003012	0.697200425	0.56821	2	90	muscle system process	BP	1	TMOD1,ACTN2	up_ACOR_EC
GO:0001704	0.697791592	0.67011	1	43	formation of primary germ layer	BP	1	FOXC2	up_ACOR_EC
GO:0007154	0.698	0.337	150	1622	cell communication	BP	1	GPR1,FZD1,ADGRD1,SEZ6L,CDON,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,INSIG2,PTGFR,SLC8B1,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,GJB5,LIMS2,ARHGEF6,IL6R,SLIT2,CRADD,LRRC28,HOXD3,SLC6A4,FGF7,ABL1,GOT1,HDAC7,EMP2,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,DTX2,PDGFD,SAV1,RHPN1,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,CCBE1,STAT5A,STAT6,RECK,CISH,KLHL24,PLPP3,CAMKK2,RASD2,F2RL1,RAB11B,GLIS2,PDK2,MFN2,ZFP36L1,TRAF7,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,MYC,PIK3IP1,ZEB1,DLC1,TBXA2R,SULF2,SHOX2,SLC12A6,HIC1,FGD4,RTN4RL1,SASH1,CREBRF,MYD88,GABBR2,LRP4,PASK,GDPD5,PTPMT1,S100A4,TSPAN5,CASTOR1,NCEH1,NTN4,ASB8,TMEM17,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CD83,PRMT2,FBLN1,ZFP36L2,HPGD,IGFBP6,RAF1,MAPKBP1,PPP2R5B,CYBA,ZNF205,NCOA2,STX4,ZFAND5,PSD4,KCNC4,QARS,ARHGAP12,ACVRL1,UBQLN2,ARHGAP10,UNC93B1,RAPGEF3,HTRA2,FLOT1,PLPP5,PPP3CB,NCK1,MAVS,IRAK1BP1,KRCC1,HMOX1,MAP2K2,TGFBR2,NPRL3,CITED2,BAG4,TRADD,DEDD2,LBH,DDIT4,RAB11FIP2,LATS2	up_VSAP_EC
GO:0080135	0.698	0.386	21	240	regulation of cellular response to stress	BP	1	FZD1,ACKR3,ARHGEF5,AXIN2,ABL1,MAP3K5,F2RL1,PIK3R1,MYC,RTN4RL1,SASH1,FBXO4,MYD88,NPAS2,FBXO7,CDK9,YPEL3,QARS,UBQLN2,NCK1,MAP2K2	up_VSAP_EC
GO:0010604	0.698	0.39	20	919	positive regulation of macromolecule metabolic process	BP	1	HOXA9,LEP,LBH,PRR16,DLL1,F3,MLLT11,THRB,GREM1,NFE2L1,TENT5C,MYBL1,DCUN1D3,BVES,RAB7A,AXIN2,PPARGC1A,CCL5,ADAM17,TNC	up_AFEM_EC
GO:0032886	0.698	0.458	6	81	regulation of microtubule-based process	BP	1	PLK2,STMN1,FES,SENP6,TAOK1,ARHGEF2	up_VCAV_EC
GO:0048511	0.698	0.46	6	72	rhythmic process	BP	1	ENOX1,SLIT2,CHRM1,NR2F6,NCOA2,ASS1	up_VSAP_EC
GO:1903532	0.698	0.492	4	78	positive regulation of secretion by cell	BP	1	NR1H4,PTPN11,HIF1A,SDC4	down_VSAP_EC
GO:0097237	0.698	0.525	3	42	cellular response to toxic substance	BP	1	TIMELESS,EZH2,SIGMAR1	down_ACOR_VSMC
GO:0070555	0.698	0.574	2	29	response to interleukin-1	BP	1	IRAK1,CACTIN	down_ACOR_VSMC
GO:0018210	0.698	0.569	2	48	peptidyl-threonine modification	BP	1	CAMK2D,SPRED1	down_VCAV_EC
GO:0051262	0.698	0.571	2	40	protein tetramerization	BP	1	VASP,GBP5	down_VSAP_EC
GO:0001953	0.698	0.679	1	14	negative regulation of cell-matrix adhesion	BP	1	HOXA7	down_ACOR_VSMC
GO:0046907	0.698	0.679	1	536	intracellular transport	BP	1	ANKRD50	down_AFEM_EC
GO:0032481	0.698	0.673	1	24	positive regulation of type I interferon production	BP	1	MAVS	down_VCAV_EC
GO:0048144	0.698	0.673	1	23	fibroblast proliferation	BP	1	DDR2	down_VCAV_EC
GO:0048145	0.698	0.673	1	23	regulation of fibroblast proliferation	BP	1	DDR2	down_VCAV_EC
GO:0048477	0.698	0.676	1	19	oogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:1902803	0.698	0.675	1	20	regulation of synaptic vesicle transport	BP	1	GSK3B	down_VSAP_EC
GO:2000300	0.698	0.675	1	20	regulation of synaptic vesicle exocytosis	BP	1	GSK3B	down_VSAP_EC
GO:0016126	0.698	0.675	1	20	sterol biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:0002285	0.698	0.669	1	50	lymphocyte activation involved in immune	BP	1	DLL1	up_AFEM_EC
GO:0010557	0.698	0.677	1	492	positive regulation of macromolecule biosynthetic process	BP	1	HOXA9	up_AORT_EC

GO:0042981	0.698	0.677	1	471	regulation of apoptotic process	BP	1	TAOK1	up_AORT_EC
GO:0006766	0.698	0.678	1	16	vitamin metabolic process	BP	1	ACPP	up_VCAV_EC
GO:0035773	0.698	0.679	1	15	insulin secretion involved in cellular response to glucose stimulus	BP	1	HIF1A	up_VCAV_EC
GO:0001667	0.698	0.669	1	146	ameboidal-type cell migration	BP	1	SEMA3A	up_VPOR_EC
GO:0072657	0.698	0.669	1	144	protein localization to membrane	BP	1	SRP54	up_VPOR_EC
GO:0034661	0.698	0.682	1	12	ncRNA catabolic process	BP	1	EXOSC7	up_VSAP_EC
GO:0042088	0.698	0.682	1	12	T-helper 1 type immune response	BP	1	STAT6	up_VSAP_EC
GO:0022408	0.698125626	0.6696	1	44	negative regulation of cell-cell adhesion	BP	1	PRKCD	up_ACOR_EC
GO:0043902	0.69851352	0.66903	1	45	positive regulation of multi-organism process	BP	1	CHMP4B	up_ACOR_EC
GO:0002819	0.698654674	0.66897	1	44	regulation of adaptive immune response	BP	1	FZD5	up_ACOR_EC
GO:0034250	0.698768637	0.66873	1	45	positive regulation of cellular amide metabolic	BP	1	PRKCD	up_ACOR_EC
GO:0001701	0.698996006	0.51816	3	134	in utero embryonic development	BP	1	FZD5,RARRES2,PYGO2	up_ACOR_EC
GO:0051603	0.699	0.375	27	305	proteolysis involved in cellular protein catabolic process	BP	1	ZRANB1,SKP2,SH3RF2,ISG15,ZNRF3,CTSS,KLHL20,CTSB,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0002250	0.699	0.473	5	68	adaptive immune response	BP	1	HMGB1,TFRC,FAM49B,EMP2,PIK3CD	down_ACOR_VSMC
GO:0071375	0.699	0.473	5	68	cellular response to peptide hormone stimulus	BP	1	SREBF1,CAV1,CDK4,SMARCC1,NCOA5	down_ACOR_VSMC
GO:0051258	0.699	0.49	4	94	protein polymerization	BP	1	KIRREL1,CLIP3,ENSCAFG00000014978,ACTR3B	down_VCAV_EC
GO:0030902	0.699	0.524	3	41	hindbrain development	BP	1	EZH2,ARCN1,GLI1	down_ACOR_VSMC
GO:0031669	0.699	0.519	3	72	cellular response to nutrient levels	BP	1	KANK2,GABARAP,CLEC16A	down_VCAV_EC
GO:0065002	0.699	0.572	2	30	intracellular protein transmembrane transport	BP	1	TIMM44,TRAM1	down_ACOR_VSMC
GO:0071806	0.699	0.572	2	30	protein transmembrane transport	BP	1	TIMM44,TRAM1	down_ACOR_VSMC
GO:0098876	0.699	0.573	2	29	vesicle-mediated transport to the plasma	BP	1	ACSL3,STXBP6	down_ACOR_VSMC
GO:0002824	0.699	0.572	2	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	GATA3,NECTIN2	up_VCAV_EC
GO:0060548	0.699	0.567	2	294	negative regulation of cell death	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0006721	0.699	0.679	1	14	terpenoid metabolic process	BP	1	FDFT1	down_ACOR_VSMC
GO:0048008	0.699	0.672	1	24	platelet-derived growth factor receptor signaling	BP	1	PDGFRB	down_VCAV_EC
GO:0009311	0.699	0.673	1	21	oligosaccharide metabolic process	BP	1	MOGS	down_VSAP_EC
GO:0007435	0.699	0.676	1	18	salivary gland morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0021772	0.699	0.683	1	11	olfactory bulb development	BP	1	CHD7	up_ACOR_VSMC
GO:0021988	0.699	0.683	1	11	olfactory lobe development	BP	1	CHD7	up_ACOR_VSMC
GO:0071622	0.699	0.68	1	13	regulation of granulocyte chemotaxis	BP	1	JAM3	up_ACOR_VSMC
GO:0048839	0.699	0.668	1	50	inner ear development	BP	1	DLL1	up_AFEM_EC
GO:0032270	0.699	0.676	1	479	positive regulation of cellular protein metabolic	BP	1	TAOK1	up_AORT_EC
GO:0042325	0.699	0.675	1	463	regulation of phosphorylation	BP	1	FBP1	up_VFEM_VSMC
GO:1902808	0.699	0.682	1	12	positive regulation of cell cycle G1/S phase	BP	1	LSM10	up_VSAP_EC
GO:2000249	0.699	0.681	1	12	regulation of actin cytoskeleton	BP	1	ABL1	up_VSAP_EC
GO:0051147	0.699468432	0.66801	1	44	regulation of muscle cell differentiation	BP	1	RBM38	up_ACOR_EC

GO:0010638	0.7	0.39	18	207	positive regulation of organelle organization	BP	1	WNT11,ARHGEF5,DDHD1,ABL1,CDC42EP5,FUZ,CDC42EP2,F2RL1,MFN2,FBXO4,PHF1,FBXO7,CDK9,PIP4K2B,ZNF205,HTRA2,NCK1,BAG4	up_VSAP_EC
GO:0071345	0.7	0.395	16	210	cellular response to cytokine stimulus	BP	1	FLNB,IRAK1,SLC29A1,SLC25A5,B3GNT2,CAV1,ADIPOR2,CDK4,TFRC,NCL,CACTIN,CDC42EP4,CORO1A,CTH,ARHGEF2,MSC	down_ACOR_VSMC
GO:0048608	0.7	0.416	11	129	reproductive structure development	BP	1	HOXA11,HOXA9,GJB5,IRX5,SLIT2,OSR1,RARG,PATZ1,DLX3,ZFP36L1,CITED2	up_VSAP_EC
GO:0051254	0.7	0.427	9	431	positive regulation of RNA metabolic process	BP	1	HOXA9,LBH,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0016311	0.7	0.428	9	106	dephosphorylation	BP	1	PPARGC1B,SH2D4A,INPP5E,PLPP3,TMEM225B,NCEH1,PLPP5,NCK1,BAG4	up_VSAP_EC
GO:0090066	0.7	0.443	7	162	regulation of anatomical structure size	BP	1	KIRREL1,ADCY6,TRPV2,ENSCAFG00000014978,AKT1S1,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0007569	0.7	0.524	3	36	cell aging	BP	1	MARCH5,CDKN1A,PRELP	up_ACOR_VSMC
GO:0009057	0.7	0.569	2	473	macromolecule catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0050868	0.7	0.572	2	28	negative regulation of T cell activation	BP	1	HMGB1,ARG2	down_ACOR_VSMC
GO:0051960	0.7	0.669	1	216	regulation of nervous system development	BP	1	LYN	down_ACOR_EC
GO:0051489	0.7	0.678	1	14	regulation of filopodium assembly	BP	1	FSCN1	down_ACOR_VSMC
GO:0032206	0.7	0.672	1	23	positive regulation of telomere maintenance	BP	1	NABP2	down_VCAV_EC
GO:0051851	0.7	0.671	1	23	modification by host of symbiont morphology or	BP	1	NAPEPLD	down_VCAV_EC
GO:0072527	0.7	0.672	1	23	pyrimidine-containing compound metabolic	BP	1	GPAM	down_VCAV_EC
GO:0070265	0.7	0.674	1	19	necrotic cell death	BP	1	ARHGEF2	down_VSAP_EC
GO:0030514	0.7	0.68	1	12	negative regulation of BMP signaling pathway	BP	1	SMAD6	up_ACOR_VSMC
GO:0007224	0.7	0.666	1	50	smoothened signaling pathway	BP	1	GAS1	up_AFEM_EC
GO:0032371	0.7	0.676	1	15	regulation of sterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0032374	0.7	0.676	1	15	regulation of cholesterol transport	BP	1	ABCA1	up_VCAV_EC
GO:1902751	0.7	0.678	1	14	positive regulation of cell cycle G2/M phase	BP	1	RAB11A	up_VCAV_EC
GO:0033365	0.7	0.67	1	276	protein localization to organelle	BP	1	SIX1	up_VFEM_EC
GO:0019637	0.7	0.671	1	342	organophosphate metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0001754	0.7	0.68	1	12	eye photoreceptor cell differentiation	BP	1	THRB	up_VSAP_EC
GO:0071985	0.7	0.68	1	12	multivesicular body sorting pathway	BP	1	VPS36	up_VSAP_EC
GO:2000108	0.7	0.68	1	12	positive regulation of leukocyte apoptotic	BP	1	CD274	up_VSAP_EC
GO:0001934	0.7	0.669	1	274	positive regulation of protein phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0040007	0.7	0.67	1	276	growth	BP	1	HOXA11	up_VSAP_VSMC

GO:0031323	0.701	0.333	167	1788	regulation of cellular metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MEIS2,MBP,RECK,LIPT2,FEZ1,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,ISG15,ZNF782,ZNF365,AR,ZNF484,SASH1,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,CDKN2B,CST3,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,BNIP3,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,LRPAP1,NPNT,OS9,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,MARF1,DKKL1,FRS2,RNF19A,CCPG1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,PPP1R26,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,MXI1,CHD7,JUP,TLE4,SPINK2,ZNF432,CCL5,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,OXR1,RNF141,AKTIP,DUSP26,CBX7,NOD2,LRRC4,ARID5B,FAM107A,ZNF629,PRKAG3,ZFP3,DDIT4,ENSCAFG00000018360,DISC1,SH3RF3,DCUN1D4,KLF11,HERPUD1,RPRD1B,ZNF461,ZNF252,FEZ2,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,WDR48,CTIF,ZKSCAN1,ZNF529,S	up_ACOR_VSMC
GO:0010556	0.701	0.339	106	1137	regulation of macromolecule biosynthetic process	BP	1	TLR1,SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,NACC2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,ORMDL3,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0000902	0.701	0.379	23	266	cell morphogenesis	BP	1	WASF3,ENPP2,RADIL,SLIT2,ABL1,CDC42EP5,PLXNA4,RILPL2,CDC42EP2,SHOX2,LRP4,DPYSL2,FRMD6,LIMD1,FBLN1,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN,LATS2	up_VSAP_EC
GO:0001667	0.701	0.414	11	146	ameboidal-type cell migration	BP	1	HMGB1,ANLN,GREM1,PRCP,PPARD,EMP2,NUP188,SGPL1,PHACTR4,NUS1,AMOTL1	down_ACOR_VSMC
GO:0008152	0.701	0.54	5	3714	metabolic process	BP	1	CYP1A1,LIMK1,GATA5,C6,ENSCAFG00000028814	up_VCAV_VSMC
GO:0046328	0.701	0.471	5	61	regulation of JNK cascade	BP	1	ARHGEF5,MAP3K5,F2RL1,SASH1,MYD88	up_VSAP_EC
GO:1903322	0.701	0.49	4	59	positive regulation of protein modification by small protein conjugation	BP	1	TNIP1,PELI1,BCL10,UBE2D1	up_VCAV_EC
GO:0060993	0.701	0.521	3	42	kidney morphogenesis	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:1901617	0.701	0.518	3	60	organic hydroxy compound biosynthetic	BP	1	NR1H4,APOE,REST	down_VSAP_EC
GO:0051345	0.701	0.515	3	151	positive regulation of hydrolase activity	BP	1	F3,RASGEF1B,CCL5	up_AFEM_EC
GO:0045833	0.701	0.57	2	29	negative regulation of lipid metabolic process	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:0006464	0.701	0.584	2	1162	cellular protein modification process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0031326	0.701	0.583	2	1176	regulation of cellular biosynthetic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0036211	0.701	0.584	2	1162	protein modification process	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0015698	0.701	0.573	2	24	inorganic anion transport	BP	1	SLC26A7,CLCN3	up_ACOR_VSMC
GO:0044267	0.701	0.594	2	1583	cellular protein metabolic process	BP	1	LIMK1,C6	up_VCAV_VSMC
GO:0006928	0.701	0.569	2	557	movement of cell or subcellular component	BP	1	EMX2,CAV1	up_VSAP_VSMC

GO:0030970	0.701	0.677	1	14	retrograde protein transport, ER to cytosol	BP	1	HM13	down_ACOR_VSMC
GO:0002090	0.701	0.676	1	14	regulation of receptor internalization	BP	1	GREM1	down_ACOR_VSMC
GO:0043666	0.701	0.677	1	14	regulation of phosphoprotein	BP	1	SLC29A1	down_ACOR_VSMC
GO:1903513	0.701	0.677	1	14	endoplasmic reticulum to cytosol transport	BP	1	HM13	down_ACOR_VSMC
GO:0032411	0.701	0.67	1	24	positive regulation of transporter activity	BP	1	PARK7	down_VCAV_EC
GO:0034764	0.701	0.666	1	50	positive regulation of transmembrane transport	BP	1	FXYD1	up_AFEM_EC
GO:1900180	0.701	0.666	1	50	regulation of protein localization to nucleus	BP	1	LEP	up_AFEM_EC
GO:0035767	0.701	0.677	1	14	endothelial cell chemotaxis	BP	1	PRKD2	up_VCAV_EC
GO:0060191	0.701	0.676	1	14	regulation of lipase activity	BP	1	SELE	up_VCAV_EC
GO:0042461	0.701	0.68	1	12	photoreceptor cell development	BP	1	THRB	up_VSAP_EC
GO:0032268	0.702	0.345	71	778	regulation of cellular protein metabolic process	BP	1	FZD1,PRR16,CDON,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,CST3,CRADD,FGF7,ABL1,EMP2,MAP3K5,PDGFD,KLF15,C1QTNF2,CNPPD1,CCBE1,RECK,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,ZFP36L1,TRAF7,GAS1,MYC,EEF2,RTN4RL1,SASH1,FBXO4,LARP6,MYD88,LRP4,ANKHD1,PHF1,FBXO7,RNF166,RPUSD4,CDK9,FBLN1,OSBPL7,SAMD4B,ZFP36L2,RAF1,EIF3K,TIMP2,QARS,EIF3D,ACVRL1,UBQLN2,HTRA2,FLOT1,TNRC6C,NCK1,MAVS,ZER1,MAP2K2,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0048729	0.702	0.388	18	209	tissue morphogenesis	BP	1	HOXA11,FZD1,WNT11,SLIT2,FGF7,ABL1,DLL1,OSR1,FUZ,RARG,IRX3,SHOX2,NTN4,KDM2B,ARHGAP12,ACVRL1,TGFBR2,CITED2	up_VSAP_EC
GO:0034220	0.702	0.4	14	188	ion transmembrane transport	BP	1	NNT,NEDD4,SLC35C2,CAV1,SLC30A1,CLIC1,GSTO1,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0044238	0.702	0.433	14	3383	primary metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0006875	0.702	0.414	11	129	cellular metal ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,FXN,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:0051961	0.702	0.455	6	73	negative regulation of nervous system	BP	1	THRB,SLIT2,DLL1,IRX3,RTN4RL1,LRP4	up_VSAP_EC
GO:0035264	0.702	0.517	3	56	multicellular organism growth	BP	1	CELF1,PTPN11,TMED2	down_VSAP_EC
GO:0051209	0.702	0.57	2	28	release of sequestered calcium ion into cytosol	BP	1	GSTO1,CORO1A	down_ACOR_VSMC
GO:0051283	0.702	0.57	2	28	negative regulation of sequestering of calcium	BP	1	GSTO1,CORO1A	down_ACOR_VSMC
GO:1903051	0.702	0.57	2	29	negative regulation of proteolysis involved in cellular protein catabolic	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC
GO:0048701	0.702	0.571	2	25	embryonic cranial skeleton morphogenesis	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0007154	0.702	0.594	2	1622	cell communication	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0044267	0.702	0.594	2	1583	cellular protein metabolic process	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0002792	0.702	0.569	2	29	negative regulation of peptide secretion	BP	1	ARG2,CD200	up_VCAV_EC
GO:0003170	0.702	0.571	2	25	heart valve development	BP	1	SHOX2,TGFBR2	up_VSAP_EC
GO:0007632	0.702	0.676	1	14	visual behavior	BP	1	HMGCR	down_ACOR_VSMC
GO:0000381	0.702	0.672	1	19	regulation of alternative mRNA splicing, via	BP	1	REST	down_VSAP_EC
GO:0055117	0.702	0.67	1	21	regulation of cardiac muscle contraction	BP	1	CALM1	down_VSAP_EC
GO:0030204	0.702	0.675	1	14	chondroitin sulfate metabolic process	BP	1	CHST7	up_VCAV_EC
GO:0031128	0.702	0.674	1	15	developmental induction	BP	1	BMP2	up_VCAV_EC
GO:0043666	0.702	0.675	1	14	regulation of phosphoprotein	BP	1	PPP1R2	up_VCAV_EC
GO:0032787	0.702	0.665	1	144	monocarboxylic acid metabolic process	BP	1	FBP1	up_VPOR_EC

GO:0044270	0.702	0.664	1	147	cellular nitrogen compound catabolic	BP	1	FBP1	up_VPOR_EC
GO:0046700	0.702	0.664	1	147	heterocycle catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0042325	0.702	0.673	1	463	regulation of phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0034103	0.702	0.678	1	12	regulation of tissue remodeling	BP	1	PPARGC1B	up_VSAP_EC
GO:0045453	0.702	0.677	1	12	bone resorption	BP	1	PPARGC1B	up_VSAP_EC
GO:0090287	0.702485139	0.56176	2	91	regulation of cellular response to growth factor	BP	1	SMAD6,ADAMTSL2	up_ACOR_EC
GO:0120035	0.703	0.4	14	160	regulation of plasma membrane bounded cell projection organization	BP	1	ITM2C,EVI5L,ZNF365,F2RL1,NRP1,ULK2,EVL,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,RREB1	up_ACOR_VSMC
GO:0023014	0.703	0.411	11	248	signal transduction by protein phosphorylation	BP	1	NOTCH2,PDGFRB,GLIPR2,CSPG4,ZFP36L1,MYDGF,SASH1,CDH2,GSDME,SPRED1,SHC1	down_VCAV_EC
GO:1901293	0.703	0.424	9	106	nucleoside phosphate biosynthetic process	BP	1	ACACB,NADK,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,PNP,DDIT4	up_VSAP_EC
GO:0045861	0.703	0.468	5	71	negative regulation of proteolysis	BP	1	SLC29A1,BIRC5,SMARCC1,DHCR24,ENSCAFG00000005299	down_ACOR_VSMC
GO:0045926	0.703	0.468	5	72	negative regulation of growth	BP	1	IFRD1,CDA,IRF8,SMARCA4,HIF1A	up_VCAV_EC
GO:0002460	0.703	0.469	5	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	CD274,EMP2,STAT6,MYD88,PPP3CB	up_VSAP_EC
GO:0022900	0.703	0.564	2	46	electron transport chain	BP	1	UQCR10,PARK7	down_VCAV_EC
GO:0000288	0.703	0.57	2	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	DCP1B,CNOT4	up_ACOR_VSMC
GO:0008219	0.703	0.569	2	611	cell death	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:2000779	0.703	0.57	2	25	regulation of double-strand break repair	BP	1	FIGNL1,TIMELESS	up_VCAV_EC
GO:0051289	0.703	0.569	2	25	protein homotetramerization	BP	1	ACACB,PCBD1	up_VSAP_EC
GO:0006414	0.703	0.673	1	15	translational elongation	BP	1	EIF5A	down_ACOR_VSMC
GO:0006903	0.703	0.674	1	14	vesicle targeting	BP	1	PREB	down_ACOR_VSMC
GO:0009112	0.703	0.674	1	14	nucleobase metabolic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0072595	0.703	0.674	1	14	maintenance of protein localization in organelle	BP	1	INSIG1	down_ACOR_VSMC
GO:0032649	0.703	0.668	1	23	regulation of interferon-gamma production	BP	1	PRNP	down_VCAV_EC
GO:0071705	0.703	0.674	1	582	nitrogen compound transport	BP	1	RAB11B	down_VPOR_EC
GO:0002204	0.703	0.67	1	18	somatic recombination of immunoglobulin genes involved in immune	BP	1	TFRC	down_VSAP_EC
GO:0002208	0.703	0.67	1	18	somatic diversification of immunoglobulins involved in immune response	BP	1	TFRC	down_VSAP_EC
GO:0032330	0.703	0.67	1	20	regulation of chondrocyte differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0032663	0.703	0.67	1	19	regulation of interleukin-2 production	BP	1	NR1H4	down_VSAP_EC
GO:0045190	0.703	0.67	1	18	isotype switching	BP	1	TFRC	down_VSAP_EC
GO:1905954	0.703	0.67	1	19	positive regulation of lipid localization	BP	1	APOE	down_VSAP_EC
GO:0002686	0.703	0.677	1	12	negative regulation of leukocyte migration	BP	1	WASL	up_ACOR_VSMC
GO:0045684	0.703	0.676	1	12	positive regulation of epidermis development	BP	1	BMP4	up_ACOR_VSMC
GO:0009156	0.703	0.664	1	50	ribonucleoside monophosphate	BP	1	PPARGC1A	up_AFEM_EC
GO:0043436	0.703	0.666	1	303	oxoacid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0010737	0.703	0.675	1	13	protein kinase A signaling	BP	1	AKAP12	up_VCAV_EC
GO:0045581	0.703	0.675	1	13	negative regulation of T cell differentiation	BP	1	HMGB1	up_VCAV_EC
GO:1902235	0.703	0.673	1	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	NCK1	up_VCAV_EC

GO:0033146	0.703	0.676	1	12	regulation of intracellular estrogen receptor signaling pathway	BP	1	LBH	up_VSAP_EC
GO:0051560	0.703	0.677	1	12	mitochondrial calcium ion homeostasis	BP	1	SLC8B1	up_VSAP_EC
GO:0035561	0.703	0.676	1	12	regulation of chromatin binding	BP	1	EBF2	up_VSAP_EC
GO:0060795	0.703	0.677	1	12	cell fate commitment involved in formation of	BP	1	HOXA11	up_VSAP_EC
GO:0071453	0.703505534	0.66296	1	46	cellular response to oxygen levels	BP	1	AQP1	up_ACOR_EC
GO:0051128	0.704	0.39	17	790	regulation of cellular component organization	BP	1	RAB20,DLL1,CRYAB,PLXNA4,MLLT11,GREM1,CLEC16A,CYLD,DCUN1D3,BVES,AXIN2,PPARGC1A,CDC42EP5,FAP,DMPK,ADAM17,KANK1	up_AFEM_EC
GO:0010035	0.704	0.423	9	107	response to inorganic substance	BP	1	TNNT2,PRKAA2,ATRX,BNIP3,EGLN1,B2M,SLC25A12,CAT,PARK7	up_ACOR_VSMC
GO:0002831	0.704	0.517	3	42	regulation of response to biotic stimulus	BP	1	HMGB1,ARG2,CACTIN	down_ACOR_VSMC
GO:0060993	0.704	0.518	3	42	kidney morphogenesis	BP	1	HOXB7,GATA3,BMP2	up_VCAV_EC
GO:0006367	0.704	0.565	2	32	transcription initiation from RNA polymerase II	BP	1	IRF8,HMGB1	up_VCAV_EC
GO:0031397	0.704	0.566	2	30	negative regulation of protein ubiquitination	BP	1	TNFAIP3,IVNS1ABP	up_VCAV_EC
GO:0033143	0.704	0.568	2	25	regulation of intracellular steroid hormone receptor signaling pathway	BP	1	PRMT2,LBH	up_VSAP_EC
GO:0016226	0.704	0.673	1	14	iron-sulfur cluster assembly	BP	1	HSPA9	down_ACOR_VSMC
GO:0031163	0.704	0.673	1	14	metallo-sulfur cluster assembly	BP	1	HSPA9	down_ACOR_VSMC
GO:0097009	0.704	0.674	1	13	energy homeostasis	BP	1	PRCP	down_ACOR_VSMC
GO:0009605	0.704	0.672	1	538	response to external stimulus	BP	1	IVNS1ABP	down_AFEM_EC
GO:1902531	0.704	0.671	1	536	regulation of intracellular signal transduction	BP	1	IVNS1ABP	down_AFEM_EC
GO:0007584	0.704	0.666	1	24	response to nutrient	BP	1	KANK2	down_VCAV_EC
GO:0031110	0.704	0.666	1	24	regulation of microtubule polymerization or depolymerization	BP	1	CLIP3	down_VCAV_EC
GO:1902750	0.704	0.666	1	24	negative regulation of cell cycle G2/M phase	BP	1	BRSK1	down_VCAV_EC
GO:0031057	0.704	0.67	1	18	negative regulation of histone modification	BP	1	KDM3A	down_VSAP_EC
GO:0006508	0.704	0.67	1	483	proteolysis	BP	1	LNPEP	up_AORT_EC
GO:0043067	0.704	0.67	1	479	regulation of programmed cell death	BP	1	TAOK1	up_AORT_EC
GO:0072528	0.704	0.673	1	14	pyrimidine-containing compound biosynthetic	BP	1	MTOR	up_VCAV_EC
GO:0048066	0.704	0.676	1	12	developmental pigmentation	BP	1	HPS4	up_VSAP_EC
GO:0120033	0.704	0.676	1	12	negative regulation of plasma membrane bounded cell projection	BP	1	SLIT2	up_VSAP_EC
GO:1902680	0.705	0.362	33	415	positive regulation of RNA biosynthetic process	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,INSIG1,THRAP3,FAM129B,GREM1,SMARCC1,DHX33,CKS2,BRCA1,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,ENSCAFG00000017103	down_ACOR_VSMC
GO:1903508	0.705	0.362	33	415	positive regulation of nucleic acid-templated transcription	BP	1	HMGB1,SREBF1,ILF3,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,INSIG1,THRAP3,FAM129B,GREM1,SMARCC1,DHX33,CKS2,BRCA1,E2F8,PPARD,NCL,NUP62,FOSL1,HMGB2,CDK2,DDX39B,CCNA2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,JMJD6,ENSCAFG00000017103	down_ACOR_VSMC
GO:0000280	0.705	0.41	11	145	nuclear division	BP	1	PDGFB,EDN1,RAB11A,FIGNL1,MZT1,CENPC,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0030162	0.705	0.42	9	202	regulation of proteolysis	BP	1	CST3,RECK,TIMP2,PSMF1,PARK7,CLEC16A,IFT57,A2M,PACSIN3	down_VCAV_EC
GO:0051186	0.705	0.429	8	159	cofactor metabolic process	BP	1	PGK1,TPI1,ENSCAFG00000028814,PGAM1,ALDH1L2,HIF1A,NMNAT2,ALDOC	down_VSAP_EC
GO:0031325	0.705	0.492	4	914	positive regulation of cellular metabolic process	BP	1	ACVRL1,LYN,HOXA1,ACSL3	down_ACOR_EC

GO:0007160	0.705	0.486	4	56	cell-matrix adhesion	BP	1	GREM1,HOXA7,RAC1,EMP2	down_ACOR_VSMC
GO:0010632	0.705	0.484	4	95	regulation of epithelial cell migration	BP	1	DCN,GLIPR2,SASH1,SPRED1	down_VCAV_EC
GO:0016202	0.705	0.562	2	39	regulation of striated muscle tissue	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0010975	0.705	0.558	2	103	regulation of neuron projection development	BP	1	PLXNA4,KANK1	up_AFEM_EC
GO:0001678	0.705	0.566	2	29	cellular glucose homeostasis	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0034198	0.705	0.566	2	27	cellular response to amino acid starvation	BP	1	ATF3,MTOR	up_VCAV_EC
GO:1990928	0.705	0.566	2	27	response to amino acid starvation	BP	1	ATF3,MTOR	up_VCAV_EC
GO:0002711	0.705	0.672	1	14	positive regulation of T cell mediated immunity	BP	1	FAM49B	down_ACOR_VSMC
GO:1901983	0.705	0.665	1	24	regulation of protein acetylation	BP	1	PARK7	down_VCAV_EC
GO:1903036	0.705	0.667	1	19	positive regulation of response to wounding	BP	1	SERPINE1	down_VSAP_EC
GO:2000780	0.705	0.676	1	11	negative regulation of double-strand break	BP	1	TP53BP1	up_ACOR_VSMC
GO:0032269	0.705	0.664	1	306	negative regulation of cellular protein metabolic	BP	1	PCSK1N	up_APUL_EC
GO:0051445	0.705	0.672	1	14	regulation of meiotic cell cycle	BP	1	FBXO5	up_VCAV_EC
GO:0051898	0.705	0.671	1	15	negative regulation of protein kinase B signaling	BP	1	RAPGEF1	up_VCAV_EC
GO:0030101	0.705	0.674	1	12	natural killer cell activation	BP	1	TOX	up_VSAP_EC
GO:0050891	0.705	0.674	1	12	multicellular organismal water homeostasis	BP	1	CLDN1	up_VSAP_EC
GO:0044092	0.705	0.663	1	270	negative regulation of molecular function	BP	1	CAV1	up_VSAP_VSMC
GO:0001501	0.705229452	0.48186	4	178	skeletal system development	BP	1	SOX9,PTH1R,FOXC2,EFEMP1	up_ACOR_EC
GO:0048704	0.705616402	0.66042	1	46	embryonic skeletal system morphogenesis	BP	1	FOXC2	up_ACOR_EC
GO:0031323	0.706	0.327	166	1788	regulation of cellular metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,TBC1D10C,CEP85,ACACB,TPCN2,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,CBX7,STAT6,RECK,GATAD1,PLPP3,ENSCAFG00000000071,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,RBL2,LMF1,GLIS2,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,BATF2,MYC,PIK3IP1,SSBP2,IRX3,ZEB1,SHOX2,TMEM225B,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,POLDIP2,CLYBL,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,NUP98,ANKHD1,TRERF1,PHF1,E2F4,NPAS2,FBXO7,LIMD1,RNF166,RPUSD4,LONP2,CDK9,PRMT2,KDM2B,FBLN1,PIP4K2B,OSBPL7,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,CYBA,ZNF205,NCOA2,EIF3K,PQBP1,TIMP2,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,UBQLN2,ZNF517,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,ZER1,MAP2K2,TGFBR2,	up_VSAP_EC
GO:0044419	0.706	0.415	10	117	interspecies interaction between organisms	BP	1	NAPEPLD,F2RL1,MYD88,MON1B,PC,EIF3G,EIF3L,EIF3D,MAVS,ULK1	up_VSAP_EC
GO:0090130	0.706	0.42	9	121	tissue migration	BP	1	HMGB1,ANLN,GREM1,PRCP,PPARD,EMP2,NUP188,NUS1,AMOTL1	down_ACOR_VSMC
GO:2000113	0.706	0.426	8	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1,SAMD4B	up_AFEM_EC
GO:0031334	0.706	0.438	7	84	positive regulation of protein complex assembly	BP	1	ARHGEF5,CDC42EP5,CDC42EP2,ICE1,NCK1,BAG4,JCHAIN	up_VSAP_EC
GO:0032271	0.706	0.45	6	73	regulation of protein polymerization	BP	1	SLIT2,ABL1,CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:0051048	0.706	0.515	3	42	negative regulation of secretion	BP	1	SREBF1,ARG2,EZR	down_ACOR_VSMC
GO:0007416	0.706	0.517	3	36	synapse assembly	BP	1	SLITRK5,APP,CRKL	up_ACOR_VSMC

GO:0008016	0.706	0.56	2	48	regulation of heart contraction	BP	1	IRX5,THRB	down_VCAV_EC
GO:0008361	0.706	0.56	2	50	regulation of cell size	BP	1	TRPV2,AKT1S1	down_VCAV_EC
GO:0051604	0.706	0.558	2	102	protein maturation	BP	1	GAS1,F3	up_AFEM_EC
GO:0072676	0.706	0.566	2	25	lymphocyte migration	BP	1	SLC8B1,HSD3B7	up_VSAP_EC
GO:0018126	0.706	0.671	1	14	protein hydroxylation	BP	1	JMJD6	down_ACOR_VSMC
GO:0106027	0.706	0.664	1	24	neuron projection organization	BP	1	PRNP	down_VCAV_EC
GO:0032008	0.706	0.667	1	19	positive regulation of TOR signaling	BP	1	SEC13	down_VSAP_EC
GO:0003073	0.706	0.666	1	20	regulation of systemic arterial blood pressure	BP	1	PRCP	down_VSAP_EC
GO:0042088	0.706	0.673	1	12	T-helper 1 type immune response	BP	1	IL18R1	up_ACOR_VSMC
GO:0097352	0.706	0.674	1	12	autophagosome maturation	BP	1	LAMP2	up_ACOR_VSMC
GO:0006082	0.706	0.663	1	305	organic acid metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0006919	0.706	0.667	1	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	PMAIP1	up_VCAV_EC
GO:0060964	0.706	0.672	1	13	regulation of gene silencing by miRNA	BP	1	PPP3CA	up_VCAV_EC
GO:0072583	0.706	0.672	1	13	clathrin-dependent endocytosis	BP	1	BMP2K	up_VCAV_EC
GO:0048568	0.706	0.66	1	148	embryonic organ development	BP	1	HOXA3	up_VPOR_EC
GO:0009127	0.706975469	0.65867	1	47	purine nucleoside monophosphate biosynthetic process	BP	1	ALDOC	up_ACOR_EC
GO:0009168	0.706975469	0.65867	1	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	ALDOC	up_ACOR_EC
GO:0044281	0.707	0.35	45	622	small molecule metabolic process	BP	1	NPR1,PANK3,CDA,PDGFB,ST6GAL1,ATF3,GK5,EDN1,PIPOX,PTGS1,ADSS,FAM3C,GUCY1A1,ODC1,SPTLC2,ARG2,TARSL2,MTOR,ACPP,BMP2,CHST7,PGM2,ABCA1,AADAT,ITPKB,PROX1,ENSCAFG00000010596,GALE,CHST1,ELOVL7,ENSCAFG00000024323,APOD,SLC25A25,GUCY1B1,PTGS2,PLCG2,GCH1,DCK,NOS2,PMAIP1,IMPA1,HIF1A,KDM3A,BCAT1,ALDH1A3	up_VCAV_EC
GO:1903047	0.707	0.393	14	257	mitotic cell cycle process	BP	1	PLK3,MZT1,NAA10,ZPR1,EIF4EBP1,KPNB1,ANLN,PDS5B,BACH1,HTT,RBBP8,CALM1,INHBA,CDKN1A	down_VSAP_EC
GO:0044255	0.707	0.446	6	293	cellular lipid metabolic process	BP	1	LEP,GPAM,ACACB,NAPEPLD,PPARGC1A,AGPAT2	up_AFEM_EC
GO:0060548	0.707	0.446	6	294	negative regulation of cell death	BP	1	ANGPT4,DLL1,CRYAB,GPAM,GREM1,PPARGC1A	up_AFEM_EC
GO:0006665	0.707	0.485	4	48	sphingolipid metabolic process	BP	1	CERS4,ENSCAFG00000000071,HACD4,B3GALT4	up_VSAP_EC
GO:0019538	0.707	0.536	3	1713	protein metabolic process	BP	1	CST3,MGAT4B,GBGT1	down_VPOR_EC
GO:0010604	0.707	0.52	3	919	positive regulation of macromolecule metabolic	BP	1	NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0050777	0.707	0.563	2	28	negative regulation of immune response	BP	1	ARG2,CACTIN	down_ACOR_VSMC
GO:0006635	0.707	0.565	2	25	fatty acid beta-oxidation	BP	1	LEP,ACAD11	up_ACOR_VSMC
GO:0098693	0.707	0.565	2	25	regulation of synaptic vesicle cycle	BP	1	FBXL20,PREPL	up_ACOR_VSMC
GO:0072507	0.707	0.555	2	103	divalent inorganic cation homeostasis	BP	1	CNNM4,DMPK	up_AFEM_EC
GO:0007006	0.707	0.561	2	35	mitochondrial membrane organization	BP	1	SH3GLB1,PMAIP1	up_VCAV_EC
GO:0044255	0.707	0.558	2	293	cellular lipid metabolic process	BP	1	ABHD5,FAM135A	up_VPOR_EC
GO:1902108	0.707	0.669	1	14	regulation of mitochondrial membrane permeability involved in	BP	1	SLC25A5	down_ACOR_VSMC
GO:0008585	0.707	0.662	1	24	female gonad development	BP	1	FOXO3	down_VCAV_EC
GO:0033209	0.707	0.662	1	24	tumor necrosis factor-mediated signaling	BP	1	FOXO3	down_VCAV_EC
GO:0046545	0.707	0.662	1	24	development of primary female sexual	BP	1	FOXO3	down_VCAV_EC

GO:0060324	0.707	0.662	1	24	face development	BP	1	CRISPLD2	down_VCAV_EC
GO:0050896	0.707	0.737	1	2346	response to stimulus	BP	1	PLCL1	down_VFEM_EC
GO:1904377	0.707	0.664	1	21	positive regulation of protein localization to cell	BP	1	KIF5B	down_VSAP_EC
GO:0040018	0.707	0.674	1	11	positive regulation of multicellular organism	BP	1	CHD7	up_ACOR_VSMC
GO:2000249	0.707	0.672	1	12	regulation of actin cytoskeleton	BP	1	NRP1	up_ACOR_VSMC
GO:0001825	0.707	0.67	1	14	blastocyst formation	BP	1	SKIL	up_VCAV_EC
GO:0051704	0.707	0.667	1	476	multi-organism process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0018345	0.707	0.672	1	12	protein palmitoylation	BP	1	ZDHHC8	up_VSAP_EC
GO:0050819	0.707	0.672	1	12	negative regulation of coagulation	BP	1	KLKB1	up_VSAP_EC
GO:0060337	0.707	0.671	1	12	type I interferon signaling pathway	BP	1	MAVS	up_VSAP_EC
GO:0061045	0.707	0.672	1	12	negative regulation of wound healing	BP	1	KLKB1	up_VSAP_EC
GO:0071357	0.707	0.671	1	12	cellular response to type I interferon	BP	1	MAVS	up_VSAP_EC
GO:0002520	0.707	0.661	1	279	immune system development	BP	1	HOXA9	up_VSAP_VSMC
GO:2000145	0.707	0.66	1	279	regulation of cell motility	BP	1	CAV1	up_VSAP_VSMC
GO:0008360	0.70705635	0.65867	1	46	regulation of cell shape	BP	1	RHOU	up_ACOR_EC
GO:0006631	0.707641238	0.55536	2	93	fatty acid metabolic process	BP	1	THNSL2,PTGDS	up_ACOR_EC
GO:0006915	0.708	0.35	43	550	apoptotic process	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,RNF152,DHCR24,NOC2L,EIF5A,B4GALT1,PPARD,CYCS,NUP62,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SGPL1,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0008152	0.708	0.427	15	3714	metabolic process	BP	1	HOXC10,TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CYP26B1,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0072594	0.708	0.406	11	155	establishment of protein localization to organelle	BP	1	HCLS1,TNFAIP3,TMEM173,FERMT1,RAB11A,PPP3CA,SH3GLB1,APOD,GCC2,NUP133,IPO11	up_VCAV_EC
GO:0032388	0.708	0.463	5	62	positive regulation of intracellular transport	BP	1	CDH1,ICE1,PIK3R1,KCNB1,MAVS	up_VSAP_EC
GO:0002285	0.708	0.483	4	50	lymphocyte activation involved in immune	BP	1	ABL1,DLL1,STAT6,F2RL1	up_VSAP_EC
GO:0002822	0.708	0.513	3	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	HMGB1,TFRC,FAM49B	down_ACOR_VSMC
GO:0080090	0.708	0.535	3	1734	regulation of primary metabolic process	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0030968	0.708	0.56	2	33	endoplasmic reticulum unfolded protein	BP	1	ATF3,NCK1	up_VCAV_EC
GO:0051149	0.708	0.563	2	25	positive regulation of muscle cell differentiation	BP	1	SHOX2,FLOT1	up_VSAP_EC
GO:0070059	0.708	0.564	2	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	1	MAP3K5,NCK1	up_VSAP_EC
GO:0060191	0.708	0.668	1	14	regulation of lipase activity	BP	1	ABHD5	down_ACOR_VSMC
GO:0008283	0.708	0.667	1	545	cell proliferation	BP	1	SRSF6	down_AFEM_EC
GO:0035306	0.708	0.661	1	24	positive regulation of dephosphorylation	BP	1	PDGFRB	down_VCAV_EC
GO:0048584	0.708	0.668	1	592	positive regulation of response to stimulus	BP	1	CITED2	down_VPOR_EC
GO:0009308	0.708	0.663	1	20	amine metabolic process	BP	1	NR1H4	down_VSAP_EC
GO:0033344	0.708	0.671	1	12	cholesterol efflux	BP	1	ABCA1	up_ACOR_VSMC
GO:2000036	0.708	0.67	1	12	regulation of stem cell population maintenance	BP	1	LBH	up_ACOR_VSMC

GO:0001933	0.708	0.657	1	146	negative regulation of protein phosphorylation	BP	1	ASPN	up_VPOR_EC
GO:0051148	0.708	0.671	1	12	negative regulation of muscle cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0045071	0.708	0.671	1	12	negative regulation of viral genome replication	BP	1	MAVS	up_VSAP_EC
GO:0042177	0.708699705	0.65657	1	47	negative regulation of protein catabolic process	BP	1	AZIN2	up_ACOR_EC
GO:0044283	0.709	0.416	9	201	small molecule biosynthetic process	BP	1	CYB5R3,UROS,ENTPD3,THNSL2,ADK,PARK7,RDH10,GLS2,ACAT1	down_VCAV_EC
GO:0009893	0.709	0.439	7	995	positive regulation of metabolic process	BP	1	ARHGEF2,ENSCAFG00000002015,ACVR2A,MTDH,ABHD5,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0035023	0.709	0.483	4	46	regulation of Rho protein signal transduction	BP	1	ABCA1,ARHGEF26,F2RL1,NRP1	up_ACOR_VSMC
GO:0048839	0.709	0.482	4	50	inner ear development	BP	1	INSIG2,LRIG3,DLL1,ZEB1	up_VSAP_EC
GO:0007368	0.709	0.512	3	37	determination of left/right symmetry	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:0070167	0.709	0.56	2	29	regulation of biomineral tissue development	BP	1	FBXO5,GREM1	down_ACOR_VSMC
GO:0050821	0.709	0.556	2	48	protein stabilization	BP	1	PARK7,NCLN	down_VCAV_EC
GO:0009889	0.709	0.574	2	1190	regulation of biosynthetic process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0009893	0.709	0.569	2	995	positive regulation of metabolic process	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0051817	0.709	0.559	2	31	modification of morphology or physiology of other organism	BP	1	TNIP1,SMARCA4	up_VCAV_EC
GO:0001707	0.709	0.563	2	25	mesoderm formation	BP	1	HOXA11,WNT11	up_VSAP_EC
GO:0070613	0.709	0.562	2	25	regulation of protein processing	BP	1	CCBE1,GAS1	up_VSAP_EC
GO:1903317	0.709	0.562	2	25	regulation of protein maturation	BP	1	CCBE1,GAS1	up_VSAP_EC
GO:1902742	0.709	0.667	1	14	apoptotic process involved in development	BP	1	B4GALT1	down_ACOR_VSMC
GO:0002286	0.709	0.66	1	24	T cell activation involved in immune response	BP	1	LOXL3	down_VCAV_EC
GO:0007156	0.709	0.659	1	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	CDH2	down_VCAV_EC
GO:0072132	0.709	0.661	1	23	mesenchyme morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:2000779	0.709	0.659	1	25	regulation of double-strand break repair	BP	1	FBH1	down_VCAV_EC
GO:2000108	0.709	0.67	1	12	positive regulation of leukocyte apoptotic	BP	1	CD274	up_ACOR_VSMC
GO:0031398	0.709	0.656	1	51	positive regulation of protein ubiquitination	BP	1	DCUN1D3	up_AFEM_EC
GO:0046890	0.709	0.657	1	51	regulation of lipid biosynthetic process	BP	1	LEP	up_AFEM_EC
GO:0009066	0.709	0.665	1	16	aspartate family amino acid metabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0006366	0.709	0.667	1	583	transcription by RNA polymerase II	BP	1	GATA5	up_VPUL_VSMC
GO:0014904	0.709	0.669	1	12	myotube cell development	BP	1	SHOX2	up_VSAP_EC
GO:0035088	0.709	0.669	1	12	establishment or maintenance of	BP	1	WNT11	up_VSAP_EC
GO:0048741	0.709	0.669	1	12	skeletal muscle fiber development	BP	1	SHOX2	up_VSAP_EC
GO:0061245	0.709	0.669	1	12	establishment or maintenance of bipolar	BP	1	WNT11	up_VSAP_EC
GO:0050830	0.709	0.67	1	12	defense response to Gram-positive bacterium	BP	1	MYD88	up_VSAP_EC
GO:0051094	0.709199444	0.41555	9	388	positive regulation of developmental process	BP	1	NR1H4,SOX9,AQP1,CCDC3,PLS1,FOXC2,TBX5,CLSTN1,NRP1	up_ACOR_EC
GO:0002699	0.709572099	0.6556	1	46	positive regulation of immune effector process	BP	1	FZD5	up_ACOR_EC
GO:0098742	0.709621021	0.65577	1	44	cell-cell adhesion via plasma-membrane	BP	1	CDH3	up_ACOR_EC
GO:1901987	0.71	0.416	9	107	regulation of cell cycle phase transition	BP	1	FAM107A,CRADD,ZFP36L1,CDC25B,FBXO7,ZFP36L2,TPRA1,CDC26,LSM10	up_VSAP_EC
GO:0043543	0.71	0.434	7	84	protein acylation	BP	1	DLST,NAA60,KLF15,DLD,ZDHHC8,EHHADH,DR1	up_VSAP_EC
GO:0060491	0.71	0.461	5	62	regulation of cell projection assembly	BP	1	SLIT2,CDC42EP5,FUZ,CDC42EP2,F2RL1	up_VSAP_EC

GO:0120032	0.71	0.461	5	62	regulation of plasma membrane bounded cell	BP	1	SLIT2,CDC42EP5,FUZ,CDC42EP2,F2RL1	up_VSAP_EC
GO:0010604	0.71	0.485	4	919	positive regulation of macromolecule metabolic	BP	1	ACVRL1,LYN,HOXA1,NEDD4	down_ACOR_EC
GO:1990138	0.71	0.513	3	35	neuron projection extension	BP	1	TMEM108,NRP1,ULK2	up_ACOR_VSMC
GO:0071322	0.71	0.559	2	29	cellular response to carbohydrate stimulus	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0061515	0.71	0.562	2	24	myeloid cell development	BP	1	CITED2,APP	up_ACOR_VSMC
GO:0030216	0.71	0.56	2	29	keratinocyte differentiation	BP	1	PRKCH,FLNB	up_VCAV_EC
GO:0031076	0.71	0.666	1	14	embryonic camera-type eye development	BP	1	PHACTR4	down_ACOR_VSMC
GO:0009888	0.71	0.664	1	545	tissue development	BP	1	SRSF6	down_AFEM_EC
GO:0006807	0.71	0.787	1	3221	nitrogen compound metabolic process	BP	1	CST3	down_AORT_EC
GO:0055008	0.71	0.659	1	24	cardiac muscle tissue morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0045010	0.71	0.662	1	19	actin nucleation	BP	1	ACTR3	down_VSAP_EC
GO:0010092	0.71	0.661	1	19	specification of animal organ identity	BP	1	CTNNB1	down_VSAP_EC
GO:0010676	0.71	0.668	1	13	positive regulation of cellular carbohydrate	BP	1	PRKCE	up_ACOR_VSMC
GO:0060795	0.71	0.668	1	12	cell fate commitment involved in formation of	BP	1	BMP4	up_ACOR_VSMC
GO:0009124	0.71	0.655	1	51	nucleoside monophosphate	BP	1	PPARGC1A	up_AFEM_EC
GO:0001890	0.71	0.655	1	51	placenta development	BP	1	LEP	up_AFEM_EC
GO:0046834	0.71	0.665	1	14	lipid phosphorylation	BP	1	IMPA1	up_VCAV_EC
GO:0019439	0.71	0.654	1	150	aromatic compound catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0042398	0.71	0.668	1	12	cellular modified amino acid biosynthetic process	BP	1	ENSCAFG00000013986	up_VSAP_EC
GO:0032459	0.71	0.668	1	12	regulation of protein oligomerization	BP	1	JCHAIN	up_VSAP_EC
GO:0009895	0.710103092	0.55228	2	94	negative regulation of catabolic process	BP	1	CHMP4B,AZIN2	up_ACOR_EC
GO:0007411	0.710266135	0.65486	1	45	axon guidance	BP	1	NRP1	up_ACOR_EC
GO:0097485	0.710266135	0.65486	1	45	neuron projection guidance	BP	1	NRP1	up_ACOR_EC
GO:0006836	0.71059895	0.65424	1	47	neurotransmitter transport	BP	1	AQP1	up_ACOR_EC
GO:0045596	0.711	0.39	14	186	negative regulation of cell differentiation	BP	1	HMGB1,HSPA9,INSIG1,PRMT1,CAV1,EZH2,GREM1,HMGB3,HOXA7,PPARD,ASPM,TWIST2,HOXA9,SIX4	down_ACOR_VSMC
GO:0044237	0.711	0.424	14	3491	cellular metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CYP26B1,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0017038	0.711	0.423	8	96	protein import	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,RPAIN	up_ACOR_VSMC
GO:0050678	0.711	0.456	5	117	regulation of epithelial cell proliferation	BP	1	BMPR1A,B4GALT1,ZFP36L1,MYDGF,IFT57	down_VCAV_EC
GO:0071705	0.711	0.479	4	582	nitrogen compound transport	BP	1	XPOT,SLC7A11,GCC2,SRP54	up_VPOR_EC
GO:0001936	0.711	0.48	4	49	regulation of endothelial cell proliferation	BP	1	STAT5A,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:0043583	0.711	0.507	3	59	ear development	BP	1	PTPN11,SDC4,SIX4	down_VSAP_EC
GO:0071901	0.711	0.51	3	37	negative regulation of protein serine/threonine	BP	1	ABL1,FBXO7,LATS2	up_VSAP_EC
GO:0031338	0.711	0.558	2	28	regulation of vesicle fusion	BP	1	STXBP6,CORO1A	down_ACOR_VSMC
GO:0033138	0.711	0.559	2	28	positive regulation of peptidyl-serine	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:0046165	0.711	0.555	2	42	alcohol biosynthetic process	BP	1	APOE,REST	down_VSAP_EC
GO:0060324	0.711	0.561	2	24	face development	BP	1	CHD7,ARID5B	up_ACOR_VSMC
GO:0019218	0.711	0.56	2	25	regulation of steroid metabolic process	BP	1	INSIG2,LMF1	up_VSAP_EC
GO:0034142	0.711	0.664	1	14	toll-like receptor 4 signaling pathway	BP	1	IRAK1	down_ACOR_VSMC
GO:0072087	0.711	0.664	1	14	renal vesicle development	BP	1	GREM1	down_ACOR_VSMC

GO:1903035	0.711	0.665	1	14	negative regulation of response to wounding	BP	1	TFPI	down_ACOR_VSMC
GO:0006915	0.711	0.664	1	550	apoptotic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0043506	0.711	0.657	1	25	regulation of JUN kinase activity	BP	1	SASH1	down_VCAV_EC
GO:0090329	0.711	0.658	1	25	regulation of DNA-dependent DNA	BP	1	FBH1	down_VCAV_EC
GO:0021591	0.711	0.667	1	12	ventricular system development	BP	1	SEMA6D	up_ACOR_VSMC
GO:0035561	0.711	0.667	1	12	regulation of chromatin binding	BP	1	PARP9	up_ACOR_VSMC
GO:0044380	0.711	0.664	1	14	protein localization to cytoskeleton	BP	1	HOOK3	up_VCAV_EC
GO:2001233	0.711	0.653	1	149	regulation of apoptotic signaling pathway	BP	1	ARHGEF2	up_VPOR_EC
GO:0032270	0.711	0.662	1	479	positive regulation of cellular protein metabolic	BP	1	ANKRD6	up_VPOR_VSMC
GO:0048878	0.711	0.656	1	283	chemical homeostasis	BP	1	CYP26B1	up_VFEM_EC
GO:0014910	0.711	0.666	1	13	regulation of smooth muscle cell migration	BP	1	SLIT2	up_VSAP_EC
GO:1903115	0.711	0.668	1	12	regulation of actin filament-based movement	BP	1	KCNE3	up_VSAP_EC
GO:2000113	0.711332739	0.41308	9	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:0071695	0.711526539	0.65332	1	45	anatomical structure maturation	BP	1	CDH3	up_ACOR_EC
GO:0071705	0.712	0.345	44	582	nitrogen compound transport	BP	1	HCLS1,GBP5,LRRC8D,TMEM173,IWS1,FERMT1,CHD7,SLC35A3,TLR4,QKI,GATA3,EDN1,RAB11A,RAB27A,EXOC6,PPP3CA,SLC38A1,ARG2,SNAP23,HHEX,RALBP1,SCAMP1,ABCA1,SNX2,THOC1,AKAP12,APOD,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,RIPK1,MCU,HIF1A,IPO11,LMTK2,RABGAP1,USP6NL	up_VCAV_EC
GO:0031344	0.712	0.39	14	161	regulation of cell projection organization	BP	1	ITM2C,EVI5L,ZNF365,F2RL1,NRP1,ULK2,EVL,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1,RREB1	up_ACOR_VSMC
GO:0051336	0.712	0.401	11	251	regulation of hydrolase activity	BP	1	CST3,PDGFRB,SNX18,RECK,AKT2,SYDE1,PARK7,IFT57,SPRED1,ARHGAP1,EVI5L	down_VCAV_EC
GO:0048232	0.712	0.422	8	95	male gamete generation	BP	1	PRDX4,ATRX,AFF4,SPINK2,DMC1,JAM3,HERPUD2,WDR48	up_ACOR_VSMC
GO:0061138	0.712	0.443	6	73	morphogenesis of a branching epithelium	BP	1	HOXA11,SLIT2,FGF7,ABL1,NTN4,TGFBR2	up_VSAP_EC
GO:0044839	0.712	0.458	5	61	cell cycle G2/M phase transition	BP	1	CDC7,SKP2,CDKN2B,CDKN1A,APP	up_ACOR_VSMC
GO:0009124	0.712	0.479	4	51	nucleoside monophosphate	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4	up_ACOR_VSMC
GO:0071772	0.712	0.478	4	50	response to BMP	BP	1	SMAD6,GATA5,BMP4,ENSCAFG00000018360	up_ACOR_VSMC
GO:0071773	0.712	0.478	4	50	cellular response to BMP stimulus	BP	1	SMAD6,GATA5,BMP4,ENSCAFG00000018360	up_ACOR_VSMC
GO:0007179	0.712	0.477	4	57	transforming growth factor beta receptor	BP	1	FERMT1,SMAD1,SKIL,ZEB1	up_VCAV_EC
GO:0072331	0.712	0.479	4	49	signal transduction by p53 class mediator	BP	1	CRADD,PDK2,KRCC1,DDIT4	up_VSAP_EC
GO:0050864	0.712	0.51	3	36	regulation of B cell activation	BP	1	TP53BP1,CDKN1A,NOD2	up_ACOR_VSMC
GO:0072028	0.712	0.509	3	37	nephron morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0009127	0.712	0.507	3	47	purine nucleoside monophosphate biosynthetic process	BP	1	ADSS,ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0009168	0.712	0.507	3	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	ADSS,ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:2000278	0.712	0.509	3	37	regulation of DNA biosynthetic process	BP	1	MYC,FBXO4,ACVRL1	up_VSAP_EC
GO:0006888	0.712	0.553	2	49	ER to Golgi vesicle-mediated transport	BP	1	ERGIC1,YIF1A	down_VCAV_EC
GO:0009161	0.712	0.55	2	103	ribonucleoside monophosphate	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0006796	0.712	0.565	2	938	phosphate-containing compound metabolic	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0046580	0.712	0.659	1	18	negative regulation of Ras protein signal	BP	1	TNFAIP1	down_VSAP_EC
GO:0051193	0.712	0.663	1	15	regulation of cofactor metabolic process	BP	1	HIF1A	up_VCAV_EC

GO:0070129	0.712	0.666	1	12	regulation of mitochondrial translation	BP	1	RPUSD4	up_VSAP_EC
GO:1902110	0.712	0.666	1	12	positive regulation of mitochondrial membrane permeability involved in apoptotic process	BP	1	ZNF205	up_VSAP_EC
GO:1902686	0.712	0.666	1	12	mitochondrial outer membrane permeabilization involved	BP	1	ZNF205	up_VSAP_EC
GO:0010862	0.712	0.666	1	12	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	1	ACVRL1	up_VSAP_EC
GO:0010876	0.712181737	0.54978	2	92	lipid localization	BP	1	CFI,PRKCD	up_ACOR_EC
GO:0001764	0.712713818	0.65185	1	45	neuron migration	BP	1	NRP1	up_ACOR_EC
GO:0010557	0.713	0.344	45	492	positive regulation of macromolecule biosynthetic process	BP	1	TLR1,SMAD6,LBH,GATA5,GATA4,CDC7,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,FAM129A,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,NGRN,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0035556	0.713	0.348	39	845	intracellular signal transduction	BP	1	NOTCH2,PDGFRB,DCN,PRNP,ADCY6,GLIPR2,BGN,ARHGEF25,RHOD,AKT1S1,AKT2,DOCK10,PLCL1,CSPG4,PRMT6,TMEM161A,ASPN,TEAD1,PARK7,ZMAT3,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,ARL2BP,CDH2,GSDME,CAMK2D,SPRED1,ARHGAP1,SHC1,FBH1,GREM1,RAC2,FOXO3,EIF4EBP1,ANKRD54,BRSK1	down_VCAV_EC
GO:0051248	0.713	0.366	23	316	negative regulation of protein metabolic process	BP	1	EDNRB,TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,EDN1,CDYL,HMG20A,HHEX,PREX2,SH3BP5,ENC1,PAK2,SWAP70,APOD,NCK1,PTGS2,CNOT7,KDM5A,KDM3A,IVNS1ABP	up_VCAV_EC
GO:0050776	0.713	0.391	13	173	regulation of immune response	BP	1	HMGB1,IRAK1,MNDA,SLC29A1,CAV1,ARG2,TFRC,FAM49B,CACTIN,HMGB2,EZR,RBM14,POLR3F	down_ACOR_VSMC
GO:0022414	0.713	0.39	13	294	reproductive process	BP	1	ADAMTS2,BMPR1A,RECK,SYDE1,MEA1,B4GALT1,ZFP36L1,ENSCAFG00000017708,IRX5,RDH10,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0042176	0.713	0.439	6	140	regulation of protein catabolic process	BP	1	LRP1,TIMP2,PSMF1,PARK7,CLEC16A,PACSIN3	down_VCAV_EC
GO:0090092	0.713	0.456	5	72	regulation of transmembrane receptor protein serine/threonine	BP	1	FERMT1,BMP2,CTDSPL2,SKIL,ZEB1	up_VCAV_EC
GO:0045931	0.713	0.478	4	49	positive regulation of mitotic cell cycle	BP	1	ABL1,POLDIP2,TTL,LSM10	up_VSAP_EC
GO:0008645	0.713	0.508	3	37	hexose transmembrane transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0015749	0.713	0.508	3	37	monosaccharide transmembrane transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0034219	0.713	0.508	3	37	carbohydrate transmembrane transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0048565	0.713	0.508	3	38	digestive tract development	BP	1	WNT11,SAV1,SHOX2	up_VSAP_EC
GO:0002824	0.713	0.556	2	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	TFRC,FAM49B	down_ACOR_VSMC
GO:0045621	0.713	0.556	2	28	positive regulation of lymphocyte	BP	1	MMP14,TOX	down_ACOR_VSMC
GO:0048583	0.713	0.568	2	1095	regulation of response to stimulus	BP	1	IVNS1ABP,SRSF6	down_AFEM_EC
GO:0009144	0.713	0.549	2	103	purine nucleoside triphosphate metabolic	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0002702	0.713	0.557	2	28	positive regulation of production of molecular mediator of immune	BP	1	TLR4,GATA3	up_VCAV_EC
GO:0006487	0.713	0.554	2	34	protein N-linked glycosylation	BP	1	ST6GAL1,ST3GAL6	up_VCAV_EC
GO:0017156	0.713	0.555	2	32	calcium ion regulated exocytosis	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0006809	0.713	0.663	1	14	nitric oxide biosynthetic process	BP	1	CAV1	down_ACOR_VSMC
GO:0010922	0.713	0.662	1	14	positive regulation of phosphatase activity	BP	1	SLC29A1	down_ACOR_VSMC

GO:0046209	0.713	0.663	1	14	nitric oxide metabolic process	BP	1	CAV1	down_ACOR_VSMC
GO:0072528	0.713	0.662	1	14	pyrimidine-containing compound biosynthetic	BP	1	CTPS1	down_ACOR_VSMC
GO:0006357	0.713	0.661	1	547	regulation of transcription by RNA polymerase II	BP	1	GABPA	down_AFEM_EC
GO:0051702	0.713	0.656	1	24	interaction with symbiont	BP	1	NAPEPLD	down_VCAV_EC
GO:0030947	0.713	0.665	1	12	regulation of vascular endothelial growth factor receptor signaling	BP	1	FGF18	up_ACOR_VSMC
GO:0031328	0.713	0.659	1	512	positive regulation of cellular biosynthetic	BP	1	HOXA9	up_AORT_EC
GO:0060325	0.713	0.663	1	13	face morphogenesis	BP	1	TIPARP	up_VCAV_EC
GO:0042327	0.713	0.653	1	289	positive regulation of phosphorylation	BP	1	MAP2K6	up_VFEM_EC
GO:0006120	0.713	0.665	1	12	mitochondrial electron transport, NADH to	BP	1	COQ9	up_VSAP_EC
GO:1901661	0.713	0.665	1	12	quinone metabolic process	BP	1	COQ9	up_VSAP_EC
GO:0045598	0.713530718	0.65063	1	47	regulation of fat cell differentiation	BP	1	CCDC3	up_ACOR_EC
GO:0051649	0.714	0.337	57	630	establishment of localization in cell	BP	1	EXPH5,SH3TC2,RHOT1,DNAJC6,ACTN2,PLCG2,LEP,HTR2B,TCAF1,USP6NL,FBXL20,FERMT1,BMP4,EVI5L,ABCA1,SCARB2,SEC24B,STX11,TMEM108,IFT43,ITPR1,KLHL20,CDKN1A,PTPN22,OS9,SCP2,PRKCE,SCG5,APP,PSEN1,SGSM2,SYNJ2BP,CHD7,PIK3C3,LAMP2,JUP,CLN8,RAB11B,DYNC1I2,AKTIP,KCNC4,LMTK2,AP2B1,SAR1B,HERPUD1,SUN1,VPS26A,INPP5K,FAF2,PREPL,RPAIN,DYNC1I1,PARK7,ENSCAFG00000013536,BVES,LMF1,PTPN14	up_ACOR_VSMC
GO:0006508	0.714	0.366	22	483	proteolysis	BP	1	PCOLCE,CST3,ADAMTS2,RECK,TIMP2,PSMF1,RHBDL1,PCSK7,RNF216,GLI3,PARK7,SEC11C,CLEC16A,RNPEP,COPS7A,IFT57,A2M,SEC61B,HM13,PCSK6,LONP2,PACSIN3	down_VCAV_EC
GO:0060828	0.714	0.44	6	82	regulation of canonical Wnt signaling pathway	BP	1	CTDNEP1,CAV1,GREM1,ASPM,GLI1,AMER1	down_ACOR_VSMC
GO:0006457	0.714	0.441	6	77	protein folding	BP	1	PRDX4,TMX3,ERO1B,PFDN5,B2M,TXNDC5	up_ACOR_VSMC
GO:0015931	0.714	0.502	3	59	nucleobase-containing compound transport	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0032874	0.714	0.503	3	57	positive regulation of stress-activated MAPK	BP	1	TNIK,SH3RF3,MID1	down_VSAP_EC
GO:0045839	0.714	0.556	2	25	negative regulation of mitotic nuclear division	BP	1	BMP4,ATRX	up_ACOR_VSMC
GO:0051149	0.714	0.556	2	25	positive regulation of muscle cell differentiation	BP	1	BMP4,EDN1	up_ACOR_VSMC
GO:0002532	0.714	0.556	2	25	production of molecular mediator involved in inflammatory response	BP	1	IL17RC,MYD88	up_VSAP_EC
GO:0032613	0.714	0.66	1	14	interleukin-10 production	BP	1	HMGB1	down_ACOR_VSMC
GO:0051438	0.714	0.655	1	24	regulation of ubiquitin-protein transferase	BP	1	PARK7	down_VCAV_EC
GO:0060711	0.714	0.655	1	21	labyrinthine layer development	BP	1	TMED2	down_VSAP_EC
GO:0034724	0.714	0.664	1	12	DNA replication-independent nucleosome	BP	1	ATRX	up_ACOR_VSMC
GO:1905475	0.714	0.649	1	52	regulation of protein localization to membrane	BP	1	LRRC15	up_AFEM_EC
GO:0034308	0.714	0.659	1	16	primary alcohol metabolic process	BP	1	BMP2	up_VCAV_EC
GO:0051338	0.714	0.652	1	288	regulation of transferase activity	BP	1	MAP2K6	up_VFEM_EC
GO:0042445	0.71416583	0.64995	1	46	hormone metabolic process	BP	1	PCSK1N	up_ACOR_EC
GO:0060255	0.715	0.399	13	1782	regulation of macromolecule metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,PUM3,EIF5,CCAR1,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0001933	0.715	0.403	10	146	negative regulation of protein phosphorylation	BP	1	TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,HHEX,PREX2,SH3BP5,NCK1	up_VCAV_EC
GO:0070838	0.715	0.427	7	96	divalent metal ion transport	BP	1	HOXA3,CAV1,SLC30A1,GSTO1,NIPA2,CORO1A,REM1	down_ACOR_VSMC
GO:0009206	0.715	0.505	3	39	purine ribonucleoside triphosphate biosynthetic	BP	1	PPARGC1A,ALDOC,DDIT4	up_ACOR_VSMC

GO:0001678	0.715	0.553	2	29	cellular glucose homeostasis	BP	1	BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0043473	0.715	0.554	2	28	pigmentation	BP	1	ARCN1,TRAPPC6A	down_ACOR_VSMC
GO:0007043	0.715	0.554	2	28	cell-cell junction assembly	BP	1	FSCN1,CAV1	down_ACOR_VSMC
GO:0097327	0.715	0.653	1	25	response to antineoplastic agent	BP	1	NR3C1	down_VCAV_EC
GO:0042490	0.715	0.656	1	19	mechanoreceptor differentiation	BP	1	SDC4	down_VSAP_EC
GO:0051972	0.715	0.655	1	20	regulation of telomerase activity	BP	1	CTNNB1	down_VSAP_EC
GO:0033059	0.715	0.663	1	12	cellular pigmentation	BP	1	RAB11B	up_ACOR_VSMC
GO:0061217	0.715	0.661	1	13	regulation of mesonephros	BP	1	BMP4	up_ACOR_VSMC
GO:0070979	0.715	0.661	1	13	protein K11-linked ubiquitination	BP	1	UBE2H	up_ACOR_VSMC
GO:0071300	0.715	0.662	1	12	cellular response to retinoic acid	BP	1	ABCA1	up_ACOR_VSMC
GO:0000910	0.715	0.649	1	52	cytokinesis	BP	1	ANXA11	up_AFEM_EC
GO:0032409	0.715	0.649	1	52	regulation of transporter activity	BP	1	FXYD1	up_AFEM_EC
GO:0043523	0.715	0.649	1	52	regulation of neuron apoptotic process	BP	1	PPARGC1A	up_AFEM_EC
GO:0009892	0.715	0.667	1	835	negative regulation of metabolic process	BP	1	HOXC10	up_AFEM_VSMC
GO:0035556	0.715	0.666	1	845	intracellular signal transduction	BP	1	TLR2	up_AFEM_VSMC
GO:0007155	0.715	0.652	1	324	cell adhesion	BP	1	NPNT	up_APUL_EC
GO:0030520	0.715	0.658	1	15	intracellular estrogen receptor signaling	BP	1	UFSP2	up_VCAV_EC
GO:0019752	0.715	0.651	1	283	carboxylic acid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0032989	0.715	0.65	1	292	cellular component morphogenesis	BP	1	SHOX2	up_VSAP_VSMC
GO:0070085	0.715702497	0.54527	2	95	glycosylation	BP	1	GALNT5,B3GNT7	up_ACOR_EC
GO:0034654	0.716	0.359	27	1236	nucleobase-containing compound biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,ACACB,PPARGC1A	up_AFEM_EC
GO:0022407	0.716	0.426	7	96	regulation of cell-cell adhesion	BP	1	HMGB1,CAV1,NF2,ARG2,TFRC,FAM49B,CORO1A	down_ACOR_VSMC
GO:0044260	0.716	0.487	5	2593	cellular macromolecule metabolic process	BP	1	IVNS1ABP,DARS,EIF3M,USP33,GABPA	down_AFEM_EC
GO:0048871	0.716	0.449	5	120	multicellular organismal homeostasis	BP	1	NDN,TRPV2,PLCL1,NCDN,NAPEPLD	down_VCAV_EC
GO:0044782	0.716	0.451	5	96	cilium organization	BP	1	EXOC5,RPGR,DYNLL1,HTT,DISC1	down_VSAP_EC
GO:0002181	0.716	0.55	2	35	cytoplasmic translation	BP	1	NCK1,DPH5	up_VCAV_EC
GO:0010466	0.716	0.551	2	32	negative regulation of peptidase activity	BP	1	PAK2,PTGS2	up_VCAV_EC
GO:0010951	0.716	0.551	2	32	negative regulation of endopeptidase activity	BP	1	PAK2,PTGS2	up_VCAV_EC
GO:0031099	0.716	0.552	2	30	regeneration	BP	1	IFRD1,APOD	up_VCAV_EC
GO:0042475	0.716	0.553	2	26	odontogenesis of dentin-containing tooth	BP	1	DLX3,LRP4	up_VSAP_EC
GO:0006940	0.716	0.659	1	14	regulation of smooth muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0009566	0.716	0.652	1	24	fertilization	BP	1	B4GALT1	down_VCAV_EC
GO:0035850	0.716	0.651	1	25	epithelial cell differentiation involved in	BP	1	GREM1	down_VCAV_EC
GO:0045921	0.716	0.652	1	24	positive regulation of exocytosis	BP	1	SDC4	down_VCAV_EC
GO:1902369	0.716	0.657	1	15	negative regulation of RNA catabolic process	BP	1	TENT2	up_VCAV_EC
GO:0071840	0.717	0.444	7	2059	cellular component organization or biogenesis	BP	1	NR1H4,TUBB4A,ARHGEF26,SLITRK5,NPNT,NTRK2,PDLIM3	up_APUL_EC
GO:0001838	0.717	0.472	4	56	embryonic epithelial tube formation	BP	1	GATA3,BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0009123	0.717	0.544	2	104	nucleoside monophosphate	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC

GO:0071804	0.717	0.55	2	31	cellular potassium ion transport	BP	1	KCNJ3,KCNJ2	up_VCAV_EC
GO:0071805	0.717	0.55	2	31	potassium ion transmembrane transport	BP	1	KCNJ3,KCNJ2	up_VCAV_EC
GO:0016064	0.717	0.552	2	26	immunoglobulin mediated immune	BP	1	STAT6,MYD88	up_VSAP_EC
GO:0019724	0.717	0.552	2	26	B cell mediated immunity	BP	1	STAT6,MYD88	up_VSAP_EC
GO:0034109	0.717	0.657	1	14	homotypic cell-cell adhesion	BP	1	ITGB3	down_ACOR_VSMC
GO:0002639	0.717	0.658	1	14	positive regulation of immunoglobulin	BP	1	TFRC	down_ACOR_VSMC
GO:0046888	0.717	0.657	1	14	negative regulation of hormone secretion	BP	1	SREBF1	down_ACOR_VSMC
GO:0006928	0.717	0.656	1	557	movement of cell or subcellular component	BP	1	FSCN1	down_AFEM_EC
GO:0051897	0.717	0.653	1	20	positive regulation of protein kinase B signaling	BP	1	MTDH	down_VSAP_EC
GO:0051899	0.717	0.651	1	22	membrane depolarization	BP	1	YWHAH	down_VSAP_EC
GO:0040019	0.717	0.66	1	12	positive regulation of embryonic development	BP	1	DAG1	up_ACOR_VSMC
GO:0051247	0.717	0.654	1	502	positive regulation of protein metabolic process	BP	1	TAOK1	up_AORT_EC
GO:0022610	0.717	0.649	1	326	biological adhesion	BP	1	NPNT	up_APUL_EC
GO:0051248	0.717	0.65	1	316	negative regulation of protein metabolic process	BP	1	PCSK1N	up_APUL_EC
GO:0097150	0.717	0.658	1	13	neuronal stem cell population maintenance	BP	1	DLL1	up_VSAP_EC
GO:0010921	0.71747786	0.64582	1	46	regulation of phosphatase activity	BP	1	PPP1R26	up_ACOR_EC
GO:1903008	0.717648556	0.6455	1	47	organelle disassembly	BP	1	ENSCAFG00000010493	up_ACOR_EC
GO:0010976	0.717717952	0.64542	1	47	positive regulation of neuron projection	BP	1	NRP1	up_ACOR_EC
GO:0065009	0.718	0.332	58	735	regulation of molecular function	BP	1	HMGB1,IRAK1,PPRC1,HMGCR,HNRNPD,UBE2S,NEDD4,SLC29A1,MTDH,HOXA3,PRELID1,RFC2,BIRC5,CAV1,RFC5,RFC3,FAM129B,NF2,AURKB,CDKN2C,ABHD5,EZH2,STMN1,GREM1,MAP3K20,RFC4,NEK2,PCNA,DHX33,CKS2,PDCD2,GMNN,DHCR24,RAP2C,YWHAB,CYCS,NUP62,EMP2,IQGAP1,IQGAP2,CACTIN,HMGB2,GSTO1,ENSCAFG00000005299,CLSPN,CDC20,REM1,CTH,AIFM1,ARHGEF2,TRAPPC6A,KNL1,DELE1,CCNB3,NUS1,HMGN1,CCT4,DCUN1D5	down_ACOR_VSMC
GO:0031328	0.718	0.351	29	512	positive regulation of cellular biosynthetic process	BP	1	ARHGEF2,VEGFA,NR1H4,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,PTGS2,HIF1A,SLC45A3,ZPR1,PTPN2,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0033043	0.718	0.356	25	446	regulation of organelle organization	BP	1	ARHGEF2,FSCN1,WDR1,MSN,LMAN1,HIF1A,DYNLL1,IWS1,NAA10,ACTR3,CTNNB1,BNIP3,TWF1,FAM162A,PLEKHG2,GSK3B,NEXN,CDC37,SH3GLB1,SDC4,HTT,CAPG,NRP1,KDM3A,MID1	down_VSAP_EC
GO:0060627	0.718	0.389	12	165	regulation of vesicle-mediated transport	BP	1	ACSL3,HMGB1,STXBP6,SDC1,ARFGAP1,INSIG1,CAV1,GREM1,PREB,HIST1H1A,EZR,CORO1A	down_ACOR_VSMC
GO:0010639	0.718	0.395	11	128	negative regulation of organelle organization	BP	1	FGF13,ARHGAP28,MID1,FEZ1,BMP4,EVI5L,TUBB4A,ATRX,BNIP3,FEZ2,INPP5K	up_ACOR_VSMC
GO:0001503	0.718	0.415	8	109	ossification	BP	1	HOXA3,FBXO5,NAB2,XYLT1,MMP14,GREM1,TWIST2,GLI1	down_ACOR_VSMC
GO:0060828	0.718	0.424	7	82	regulation of canonical Wnt signaling pathway	BP	1	RECK,MLLT3,FERMT1,FGFR2,LATS2,ZNRF3,PSEN1	up_ACOR_VSMC
GO:0072659	0.718	0.468	4	82	protein localization to plasma membrane	BP	1	EXOC5,KIF5B,TNIK,BLZF1	down_VSAP_EC
GO:0050680	0.718	0.499	3	44	negative regulation of epithelial cell proliferation	BP	1	CAV1,PPARD,TINF2	down_ACOR_VSMC
GO:0006793	0.718	0.557	2	948	phosphorus metabolic process	BP	1	EYA1,FBP1	up_VFEM_VSMC
GO:0002377	0.718	0.551	2	26	immunoglobulin production	BP	1	STAT6,STX4	up_VSAP_EC
GO:0030837	0.718	0.655	1	14	negative regulation of actin filament	BP	1	CAPG	down_ACOR_VSMC
GO:0042698	0.718	0.656	1	14	ovulation cycle	BP	1	SGPL1	down_ACOR_VSMC

GO:0048635	0.718	0.655	1	14	negative regulation of muscle organ	BP	1	SIX4	down_ACOR_VSMC
GO:0071398	0.718	0.656	1	14	cellular response to fatty acid	BP	1	CDK4	down_ACOR_VSMC
GO:1901862	0.718	0.656	1	14	negative regulation of muscle tissue	BP	1	SIX4	down_ACOR_VSMC
GO:0012501	0.718	0.655	1	561	programmed cell death	BP	1	IVNS1ABP	down_AFEM_EC
GO:0010591	0.718	0.659	1	12	regulation of lamellipodium assembly	BP	1	SSH3	up_ACOR_VSMC
GO:0042304	0.718	0.655	1	15	regulation of fatty acid biosynthetic process	BP	1	PTGS2	up_VCAV_EC
GO:0042981	0.718	0.652	1	471	regulation of apoptotic process	BP	1	EYA1	up_VFEM_VSMC
GO:0051049	0.718	0.653	1	479	regulation of transport	BP	1	NETO1	up_VFEM_VSMC
GO:0002703	0.718413968	0.64454	1	47	regulation of leukocyte mediated immunity	BP	1	FZD5	up_ACOR_EC
GO:0009056	0.719	0.345	35	755	catabolic process	BP	1	LRP1,DCN,MAOA,CHID1,GABARAP,TIMP2,AKT2,PSMF1,SAMD4B,ACAA1,PLCL1,EPHX1,ENTPD3,THNSL2,POLDIP2,RNF216,WDR45,PEX5,PARK7,ZFP36L1,CLEC16A,RETREG1,RNPEP,EMC6,ENSCAFG00000002977,ENSCAFG00000017708,SEC61B,HM13,PYM1,FBH1,LONP2,GLS2,PACSIN3,BCKDHB,ACAT1	down_VCAV_EC
GO:0044093	0.719	0.404	9	437	positive regulation of molecular function	BP	1	LEP,F3,GREM1,CAMK2A,RASGEF1B,DCUN1D3,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0009150	0.719	0.412	8	161	purine ribonucleotide metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1,AK5	down_VSAP_EC
GO:0046034	0.719	0.434	6	88	ATP metabolic process	BP	1	CDK1,CYCS,CYC1,ATP5F1A,ENSCAFG00000013366,ATP5F1D	down_ACOR_VSMC
GO:0072073	0.719	0.45	5	60	kidney epithelium development	BP	1	SMAD6,BMP4,FGFR2,CLSTN1,NPNT	up_ACOR_VSMC
GO:0008202	0.719	0.467	4	80	steroid metabolic process	BP	1	NR1H4,APOE,REST,YWHAH	down_VSAP_EC
GO:0010563	0.719	0.465	4	203	negative regulation of phosphorus metabolic	BP	1	MYO1D,GREM1,CYLD,LRRC15	up_AFEM_EC
GO:0045936	0.719	0.465	4	203	negative regulation of phosphate metabolic	BP	1	MYO1D,GREM1,CYLD,LRRC15	up_AFEM_EC
GO:0071229	0.719	0.544	2	51	cellular response to acid chemical	BP	1	ADCY6,COL6A1	down_VCAV_EC
GO:0051603	0.719	0.543	2	305	proteolysis involved in cellular protein catabolic	BP	1	USP33,RNF6	up_VPOR_EC
GO:0042278	0.719	0.55	2	25	purine nucleoside metabolic process	BP	1	NT5C2,PNP	up_VSAP_EC
GO:0001937	0.719	0.654	1	15	negative regulation of endothelial cell	BP	1	CAV1	down_ACOR_VSMC
GO:0046718	0.719	0.656	1	13	viral entry into host cell	BP	1	CTSB	up_ACOR_VSMC
GO:0072283	0.719	0.658	1	12	metanephric renal vesicle morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0007626	0.719	0.644	1	53	locomotory behavior	BP	1	LGI4	up_AFEM_EC
GO:0046822	0.719	0.643	1	53	regulation of nucleocytoplasmic	BP	1	LEP	up_AFEM_EC
GO:0045740	0.719	0.658	1	12	positive regulation of DNA replication	BP	1	ATRX	up_VCAV_EC
GO:2000401	0.719	0.656	1	13	regulation of lymphocyte migration	BP	1	SLC8B1	up_VSAP_EC
GO:0042327	0.719	0.646	1	289	positive regulation of phosphorylation	BP	1	CAV1	up_VSAP_VSMC

GO:0065007	0.72	0.318	170	3499	biological regulation	BP	1	CST3,GPAM,NOTCH2,HSPB6,PDGFRB,SLC35F6,KIRREL1,SNX18,FBLN2,SMAD9,ITGB5,LRP1,DCN,MAOA,CFD,NAB2,NDN,ANGPT1,PRNP,LUM,MT2A,SDC4,VASN,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,SH3BP1,BMPR1A,TLN2,VKORC1,NABP2,LMO4,EVC,RECK,FXYD1,IGFBP6,TRPV2,CLIP3,NUMBL,CHID1,ARHGEF25,RHOD,OSMR,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,DOCK10,PSMF1,LCAT,SAMD4B,EEF2K,TFE3,ENSCAFG00000018277,NR3C1,SYDE1,HR,SCP2,PDIA4,SLC39A6,LAMA3,CLSTN1,PLCL1,CACNB3,CSPG4,TRIM8,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,CXXC5,SEMA3C,ASPN,POLDIP2,LRPAP1,GNAZ,EIF3K,THY1,NECAB3,RNF216,TEAD1,CYP1B1,PEX5,ARHGAP10,TLX2,CC2D1A,ATP6V0C,B4GALT1,RETSAT,GLI3,PARK7,ZMAT3,ADAMTSL4,EEF2,MAST2,SCARA5,ZFP36L1,MYDGF,SASH1,CLEC16A,NCDN,BPI,TPC3,RNPEP,CYBA,ENSCAFG00000018194,RBM38,ARL2BP,IFT57,MAVS,CDH2,EDIL3,LOXL3,MPV17,ORMDL3,GSDME,LSM10,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,MGARP,ACTR3B,RAB7B,A2M,SPNS1,IRX5,TSC22D3,UST,MAPRE3,GLIS2,TWIST2,ARHGAP1,PRKCSH,DDR2,SHC1,RDH10,PCSK6,PYM1,CRCP,F	down_VCAV_EC
GO:0032787	0.72	0.387	12	144	monocarboxylic acid metabolic process	BP	1	LEP,PPARGC1A,NIT2,ACAD11,CYP2J2,PRKCE,EDN1,ALDOC,HPGD,DDIT4,PARK7,ELOVL7	up_ACOR_VSMC
GO:0010558	0.72	0.41	8	392	negative regulation of macromolecule biosynthetic process	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1,SAMD4B	up_AFEM_EC
GO:0051186	0.72	0.419	7	159	cofactor metabolic process	BP	1	GPAM,H6PD,UROS,PGLS,PARK7,ACSS2,ACAT1	down_VCAV_EC
GO:0016043	0.72	0.453	6	1973	cellular component organization	BP	1	NR1H4,MYBPC2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0043491	0.72	0.469	4	50	protein kinase B signaling	BP	1	LEP,SESN3,DAG1,INPP5K	up_ACOR_VSMC
GO:0032501	0.72	0.521	3	1782	multicellular organismal process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0072594	0.72	0.493	3	155	establishment of protein localization to organelle	BP	1	LEP,CRY2,RAB7A	up_AFEM_EC
GO:0032092	0.72	0.498	3	38	positive regulation of protein binding	BP	1	ABL1,TIAM1,FLOT1	up_VSAP_EC
GO:0051208	0.72	0.547	2	29	sequestering of calcium ion	BP	1	GSTO1,CORO1A	down_ACOR_VSMC
GO:0051282	0.72	0.547	2	29	regulation of sequestering of calcium ion	BP	1	GSTO1,CORO1A	down_ACOR_VSMC
GO:0006665	0.72	0.542	2	48	sphingolipid metabolic process	BP	1	ORMDL3,ENSCAFG00000017708	down_VCAV_EC
GO:0050794	0.72	0.621	2	3075	regulation of cellular process	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0002821	0.72	0.546	2	30	positive regulation of adaptive immune	BP	1	GATA3,NECTIN2	up_VCAV_EC
GO:0006637	0.72	0.546	2	32	acyl-CoA metabolic process	BP	1	PIPOX,ELOVL7	up_VCAV_EC
GO:0035383	0.72	0.546	2	32	thioester metabolic process	BP	1	PIPOX,ELOVL7	up_VCAV_EC
GO:0090100	0.72	0.546	2	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FERMT1,BMP2	up_VCAV_EC
GO:0030029	0.72	0.645	1	239	actin filament-based process	BP	1	PDPN	down_ACOR_EC
GO:0030204	0.72	0.653	1	14	chondroitin sulfate metabolic process	BP	1	XYLT1	down_ACOR_VSMC
GO:0098900	0.72	0.653	1	15	regulation of action potential	BP	1	CAV1	down_ACOR_VSMC
GO:0031399	0.72	0.652	1	559	regulation of protein modification process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0032210	0.72	0.649	1	20	regulation of telomere maintenance via	BP	1	CTNNB1	down_VSAP_EC
GO:1904356	0.72	0.649	1	20	regulation of telomere maintenance via telomere lengthening	BP	1	CTNNB1	down_VSAP_EC
GO:0033522	0.72	0.657	1	12	histone H2A ubiquitination	BP	1	PCGF5	up_ACOR_VSMC
GO:0048333	0.72	0.657	1	12	mesodermal cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0023052	0.72	0.686	1	1602	signaling	BP	1	TBX5	up_APUL_VSMC

GO:0032410	0.72	0.651	1	17	negative regulation of transporter activity	BP	1	CTTNBP2NL	up_VCAV_EC
GO:1901361	0.72	0.642	1	154	organic cyclic compound catabolic process	BP	1	FBP1	up_VPOR_EC
GO:0048705	0.720101354	0.53974	2	95	skeletal system morphogenesis	BP	1	SOX9,FOXC2	up_ACOR_EC
GO:0050821	0.72043341	0.6419	1	48	protein stabilization	BP	1	CLU	up_ACOR_EC
GO:0051347	0.720575045	0.46322	4	182	positive regulation of transferase activity	BP	1	PKIB,FZD5,PAK3,PRKCD	up_ACOR_EC
GO:1902107	0.720948177	0.64135	1	47	positive regulation of leukocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0051130	0.721	0.348	30	342	positive regulation of cellular component organization	BP	1	WNT11,ARHGEF5,AMIGO1,ENPP2,LRRN3,DDHD1,ABL1,DLL1,CDC42EP5,FUZ,CDC42EP2,F2RL1,DDR2,MFN2,ICE1,SHOX2,FBXO4,LRP4,PHF1,FBXO7,CDK9,PIP4K2B,CYBA,ZNF205,HTRA2,FLOT1,NCK1,MAP2K2,BAG4,JCHAIN	up_VSAP_EC
GO:0031175	0.721	0.364	19	224	neuron projection development	BP	1	AMIGO1,SLIT2,ABL1,PLXNA4,SHOX2,RTN4RL1,LRP4,DPYSL2,GDPD5,FBXO7,NFIB,CDNF,PQBP1,TTL,FLOT1,NCK1,ULK1,MAP2K2,OGN	up_VSAP_EC
GO:0045930	0.721	0.412	8	97	negative regulation of mitotic cell cycle	BP	1	NACC2,BMP4,ATRX,PTPN3,CDKN2B,CDKN1A,FZD3,FAM107A	up_ACOR_VSMC
GO:0072503	0.721	0.42	7	97	cellular divalent inorganic cation homeostasis	BP	1	HMGB1,CAV1,SLC30A1,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0045930	0.721	0.463	4	97	negative regulation of mitotic cell cycle	BP	1	KANK2,NABP2,ZFP36L1,BRSK1	down_VCAV_EC
GO:0110053	0.721	0.463	4	98	regulation of actin filament organization	BP	1	KIRREL1,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0050803	0.721	0.467	4	55	regulation of synapse structure or activity	BP	1	EPHB1,ARHGEF15,RELN,MEF2C	up_VCAV_EC
GO:0050807	0.721	0.467	4	55	regulation of synapse organization	BP	1	EPHB1,ARHGEF15,RELN,MEF2C	up_VCAV_EC
GO:0014020	0.721	0.496	3	41	primary neural tube formation	BP	1	BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0032640	0.721	0.543	2	39	tumor necrosis factor production	BP	1	ARHGEF2,NR1H4	down_VSAP_EC
GO:0048634	0.721	0.543	2	40	regulation of muscle organ development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0006090	0.721	0.547	2	26	pyruvate metabolic process	BP	1	ALDOC,DDIT4	up_ACOR_VSMC
GO:1901564	0.721	0.581	2	2053	organonitrogen compound metabolic	BP	1	WNT7A,ARG2	up_AORT_VSMC
GO:0006383	0.721	0.545	2	28	transcription by RNA polymerase III	BP	1	MTOR,BDP1	up_VCAV_EC
GO:0033554	0.721	0.548	2	708	cellular response to stress	BP	1	PTGER2,ARHGEF2	up_VPUL_EC
GO:0045191	0.721	0.653	1	14	regulation of isotype switching	BP	1	TFRC	down_ACOR_VSMC
GO:0060323	0.721	0.652	1	14	head morphogenesis	BP	1	SGPL1	down_ACOR_VSMC
GO:0007049	0.721	0.652	1	560	cell cycle	BP	1	GPSM2	down_AFEM_EC
GO:0098693	0.721	0.645	1	25	regulation of synaptic vesicle cycle	BP	1	CDH2	down_VCAV_EC
GO:0007431	0.721	0.648	1	19	salivary gland development	BP	1	NRP1	down_VSAP_EC
GO:0007063	0.721	0.655	1	12	regulation of sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0043030	0.721	0.655	1	12	regulation of macrophage activation	BP	1	APP	up_ACOR_VSMC
GO:0002449	0.721	0.641	1	53	lymphocyte mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0009891	0.721	0.65	1	521	positive regulation of biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0044087	0.722	0.373	15	339	regulation of cellular component biogenesis	BP	1	KIRREL1,SDC4,LMO4,CLIP3,RHOD,ENSCAFG00000014978,LCAT,CLSTN1,THY1,ORMDL3,NCLN,ACTR3B,GREM1,EVI5L,RAC2	down_VCAV_EC
GO:1901361	0.722	0.39	11	154	organic cyclic compound catabolic process	BP	1	CDA,TENT2,CNOT6,ENSCAFG00000024323,PAN3,CNOT7,SMG7,BLVRA,HIF1A,DCP2,TET2	up_VCAV_EC
GO:0023052	0.722	0.443	6	1602	signaling	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0048863	0.722	0.445	5	70	stem cell differentiation	BP	1	HSPA9,GREM1,HOXA7,NOLC1,PHACTR4	down_ACOR_VSMC
GO:0022604	0.722	0.442	5	122	regulation of cell morphogenesis	BP	1	TRPV2,THY1,TLX2,UST,BRSK1	down_VCAV_EC
GO:0072503	0.722	0.463	4	97	cellular divalent inorganic cation homeostasis	BP	1	PRNP,SLC39A6,THY1,CYBA	down_VCAV_EC

GO:0097529	0.722	0.467	4	52	myeloid leukocyte migration	BP	1	VEGFD,HRH1,CCL5,JAM3	up_ACOR_VSMC
GO:0035265	0.722	0.467	4	54	organ growth	BP	1	MEF2C,STC1,EDN1,PROX1	up_VCAV_EC
GO:2001234	0.722	0.491	3	75	negative regulation of apoptotic signaling	BP	1	SLC35F6,TMEM161A,PARK7	down_VCAV_EC
GO:0003158	0.722	0.496	3	38	endothelium development	BP	1	BMP4,ARHGEF26,F2RL1	up_ACOR_VSMC
GO:0033013	0.722	0.65	1	15	tetrapyrrole metabolic process	BP	1	ENSCAFG00000005637	down_ACOR_VSMC
GO:0050789	0.722	0.777	1	3295	regulation of biological process	BP	1	CST3	down_AORT_EC
GO:0043200	0.722	0.644	1	26	response to amino acid	BP	1	COL6A1	down_VCAV_EC
GO:0070059	0.722	0.644	1	25	intrinsic apoptotic signaling pathway in response to endoplasmic	BP	1	PARK7	down_VCAV_EC
GO:0070301	0.722	0.644	1	25	cellular response to hydrogen peroxide	BP	1	PARK7	down_VCAV_EC
GO:0008631	0.722	0.652	1	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	PARK7	up_ACOR_VSMC
GO:0042531	0.722	0.652	1	13	positive regulation of tyrosine phosphorylation	BP	1	PARP9	up_ACOR_VSMC
GO:0002714	0.722	0.654	1	12	positive regulation of B cell mediated immunity	BP	1	TP53BP1	up_ACOR_VSMC
GO:0002891	0.722	0.654	1	12	positive regulation of immunoglobulin mediated immune	BP	1	TP53BP1	up_ACOR_VSMC
GO:0033036	0.722	0.658	1	852	macromolecule localization	BP	1	TLR2	up_AFEM_VSMC
GO:0043085	0.722	0.644	1	323	positive regulation of catalytic activity	BP	1	NPNT	up_APUL_EC
GO:0006084	0.722	0.65	1	15	acetyl-CoA metabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0006298	0.722	0.652	1	13	mismatch repair	BP	1	HMGB1	up_VCAV_EC
GO:0060043	0.722	0.651	1	14	regulation of cardiac muscle cell proliferation	BP	1	MEF2C	up_VCAV_EC
GO:0034470	0.722	0.639	1	154	ncRNA processing	BP	1	RRP15	up_VPOR_EC
GO:0051253	0.722	0.644	1	359	negative regulation of RNA metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0072202	0.722	0.653	1	13	cell differentiation involved in metanephros	BP	1	OSR1	up_VSAP_EC
GO:0051338	0.722	0.643	1	288	regulation of transferase activity	BP	1	CAV1	up_VSAP_VSMC
GO:0009117	0.723	0.375	14	208	nucleotide metabolic process	BP	1	NPR1,PANK3,CDA,PIPOX,ADSS,GUCY1A1,ACPP,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,DCK,NOS2,HIF1A	up_VCAV_EC
GO:0010594	0.723	0.444	5	71	regulation of endothelial cell migration	BP	1	HMGB1,PRCP,EMP2,NUS1,AMOTL1	down_ACOR_VSMC
GO:0002443	0.723	0.444	5	71	leukocyte mediated immunity	BP	1	HMGB1,TFRC,FAM49B,EMP2,CORO1A	down_ACOR_VSMC
GO:0051216	0.723	0.444	5	70	cartilage development	BP	1	HOXA3,GREM1,POC1A,HOXC4,SERPINH1	down_ACOR_VSMC
GO:1903364	0.723	0.445	5	61	positive regulation of cellular protein catabolic	BP	1	SH3RF2,RNF19A,PSEN1,DISC1,HERPUD1	up_ACOR_VSMC
GO:0008654	0.723	0.465	4	58	phospholipid biosynthetic process	BP	1	ACSL3,MVD,VAC14,NUS1	down_ACOR_VSMC
GO:0051179	0.723	0.517	3	1747	localization	BP	1	HOXA3,TBX5,SLIT2	up_VPUL_VSMC
GO:0051250	0.723	0.495	3	38	negative regulation of lymphocyte activation	BP	1	CD274,TBC1D10C,FBXO7	up_VSAP_EC
GO:0048864	0.723	0.544	2	29	stem cell development	BP	1	NOLC1,PHACTR4	down_ACOR_VSMC
GO:0030216	0.723	0.543	2	29	keratinocyte differentiation	BP	1	FLNB,HOXA7	down_ACOR_VSMC
GO:0002312	0.723	0.545	2	24	B cell activation involved in immune response	BP	1	PLCG2,TP53BP1	up_ACOR_VSMC
GO:0006638	0.723	0.543	2	30	neutral lipid metabolic process	BP	1	GK5,ENSCAFG00000010596	up_VCAV_EC
GO:0006639	0.723	0.543	2	30	acylglycerol metabolic process	BP	1	GK5,ENSCAFG00000010596	up_VCAV_EC
GO:0015718	0.723	0.542	2	30	monocarboxylic acid transport	BP	1	SLCO3A1,NOS2	up_VCAV_EC
GO:0031058	0.723	0.543	2	28	positive regulation of histone modification	BP	1	GATA3,PRKD2	up_VCAV_EC
GO:0048675	0.723	0.545	2	26	axon extension	BP	1	IFRD1,RAB11A	up_VCAV_EC

GO:0006826	0.723	0.648	1	15	iron ion transport	BP	1	TFRC	down_ACOR_VSMC
GO:0060043	0.723	0.65	1	14	regulation of cardiac muscle cell proliferation	BP	1	GLI1	down_ACOR_VSMC
GO:0006641	0.723	0.642	1	25	triglyceride metabolic process	BP	1	GPAM	down_VCAV_EC
GO:1990266	0.723	0.643	1	24	neutrophil migration	BP	1	RAC2	down_VCAV_EC
GO:0007613	0.723	0.644	1	20	memory	BP	1	APOE	down_VSAP_EC
GO:0007050	0.723	0.638	1	53	cell cycle arrest	BP	1	FAP	up_AFEM_EC
GO:0051924	0.723	0.639	1	53	regulation of calcium ion transport	BP	1	CAMK2A	up_AFEM_EC
GO:0010660	0.723	0.65	1	14	regulation of muscle cell apoptotic process	BP	1	RGL2	up_VCAV_EC
GO:0016925	0.723	0.648	1	16	protein sumoylation	BP	1	HMG20A	up_VCAV_EC
GO:0035556	0.723	0.657	1	845	intracellular signal transduction	BP	1	LIMK1	up_VCAV_VSMC
GO:0043067	0.723	0.646	1	479	regulation of programmed cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0006298	0.723	0.651	1	13	mismatch repair	BP	1	AXIN2	up_VSAP_EC
GO:0007596	0.723040243	0.6387	1	47	blood coagulation	BP	1	PRKCD	up_ACOR_EC
GO:0055074	0.723118134	0.53591	2	95	calcium ion homeostasis	BP	1	PTH1R,TMTC2	up_ACOR_EC
GO:0006665	0.723121346	0.6385	1	48	sphingolipid metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0017038	0.723236079	0.53573	2	96	protein import	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0006605	0.723520605	0.53526	2	99	protein targeting	BP	1	KCNB1,CHMP4B	up_ACOR_EC
GO:0031497	0.723846477	0.63747	1	49	chromatin assembly	BP	1	SOX9	up_ACOR_EC
GO:0051094	0.724	0.343	30	388	positive regulation of developmental process	BP	1	HMGB1,HMGA1,SLC29A1,MTDH,SRRT,FBXO5,PRMT1,NF2,MMP14,EZH2,GREM1,ARG2,PDCD2,HOXB7,B4GALT1,TFRC,PPARD,RAC1,HMGB2,EZR,TOX,RBM14,BEND6,CDC20,ASPM,CTH,ARHGEF2,GLI1,SIX4,TPBG	down_ACOR_VSMC
GO:0031324	0.724	0.444	5	735	negative regulation of cellular metabolic process	BP	1	CXHXorf57,ENSCAFG00000002015,ASPN,FBP1,MTDH	up_VPOR_EC
GO:0019222	0.724	0.486	4	1934	regulation of metabolic process	BP	1	HOXC10,HOXA9,LNPEP,TAOK1	up_AORT_EC
GO:1903046	0.724	0.463	4	55	meiotic cell cycle process	BP	1	FIGNL1,CENPC,ATRX,FBXO5	up_VCAV_EC
GO:0042147	0.724	0.494	3	38	retrograde transport, endosome to Golgi	BP	1	TBC1D10C,DENND5A,ZFYVE21	up_VSAP_EC
GO:0048639	0.724	0.539	2	39	positive regulation of developmental growth	BP	1	CELF1,NRP1	down_VSAP_EC
GO:1900076	0.724	0.542	2	29	regulation of cellular response to insulin	BP	1	BAIAP2L1,NCK1	up_VCAV_EC
GO:0048332	0.724	0.543	2	26	mesoderm morphogenesis	BP	1	HOXA11,WNT11	up_VSAP_EC
GO:0045880	0.724	0.649	1	14	positive regulation of smoothened signaling	BP	1	GLI1	down_ACOR_VSMC
GO:0048708	0.724	0.644	1	20	astrocyte differentiation	BP	1	PTPN11	down_VSAP_EC
GO:1901655	0.724	0.643	1	20	cellular response to ketone	BP	1	MSN	down_VSAP_EC
GO:1990266	0.724	0.641	1	24	neutrophil migration	BP	1	WDR1	down_VSAP_EC
GO:2000756	0.724	0.644	1	20	regulation of peptidyl-lysine acetylation	BP	1	IWS1	down_VSAP_EC
GO:0044319	0.724	0.652	1	12	wound healing, spreading of cells	BP	1	RREB1	up_ACOR_VSMC
GO:0046470	0.724	0.65	1	13	phosphatidylcholine metabolic process	BP	1	LCAT	up_ACOR_VSMC
GO:0048663	0.724	0.65	1	13	neuron fate commitment	BP	1	BMP4	up_ACOR_VSMC
GO:0090504	0.724	0.652	1	12	epiboly	BP	1	RREB1	up_ACOR_VSMC
GO:0090505	0.724	0.652	1	12	epiboly involved in wound healing	BP	1	RREB1	up_ACOR_VSMC
GO:0006575	0.724	0.637	1	53	cellular modified amino acid metabolic process	BP	1	GCNT4	up_AFEM_EC
GO:0050654	0.724	0.648	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	CHST7	up_VCAV_EC

GO:0090169	0.724	0.65	1	13	regulation of spindle assembly	BP	1	SENP6	up_VCAV_EC
GO:0010629	0.724	0.645	1	502	negative regulation of gene expression	BP	1	SHOX2	up_VFEM_VSMC
GO:0008219	0.724	0.649	1	611	cell death	BP	1	SLIT2	up_VPUL_VSMC
GO:0006888	0.724843124	0.6362	1	49	ER to Golgi vesicle-mediated transport	BP	1	PREB	up_ACOR_EC
GO:0051172	0.725	0.324	60	663	negative regulation of nitrogen compound metabolic process	BP	1	SMAD6,LEP,RASSF2,RECK,NACC2,PRKAA2,ITM2C,BMP4,FGFR2,TP53BP1,EIF4A2,ATRX,TRPS1,SH3RF2,LATS2,ISG15,PTPN3,NDRG2,CST3,ZNF174,ANKRD1,F2RL1,FAM129A,DAPK1,CDKN1A,ENSCAFG00000006238,CLSTN1,PTPN22,OS9,ORMDL3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,DAG1,PARP9,PSEN1,SYNJ2BP,MXI1,SPINK2,NR3C1,WWC2,DUSP22,EDN1,OXR1,DUSP26,CBX7,LRRC4,DDIT4,KLF11,INPP5K,WFS1,AZIN2,ENSCAFG00000029553,ID3,PARK7,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0018205	0.725	0.398	9	122	peptidyl-lysine modification	BP	1	POLE3,EZH2,BRCA1,NOC2L,DMAP1,CTH,TADA2A,JMJD6,UBA2	down_ACOR_VSMC
GO:0044260	0.725	0.423	9	2593	cellular macromolecule metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0044260	0.725	0.432	8	2593	cellular macromolecule metabolic process	BP	1	NR1H4,STK32B,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0072511	0.725	0.415	7	97	divalent inorganic cation transport	BP	1	HOXA3,CAV1,SLC30A1,GSTO1,NIPA2,CORO1A,REM1	down_ACOR_VSMC
GO:0045787	0.725	0.426	6	117	positive regulation of cell cycle	BP	1	ASNS,PTPN11,DDX39B,EIF4EBP1,RAD23A,CDKN1A	down_VSAP_EC
GO:0001819	0.725	0.439	5	120	positive regulation of cytokine production	BP	1	LUM,PARK7,CYBA,MAVS,RAB7B	down_VCAV_EC
GO:0060491	0.725	0.443	5	62	regulation of cell projection assembly	BP	1	EVI5L,F2RL1,NRP1,EVL,SSH3	up_ACOR_VSMC
GO:0120032	0.725	0.443	5	62	regulation of plasma membrane bounded cell	BP	1	EVI5L,F2RL1,NRP1,EVL,SSH3	up_ACOR_VSMC
GO:0016458	0.725	0.489	3	59	gene silencing	BP	1	MORF4L2,CNOT7,SND1	down_VSAP_EC
GO:0044839	0.725	0.488	3	61	cell cycle G2/M phase transition	BP	1	BACH1,CALM1,CDKN1A	down_VSAP_EC
GO:0048522	0.725	0.508	3	1484	positive regulation of cellular process	BP	1	DKK2,HOXA9,TAOK1	up_AORT_EC
GO:0050657	0.725	0.536	2	51	nucleic acid transport	BP	1	SNUPN,ZFP36L1	down_VCAV_EC
GO:0050658	0.725	0.536	2	51	RNA transport	BP	1	SNUPN,ZFP36L1	down_VCAV_EC
GO:0051236	0.725	0.536	2	51	establishment of RNA localization	BP	1	SNUPN,ZFP36L1	down_VCAV_EC
GO:0015980	0.725	0.533	2	106	energy derivation by oxidation of organic	BP	1	LEP,PPARGC1A	up_AFEM_EC
GO:0032007	0.725	0.541	2	27	negative regulation of TOR signaling	BP	1	PREX2,HIF1A	up_VCAV_EC
GO:0001508	0.725	0.64	1	25	action potential	BP	1	TPC3	down_VCAV_EC
GO:0021549	0.725	0.64	1	26	cerebellum development	BP	1	NAGLU	down_VCAV_EC
GO:0051149	0.725	0.64	1	25	positive regulation of muscle cell differentiation	BP	1	GREM1	down_VCAV_EC
GO:0008219	0.725	0.648	1	611	cell death	BP	1	CITED2	down_VPOR_EC
GO:0061180	0.725	0.642	1	20	mammary gland epithelium development	BP	1	HIF1A	down_VSAP_EC
GO:0010628	0.725	0.644	1	527	positive regulation of gene expression	BP	1	HOXA9	up_AORT_EC
GO:0007154	0.725	0.68	1	1622	cell communication	BP	1	TBX5	up_APUL_VSMC
GO:0001974	0.725	0.649	1	13	blood vessel remodeling	BP	1	ACVRL1	up_VSAP_EC
GO:0036465	0.725	0.649	1	13	synaptic vesicle recycling	BP	1	PPP3CB	up_VSAP_EC
GO:0007215	0.725	0.648	1	13	glutamate receptor signaling pathway	BP	1	KLHL24	up_VSAP_EC
GO:0010558	0.725078342	0.39703	9	392	negative regulation of macromolecule biosynthetic process	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:0098609	0.725447809	0.45725	4	181	cell-cell adhesion	BP	1	CDH3,ELMO2,VCAM1,PRKCD	up_ACOR_EC
GO:0009913	0.725594901	0.63544	1	47	epidermal cell differentiation	BP	1	CDH3	up_ACOR_EC
GO:0048872	0.726	0.414	7	85	homeostasis of number of cells	BP	1	NAPEPLD,ABL1,ANKRD54,ZFP36L1,PPP3CB,HMOX1,CITED2	up_VSAP_EC

GO:0016050	0.726	0.424	6	119	vesicle organization	BP	1	SEC24D,SEC23A,HOOK3,USO1,SDC4,SEC13	down_VSAP_EC
GO:0008015	0.726	0.438	5	120	blood circulation	BP	1	ADCY6,CLSTN1,RNPEP,IRX5,THRB	down_VCAV_EC
GO:0071772	0.726	0.462	4	50	response to BMP	BP	1	FZD1,ABL1,LRP4,ACVRL1	up_VSAP_EC
GO:0071773	0.726	0.462	4	50	cellular response to BMP stimulus	BP	1	FZD1,ABL1,LRP4,ACVRL1	up_VSAP_EC
GO:0060255	0.726	0.513	3	1782	regulation of macromolecule metabolic	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0045910	0.726	0.646	1	14	negative regulation of DNA recombination	BP	1	PARPBP	down_ACOR_VSMC
GO:0140112	0.726	0.645	1	15	extracellular vesicle biogenesis	BP	1	SDC1	down_ACOR_VSMC
GO:0005977	0.726	0.638	1	26	glycogen metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0006073	0.726	0.638	1	26	cellular glucan metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0044042	0.726	0.638	1	26	glucan metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0009247	0.726	0.64	1	22	glycolipid biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0038034	0.726	0.64	1	21	signal transduction in absence of ligand	BP	1	INHBA	down_VSAP_EC
GO:0097192	0.726	0.64	1	21	extrinsic apoptotic signaling pathway in	BP	1	INHBA	down_VSAP_EC
GO:0045911	0.726	0.649	1	12	positive regulation of DNA recombination	BP	1	TP53BP1	up_ACOR_VSMC
GO:0098659	0.726	0.647	1	13	inorganic cation import across plasma membrane	BP	1	SLC8A1	up_ACOR_VSMC
GO:0099587	0.726	0.647	1	13	inorganic ion import across plasma membrane	BP	1	SLC8A1	up_ACOR_VSMC
GO:0065003	0.726	0.647	1	616	protein-containing complex assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0021532	0.726	0.648	1	13	neural tube patterning	BP	1	KDM2B	up_VSAP_EC
GO:0031113	0.726	0.648	1	13	regulation of microtubule polymerization	BP	1	ABL1	up_VSAP_EC
GO:0001837	0.726852175	0.63373	1	48	epithelial to mesenchymal transition	BP	1	SOX9	up_ACOR_EC
GO:0051248	0.727	0.349	24	316	negative regulation of protein metabolic process	BP	1	ILF3,USP4,EIF4A3,HMGCR,U2AF2,SLC29A1,PPP1R15B,BIRC5,CAV1,NF2,CDKN2C,GREM1,SMARCC1,DHCR24,BRCA1,NOC2L,YWHAB,NCL,NUP62,CACTIN,ENSCAFG00000005299,EZR,RBM14,TINF2	down_ACOR_VSMC
GO:0001935	0.727	0.461	4	50	endothelial cell proliferation	BP	1	STAT5A,ZNF580,ACVRL1,HMOX1	up_VSAP_EC
GO:1900076	0.727	0.538	2	29	regulation of cellular response to insulin	BP	1	CDK4,NCOA5	down_ACOR_VSMC
GO:1990845	0.727	0.533	2	51	adaptive thermogenesis	BP	1	TRPV2,PLCL1	down_VCAV_EC
GO:0033865	0.727	0.535	2	43	nucleoside bisphosphate metabolic process	BP	1	ENPP1,PAPSS1	down_VSAP_EC
GO:0033875	0.727	0.535	2	43	ribonucleoside bisphosphate metabolic	BP	1	ENPP1,PAPSS1	down_VSAP_EC
GO:0034032	0.727	0.535	2	43	purine nucleoside bisphosphate metabolic	BP	1	ENPP1,PAPSS1	down_VSAP_EC
GO:0043648	0.727	0.54	2	26	dicarboxylic acid metabolic process	BP	1	NIT2,NMNAT1	up_ACOR_VSMC
GO:0007155	0.727	0.533	2	324	cell adhesion	BP	1	ENSCAFG00000002015,SLC7A11	up_VPOR_EC
GO:0030260	0.727	0.643	1	15	entry into host cell	BP	1	CAV1	down_ACOR_VSMC
GO:0044409	0.727	0.643	1	15	entry into host	BP	1	CAV1	down_ACOR_VSMC
GO:0051806	0.727	0.643	1	15	entry into cell of other organism involved in	BP	1	CAV1	down_ACOR_VSMC
GO:0051828	0.727	0.643	1	15	entry into other organism involved in symbiotic	BP	1	CAV1	down_ACOR_VSMC
GO:0060421	0.727	0.645	1	14	positive regulation of heart growth	BP	1	GLI1	down_ACOR_VSMC
GO:0002532	0.727	0.638	1	25	production of molecular mediator involved in inflammatory response	BP	1	CHID1	down_VCAV_EC
GO:0070613	0.727	0.637	1	25	regulation of protein processing	BP	1	A2M	down_VCAV_EC
GO:0072676	0.727	0.638	1	25	lymphocyte migration	BP	1	HSD3B7	down_VCAV_EC
GO:1903317	0.727	0.637	1	25	regulation of protein maturation	BP	1	A2M	down_VCAV_EC

GO:0046677	0.727	0.633	1	54	response to antibiotic	BP	1	CRYAB	up_AFEM_EC
GO:0071897	0.727	0.633	1	54	DNA biosynthetic process	BP	1	GREM1	up_AFEM_EC
GO:0006974	0.727	0.637	1	333	cellular response to DNA damage stimulus	BP	1	ZDHHC16	up_APUL_EC
GO:0045892	0.727	0.636	1	328	negative regulation of transcription, DNA-	BP	1	NR1H4	up_APUL_EC
GO:0002684	0.728	0.358	18	239	positive regulation of immune system process	BP	1	HMGB1,IRAK1,MNDA,PRMT1,CAV1,MMP14,PDCD2,TFRC,FAM49B,RAC1,CACTIN,HMGB2,EZR,TOX,RBM14,CORO1A,POLR3F,PIK3CD	down_ACOR_VSMC
GO:0006816	0.728	0.423	6	84	calcium ion transport	BP	1	HOXA3,CAV1,SLC30A1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0032869	0.728	0.458	4	57	cellular response to insulin stimulus	BP	1	SREBF1,CDK4,SMARCC1,NCOA5	down_ACOR_VSMC
GO:0071236	0.728	0.488	3	39	cellular response to antibiotic	BP	1	ABL1,MAP3K5,ZNF580	up_VSAP_EC
GO:0048869	0.728	0.549	2	1119	cellular developmental process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0071706	0.728	0.534	2	40	tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2,NR1H4	down_VSAP_EC
GO:1901987	0.728	0.53	2	107	regulation of cell cycle phase transition	BP	1	OVOL1,DCUN1D3	up_AFEM_EC
GO:0006672	0.728	0.535	2	33	ceramide metabolic process	BP	1	SPTLC2,SAMD8	up_VCAV_EC
GO:0034613	0.728	0.642	1	576	cellular protein localization	BP	1	GPSM2	down_AFEM_EC
GO:0001708	0.728	0.639	1	20	cell fate specification	BP	1	CTNNB1	down_VSAP_EC
GO:0002637	0.728	0.638	1	20	regulation of immunoglobulin	BP	1	TFRC	down_VSAP_EC
GO:0033559	0.728	0.638	1	21	unsaturated fatty acid metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0071156	0.728	0.639	1	21	regulation of cell cycle arrest	BP	1	CDKN1A	down_VSAP_EC
GO:0032651	0.728	0.645	1	13	regulation of interleukin-1 beta production	BP	1	NOD2	up_ACOR_VSMC
GO:0060972	0.728	0.645	1	13	left/right pattern formation	BP	1	CITED2	up_ACOR_VSMC
GO:0060612	0.728	0.643	1	14	adipose tissue development	BP	1	SLC25A25	up_VCAV_EC
GO:1900408	0.728	0.643	1	15	negative regulation of cellular response to	BP	1	HIF1A	up_VCAV_EC
GO:1903202	0.728	0.643	1	15	negative regulation of oxidative stress-induced	BP	1	HIF1A	up_VCAV_EC
GO:1901699	0.728	0.631	1	164	cellular response to nitrogen compound	BP	1	ARHGEF2	up_VPOR_EC
GO:0051247	0.728	0.641	1	502	positive regulation of protein metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0048566	0.728	0.645	1	13	embryonic digestive tract development	BP	1	SHOX2	up_VSAP_EC
GO:0031328	0.728166108	0.37759	12	512	positive regulation of cellular biosynthetic	BP	1	CDH3,NR1H4,GATA4,PKIB,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2,PRKCD	up_ACOR_EC
GO:0032502	0.729	0.306	135	1661	developmental process	BP	1	ELK3,FSCN1,HMGB1,SREBF1,FLNB,USP1,ANLN,FMNL3,ACSL4,HMGA1,EIF4A3,SMC1A,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,HOXA3,TRIP13,SF1,SRRT,GINS4,SDC1,CTDNEP1,RAD54L,FBXO5,HSPA9,NAB2,HNRNPH3,B3GNT2,CFAP298,PRELID1,INSIG1,PRMT1,CAV1,CDK1,CASP2,XYLT1,TIMELESS,NF2,ANPEP,PFAS,MMP14,EZH2,STMN1,SLC30A1,GREM1,MAP3K20,NEK2,ADIPOR2,CDK4,SMARCC1,RNASEH2B,HMGB3,PCNA,HOXA7,SMG9,ARG2,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,POC1A,BRCA1,WDR62,E2F8,B4GALT1,NAV2,PRCP,TFRC,ADAMTS6,PPARD,RAP2C,NCL,RAC1,NUP62,UGDH,EMP2,FOSL1,PLK4,IQGAP1,RSL1D1,HOXC6,HMGB2,CDC42EP4,ARCN1,SMC3,CDK2,SMARCB1,RAB35,HOXB5,RBBP8,EZR,SMC6,TOX,HOXC4,RBM14,CORO1A,SGPL1,NOLC1,BEND6,PHACTR4,CDC20,SLC20A1,ERF,ASPM,PRPS1,TBX15,ENSCAFG00000010224,ELF4,TXNDC12,RADIL,ITGA2,CTH,ARHGEF2,TWIST2,HOXA9,SERPINH1,GLI1,JMJD6,MSC,CDC5L,EMG1,RTTN,RTCB,NUS1,HMGN1,TBCC,SIX4,TTLL1,TPBG,AMER1,ANXA7	down_ACOR_VSMC

GO:0010557	0.729	0.349	22	492	positive regulation of macromolecule biosynthetic process	BP	1	DCN,LUM,LARP6,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,AKT2,TFE3,TEAD1,GLI3,PARK7,EEF2,MYDGF,MAVS,MAPRE3,SHC1,PYM1,GREM1,SOAT1,THRB,ZBTB16	down_VCAV_EC
GO:0006511	0.729	0.35	22	253	ubiquitin-dependent protein catabolic process	BP	1	ZRANB1,SKP2,SH3RF2,ZNRF3,KLHL20,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,SIAH1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0042326	0.729	0.381	11	163	negative regulation of phosphorylation	BP	1	PPP2R5A,TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,HHEX,PREX2,SH3BP5,NCK1	up_VCAV_EC
GO:0060070	0.729	0.395	9	105	canonical Wnt signaling pathway	BP	1	RECK,MLLT3,FERMT1,FGFR2,LATS2,ZNRF3,FZD3,PSEN1,DISC1	up_ACOR_VSMC
GO:0043542	0.729	0.412	7	86	endothelial cell migration	BP	1	BMP4,SASH1,FGF18,NRP1,SYNJ2BP,JUP,PIK3C2A	up_ACOR_VSMC
GO:0048732	0.729	0.421	6	116	gland development	BP	1	SULF1,MSN,HIF1A,CTNNB1,SIX4,NRP1	down_VSAP_EC
GO:0002696	0.729	0.455	4	80	positive regulation of leukocyte activation	BP	1	SOCS5,FAM49B,TFRC,CDKN1A	down_VSAP_EC
GO:0006109	0.729	0.457	4	51	regulation of carbohydrate metabolic	BP	1	LEP,PRKCE,DDIT4,INPP5K	up_ACOR_VSMC
GO:0051252	0.729	0.495	3	1051	regulation of RNA metabolic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0009156	0.729	0.531	2	50	ribonucleoside monophosphate	BP	1	ATP5MC1,AMPD2	down_VCAV_EC
GO:0046323	0.729	0.536	2	26	glucose import	BP	1	LEP,SLC2A12	up_ACOR_VSMC
GO:0006884	0.729	0.642	1	14	cell volume homeostasis	BP	1	ANXA7	down_ACOR_VSMC
GO:0001836	0.729	0.638	1	18	release of cytochrome c from mitochondria	BP	1	PRELID1	down_ACOR_VSMC
GO:0050849	0.729	0.641	1	15	negative regulation of calcium-mediated	BP	1	GSTO1	down_ACOR_VSMC
GO:0045738	0.729	0.645	1	12	negative regulation of DNA repair	BP	1	TP53BP1	up_ACOR_VSMC
GO:0051187	0.729	0.644	1	13	cofactor catabolic process	BP	1	CAT	up_ACOR_VSMC
GO:0051196	0.729	0.644	1	13	regulation of coenzyme metabolic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0051646	0.729	0.645	1	12	mitochondrion localization	BP	1	RHOT1	up_ACOR_VSMC
GO:0051785	0.729	0.642	1	14	positive regulation of nuclear division	BP	1	EDN1	up_ACOR_VSMC
GO:0070098	0.729	0.642	1	14	chemokine-mediated signaling pathway	BP	1	CCL5	up_ACOR_VSMC
GO:0019220	0.729	0.639	1	525	regulation of phosphate metabolic process	BP	1	TAOK1	up_AORT_EC
GO:0051174	0.729	0.639	1	525	regulation of phosphorus metabolic process	BP	1	TAOK1	up_AORT_EC
GO:0000278	0.729	0.635	1	331	mitotic cell cycle	BP	1	LZTS1	up_APUL_EC
GO:1902679	0.729	0.635	1	329	negative regulation of RNA biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:1903507	0.729	0.635	1	329	negative regulation of nucleic acid-templated	BP	1	NR1H4	up_APUL_EC
GO:0002183	0.729	0.64	1	16	cytoplasmic translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0040011	0.729	0.638	1	505	locomotion	BP	1	EMX2	up_VFEM_VSMC
GO:0042130	0.729	0.644	1	13	negative regulation of T cell proliferation	BP	1	CD274	up_VSAP_EC
GO:0050686	0.729	0.643	1	13	negative regulation of mRNA processing	BP	1	CDK9	up_VSAP_EC
GO:0050702	0.729	0.644	1	13	interleukin-1 beta secretion	BP	1	F2RL1	up_VSAP_EC
GO:0060740	0.729	0.644	1	13	prostate gland epithelium morphogenesis	BP	1	RARG	up_VSAP_EC
GO:0050866	0.729200255	0.6307	1	48	negative regulation of cell activation	BP	1	PRKCD	up_ACOR_EC
GO:0010970	0.729385487	0.63046	1	48	transport along microtubule	BP	1	DYNC1I1	up_ACOR_EC
GO:0099111	0.729385487	0.63046	1	48	microtubule-based transport	BP	1	DYNC1I1	up_ACOR_EC
GO:0043009	0.72952355	0.4329	5	227	chordate embryonic development	BP	1	SOX9,FZD5,FOXC2,RARRES2,PYGO2	up_ACOR_EC
GO:0009156	0.729907657	0.62959	1	50	ribonucleoside monophosphate	BP	1	ALDOC	up_ACOR_EC
GO:0034660	0.73	0.379	11	211	ncRNA metabolic process	BP	1	CARS,SARS,AARS,SMARCA4,MRPL1,YARS,TARS,NARS,SND1,PDCD11,RTCB	down_VSAP_EC
GO:0045930	0.73	0.401	8	97	negative regulation of mitotic cell cycle	BP	1	FAM107A,CRADD,ABL1,ZFP36L1,GAS1,FBXO7,ZFP36L2,TPRA1	up_VSAP_EC

GO:1901653	0.73	0.41	7	84	cellular response to peptide	BP	1	ACTN2,PTPN22,SESN3,APP,PSEN1,NOD2,INPP5K	up_ACOR_VSMC
GO:0006164	0.73	0.41	7	86	purine nucleotide biosynthetic process	BP	1	ACACB,PDK2,GALK1,ACSS2,DCAKD,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:1901215	0.73	0.455	4	57	negative regulation of neuron death	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIX4	down_ACOR_VSMC
GO:0010638	0.73	0.451	4	207	positive regulation of organelle organization	BP	1	MLLT11,CLEC16A,PPARGC1A,CDC42EP5	up_AFEM_EC
GO:0031323	0.73	0.508	3	1788	regulation of cellular metabolic process	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0055114	0.73	0.48	3	157	oxidation-reduction process	BP	1	LEP,ACACB,PPARGC1A	up_AFEM_EC
GO:0030518	0.73	0.486	3	42	intracellular steroid hormone receptor	BP	1	SMARCA4,UFSP2,KDM3A	up_VCAV_EC
GO:0009966	0.73	0.49	3	868	regulation of signal transduction	BP	1	EYA1,TIAM1,CYP26B1	up_VFEM_EC
GO:1901136	0.73	0.486	3	38	carbohydrate derivative catabolic process	BP	1	HPSE,PNP,GNPDA1	up_VSAP_EC
GO:0006997	0.73	0.531	2	42	nucleus organization	BP	1	ZPR1,KDM3A	down_VSAP_EC
GO:0022610	0.73	0.529	2	326	biological adhesion	BP	1	ENSCAFG00000002015,SLC7A11	up_VPOR_EC
GO:0070727	0.73	0.64	1	579	cellular macromolecule localization	BP	1	GPSM2	down_AFEM_EC
GO:0060425	0.73	0.634	1	25	lung morphogenesis	BP	1	RDH10	down_VCAV_EC
GO:0000462	0.73	0.635	1	22	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	PDCD11	down_VSAP_EC
GO:0008306	0.73	0.636	1	21	associative learning	BP	1	HIF1A	down_VSAP_EC
GO:1903533	0.73	0.635	1	21	regulation of protein targeting	BP	1	MYO1C	down_VSAP_EC
GO:0016572	0.73	0.642	1	13	histone phosphorylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0002262	0.73	0.63	1	54	myeloid cell homeostasis	BP	1	NFE2L1	up_AFEM_EC
GO:0043409	0.73	0.63	1	54	negative regulation of MAPK cascade	BP	1	CYLD	up_AFEM_EC
GO:0006518	0.73	0.632	1	290	peptide metabolic process	BP	1	MME	up_VFEM_EC
GO:0050906	0.73	0.642	1	13	detection of stimulus involved in sensory	BP	1	NR2F6	up_VSAP_EC
GO:0051187	0.73	0.642	1	13	cofactor catabolic process	BP	1	HMOX1	up_VSAP_EC
GO:1902476	0.73	0.643	1	13	chloride transmembrane transport	BP	1	CLCN2	up_VSAP_EC
GO:0051270	0.73	0.632	1	296	regulation of cellular component movement	BP	1	CAV1	up_VSAP_VSMC
GO:0060548	0.73	0.632	1	294	negative regulation of cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0007599	0.730584296	0.6289	1	48	hemostasis	BP	1	PRKCD	up_ACOR_EC
GO:0019222	0.731	0.3	179	1934	regulation of metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,HNF4A,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PTGFR,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,TBC1D10C,CEP85,ACACB,TPCN2,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,EBF2,HDAC7,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,CBX7,STAT6,RECK,GATAD1,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,RBL2,LMF1,GLIS2,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,BATF2,MYC,PIK3IP1,SSBP2,IRX3,ZEB1,SHOX2,TMEM225B,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,HOXC10,POLDIP2,CLYBL,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,PHF1,E2F4,NPAS2,PRKAB1,SMG9,FBXO7,LIMD1,RNF166,RPUSD4,LONP2,PC,CDK9,PRMT2,KDM2B,FBLN1,PIP4K2B,OSBPL7,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,CYBA,ZNF205,NCOA2,EIF3K,PQBP1,TIMP2,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,UBQLN2,ZNF517,HT	up_VSAP_EC

GO:1902531	0.731	0.343	24	536	regulation of intracellular signal transduction	BP	1	NOTCH2,PDGFRB,DCN,PRNP,GLIPR2,BGN,ARHGEF25,AKT1S1,CSPG4,PRMT6,TMEM161A,ASPN,PARK7,MYDGF,SASH1,CLEC16A,ARL2BP,CDH2,GSDME,SPRED1,SHC1,FBH1,GREM1,ANKRD54	down_VCAV_EC
GO:0048514	0.731	0.361	16	214	blood vessel morphogenesis	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,NCL,EMP2,SGPL1,JMJD6,NUS1	down_ACOR_VSMC
GO:0032386	0.731	0.385	10	137	regulation of intracellular transport	BP	1	SREBF1,NEDD4,RAN,INSIG1,PLK3,PREB,DMAP1,EZR,RBM14,NUS1	down_ACOR_VSMC
GO:0034504	0.731	0.399	8	111	protein localization to nucleus	BP	1	HCLS1,TMEM173,FERMT1,PPP3CA,HHEX,APOD,NUP133,IPO11	up_VCAV_EC
GO:0009628	0.731	0.417	6	302	response to abiotic stimulus	BP	1	CRY2,ANGPT4,CRYAB,MFAP4,DCUN1D3,ADAM17	up_AFEM_EC
GO:0030198	0.731	0.42	6	81	extracellular matrix organization	BP	1	ADAMTS9,LAMC2,FERMT1,SERAC1,OLFML2A,FSCN1	up_VCAV_EC
GO:0007219	0.731	0.453	4	59	Notch signaling pathway	BP	1	HEY1,SLC35C2,MMP14,BEND6	down_ACOR_VSMC
GO:0032006	0.731	0.455	4	52	regulation of TOR signaling	BP	1	SESN1,CASTOR1,NPRL3,DDIT4	up_VSAP_EC
GO:0010467	0.731	0.507	3	1787	gene expression	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0016054	0.731	0.481	3	61	organic acid catabolic process	BP	1	ALDH1L2,SESN2,CEMIP2	down_VSAP_EC
GO:0046395	0.731	0.481	3	61	carboxylic acid catabolic process	BP	1	ALDH1L2,SESN2,CEMIP2	down_VSAP_EC
GO:0009145	0.731	0.485	3	40	purine nucleoside triphosphate biosynthetic	BP	1	PPARGC1A,ALDOC,DDIT4	up_ACOR_VSMC
GO:0032006	0.731	0.528	2	52	regulation of TOR signaling	BP	1	AKT1S1,CLEC16A	down_VCAV_EC
GO:0043412	0.731	0.546	2	1225	macromolecule modification	BP	1	MGAT4B,GBGT1	down_VPOR_EC
GO:0006732	0.731	0.526	2	107	coenzyme metabolic process	BP	1	GPAM,ACACB	up_AFEM_EC
GO:0019319	0.731	0.534	2	26	hexose biosynthetic process	BP	1	PDK2,PC	up_VSAP_EC
GO:0032729	0.731	0.638	1	15	positive regulation of interferon-gamma	BP	1	FAM49B	down_ACOR_VSMC
GO:0009987	0.731	1	1	5086	cellular process	BP	1	GATA5	down_AFEM_VSMC
GO:0014074	0.731	0.633	1	26	response to purine-containing compound	BP	1	ZFP36L1	down_VCAV_EC
GO:0046683	0.731	0.633	1	26	response to organophosphorus	BP	1	ZFP36L1	down_VCAV_EC
GO:0007586	0.731	0.635	1	20	digestion	BP	1	STRAP	down_VSAP_EC
GO:0022600	0.731	0.635	1	20	digestive system process	BP	1	STRAP	down_VSAP_EC
GO:0033866	0.731	0.634	1	22	nucleoside bisphosphate biosynthetic process	BP	1	PAPSS1	down_VSAP_EC
GO:0034030	0.731	0.634	1	22	ribonucleoside bisphosphate biosynthetic	BP	1	PAPSS1	down_VSAP_EC
GO:0034033	0.731	0.634	1	22	purine nucleoside bisphosphate biosynthetic	BP	1	PAPSS1	down_VSAP_EC
GO:0007193	0.731	0.641	1	13	adenylate cyclase-inhibiting G protein-coupled receptor signaling	BP	1	EDN1	up_ACOR_VSMC
GO:0031113	0.731	0.641	1	13	regulation of microtubule polymerization	BP	1	TUBB4A	up_ACOR_VSMC
GO:0070528	0.731	0.641	1	13	protein kinase C signaling	BP	1	HTR2B	up_ACOR_VSMC
GO:1901890	0.731	0.641	1	13	positive regulation of cell junction assembly	BP	1	NRP1	up_ACOR_VSMC
GO:1902531	0.731	0.636	1	536	regulation of intracellular signal transduction	BP	1	TAOK1	up_AORT_EC
GO:0044255	0.731	0.631	1	293	cellular lipid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0008631	0.731	0.641	1	13	intrinsic apoptotic signaling pathway in response to oxidative	BP	1	MAP3K5	up_VSAP_EC
GO:0048854	0.731	0.642	1	13	brain morphogenesis	BP	1	SLC6A4	up_VSAP_EC
GO:0003148	0.731	0.641	1	13	outflow tract septum morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0070232	0.731	0.641	1	13	regulation of T cell apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0051353	0.731	0.642	1	13	positive regulation of oxidoreductase activity	BP	1	ABL1	up_VSAP_EC
GO:1902186	0.731	0.641	1	13	regulation of viral release from host cell	BP	1	PC	up_VSAP_EC

GO:0030308	0.731146684	0.62807	1	49	negative regulation of cell growth	BP	1	NRP1	up_ACOR_EC
GO:1901137	0.731922689	0.42992	5	232	carbohydrate derivative biosynthetic process	BP	1	GALNT5,B3GNT7,GUCY1B1,PIGS,ALDOC	up_ACOR_EC
GO:0048522	0.732	0.314	70	1484	positive regulation of cellular process	BP	1	GPAM,NOTCH2,PDGFRB,SLC35F6,KIRREL1,LRP1,DCN,PRNP,LUM,SDC4,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,EVC,TRPV2,CLIP3,NUMBL,RHOD,OSMR,ENSCAFG00000014978,SSBP2,AKT2,TFE3,SYDE1,CLSTN1,CSPG4,TMEM161A,SEMA3C,POLDIP2,THY1,TEAD1,ATP6V0C,B4GALT1,GLI3,PARK7,ADAMTSL4,EEF2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,IFT57,MAVS,CDH2,LOXL3,GSDME,LSM10,SPRED1,ACTR3B,RAB7B,MAPRE3,TWIST2,DDR2,SHC1,PYM1,FBH1,GREM1,RAC2,NAPEPLD,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,ANKRD54	down_VCAV_EC
GO:1901566	0.732	0.325	42	598	organonitrogen compound biosynthetic process	BP	1	NPR1,ST8SIA6,PANK3,TNIP1,PDGFB,ST6GAL1,TLR4,QKI,GATA3,ZDHHC22,ADSS,GUCY1A1,ODC1,SPTLC2,ARG2,B3GNT5,TARSL2,MTOR,SAMD8,HHAT,CHST7,ST3GAL6,ENC1,ABCA1,SECISBP2L,GALNT18,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,NCK1,DPH5,GUCY1B1,MRRF,BCL10,CNOT7,GCH1,NOS2,HIF1A,BCAT1,ZDHHC6,TET2	up_VCAV_EC
GO:0032269	0.732	0.346	22	306	negative regulation of cellular protein metabolic process	BP	1	EDNRB,TNFAIP3,TNIP1,PDE4D,ATF3,RAPGEF1,TLR4,EDN1,CDYL,HMG20A,HHEX,PREX2,SH3BP5,ENC1,PAK2,SWAP70,NCK1,PTGS2,CNOT7,KDM5A,KDM3A,IVNS1ABP	up_VCAV_EC
GO:0010038	0.732	0.434	5	62	response to metal ion	BP	1	ENSCAFG00000009113,CDH1,SLC25A12,MT2A,HMOX1	up_VSAP_EC
GO:0002821	0.732	0.532	2	30	positive regulation of adaptive immune	BP	1	TFRC,FAM49B	down_ACOR_VSMC
GO:0042632	0.732	0.533	2	27	cholesterol homeostasis	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:0060395	0.732	0.532	2	27	SMAD protein signal transduction	BP	1	BMP4,NCEH1	up_ACOR_VSMC
GO:0010243	0.732	0.628	1	238	response to organonitrogen	BP	1	IGF1R	down_ACOR_EC
GO:1902369	0.732	0.638	1	15	negative regulation of RNA catabolic process	BP	1	THRAP3	down_ACOR_VSMC
GO:0032720	0.732	0.64	1	13	negative regulation of tumor necrosis factor	BP	1	PTPN22	up_ACOR_VSMC
GO:0050772	0.732	0.64	1	13	positive regulation of axonogenesis	BP	1	NRP1	up_ACOR_VSMC
GO:0022602	0.732	0.64	1	13	ovulation cycle process	BP	1	SLIT2	up_VSAP_EC
GO:0034404	0.732056754	0.62679	1	50	nucleobase-containing small molecule	BP	1	ALDOC	up_ACOR_EC
GO:0010941	0.733	0.321	47	524	regulation of cell death	BP	1	FZD1,WNT11,CD274,ACKR3,MAP3K14,AXIN2,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,PTPMT1,NPAS2,FBXO7,WISP2,ENSCAFG00000011993,PRMT2,KDM2B,RAF1,ZNF205,STX4,QARS,ARHGAP10,HTRA2,NCK1,HMOX1,MAP2K2,CITED2,DEDD2,LATS2	up_VSAP_EC
GO:0048638	0.733	0.418	6	82	regulation of developmental growth	BP	1	CDK4,PPARD,EZR,SGPL1,GLI1,SIX4	down_ACOR_VSMC
GO:0044772	0.733	0.415	6	144	mitotic cell cycle phase transition	BP	1	KANK2,ZFP36L1,LSM10,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0031669	0.733	0.431	5	72	cellular response to nutrient levels	BP	1	SREBF1,SREBF2,RNF152,PDXP,MIOS	down_ACOR_VSMC
GO:0003013	0.733	0.429	5	121	circulatory system process	BP	1	ADCY6,CLSTN1,RNPEP,IRX5,THRB	down_VCAV_EC
GO:0050896	0.733	0.483	4	2346	response to stimulus	BP	1	HDAC7,CITED2,RAB11B,HSD3B7	down_VPOR_EC
GO:0007409	0.733	0.523	2	109	axonogenesis	BP	1	PLXNA4,LRRN2	up_AFEM_EC
GO:1900542	0.733	0.531	2	26	regulation of purine nucleotide metabolic	BP	1	PDK2,DDIT4	up_VSAP_EC
GO:0009132	0.733	0.63	1	25	nucleoside diphosphate metabolic process	BP	1	ENTPD3	down_VCAV_EC
GO:0008299	0.733	0.637	1	14	isoprenoid biosynthetic process	BP	1	GGPS1	up_ACOR_VSMC
GO:0033962	0.733	0.64	1	12	cytoplasmic mRNA processing body assembly	BP	1	ATXN2	up_ACOR_VSMC
GO:0070229	0.733	0.638	1	13	negative regulation of lymphocyte apoptotic	BP	1	BMP4	up_ACOR_VSMC

GO:0050803	0.733	0.625	1	55	regulation of synapse structure or activity	BP	1	DMPK	up_AFEM_EC
GO:0050807	0.733	0.625	1	55	regulation of synapse organization	BP	1	DMPK	up_AFEM_EC
GO:1903046	0.733	0.626	1	55	meiotic cell cycle process	BP	1	OVOL1	up_AFEM_EC
GO:0032786	0.733	0.639	1	13	positive regulation of DNA-templated transcription, elongation	BP	1	THOC1	up_VCAV_EC
GO:0032870	0.733	0.625	1	162	cellular response to hormone stimulus	BP	1	RNF6	up_VPOR_EC
GO:2000001	0.733	0.638	1	13	regulation of DNA damage checkpoint	BP	1	FBXO4	up_VSAP_EC
GO:0016572	0.733	0.639	1	13	histone phosphorylation	BP	1	CDK9	up_VSAP_EC
GO:0006282	0.733784106	0.62473	1	48	regulation of DNA repair	BP	1	FIGNL1	up_ACOR_EC
GO:1905330	0.73384185	0.62465	1	48	regulation of morphogenesis of an	BP	1	SOX9	up_ACOR_EC
GO:0010468	0.734	0.302	116	1270	regulation of gene expression	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,HNF4A,ARHGEF5,AXIN2,OSR2,INSIG2,PTGFR,ZNF367,PPARGC1B,ACACB,IRX5,ZHX3,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,TENT5C,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CCBE1,CBX7,STAT6,GATAD1,PLPP3,EXOSC7,PYM1,F2RL1,RBL2,GLIS2,DDR2,ICE1,ZFP36L1,PIK3R1,RBCK1,GAS1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,ANKHD1,TRERF1,E2F4,NPAS2,PRKAB1,SMG9,LIMD1,RPUSD4,PC,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,ZNF205,NCOA2,EIF3K,PQBP1,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,TGFBR2,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0071704	0.734	0.397	14	3535	organic substance metabolic process	BP	1	TBX15,EYA1,HOXA9,MAP2K6,MME,HOXA10,TRIM9,HOXA7,SIX1,YBX3,CYP26B1,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0009611	0.734	0.429	5	122	response to wounding	BP	1	SDC4,VKORC1,B4GALT1,ZFP36L1,RGMA	down_VCAV_EC
GO:0010675	0.734	0.48	3	46	regulation of cellular carbohydrate metabolic	BP	1	FAM3C,ENSCAFG00000010596,PMAIP1	up_VCAV_EC
GO:0072331	0.734	0.479	3	49	signal transduction by p53 class mediator	BP	1	USP28,PMAIP1,ATRX	up_VCAV_EC
GO:1901861	0.734	0.526	2	41	regulation of muscle tissue development	BP	1	CTNNB1,SIX4	down_VSAP_EC
GO:0016043	0.734	0.565	2	1973	cellular component organization	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0002705	0.734	0.528	2	31	positive regulation of leukocyte mediated	BP	1	GATA3,NECTIN2	up_VCAV_EC
GO:0040014	0.734	0.53	2	27	regulation of multicellular organism growth	BP	1	FXN,HTRA2	up_VSAP_EC
GO:0043604	0.734	0.626	1	288	amide biosynthetic process	BP	1	RPSA	down_ACOR_EC
GO:0010469	0.734	0.629	1	26	regulation of signaling receptor activity	BP	1	PARK7	down_VCAV_EC
GO:0032609	0.734	0.629	1	25	interferon-gamma production	BP	1	PRNP	down_VCAV_EC
GO:1901879	0.734	0.628	1	26	regulation of protein depolymerization	BP	1	PLEKHH2	down_VCAV_EC
GO:0033046	0.734	0.63	1	21	negative regulation of sister chromatid	BP	1	NAA10	down_VSAP_EC
GO:0033048	0.734	0.63	1	21	negative regulation of mitotic sister chromatid	BP	1	NAA10	down_VSAP_EC
GO:0051985	0.734	0.63	1	21	negative regulation of chromosome segregation	BP	1	NAA10	down_VSAP_EC
GO:0051291	0.734	0.63	1	21	protein heterooligomerization	BP	1	C1QTNF6	down_VSAP_EC
GO:0038084	0.734	0.637	1	13	vascular endothelial growth factor signaling	BP	1	NRP1	up_ACOR_VSMC
GO:0051926	0.734	0.636	1	14	negative regulation of calcium ion transport	BP	1	INPP5K	up_ACOR_VSMC
GO:0090199	0.734	0.634	1	15	regulation of release of cytochrome c from	BP	1	BNIP3	up_ACOR_VSMC
GO:0007034	0.734	0.624	1	55	vacuolar transport	BP	1	RAB7A	up_AFEM_EC

GO:0045880	0.734	0.635	1	14	positive regulation of smoothened signaling	BP	1	CTNNA1	up_VCAV_EC
GO:0009966	0.734	0.643	1	868	regulation of signal transduction	BP	1	GATA5	up_VCAV_VSMC
GO:1903827	0.734	0.624	1	164	regulation of cellular protein localization	BP	1	GCC2	up_VPOR_EC
GO:0007193	0.734	0.638	1	13	adenylate cyclase-inhibiting G protein-coupled receptor signaling	BP	1	CHRM1	up_VSAP_EC
GO:0051150	0.734	0.637	1	13	regulation of smooth muscle cell differentiation	BP	1	ZEB1	up_VSAP_EC
GO:0090502	0.734	0.637	1	13	RNA phosphodiester bond hydrolysis,	BP	1	RCL1	up_VSAP_EC
GO:0006835	0.734	0.637	1	13	dicarboxylic acid transport	BP	1	SLC25A12	up_VSAP_EC
GO:0030104	0.734	0.637	1	13	water homeostasis	BP	1	CLDN1	up_VSAP_EC
GO:0099003	0.73491042	0.62305	1	50	vesicle-mediated transport in synapse	BP	1	CALY	up_ACOR_EC
GO:0051173	0.735	0.307	80	874	positive regulation of nitrogen compound metabolic process	BP	1	ADRA1B,TLR1,SMAD6,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MBP,SKP2,PRKAA2,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,SH3RF2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,AR,SASH1,LMO4,FGF18,PLAC8B,F2RL1,FAM129A,DAPK1,EGLN1,CRLF3,NRP1,PTPN22,NPNT,SMARCD3,SMPD1,PRKCE,CCNT1,FRS2,RNF19A,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,ZKSCAN1,ENSCAFG00000029553,PARK7,TEAD1,NGRN,HMBOX1,SSBP2,CRKL	up_ACOR_VSMC
GO:0006886	0.735	0.333	29	332	intracellular protein transport	BP	1	EXPH5,SH3TC2,LEP,TCAF1,USP6NL,FERMT1,BMP4,EVI5L,SCARB2,SEC24B,STX11,CDKN1A,PTPN22,OS9,SCG5,PSEN1,SGSM2,SYNJ2BP,LAMP2,JUP,AP2B1,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RPAIN,PARK7,PTPN14	up_ACOR_VSMC
GO:0009894	0.735	0.339	24	277	regulation of catabolic process	BP	1	AXIN2,PLEKHF1,ACACB,TPCN2,TENT5C,MFN2,ZFP36L1,POLDIP2,AZIN2,FBXO7,RNF166,LONP2,PIP4K2B,OSBPL7,SAMD4B,ZFP36L2,TIMP2,IDH1,UBQLN2,HTRA2,TNRC6C,HMOX1,NPRL3,DDIT4	up_VSAP_EC
GO:0051188	0.735	0.428	5	81	cofactor biosynthetic process	BP	1	PANK3,ELOVL7,ENSCAFG00000024323,GCH1,HIF1A	up_VCAV_EC
GO:0001704	0.735	0.479	3	43	formation of primary germ layer	BP	1	NF2,MMP14,ITGA2	down_ACOR_VSMC
GO:0051146	0.735	0.474	3	76	striated muscle cell differentiation	BP	1	RBM38,CDH2,GREM1	down_VCAV_EC
GO:0006892	0.735	0.479	3	39	post-Golgi vesicle-mediated transport	BP	1	CCDC93,DOP1B,MYO1B	up_VSAP_EC
GO:0009755	0.735	0.523	2	52	hormone-mediated signaling pathway	BP	1	KANK2,PARK7	down_VCAV_EC
GO:0050663	0.735	0.522	2	52	cytokine secretion	BP	1	GPAM,MAVS	down_VCAV_EC
GO:0003401	0.735	0.634	1	15	axis elongation	BP	1	SIX4	down_ACOR_VSMC
GO:1900744	0.735	0.634	1	15	regulation of p38MAPK cascade	BP	1	EZR	down_ACOR_VSMC
GO:1902235	0.735	0.633	1	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	TXNDC12	down_ACOR_VSMC
GO:0044238	0.735	0.765	1	3383	primary metabolic process	BP	1	CST3	down_AORT_EC
GO:0010464	0.735	0.629	1	21	regulation of mesenchymal cell	BP	1	CTNNB1	down_VSAP_EC
GO:0048566	0.735	0.636	1	13	embryonic digestive tract development	BP	1	FGFR2	up_ACOR_VSMC
GO:1901796	0.735	0.63	1	18	regulation of signal transduction by p53 class	BP	1	PMAIP1	up_VCAV_EC
GO:0032212	0.735	0.632	1	16	positive regulation of telomere maintenance via	BP	1	HMBOX1	up_VCAV_EC
GO:1904358	0.735	0.632	1	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	HMBOX1	up_VCAV_EC
GO:0045648	0.735	0.636	1	13	positive regulation of erythrocyte	BP	1	ANKRD54	up_VSAP_EC
GO:2000179	0.735	0.634	1	14	positive regulation of neural precursor cell	BP	1	CDON	up_VSAP_EC

GO:0048339	0.735	0.636	1	13	paraxial mesoderm development	BP	1	WNT11	up_VSAP_EC
GO:0071675	0.735	0.636	1	13	regulation of mononuclear cell	BP	1	SLIT2	up_VSAP_EC
GO:0035556	0.736	0.307	76	845	intracellular signal transduction	BP	1	ADGRD1,SEZ6L,CDON,WNT11,ACKR3,MAP3K14,ARHGEF5,C5AR2,PTGFR,PLEKHF1,TBC1D10C,ARHGEF6,IL6R,SLIT2,CRADD,ABL1,HDAC7,SESN1,MAP3K5,CDC42EP5,PDGFD,SAV1,C1QTNF2,HPSE,RASGRP2,ANKRD54,CDC42EP2,STAT5A,CISH,CAMKK2,F2RL1,PDK2,MFN2,ZFP36L1,TRAF7,RGL1,PIK3R1,RBCK1,TIAM1,MYC,PIK3IP1,DLC1,TBXA2R,HIC1,FGD4,RTN4RL1,SASH1,MYD88,PTPMT1,S100A4,CASTOR1,ASB8,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,FBLN1,ZFP36L2,RAF1,MAPKBP1,PSD4,QARS,ARHGAP12,RAPGEF3,HTRA2,FLOT1,PPP3CB,NCK1,IRAK1BP1,KRCC1,MAP2K2,NPRL3,BAG4,TRADD,DDIT4,LATS2	up_VSAP_EC
GO:0008150	0.736	0.476	14	5646	biological_process	BP	1	HOXC10,EYA1,GATM,HOXA10,HOXA9,SPINK5,NETO1,TBX15,SLC16A12,FBP1,EMX2,HOXA11,SHOX2,ATP8B4	up_VFEM_VSMC
GO:0032386	0.736	0.379	10	137	regulation of intracellular transport	BP	1	HCLS1,MX2,TMEM173,IWS1,FERMT1,APOD,FES,CTDSPL2,GCC2,DNAJC13	up_VCAV_EC
GO:0014070	0.736	0.384	9	172	response to organic cyclic compound	BP	1	SMARCA4,MSN,CTNNB1,UBA5,REST,PAK2,YWHAH,KDM3A,HOMER1	down_VSAP_EC
GO:0006399	0.736	0.413	6	87	tRNA metabolic process	BP	1	VARS,FARSA,THUMPD2,OSGEP,RARS,RTCB	down_ACOR_VSMC
GO:0016482	0.736	0.429	5	63	cytosolic transport	BP	1	TBC1D10C,EMP2,DOP1B,DENND5A,ZFYVE21	up_VSAP_EC
GO:0071383	0.736	0.448	4	58	cellular response to steroid hormone stimulus	BP	1	TFPI,SMARCA4,UFSP2,KDM3A	up_VCAV_EC
GO:0043484	0.736	0.523	2	43	regulation of RNA splicing	BP	1	ZPR1,REST	down_VSAP_EC
GO:0090317	0.736	0.63	1	16	negative regulation of intracellular protein	BP	1	INSIG1	down_ACOR_VSMC
GO:0006366	0.736	0.632	1	583	transcription by RNA polymerase II	BP	1	GABPA	down_AFEM_EC
GO:0045739	0.736	0.626	1	26	positive regulation of DNA repair	BP	1	TMEM161A	down_VCAV_EC
GO:0010718	0.736	0.627	1	21	positive regulation of epithelial to mesenchymal	BP	1	CTNNB1	down_VSAP_EC
GO:0071526	0.736	0.636	1	12	semaphorin-plexin signaling pathway	BP	1	NRP1	up_ACOR_VSMC
GO:0072698	0.736	0.635	1	13	protein localization to microtubule cytoskeleton	BP	1	MID1	up_ACOR_VSMC
GO:0050792	0.736	0.621	1	55	regulation of viral process	BP	1	RAB7A	up_AFEM_EC
GO:0001941	0.736	0.633	1	14	postsynaptic membrane organization	BP	1	RELN	up_VCAV_EC
GO:0060323	0.736	0.633	1	14	head morphogenesis	BP	1	TIPARP	up_VCAV_EC
GO:0019748	0.736	0.635	1	13	secondary metabolic process	BP	1	MPST	up_VSAP_EC
GO:1904292	0.736	0.634	1	13	regulation of ERAD pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0009059	0.737	0.309	74	1563	macromolecule biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,LMO4,CLIP3,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,AKT2,LCAT,SAMD4B,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,DDOST,VDR,PRMT6,CXXC5,GFPT2,PIGS,EIF3K,NECAB3,TEAD1,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,RPL27,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,FUT8,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0048518	0.737	0.377	12	1676	positive regulation of biological process	BP	1	C3AR1,HOXA3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,MTDH,ABHD5,CCAR1,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0006310	0.737	0.401	7	93	DNA recombination	BP	1	FIGNL1,THOC1,SWAP70,HMGB1,BLM,SMC5,GINS4	up_VCAV_EC
GO:0015711	0.737	0.445	4	81	organic anion transport	BP	1	SLC7A5,SLC38A1,APOE,SLC7A11	down_VSAP_EC
GO:1903038	0.737	0.524	2	30	negative regulation of leukocyte cell-cell	BP	1	HMGB1,ARG2	down_ACOR_VSMC

GO:0010761	0.737	0.631	1	15	fibroblast migration	BP	1	SGPL1	down_ACOR_VSMC
GO:0002762	0.737	0.63	1	15	negative regulation of myeloid leukocyte	BP	1	HOXA7	down_ACOR_VSMC
GO:0022037	0.737	0.624	1	27	metencephalon development	BP	1	NAGLU	down_VCAV_EC
GO:0051145	0.737	0.627	1	21	smooth muscle cell differentiation	BP	1	CTNNB1	down_VSAP_EC
GO:0010941	0.737	0.629	1	524	regulation of cell death	BP	1	TAOK1	up_AORT_EC
GO:0010629	0.737	0.629	1	502	negative regulation of gene expression	BP	1	NKX2-5	up_VPOR_VSMC
GO:0008542	0.737	0.633	1	13	visual learning	BP	1	CTNS	up_VSAP_EC
GO:0002720	0.737	0.633	1	13	positive regulation of cytokine production involved in immune	BP	1	F2RL1	up_VSAP_EC
GO:0032720	0.737	0.633	1	13	negative regulation of tumor necrosis factor	BP	1	C5AR2	up_VSAP_EC
GO:0042531	0.737	0.633	1	13	positive regulation of tyrosine phosphorylation	BP	1	IL6R	up_VSAP_EC
GO:0009124	0.73726378	0.61985	1	51	nucleoside monophosphate	BP	1	ALDOC	up_ACOR_EC
GO:0071702	0.738	0.313	52	687	organic substance transport	BP	1	HCLS1,GBP5,OSBPL9,ATP8A1,LRRC8D,TMEM173,IWS1,FERMT1,CHD7,SLC35A3,TLR4,QKI,GATA3,EDN1,RAB11A,RAB27A,EXOC6,PPP3CA,YES1,SLC38A1,ARG2,SNAP23,HHEX,RALBP1,SCAMP1,RSC1A1,PDZD8,ABCA1,OSBPL6,SNX2,SLCO3A1,THOC1,AKAP12,APOD,SLC2A3,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,RIPK1,MCU,HIF1A,IPO11,LMTK2,RABGAP1,USP6NL	up_VCAV_EC
GO:0045184	0.738	0.316	47	532	establishment of protein localization	BP	1	EXPH5,SH3TC2,TLR1,LEP,HTR2B,TCAF1,USP6NL,MBP,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,SEC24B,CD274,STX11,ANKRD1,F2RL1,CDKN1A,PTPN22,NPNT,OS9,PRKCE,SCG5,PSEN1,SGSM2,SYNJ2BP,LAMP2,JUP,CCL5,RAB11B,NOD2,LMTK2,AP2B1,SCAMP5,SAR1B,HERPUD1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0009628	0.738	0.337	23	302	response to abiotic stimulus	BP	1	USP1,HMGCR,SMC1A,NEDD4,INTS7,RAD54L,CAV1,RAD51,CASP2,AURKB,TOPBP1,MAP3K20,PLK3,PCNA,NOC2L,PPARD,POLH,DTL,SUV39H1,ARHGEF2,CDC25A,HMGN1,ANXA7	down_ACOR_VSMC
GO:0032446	0.738	0.345	19	255	protein modification by small protein conjugation	BP	1	USP4,UBE2S,U2AF2,SLC29A1,UBE2T,CAV1,FANCI,UHRF1,RNF152,BRCA1,UBE2J2,DTL,UBE2K,CDC20,UBE2C,UBA2,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0009894	0.738	0.366	12	277	regulation of catabolic process	BP	1	LRP1,DCN,TIMP2,AKT2,PSMF1,SAMD4B,POLDIP2,PARK7,ZFP36L1,CLEC16A,LONP2,PACSIN3	down_VCAV_EC
GO:0046907	0.738	0.371	11	536	intracellular transport	BP	1	LEP,CRY2,VPS26C,GAS1,CRYAB,CHRM2,MYO1D,CAMK2A,REEP2,BVES,RAB7A	up_AFEM_EC
GO:0050896	0.738	0.402	9	2346	response to stimulus	BP	1	EMX2,NETO1,GATM,SALL1,TLR2,CAV1,SHOX2,F5,FGF5	up_VSAP_VSMC
GO:0050817	0.738	0.447	4	50	coagulation	BP	1	LNPK,F2RL1,ENPP4,PSEN1	up_ACOR_VSMC
GO:0009117	0.738	0.441	4	208	nucleotide metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:1905475	0.738	0.446	4	52	regulation of protein localization to membrane	BP	1	PIK3R1,LRP4,KCNB1,STX4	up_VSAP_EC
GO:0002819	0.738	0.474	3	44	regulation of adaptive immune response	BP	1	HMGB1,TFRC,FAM49B	down_ACOR_VSMC
GO:1903900	0.738	0.475	3	40	regulation of viral life cycle	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0002690	0.738	0.525	2	26	positive regulation of leukocyte chemotaxis	BP	1	F2RL1,ZNF580	up_VSAP_EC
GO:0007009	0.738	0.524	2	27	plasma membrane organization	BP	1	XKR8,FLOT1	up_VSAP_EC
GO:0006518	0.738	0.621	1	290	peptide metabolic process	BP	1	RPSA	down_ACOR_EC
GO:0009163	0.738	0.629	1	16	nucleoside biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0032495	0.738	0.63	1	15	response to muramyl dipeptide	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0042455	0.738	0.629	1	16	ribonucleoside biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0019080	0.738	0.623	1	26	viral gene expression	BP	1	TRIM8	down_VCAV_EC

GO:0031124	0.738	0.622	1	27	mRNA 3'-end processing	BP	1	ZFP36L1	down_VCAV_EC
GO:0016445	0.738	0.625	1	20	somatic diversification of immunoglobulins	BP	1	TFRC	down_VSAP_EC
GO:0016447	0.738	0.625	1	20	somatic recombination of immunoglobulin gene	BP	1	TFRC	down_VSAP_EC
GO:0051341	0.738	0.625	1	22	regulation of oxidoreductase activity	BP	1	APOE	down_VSAP_EC
GO:0097061	0.738	0.625	1	21	dendritic spine organization	BP	1	APOE	down_VSAP_EC
GO:0072202	0.738	0.633	1	13	cell differentiation involved in metanephros	BP	1	BMP4	up_ACOR_VSMC
GO:0035264	0.738	0.618	1	56	multicellular organism growth	BP	1	GPAM	up_AFEM_EC
GO:0042181	0.738	0.628	1	17	ketone biosynthetic process	BP	1	BMP2	up_VCAV_EC
GO:0051781	0.738	0.627	1	18	positive regulation of cell division	BP	1	PDGFB	up_VCAV_EC
GO:0051603	0.738	0.621	1	305	proteolysis involved in cellular protein catabolic	BP	1	TRIM9	up_VFEM_EC
GO:0001759	0.738	0.632	1	13	organ induction	BP	1	HOXA11	up_VSAP_EC
GO:0015985	0.738	0.633	1	13	energy coupled proton transport, down	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0015986	0.738	0.633	1	13	ATP synthesis coupled proton transport	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0070979	0.738	0.632	1	13	protein K11-linked ubiquitination	BP	1	CDC26	up_VSAP_EC
GO:0040012	0.738	0.621	1	303	regulation of locomotion	BP	1	CAV1	up_VSAP_VSMC
GO:0060341	0.739	0.344	19	255	regulation of cellular localization	BP	1	HCLS1,PPP2R5A,MX2,TMEM173,PDE4D,IWS1,MEF2C,FERMT1,CHD7,APLNR,SNCAIP,EPB41,SH3GLB1,APOD,FES,CTDSPL2,GCC2,DNAJC13,HIF1A	up_VCAV_EC
GO:0010557	0.739	0.375	10	492	positive regulation of macromolecule biosynthetic process	BP	1	HOXA9,LBH,PRR16,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0022408	0.739	0.474	3	44	negative regulation of cell-cell adhesion	BP	1	HMGB1,NF2,ARG2	down_ACOR_VSMC
GO:0043902	0.739	0.473	3	45	positive regulation of multi-organism process	BP	1	SMC3,RAD23A,PPIH	down_ACOR_VSMC
GO:0032502	0.739	0.494	3	1661	developmental process	BP	1	SRSF6,GABPA,FSCN1	down_AFEM_EC
GO:0000041	0.739	0.522	2	31	transition metal ion transport	BP	1	SLC30A1,TFRC	down_ACOR_VSMC
GO:0009119	0.739	0.521	2	32	ribonucleoside metabolic process	BP	1	RAN,CTPS1	down_ACOR_VSMC
GO:0009124	0.739	0.517	2	51	nucleoside monophosphate	BP	1	ATP5MC1,AMPD2	down_VCAV_EC
GO:0045445	0.739	0.523	2	27	myoblast differentiation	BP	1	BMP4,ANKRD1	up_ACOR_VSMC
GO:0051963	0.739	0.524	2	26	regulation of synapse assembly	BP	1	SLITRK5,APP	up_ACOR_VSMC
GO:0008543	0.739	0.524	2	27	fibroblast growth factor receptor signaling	BP	1	FGF7,SULF2	up_VSAP_EC
GO:0043537	0.739	0.628	1	15	negative regulation of blood vessel endothelial	BP	1	HMGB1	down_ACOR_VSMC
GO:0061951	0.739	0.627	1	16	establishment of protein localization to plasma	BP	1	ACSL3	down_ACOR_VSMC
GO:0032623	0.739	0.623	1	21	interleukin-2 production	BP	1	NR1H4	down_VSAP_EC
GO:0061383	0.739	0.624	1	20	trabecula morphogenesis	BP	1	FHL2	down_VSAP_EC
GO:0043949	0.739	0.631	1	13	regulation of cAMP-mediated signaling	BP	1	APLP1	up_ACOR_VSMC
GO:0050686	0.739	0.631	1	13	negative regulation of mRNA processing	BP	1	CCNT1	up_ACOR_VSMC
GO:0006357	0.739	0.626	1	547	regulation of transcription by RNA polymerase II	BP	1	HOXA9	up_AORT_EC
GO:0048468	0.739	0.627	1	553	cell development	BP	1	SGCD	up_AORT_EC
GO:0006904	0.739	0.629	1	15	vesicle docking involved in exocytosis	BP	1	EXOC6	up_VCAV_EC
GO:0006739	0.739	0.631	1	13	NADP metabolic process	BP	1	NADK	up_VSAP_EC

GO:0006807	0.739477	0.31164	81	3221	nitrogen compound metabolic process	BP	1	C7,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,BTD,LHX9,ENSCAFG00000028814,SMAD6,B3GNT7,KLHL25,ZMYND8,NIT2,PAK3,GUCY1B1,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,RBM38,CLU,SFMBT2,ALDOC,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,HM13,PRKCD,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0051225	0.739719249	0.61677	1	49	spindle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0051130	0.74	0.352	15	342	positive regulation of cellular component organization	BP	1	KIRREL1,LRP1,DCN,SDC4,NABP2,TRPV2,CLIP3,AKT2,THY1,CLEC16A,CYBA,ACTR3B,DDR2,GREM1,RAC2	down_VCAV_EC
GO:0072657	0.74	0.365	12	144	protein localization to membrane	BP	1	PLEKHF1,CDH1,EMP2,RILPL2,RAB11B,PIK3R1,LRP4,TSPAN5,KCNB1,STX4,FLOT1,BAG4	up_VSAP_EC
GO:1901653	0.74	0.408	6	84	cellular response to peptide	BP	1	PPARG,BAIAP2L1,NCK1,TIMELESS,NR4A1,ARHGEF2	up_VCAV_EC
GO:0002064	0.74	0.423	5	71	epithelial cell development	BP	1	FLNB,B4GALT1,RAP2C,IQGAP1,EZR	down_ACOR_VSMC
GO:0032886	0.74	0.441	4	81	regulation of microtubule-based process	BP	1	ARHGEF2,CTNNB1,GSK3B,MID1	down_VSAP_EC
GO:0050707	0.74	0.472	3	44	regulation of cytokine secretion	BP	1	HMGB1,ARG2,EZR	down_ACOR_VSMC
GO:0032147	0.74	0.468	3	77	activation of protein kinase activity	BP	1	PRNP,CSPG4,SHC1	down_VCAV_EC
GO:0006885	0.74	0.473	3	39	regulation of pH	BP	1	SLC26A7,DMXL1,EDN1	up_ACOR_VSMC
GO:0010821	0.74	0.471	3	49	regulation of mitochondrion	BP	1	SH3GLB1,PMAIP1,HIF1A	up_VCAV_EC
GO:0015718	0.74	0.521	2	30	monocarboxylic acid transport	BP	1	ACSL3,PPARD	down_ACOR_VSMC
GO:0006810	0.74	0.535	2	1244	transport	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:0007052	0.74	0.518	2	42	mitotic spindle organization	BP	1	MZT1,KPNB1	down_VSAP_EC
GO:0140029	0.74	0.521	2	28	exocytic process	BP	1	STX11,PSEN1	up_ACOR_VSMC
GO:0002260	0.74	0.626	1	15	lymphocyte homeostasis	BP	1	CORO1A	down_ACOR_VSMC
GO:0000079	0.74	0.62	1	26	regulation of cyclin-dependent protein serine/threonine kinase	BP	1	MAPRE3	down_VCAV_EC
GO:0001738	0.74	0.62	1	27	morphogenesis of a polarized epithelium	BP	1	BRSK1	down_VCAV_EC
GO:0021536	0.74	0.622	1	21	diencephalon development	BP	1	NRP1	down_VSAP_EC
GO:0051310	0.74	0.621	1	22	metaphase plate congression	BP	1	KPNB1	down_VSAP_EC
GO:0048854	0.74	0.629	1	13	brain morphogenesis	BP	1	PSEN1	up_ACOR_VSMC
GO:0009605	0.74	0.625	1	538	response to external stimulus	BP	1	BPI	up_AORT_EC
GO:0046635	0.74	0.626	1	15	positive regulation of alpha-beta T cell	BP	1	ITPKB	up_VCAV_EC
GO:0043254	0.74	0.616	1	164	regulation of protein complex assembly	BP	1	TWF1	up_VPOR_EC
GO:0048285	0.74	0.616	1	166	organelle fission	BP	1	MZT1	up_VPOR_EC
GO:0010676	0.74	0.63	1	13	positive regulation of cellular carbohydrate	BP	1	C1QTNF2	up_VSAP_EC
GO:0045191	0.74	0.628	1	14	regulation of isotype switching	BP	1	STAT6	up_VSAP_EC
GO:0051960	0.741	0.342	19	216	regulation of nervous system development	BP	1	ITM2C,BMP4,SEC24B,WASF3,ZNF365,NRP1,ULK2,SMARCD3,SLITRK5,FZD3,APP,PSEN1,CHD7,SIPA1L1,SSH3,ASAP1,B2M,DISC1,CRKL	up_ACOR_VSMC
GO:0043542	0.741	0.407	6	86	endothelial cell migration	BP	1	HMGB1,GREM1,PRCP,EMP2,NUS1,AMOTL1	down_ACOR_VSMC
GO:0001890	0.741	0.443	4	51	placenta development	BP	1	GJB5,DLX3,ZFP36L1,CITED2	up_VSAP_EC
GO:0000077	0.741	0.468	3	60	DNA damage checkpoint	BP	1	PTPN11,DDX39B,CDKN1A	down_VSAP_EC

GO:0022904	0.741	0.471	3	43	respiratory electron transport chain	BP	1	PPARGC1A,SLC25A12,PARK7	up_ACOR_VSMC
GO:0014033	0.741	0.519	2	30	neural crest cell differentiation	BP	1	NOLC1,PHACTR4	down_ACOR_VSMC
GO:0000910	0.741	0.515	2	52	cytokinesis	BP	1	SNX18,ANXA11	down_VCAV_EC
GO:0000086	0.741	0.515	2	52	G2/M transition of mitotic cell cycle	BP	1	BRSK1,CDK14	down_VCAV_EC
GO:0034644	0.741	0.518	2	32	cellular response to UV	BP	1	MAPK13,USP28	up_VCAV_EC
GO:0019752	0.741	0.617	1	283	carboxylic acid metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0035725	0.741	0.625	1	16	sodium ion transmembrane transport	BP	1	NEDD4	down_ACOR_VSMC
GO:0006959	0.741	0.621	1	21	humoral immune response	BP	1	A2M	down_VSAP_EC
GO:0061640	0.741	0.62	1	23	cytoskeleton-dependent cytokinesis	BP	1	ANLN	down_VSAP_EC
GO:0009409	0.741	0.628	1	13	response to cold	BP	1	PLAC8B	up_ACOR_VSMC
GO:0090184	0.741	0.627	1	14	positive regulation of kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:0060147	0.741	0.626	1	14	regulation of posttranscriptional gene	BP	1	PPP3CA	up_VCAV_EC
GO:0060428	0.741	0.623	1	17	lung epithelium development	BP	1	CREB1	up_VCAV_EC
GO:0060966	0.741	0.626	1	14	regulation of gene silencing by RNA	BP	1	PPP3CA	up_VCAV_EC
GO:0010562	0.741	0.618	1	312	positive regulation of phosphorus metabolic	BP	1	MAP2K6	up_VFEM_EC
GO:0045937	0.741	0.618	1	312	positive regulation of phosphate metabolic	BP	1	MAP2K6	up_VFEM_EC
GO:0006629	0.741	0.62	1	382	lipid metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0035794	0.741	0.628	1	13	positive regulation of mitochondrial membrane permeability	BP	1	ZNF205	up_VSAP_EC
GO:1905710	0.741	0.628	1	13	positive regulation of membrane permeability	BP	1	ZNF205	up_VSAP_EC
GO:0031325	0.742	0.314	42	914	positive regulation of cellular metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,DCN,PRNP,LUM,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,CLIP3,ENSCAFG00000014978,SSBP2,AKT2,TFE3,CSPG4,TMEM161A,TEAD1,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,SOAT1,THRB,PACSIN3,ZBTB16	down_VCAV_EC
GO:0006753	0.742	0.353	14	211	nucleoside phosphate metabolic process	BP	1	NPR1,PANK3,CDA,PIPOX,ADSS,GUCY1A1,ACPP,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,DCK,NOS2,HIF1A	up_VCAV_EC
GO:0062012	0.742	0.386	8	100	regulation of small molecule metabolic	BP	1	LEP,PPARGC1A,PRKCE,DKKL1,DDIT4,INPP5K,PARK7,LMF1	up_ACOR_VSMC
GO:0055065	0.742	0.403	6	145	metal ion homeostasis	BP	1	PRNP,SLC39A6,THY1,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0006403	0.742	0.421	5	64	RNA localization	BP	1	ZFP36L1,NUP98,SNUPN,FLOT1,TGFBR2	up_VSAP_EC
GO:0048518	0.742	0.49	3	1676	positive regulation of biological process	BP	1	GPSM2,SRSF6,FSCN1	down_AFEM_EC
GO:0006402	0.742	0.466	3	77	mRNA catabolic process	BP	1	SAMD4B,ZFP36L1,PYM1	down_VCAV_EC
GO:0001824	0.742	0.519	2	27	blastocyst development	BP	1	LATS2,CITED2	up_ACOR_VSMC
GO:0045682	0.742	0.52	2	27	regulation of epidermis development	BP	1	FERMT1,BMP4	up_ACOR_VSMC
GO:0051172	0.742	0.519	2	663	negative regulation of nitrogen compound	BP	1	NR1H4,PCSK1N	up_APUL_EC
GO:0003338	0.742	0.625	1	15	metanephros morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:1901568	0.742	0.617	1	26	fatty acid derivative metabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0072583	0.742	0.626	1	13	clathrin-dependent endocytosis	BP	1	DNAJC6	up_ACOR_VSMC
GO:1901991	0.742	0.614	1	56	negative regulation of mitotic cell cycle phase	BP	1	DCUN1D3	up_AFEM_EC
GO:0007585	0.742	0.623	1	16	respiratory gaseous exchange	BP	1	EDN1	up_VCAV_EC
GO:0035116	0.742	0.625	1	15	embryonic hindlimb morphogenesis	BP	1	CHD7	up_VCAV_EC
GO:0035136	0.742	0.623	1	16	forelimb morphogenesis	BP	1	ATRX	up_VCAV_EC

GO:0044255	0.742	0.615	1	293	cellular lipid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0016579	0.742171371	0.61349	1	49	protein deubiquitination	BP	1	USP53	up_ACOR_EC
GO:0033365	0.742816213	0.40249	6	276	protein localization to organelle	BP	1	TRIM8,DCLK2,MAVS,CHMP4B,NRP1,PRKCD	up_ACOR_EC
GO:1903050	0.743	0.394	7	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	SH3RF2,OS9,RNF19A,PSEN1,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0010810	0.743	0.439	4	60	regulation of cell-substrate adhesion	BP	1	GREM1,HOXA7,RAC1,EMP2	down_ACOR_VSMC
GO:0044770	0.743	0.464	3	161	cell cycle phase transition	BP	1	OVOL1,CAMK2A,DCUN1D3	up_AFEM_EC
GO:0010557	0.743	0.516	2	492	positive regulation of macromolecule biosynthetic process	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0051651	0.743	0.517	2	31	maintenance of location in cell	BP	1	INSIG1,ASPM	down_ACOR_VSMC
GO:0071804	0.743	0.516	2	31	cellular potassium ion transport	BP	1	NEDD4,CAV1	down_ACOR_VSMC
GO:0071805	0.743	0.516	2	31	potassium ion transmembrane transport	BP	1	NEDD4,CAV1	down_ACOR_VSMC
GO:0009798	0.743	0.517	2	31	axis specification	BP	1	STC1,HHEX	up_VCAV_EC
GO:0030307	0.743	0.516	2	31	positive regulation of cell growth	BP	1	EDN1,RAB11A	up_VCAV_EC
GO:0010390	0.743	0.623	1	15	histone monoubiquitination	BP	1	UHRF1	down_ACOR_VSMC
GO:0061337	0.743	0.622	1	16	cardiac conduction	BP	1	CAV1	down_ACOR_VSMC
GO:0006090	0.743	0.616	1	26	pyruvate metabolic process	BP	1	ME3	down_VCAV_EC
GO:0032007	0.743	0.616	1	27	negative regulation of TOR signaling	BP	1	AKT1S1	down_VCAV_EC
GO:1900542	0.743	0.616	1	26	regulation of purine nucleotide metabolic	BP	1	PARK7	down_VCAV_EC
GO:0006356	0.743	0.619	1	20	regulation of transcription by RNA polymerase I	BP	1	SMARCA4	down_VSAP_EC
GO:0032233	0.743	0.618	1	21	positive regulation of actin filament bundle	BP	1	NRP1	down_VSAP_EC
GO:0044070	0.743	0.618	1	22	regulation of anion transport	BP	1	APOE	down_VSAP_EC
GO:0046638	0.743	0.625	1	13	positive regulation of alpha-beta T cell	BP	1	CD83	up_ACOR_VSMC
GO:1901021	0.743	0.625	1	13	positive regulation of calcium ion transmembrane	BP	1	PLCG2	up_ACOR_VSMC
GO:0002252	0.743	0.612	1	166	immune effector process	BP	1	OAS3	up_VPOR_EC
GO:0051186	0.743	0.612	1	159	cofactor metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0016310	0.743	0.624	1	641	phosphorylation	BP	1	SLIT2	up_VPUL_VSMC
GO:0009792	0.743243862	0.41593	5	231	embryo development ending in birth or egg	BP	1	SOX9,FZD5,FOXC2,RARRES2,PYGO2	up_ACOR_EC
GO:0016573	0.74335025	0.6118	1	50	histone acetylation	BP	1	PHF20	up_ACOR_EC
GO:0031398	0.743484272	0.61153	1	51	positive regulation of protein ubiquitination	BP	1	NOD2	up_ACOR_EC
GO:0050817	0.743753926	0.61126	1	50	coagulation	BP	1	PRKCD	up_ACOR_EC
GO:0051173	0.744	0.313	40	874	positive regulation of nitrogen compound metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,DCN,PRNP,LUM,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,CLIP3,ENSCAFG00000014978,SSBP2,AKT2,TFE3,CSPG4,TMEM161A,TEAD1,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,SASH1,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,SOAT1,THRB,PACSIN3,ZBTB16	down_VCAV_EC
GO:0006366	0.744	0.326	26	583	transcription by RNA polymerase II	BP	1	SMAD9,DCN,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TFE3,NR3C1,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,TSC22D3,GLIS2,GREM1,THRB,RGMA	down_VCAV_EC
GO:0043085	0.744	0.351	14	323	positive regulation of catalytic activity	BP	1	PDGFRB,SNX18,PRNP,LMO4,AKT2,CSPG4,PARK7,SASH1,IFT57,MAPRE3,DDR2,SHC1,GREM1,EVI5L	down_VCAV_EC
GO:0044057	0.744	0.377	9	110	regulation of system process	BP	1	THRB,WASF3,IRX5,EMP2,KCNE3,CHRM1,F2RL1,TBXA2R,AGTR1	up_VSAP_EC

GO:2001020	0.744	0.393	7	88	regulation of response to DNA damage stimulus	BP	1	ACKR3,AXIN2,ABL1,MYC,FBXO4,NPAS2,CDK9	up_VSAP_EC
GO:0007610	0.744	0.402	6	146	behavior	BP	1	PRNP,NAGLU,PARK7,ENSCAFG00000017708,THRB,BRSK1	down_VCAV_EC
GO:0048562	0.744	0.416	5	102	embryonic organ morphogenesis	BP	1	TMED2,HOXB7,HIF1A,CTNNB1,SIX4	down_VSAP_EC
GO:0016051	0.744	0.419	5	63	carbohydrate biosynthetic process	BP	1	GOT1,C1QTNF2,PDK2,PASK,PC	up_VSAP_EC
GO:0051047	0.744	0.436	4	84	positive regulation of secretion	BP	1	NR1H4,PTPN11,HIF1A,SDC4	down_VSAP_EC
GO:0070302	0.744	0.437	4	78	regulation of stress-activated protein kinase	BP	1	TNIK,LYN,SH3RF3,MID1	down_VSAP_EC
GO:0045216	0.744	0.467	3	44	cell-cell junction organization	BP	1	FSCN1,CAV1,NF2	down_ACOR_VSMC
GO:0030183	0.744	0.515	2	30	B cell differentiation	BP	1	MMP14,HMGB3	down_ACOR_VSMC
GO:0000302	0.744	0.511	2	52	response to reactive oxygen species	BP	1	PARK7,MPV17	down_VCAV_EC
GO:0010468	0.744	0.529	2	1270	regulation of gene expression	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0060415	0.744	0.517	2	27	muscle tissue morphogenesis	BP	1	FZD1,SHOX2	up_VSAP_EC
GO:0015991	0.744	0.62	1	16	ATP hydrolysis coupled proton transport	BP	1	ENSCAFG00000013366	down_ACOR_VSMC
GO:0050654	0.744	0.622	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	XYLT1	down_ACOR_VSMC
GO:0050854	0.744	0.621	1	16	regulation of antigen receptor-mediated	BP	1	EZR	down_ACOR_VSMC
GO:0070542	0.744	0.622	1	15	response to fatty acid	BP	1	CDK4	down_ACOR_VSMC
GO:0071277	0.744	0.622	1	15	cellular response to calcium ion	BP	1	IQGAP1	down_ACOR_VSMC
GO:0090662	0.744	0.62	1	16	ATP hydrolysis coupled transmembrane transport	BP	1	ENSCAFG00000013366	down_ACOR_VSMC
GO:0099131	0.744	0.62	1	16	ATP hydrolysis coupled ion transmembrane	BP	1	ENSCAFG00000013366	down_ACOR_VSMC
GO:0070373	0.744	0.614	1	26	negative regulation of ERK1 and ERK2 cascade	BP	1	SPRED1	down_VCAV_EC
GO:0007017	0.744563634	0.40037	6	273	microtubule-based process	BP	1	BRSK1,DIXDC1,DYNC1I1,DCLK2,CHMP4B,TUBB4A	up_ACOR_EC
GO:0010604	0.745	0.296	84	919	positive regulation of macromolecule metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MBP,SKP2,PRKAA2,MLLT3,BMP4,FGFR2,TP53BP1,GJA1,ATRX,MED14,TLR3,SH3RF2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,AR,SASH1,LMO4,FGF18,PLAC8B,F2RL1,FAM129A,DAPK1,RBM4B,EGLN1,CRLF3,NRP1,PTPN22,NPNT,SMARCD3,SMPD1,PRKCE,CCNT1,FRS2,RNF19A,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,ZKSCAN1,ENSCAFG00000029553,PARK7,TEAD1,NGRN,HMBOX1,SSBP2,BVES,CRKL	up_ACOR_VSMC
GO:0051604	0.745	0.391	7	102	protein maturation	BP	1	BIRC5,CASP2,MMP14,DHCR24,ENSCAFG00000005299,PMPCA,SERPINH1	down_ACOR_VSMC
GO:0034645	0.745	0.429	5	1546	cellular macromolecule biosynthetic process	BP	1	NR1H4,GALNT17,ZDHHC16,NPNT,HOXA1	up_APUL_EC
GO:0032434	0.745	0.436	4	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	SLC29A1,SMARCC1,PLK3,RAD23A	down_ACOR_VSMC
GO:0032409	0.745	0.437	4	52	regulation of transporter activity	BP	1	KCNE3,OSR1,KLHL24,FXYD1	up_VSAP_EC
GO:0008630	0.745	0.466	3	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	NACC2,CDKN1A,DDIT4	up_ACOR_VSMC
GO:0007041	0.745	0.467	3	41	lysosomal transport	BP	1	HOOK3,GCC2,VPS54	up_VCAV_EC
GO:0009206	0.745	0.466	3	39	purine ribonucleoside triphosphate biosynthetic	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0009166	0.745	0.514	2	31	nucleotide catabolic process	BP	1	NUDT1,NUDT3	down_ACOR_VSMC
GO:0002705	0.745	0.514	2	31	positive regulation of leukocyte mediated	BP	1	TFRC,FAM49B	down_ACOR_VSMC
GO:0019219	0.745	0.527	2	1151	regulation of nucleobase-containing compound metabolic process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0046434	0.745	0.51	2	52	organophosphate catabolic process	BP	1	ENTPD3,ACAT1	down_VCAV_EC

GO:0034504	0.745	0.507	2	111	protein localization to nucleus	BP	1	LEP,CRY2	up_AFEM_EC
GO:0031124	0.745	0.516	2	27	mRNA 3'-end processing	BP	1	ZFP36L1,CDK9	up_VSAP_EC
GO:0050000	0.745	0.516	2	27	chromosome localization	BP	1	NUP98,TTL	up_VSAP_EC
GO:0021955	0.745	0.621	1	15	central nervous system neuron axonogenesis	BP	1	SLC29A1	down_ACOR_VSMC
GO:0002712	0.745	0.621	1	15	regulation of B cell mediated immunity	BP	1	TFRC	down_ACOR_VSMC
GO:0002889	0.745	0.621	1	15	regulation of immunoglobulin	BP	1	TFRC	down_ACOR_VSMC
GO:0010257	0.745	0.614	1	25	NADH dehydrogenase complex assembly	BP	1	COA1	down_VCAV_EC
GO:0021761	0.745	0.613	1	27	limbic system development	BP	1	GLI3	down_VCAV_EC
GO:0032981	0.745	0.614	1	25	mitochondrial respiratory chain complex I assembly	BP	1	COA1	down_VCAV_EC
GO:0010737	0.745	0.623	1	13	protein kinase A signaling	BP	1	ENSCAFG00000029553	up_ACOR_VSMC
GO:0030888	0.745	0.623	1	13	regulation of B cell proliferation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0072077	0.745	0.622	1	13	renal vesicle morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0072273	0.745	0.622	1	13	metanephric nephron morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0033260	0.745	0.62	1	15	nuclear DNA replication	BP	1	ATRX	up_VCAV_EC
GO:0044106	0.745	0.619	1	17	cellular amine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0051293	0.745	0.623	1	13	establishment of spindle localization	BP	1	ZW10	up_VCAV_EC
GO:0070647	0.745	0.612	1	311	protein modification by small protein conjugation	BP	1	EYA1	up_VFEM_EC
GO:0007517	0.745686042	0.50639	2	100	muscle organ development	BP	1	FOXC2,TBX5	up_ACOR_EC
GO:0140013	0.745886009	0.60837	1	50	meiotic nuclear division	BP	1	FIGNL1	up_ACOR_EC
GO:0051276	0.745949422	0.37224	9	398	chromosome organization	BP	1	NR1H4,PKIB,SOX9,PHF20,ZMYND8,CHMP4B,RIOX2,PRKCD,PYGO2	up_ACOR_EC
GO:0000278	0.746	0.325	25	331	mitotic cell cycle	BP	1	PLK2,PDGFB,STK10,EDN1,RAB11A,PPP3CA,MAP3K3,SLK,MZT1,ENSCAFG00000010596,STMN1,PAK2,CENPC,TAOK1,BLM,SMC5,RAD21,RAD17,USP37,CUL4A,ZW10,ATRX,TOPBP1,TMOD3,FBXO5	up_VCAV_EC
GO:0030154	0.746	0.394	7	1040	cell differentiation	BP	1	BARX1,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,RNF6	up_VPOR_EC
GO:0043405	0.746	0.402	6	85	regulation of MAP kinase activity	BP	1	IRAK1,HMGCR,CAV1,EZH2,MAP3K20,NUP62	down_ACOR_VSMC
GO:0001818	0.746	0.416	5	65	negative regulation of cytokine production	BP	1	CD83,CD274,NDRG2,F2RL1,PTPN22	up_ACOR_VSMC
GO:0015672	0.746	0.432	4	89	monovalent inorganic cation transport	BP	1	KIF5B,NDUFA4L2,NKAIN1,YWHAH	down_VSAP_EC
GO:0006355	0.746	0.471	3	974	regulation of transcription, DNA-	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0055123	0.746	0.465	3	40	digestive system development	BP	1	WNT11,SAV1,SHOX2	up_VSAP_EC
GO:0009141	0.746	0.506	2	110	nucleoside triphosphate metabolic process	BP	1	ATP6V1B2,PPARGC1A	up_AFEM_EC
GO:0034121	0.746	0.614	1	22	regulation of toll-like receptor signaling	BP	1	LYN	down_VSAP_EC
GO:1905268	0.746	0.615	1	20	negative regulation of chromatin organization	BP	1	KDM3A	down_VSAP_EC
GO:0045581	0.746	0.622	1	13	negative regulation of T cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0032874	0.746	0.608	1	57	positive regulation of stress-activated MAPK	BP	1	LEP	up_AFEM_EC
GO:0019637	0.746	0.611	1	342	organophosphate metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0045620	0.746	0.619	1	15	negative regulation of lymphocyte	BP	1	HMGB1	up_VCAV_EC
GO:0019220	0.746	0.616	1	525	regulation of phosphate metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0051174	0.746	0.616	1	525	regulation of phosphorus metabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0010562	0.746	0.61	1	312	positive regulation of phosphorus metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0043604	0.746	0.611	1	288	amide biosynthetic process	BP	1	PRR16	up_VSAP_VSMC

GO:0045937	0.746	0.61	1	312	positive regulation of phosphate metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0048839	0.746978629	0.60688	1	50	inner ear development	BP	1	SOX9	up_ACOR_EC
GO:0009891	0.747	0.306	47	521	positive regulation of biosynthetic process	BP	1	TLR1,SMAD6,LBH,GATA5,GATA4,CDC7,PCGF5,HTR2B,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,FAM129A,EGLN1,CRLF3,NPNT,SMARCD3,CCDC3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,NGRN,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0055065	0.747	0.357	12	145	metal ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,FXN,SLC25A28,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:1902903	0.747	0.411	5	125	regulation of supramolecular fiber	BP	1	KIRREL1,CLIP3,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0045333	0.747	0.459	3	74	cellular respiration	BP	1	UQCR10,PARK7,MTFR1L	down_VCAV_EC
GO:0043122	0.747	0.46	3	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	NR1H4,MTDH,CTNNB1	down_VSAP_EC
GO:0043170	0.747	0.52	3	2980	macromolecule metabolic process	BP	1	HOXA9,WNT7A,ESR1	up_AORT_VSMC
GO:0031345	0.747	0.463	3	46	negative regulation of cell projection organization	BP	1	IFRD1,PPP3CA,RAPGEF2	up_VCAV_EC
GO:0045935	0.747	0.51	2	491	positive regulation of nucleobase-containing compound metabolic	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:2001021	0.747	0.511	2	30	negative regulation of response to DNA damage	BP	1	PARPBP,DDX39B	down_ACOR_VSMC
GO:0006464	0.747	0.524	2	1162	cellular protein modification process	BP	1	IVNS1ABP,USP33	down_AFEM_EC
GO:0036211	0.747	0.524	2	1162	protein modification process	BP	1	IVNS1ABP,USP33	down_AFEM_EC
GO:0019538	0.747	0.538	2	1713	protein metabolic process	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0006029	0.747	0.512	2	29	proteoglycan metabolic process	BP	1	BMP2,CHST7	up_VCAV_EC
GO:1901292	0.747	0.51	2	34	nucleoside phosphate catabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0019538	0.747	0.537	2	1713	protein metabolic process	BP	1	LIMK1,C6	up_VCAV_VSMC
GO:0055021	0.747	0.617	1	15	regulation of cardiac muscle tissue growth	BP	1	GLI1	down_ACOR_VSMC
GO:0007173	0.747	0.611	1	27	epidermal growth factor receptor signaling	BP	1	SHC1	down_VCAV_EC
GO:0007032	0.747	0.612	1	22	endosome organization	BP	1	HOOK3	down_VSAP_EC
GO:0006903	0.747	0.618	1	14	vesicle targeting	BP	1	PSEN1	up_ACOR_VSMC
GO:0001974	0.747	0.62	1	13	blood vessel remodeling	BP	1	CHD7	up_ACOR_VSMC
GO:0060964	0.747	0.62	1	13	regulation of gene silencing by miRNA	BP	1	BMP4	up_ACOR_VSMC
GO:0007179	0.747	0.606	1	57	transforming growth factor beta receptor	BP	1	ADAM17	up_AFEM_EC
GO:0032869	0.747	0.606	1	57	cellular response to insulin stimulus	BP	1	KANK1	up_AFEM_EC
GO:0048754	0.747	0.606	1	57	branching morphogenesis of an epithelial tube	BP	1	GREM1	up_AFEM_EC
GO:1901215	0.747	0.606	1	57	negative regulation of neuron death	BP	1	PPARGC1A	up_AFEM_EC
GO:0007049	0.747	0.615	1	560	cell cycle	BP	1	TAOK1	up_AORT_EC
GO:0010657	0.747	0.617	1	15	muscle cell apoptotic process	BP	1	RGL2	up_VCAV_EC
GO:0050885	0.747	0.619	1	14	neuromuscular process controlling balance	BP	1	ALDH1A3	up_VCAV_EC
GO:0019220	0.747	0.615	1	525	regulation of phosphate metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0051174	0.747	0.615	1	525	regulation of phosphorus metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:1902531	0.747	0.615	1	536	regulation of intracellular signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0006518	0.747	0.609	1	290	peptide metabolic process	BP	1	PRR16	up_VSAP_VSMC
GO:0033674	0.74776162	0.45703	3	144	positive regulation of kinase activity	BP	1	FZD5,PAK3,PRKCD	up_ACOR_EC
GO:0050767	0.748	0.341	16	184	regulation of neurogenesis	BP	1	ITM2C,BMP4,ZNF365,NRP1,ULK2,SMARCD3,FZD3,APP,PSEN1,CHD7,SIPA1L1,SSH3,ASAP1,B2M,DISC1,CRKL	up_ACOR_VSMC

GO:2000027	0.748	0.414	5	72	regulation of animal organ morphogenesis	BP	1	GREM1,HOXB7,B4GALT1,GLI1,SIX4	down_ACOR_VSMC
GO:1903362	0.748	0.43	4	100	regulation of cellular protein catabolic process	BP	1	LRP1,PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:0044843	0.748	0.432	4	62	cell cycle G1/S phase transition	BP	1	PLK2,PPP3CA,USP37,CUL4A	up_VCAV_EC
GO:0043547	0.748	0.46	3	61	positive regulation of GTPase activity	BP	1	ENSCAFG00000002015,GSK3B,TAX1BP3	down_VSAP_EC
GO:0007264	0.748	0.456	3	164	small GTPase mediated signal transduction	BP	1	RASGEF1B,CDC42EP5,KANK1	up_AFEM_EC
GO:1903506	0.748	0.468	3	977	regulation of nucleic acid-templated transcription	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0009156	0.748	0.461	3	50	ribonucleoside monophosphate	BP	1	ADSS,ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0002700	0.748	0.463	3	40	regulation of production of molecular mediator of immune response	BP	1	STAT6,F2RL1,STX4	up_VSAP_EC
GO:0036473	0.748	0.511	2	27	cell death in response to oxidative stress	BP	1	OXR1,PARK7	up_ACOR_VSMC
GO:0050796	0.748	0.509	2	33	regulation of insulin secretion	BP	1	MCU,HIF1A	up_VCAV_EC
GO:0007589	0.748	0.616	1	16	body fluid secretion	BP	1	CAV1	down_ACOR_VSMC
GO:0010324	0.748	0.616	1	16	membrane invagination	BP	1	AURKB	down_ACOR_VSMC
GO:0002548	0.748	0.614	1	17	monocyte chemotaxis	BP	1	HMGB1	down_ACOR_VSMC
GO:0036473	0.748	0.609	1	27	cell death in response to oxidative stress	BP	1	PARK7	down_VCAV_EC
GO:0045921	0.748	0.61	1	24	positive regulation of exocytosis	BP	1	SDC4	down_VSAP_EC
GO:0031440	0.748	0.619	1	13	regulation of mRNA 3'-end processing	BP	1	CCNT1	up_ACOR_VSMC
GO:0033628	0.748	0.617	1	14	regulation of cell adhesion mediated by integrin	BP	1	FERMT1	up_ACOR_VSMC
GO:0006898	0.748	0.605	1	57	receptor-mediated endocytosis	BP	1	GREM1	up_AFEM_EC
GO:0070374	0.748	0.606	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	CCL5	up_AFEM_EC
GO:0001941	0.748	0.618	1	14	postsynaptic membrane organization	BP	1	LRP4	up_VSAP_EC
GO:0090313	0.748	0.618	1	14	regulation of protein targeting to membrane	BP	1	KCNB1	up_VSAP_EC
GO:0001558	0.748240773	0.50294	2	101	regulation of cell growth	BP	1	ESM1,NRP1	up_ACOR_EC
GO:0002285	0.748740724	0.60448	1	50	lymphocyte activation involved in immune	BP	1	PTGER4	up_ACOR_EC
GO:0019538	0.749	0.286	131	1713	protein metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,ST8SIA6,KIT,PRCP,PPP2R5A,PRKCH,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,CTSC,PDE4D,IWS1,MEF2C,ATF3,KLKB1,TIPARP,RAPGEF1,WWP1,TLR4,QKI,TSPAN15,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,ZDHHC22,PSME4,NEDD9,PELI1,YES1,ENSCAFG00000010893,ODC1,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,ENSCAFG00000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,TLR3,MFNG,APOD,NCK1,ESCO1,DPH5,VHL,OTUD4,WSB1,PARP4,FES,NSD1,MRRF,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,HMGB1,NOS2,PMAIP1,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,HIF1A,KDM3A,LMTK2,ATRX,RBBP6,ZDHHC6,TNFAIP1,IVNS1ABP,JCAD,PSMB9,PSMD12,TET2,ARHGEF2,ITCH,CDON	up_VCAV_EC

GO:0051246	0.749	0.293	75	832	regulation of protein metabolic process	BP	1	FZD1,PRR16,CDON,NECAB3,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,CST3,CRADD,ABTB1,FGF7,ABL1,EMP2,MAP3K5,PDGFD,KLF15,C1QTNF2,CNPPD1,CCBE1,RECK,PLPP3,CAMKK2,TNKS1BP1,PYM1,F2RL1,DDR2,ZFP36L1,TRAF7,GAS1,MYC,EEF2,RTN4RL1,SASH1,FBXO4,LARP6,MYD88,LRP4,ANKHD1,AZIN2,PHF1,FBXO7,RNF166,RPUSD4,CDK9,FBLN1,OSBPL7,SAMD4B,ZFP36L2,RAF1,EIF3K,TIMP2,QARS,EIF3D,ACVRL1,UBQLN2,HTRA2,FLOT1,TNRC6C,NCK1,MAVS,ZER1,MAP2K2,TGFBR2,BAG4,SOAT1,LATS2	up_VSAP_EC
GO:0043543	0.749	0.429	4	84	protein acylation	BP	1	IWS1,NAA10,MORF4L2,CDYL	down_VSAP_EC
GO:0006753	0.749	0.428	4	211	nucleoside phosphate metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0009201	0.749	0.462	3	41	ribonucleoside triphosphate biosynthetic	BP	1	PPARGC1A,ALDOC,DDIT4	up_ACOR_VSMC
GO:2001141	0.749	0.466	3	979	regulation of RNA biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0046474	0.749	0.506	2	44	glycerophospholipid biosynthetic process	BP	1	NR1H4,SH3GLB1	down_VSAP_EC
GO:0051179	0.749	0.534	2	1747	localization	BP	1	TLR2,SLC16A12	up_AFEM_VSMC
GO:0006360	0.749	0.51	2	28	transcription by RNA polymerase I	BP	1	MTOR,SMARCA4	up_VCAV_EC
GO:0045892	0.749	0.503	2	328	negative regulation of transcription, DNA-	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0042221	0.749	0.517	2	1012	response to chemical	BP	1	FBP1,EMX2	up_VFEM_VSMC
GO:0002011	0.749	0.51	2	28	morphogenesis of an epithelial sheet	BP	1	ARHGAP12,ACVRL1	up_VSAP_EC
GO:0043330	0.749	0.614	1	16	response to exogenous dsRNA	BP	1	CAV1	down_ACOR_VSMC
GO:1900024	0.749	0.614	1	16	regulation of substrate adhesion-dependent cell	BP	1	RAC1	down_ACOR_VSMC
GO:0002690	0.749	0.608	1	26	positive regulation of leukocyte chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0000060	0.749	0.614	1	15	protein import into nucleus, translocation	BP	1	TMEM173	up_VCAV_EC
GO:0030837	0.749	0.617	1	14	negative regulation of actin filament	BP	1	SLIT2	up_VSAP_EC
GO:0060421	0.749	0.616	1	14	positive regulation of heart growth	BP	1	ACACB	up_VSAP_EC
GO:0048285	0.75	0.352	12	166	organelle fission	BP	1	MX2,PDGFB,EDN1,RAB11A,FIGNL1,MZT1,CENPC,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0046700	0.75	0.394	6	147	heterocycle catabolic process	BP	1	SAMD4B,ENTPD3,ZFP36L1,PYM1,FBH1,ACAT1	down_VCAV_EC
GO:0000910	0.75	0.431	4	52	cytokinesis	BP	1	PKP4,PRKCE,PIK3C3,MITD1	up_ACOR_VSMC
GO:0050896	0.75	0.461	4	2346	response to stimulus	BP	1	GATA5,IL22RA1,LRRN4,SLIT2	up_VPUL_VSMC
GO:1901699	0.75	0.455	3	164	cellular response to nitrogen compound	BP	1	CHRM2,CAMK2A,KANK1	up_AFEM_EC
GO:0016073	0.75	0.51	2	26	snRNA metabolic process	BP	1	INTS9,ELL2	up_ACOR_VSMC
GO:0021549	0.75	0.51	2	26	cerebellum development	BP	1	ZNF365,ATRN	up_ACOR_VSMC
GO:0021575	0.75	0.614	1	15	hindbrain morphogenesis	BP	1	GLI1	down_ACOR_VSMC
GO:0021587	0.75	0.614	1	15	cerebellum morphogenesis	BP	1	GLI1	down_ACOR_VSMC
GO:0046785	0.75	0.608	1	23	microtubule polymerization	BP	1	MZT1	down_VSAP_EC
GO:0035249	0.75	0.616	1	13	synaptic transmission, glutamatergic	BP	1	PSEN1	up_ACOR_VSMC
GO:0051489	0.75	0.614	1	14	regulation of filopodium assembly	BP	1	NRP1	up_ACOR_VSMC
GO:1904705	0.75	0.615	1	14	regulation of vascular smooth muscle cell	BP	1	CDKN1A	up_ACOR_VSMC
GO:1990874	0.75	0.615	1	14	vascular smooth muscle cell proliferation	BP	1	CDKN1A	up_ACOR_VSMC
GO:2000026	0.75	0.611	1	560	regulation of multicellular organismal development	BP	1	HOXA9	up_AORT_EC
GO:0000266	0.75	0.611	1	17	mitochondrial fission	BP	1	MX2	up_VCAV_EC
GO:0007094	0.75	0.613	1	16	mitotic spindle assembly checkpoint	BP	1	ZW10	up_VCAV_EC

GO:0071173	0.75	0.613	1	16	spindle assembly checkpoint	BP	1	ZW10	up_VCAV_EC
GO:0071174	0.75	0.613	1	16	mitotic spindle checkpoint	BP	1	ZW10	up_VCAV_EC
GO:0045604	0.75	0.611	1	17	regulation of epidermal cell differentiation	BP	1	PRKCH	up_VCAV_EC
GO:0046148	0.75	0.611	1	17	pigment biosynthetic process	BP	1	RAPGEF2	up_VCAV_EC
GO:0051705	0.75	0.612	1	16	multi-organism behavior	BP	1	PTCHD1	up_VCAV_EC
GO:2000113	0.75	0.608	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0003341	0.75	0.615	1	14	cilium movement	BP	1	KIF27	up_VSAP_EC
GO:0071398	0.75	0.615	1	14	cellular response to fatty acid	BP	1	PTGFR	up_VSAP_EC
GO:0072087	0.75	0.615	1	14	renal vesicle development	BP	1	OSR1	up_VSAP_EC
GO:0070647	0.75	0.605	1	311	protein modification by small protein conjugation	BP	1	CAV1	up_VSAP_VSMC
GO:0018393	0.750226659	0.60234	1	51	internal peptidyl-lysine acetylation	BP	1	PHF20	up_ACOR_EC
GO:0031056	0.750272983	0.60237	1	50	regulation of histone modification	BP	1	PYGO2	up_ACOR_EC
GO:2000112	0.751	0.286	103	1119	regulation of cellular macromolecule biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,NACC2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0031400	0.751	0.34	15	205	negative regulation of protein modification process	BP	1	USP4,HMGCR,U2AF2,PPP1R15B,CAV1,NF2,CDKN2C,GREM1,BRCA1,NOC2L,YWHAB,NUP62,CACTIN,EZR,TINF2	down_ACOR_VSMC
GO:0043207	0.751	0.355	11	216	response to external biotic stimulus	BP	1	NR1H4,SERPINE1,COTL1,MTDH,ADAM17,ACTA2,CNOT7,LYN,BNIP3,GBP5,DEFB124	down_VSAP_EC
GO:0051707	0.751	0.355	11	216	response to other organism	BP	1	NR1H4,SERPINE1,COTL1,MTDH,ADAM17,ACTA2,CNOT7,LYN,BNIP3,GBP5,DEFB124	down_VSAP_EC
GO:0044270	0.751	0.393	6	147	cellular nitrogen compound catabolic	BP	1	SAMD4B,ENTPD3,ZFP36L1,PYM1,FBH1,ACAT1	down_VCAV_EC
GO:0009056	0.751	0.411	5	755	catabolic process	BP	1	FBP1,MTDH,ABHD5,USP33,RNF6	up_VPOR_EC
GO:0008150	0.751	0.658	4	5646	biological_process	BP	1	HOXA3,TBX5,HOXA2,HOXB5	up_APUL_VSMC
GO:0022612	0.751	0.458	3	44	gland morphogenesis	BP	1	CAV1,B4GALT1,GLI1	down_ACOR_VSMC
GO:0031570	0.751	0.455	3	61	DNA integrity checkpoint	BP	1	PTPN11,DDX39B,CDKN1A	down_VSAP_EC
GO:1903827	0.751	0.452	3	164	regulation of cellular protein localization	BP	1	LEP,CYLD,LRRC15	up_AFEM_EC
GO:1905477	0.751	0.505	2	32	positive regulation of protein localization to	BP	1	ACSL3,EZR	down_ACOR_VSMC
GO:0045055	0.751	0.501	2	52	regulated exocytosis	BP	1	RAB31,RAC2	down_VCAV_EC
GO:0030510	0.751	0.508	2	27	regulation of BMP signaling pathway	BP	1	SMAD6,BMP4	up_ACOR_VSMC
GO:1902679	0.751	0.501	2	329	negative regulation of RNA biosynthetic process	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:1903507	0.751	0.501	2	329	negative regulation of nucleic acid-templated	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0046364	0.751	0.508	2	27	monosaccharide biosynthetic process	BP	1	PDK2,PC	up_VSAP_EC
GO:0046622	0.751	0.612	1	15	positive regulation of organ growth	BP	1	GLI1	down_ACOR_VSMC
GO:0044237	0.751	0.749	1	3491	cellular metabolic process	BP	1	CST3	down_AORT_EC

GO:0060415	0.751	0.605	1	27	muscle tissue morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0000380	0.751	0.607	1	22	alternative mRNA splicing, via spliceosome	BP	1	REST	down_VSAP_EC
GO:0033555	0.751	0.614	1	13	multicellular organismal response to stress	BP	1	FBXL20	up_ACOR_VSMC
GO:0035384	0.751	0.613	1	14	thioester biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0071616	0.751	0.613	1	14	acyl-CoA biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0060560	0.751	0.602	1	58	developmental growth involved in	BP	1	PLXNA4	up_AFEM_EC
GO:0042771	0.751	0.612	1	16	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	USP28	up_VCAV_EC
GO:0110111	0.751	0.61	1	17	negative regulation of animal organ	BP	1	GATA3	up_VCAV_EC
GO:1902883	0.751	0.611	1	16	negative regulation of response to oxidative	BP	1	HIF1A	up_VCAV_EC
GO:0044089	0.751	0.601	1	170	positive regulation of cellular component	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0006809	0.751	0.613	1	14	nitric oxide biosynthetic process	BP	1	ASS1	up_VSAP_EC
GO:0046209	0.751	0.613	1	14	nitric oxide metabolic process	BP	1	ASS1	up_VSAP_EC
GO:0032269	0.751	0.604	1	306	negative regulation of cellular protein metabolic	BP	1	CAV1	up_VSAP_VSMC
GO:0061351	0.751054465	0.6013	1	50	neural precursor cell proliferation	BP	1	DIXDC1	up_ACOR_EC
GO:0000910	0.751087708	0.60106	1	52	cytokinesis	BP	1	CHMP4B	up_ACOR_EC
GO:1903320	0.752	0.407	5	102	regulation of protein modification by small protein conjugation or	BP	1	PRICKLE1,HSPA5,TRIB3,NXN,SPOPL	down_VSAP_EC
GO:0050867	0.752	0.426	4	83	positive regulation of cell activation	BP	1	SOCS5,FAM49B,TFRC,CDKN1A	down_VSAP_EC
GO:0042326	0.752	0.451	3	163	negative regulation of phosphorylation	BP	1	GREM1,CYLD,LRRC15	up_AFEM_EC
GO:0051302	0.752	0.456	3	47	regulation of cell division	BP	1	PDGFB,RAB11A,BLM	up_VCAV_EC
GO:0046677	0.752	0.5	2	54	response to antibiotic	BP	1	ADCY6,PARK7	down_VCAV_EC
GO:0016064	0.752	0.507	2	26	immunoglobulin mediated immune	BP	1	TP53BP1,C1S	up_ACOR_VSMC
GO:0019724	0.752	0.507	2	26	B cell mediated immunity	BP	1	TP53BP1,C1S	up_ACOR_VSMC
GO:0055092	0.752	0.506	2	28	sterol homeostasis	BP	1	LCAT,ABCA1	up_ACOR_VSMC
GO:1901659	0.752	0.609	1	17	glycosyl compound biosynthetic process	BP	1	CTPS1	down_ACOR_VSMC
GO:0065007	0.752	0.748	1	3499	biological regulation	BP	1	CST3	down_AORT_EC
GO:0033138	0.752	0.603	1	28	positive regulation of peptidyl-serine	BP	1	PARK7	down_VCAV_EC
GO:0016358	0.752	0.6	1	58	dendrite development	BP	1	CAMK2A	up_AFEM_EC
GO:0021915	0.752	0.6	1	58	neural tube development	BP	1	LUZP1	up_AFEM_EC
GO:0070304	0.752	0.6	1	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	LEP	up_AFEM_EC
GO:0031399	0.752	0.609	1	559	regulation of protein modification process	BP	1	TAOK1	up_AORT_EC
GO:0030901	0.752	0.612	1	14	midbrain development	BP	1	KDM2B	up_VSAP_EC
GO:0045880	0.752	0.612	1	14	positive regulation of smoothened signaling	BP	1	SHOX2	up_VSAP_EC
GO:0050885	0.752	0.612	1	14	neuromuscular process controlling balance	BP	1	ABL1	up_VSAP_EC
GO:0000086	0.752571284	0.59901	1	52	G2/M transition of mitotic cell cycle	BP	1	BRSK1	up_ACOR_EC
GO:0019752	0.753	0.318	24	283	carboxylic acid metabolic process	BP	1	LEP,ENOSF1,PRDX4,ENSCAFG00000002977,TARSL2,PPARGC1A,NIT2,ACAD11,ERO1B,EGLN1,CYP2J2,P4HA1,PRKCE,SARDH,SGSM2,EDN1,ALDOC,HPGD,PCYOX1,DDIT4,AZIN2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0061061	0.753	0.344	13	179	muscle structure development	BP	1	FLNB,HINFP,SDC1,CAV1,MMP14,EZH2,GREM1,PPARD,RBM14,CTH,GLI1,MSC,SIX4	down_ACOR_VSMC
GO:0050900	0.753	0.392	6	89	leukocyte migration	BP	1	HMGB1,MMP14,HOXA7,B4GALT1,RAC1,CORO1A	down_ACOR_VSMC

GO:0048513	0.753	0.396	6	906	animal organ development	BP	1	BARX1,HOOK3,HOXA3,SEMA3A,ASPN,ACVR2A	up_VPOR_EC
GO:2000116	0.753	0.407	5	67	regulation of cysteine-type endopeptidase	BP	1	CST3,DAPK1,SH3RF1,PERP,PARK7	up_ACOR_VSMC
GO:0002366	0.753	0.407	5	65	leukocyte activation involved in immune	BP	1	ABL1,DLL1,STAT6,F2RL1,STX4	up_VSAP_EC
GO:0043254	0.753	0.45	3	164	regulation of protein complex assembly	BP	1	CRYAB,CDC42EP5,KANK1	up_AFEM_EC
GO:0044271	0.753	0.472	3	1501	cellular nitrogen compound biosynthetic	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0019362	0.753	0.502	2	35	pyridine nucleotide metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0046496	0.753	0.502	2	35	nicotinamide nucleotide metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0044257	0.753	0.498	2	327	cellular protein catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0034763	0.753	0.505	2	27	negative regulation of transmembrane transport	BP	1	KCNE3,OSR1	up_VSAP_EC
GO:0009066	0.753	0.608	1	16	aspartate family amino acid metabolic process	BP	1	CTH	down_ACOR_VSMC
GO:0061462	0.753	0.609	1	15	protein localization to lysosome	BP	1	NEDD4	down_ACOR_VSMC
GO:0061097	0.753	0.602	1	27	regulation of protein tyrosine kinase activity	BP	1	PRNP	down_VCAV_EC
GO:0035710	0.753	0.604	1	22	CD4-positive, alpha-beta T cell activation	BP	1	SOCS5	down_VSAP_EC
GO:0060325	0.753	0.613	1	13	face morphogenesis	BP	1	ARID5B	up_ACOR_VSMC
GO:0042446	0.753	0.61	1	14	hormone biosynthetic process	BP	1	HSD17B8	up_VSAP_EC
GO:0043954	0.753	0.611	1	14	cellular component maintenance	BP	1	F2RL1	up_VSAP_EC
GO:0043523	0.753811011	0.59729	1	52	regulation of neuron apoptotic process	BP	1	NRP1	up_ACOR_EC
GO:0016043	0.754	0.287	93	1973	cellular component organization	BP	1	ADAMTS2,SLC35F6,KIRREL1,SNX18,FBLN2,LRP1,DCN,NDN,PRNP,LUM,SDC4,ATP8B2,COA1,LOX,TLN2,NABP2,LMO4,RECK,IGFBP6,RPS10,TRPV2,COL6A1,CLIP3,NUMBL,NAGLU,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,AKT2,TTC8,LCAT,CHCHD10,SYDE1,HR,SCP2,CLSTN1,CACNB3,PRMT6,CABIN1,WIPF1,RASSF8,SEMA3C,POLDIP2,CRISPLD2,LRPAP1,EIF3K,THY1,WDR45,PEX5,ARHGAP10,TLX2,ATP6V0C,MYO1B,B4GALT1,GLI3,PARK7,ADAMTSL4,MAST2,SCARA5,CLEC16A,NCDN,RETREG1,CYBA,IFT57,MAVS,MRPS11,EMC6,CDH2,LOXL3,MPV17,RPS27,NCLN,ENSCAFG00000017708,MGARP,ACTR3B,UST,MTFR1L,RAB31,PRKCSH,DDR2,SHC1,PYM1,GREM1,PLEKHH2,EVI5L,LONP2,RAC2,SOAT1,PACSIN3,RGMA,ECM2,BRSK1	down_VCAV_EC
GO:0042592	0.754	0.298	46	522	homeostatic process	BP	1	NAPEPLD,HNF4A,C5AR2,LIPC,SLC8B1,PPARGC1B,ACACB,ABL1,GOT1,EBF2,DLL1,ANKRD54,CLDN1,PTGES2,STAT6,ENSCAFG00000000071,F2RL1,RAB11B,PDK2,MFN2,ZFP36L1,FXN,PIK3R1,SLC25A28,MYC,DLD,SCARA5,FBXO4,HOXC10,PASK,E2F4,PRKAB1,KCNB1,LCAT,TXNDC16,FTL,RAF1,CYBA,STX4,PPP3CB,HMOX1,CITED2,ENSCAFG00000006478,NCOA4,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0072521	0.754	0.347	12	185	purine-containing compound metabolic process	BP	1	NPR1,PANK3,PIPOX,ADSS,GUCY1A1,ACPP,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,NOS2,HIF1A	up_VCAV_EC
GO:0006468	0.754	0.352	11	544	protein phosphorylation	BP	1	LEP,HCK,GREM1,CAMK2A,CYLD,LRRC15,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17	up_AFEM_EC
GO:0048871	0.754	0.358	10	120	multicellular organismal homeostasis	BP	1	LEP,PLCL1,GJA1,PPARGC1A,PLAC8B,CLN8,NOD2,INPP5K,WFS1,IL18R1	up_ACOR_VSMC
GO:0051171	0.754	0.475	3	1697	regulation of nitrogen compound metabolic	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0018107	0.754	0.454	3	45	peptidyl-threonine phosphorylation	BP	1	MTOR,PRKD2,LMTK2	up_VCAV_EC
GO:0006937	0.754	0.455	3	40	regulation of muscle contraction	BP	1	KCNE3,CHRM1,TBXA2R	up_VSAP_EC
GO:0006400	0.754	0.501	2	33	tRNA modification	BP	1	THUMPD2,OSGEP	down_ACOR_VSMC
GO:1901654	0.754	0.502	2	31	response to ketone	BP	1	CAV1,CDK4	down_ACOR_VSMC
GO:1903363	0.754	0.502	2	32	negative regulation of cellular protein catabolic	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC

GO:0048645	0.754	0.501	2	33	animal organ formation	BP	1	MEF2C,HHEX	up_VCAV_EC
GO:1901566	0.754	0.502	2	598	organonitrogen compound biosynthetic	BP	1	ADCY3,CHST7	up_VFEM_EC
GO:2001244	0.754	0.503	2	27	positive regulation of intrinsic apoptotic	BP	1	PLEKHF1,NCK1	up_VSAP_EC
GO:0034763	0.754	0.601	1	27	negative regulation of transmembrane transport	BP	1	AKT2	down_VCAV_EC
GO:0043473	0.754	0.601	1	28	pigmentation	BP	1	GLI3	down_VCAV_EC
GO:0051607	0.754	0.597	1	58	defense response to virus	BP	1	GPAM	up_AFEM_EC
GO:0009948	0.754	0.607	1	16	anterior/posterior axis specification	BP	1	HHEX	up_VCAV_EC
GO:0010558	0.754	0.601	1	392	negative regulation of macromolecule biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0006884	0.754	0.61	1	14	cell volume homeostasis	BP	1	E2F4	up_VSAP_EC
GO:0060612	0.754	0.609	1	14	adipose tissue development	BP	1	EBF2	up_VSAP_EC
GO:0065007	0.755	0.273	287	3499	biological regulation	BP	1	ELK3,ACSL3,FSCN1,HMGB1,RNPS1,LSS,SREBF1,USP1,IRAK1,MCM7,RPA1,ANLN,ILF3,DDX39A,STXBP6,CBX5,PPRC1,USP4,FMNL3,RACGAP1,ATAD2,HMGA1,EIF4A3,HMGCR,EDC3,TFPI,HNRNPD,SREBF2,SMC1A,TFPI2,HINFP,RALY,UBE2S,NEDD4,SRSF2,WDR76,MED17,U2AF2,ZW10,INTS7,QSOX2,MNDA,CAPG,PSMD3,SLC29A1,MTDH,HEY1,HOXA3,PPM1G,RRBP1,TRIP13,COLGALT1,SLC25A5,PPP1R15B,SF1,PARPBP,SRRT,SDC1,ARFGAP1,CTDNEP1,RANGAP1,FBXO5,HSPA9,NAB2,SLC35C2,RAN,CFAP298,PRELID1,CDCA7L,FUS,RFC2,BIRC5,MYBBP1A,INSIG1,PRMT1,ENSCAFG00000030005,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,TIMELESS,THRAP3,LIMA1,TRUB2,FAM129B,TCEA1,ENSCAFG00000008236,NF2,EDC4,AURKB,PSD4,NONO,MMP14,HNRNPL,CDKN2C,TOPBP1,ABHD5,EZH2,STMN1,DEPDC1,SLC30A1,PPP2R5D,GREM1,MAP3K20,RFC4,NEK2,ADIPOR2,CLIC1,FEN1,CDK4,TRIM35,SMARCC1,RNASEH2B,PLK3,HMGB3,RCC1,PCNA,DHX33,HOXA7,SMG9,BID,ARG2,ANXA5,SF3B4,UHRF1,CKS2,PDCD2,HOXC10,RNF152,NKAIN1,HOXB7,TKT,GMNN,DHCR24,POC1A,TRPV4,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,E2F8,B4GALT1,NAV2,PRCP,PREB,TFRC,NRAS,PPARD,CDC6,NDC80,IT	down_ACOR_VSMC
GO:0051252	0.755	0.283	95	1051	regulation of RNA metabolic process	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,TENT5C,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,F2RL1,RBL2,GLIS2,DDR2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,NUP98,TRERF1,E2F4,NPAS2,LIMD1,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:1901135	0.755	0.323	20	390	carbohydrate derivative metabolic process	BP	1	SULF1,ENPP1,PGK1,TPI1,ENSCAFG00000032470,PGAM1,UGCG,CEMIP2,CHSY1,HIF1A,GALNT1,ENTPD4,ALDOC,CTNNB1,PAPSS1,PLOD3,STT3A,AK5,EXT1,RPN1	down_VSAP_EC
GO:1901564	0.755	0.347	15	2053	organonitrogen compound metabolic process	BP	1	OSTC,OGA,ARHGEF2,AK5,ASPN,ACVR2A,FBP1,RSL24D1,RPL10L,KLHL28,PUM3,EIF5,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0009059	0.755	0.417	5	1563	macromolecule biosynthetic process	BP	1	NR1H4,GALNT17,ZDHHC16,NPNT,HOXA1	up_APUL_EC
GO:0034332	0.755	0.501	2	32	adherens junction organization	BP	1	GREM1,RAC1	down_ACOR_VSMC
GO:0006623	0.755	0.606	1	16	protein targeting to vacuole	BP	1	NEDD4	down_ACOR_VSMC
GO:1901998	0.755	0.606	1	16	toxin transport	BP	1	CCT4	down_ACOR_VSMC
GO:1901976	0.755	0.603	1	21	regulation of cell cycle checkpoint	BP	1	DDX39B	down_VSAP_EC

GO:0036465	0.755	0.609	1	13	synaptic vesicle recycling	BP	1	DNAJC6	up_ACOR_VSMC
GO:2001239	0.755	0.607	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	UNC5B	up_ACOR_VSMC
GO:0006915	0.755	0.605	1	550	apoptotic process	BP	1	TAOK1	up_AORT_EC
GO:0048546	0.755	0.605	1	16	digestive tract morphogenesis	BP	1	HIF1A	up_VCAV_EC
GO:0014070	0.755	0.595	1	172	response to organic cyclic compound	BP	1	RNF6	up_VPOR_EC
GO:0051172	0.755	0.608	1	663	negative regulation of nitrogen compound	BP	1	SLIT2	up_VPUL_VSMC
GO:0010955	0.755	0.608	1	14	negative regulation of protein processing	BP	1	GAS1	up_VSAP_EC
GO:1903318	0.755	0.608	1	14	negative regulation of protein maturation	BP	1	GAS1	up_VSAP_EC
GO:0044238	0.755058925	0.29443	85	3383	primary metabolic process	BP	1	C7,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,CCDC3,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,PLCE1,ZMYND8,NIT2,PTGDS,PAK3,CFI,GUCY1B1,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,CHPT1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,RBM38,CLU,SFMBT2,ALDOC,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,PRKCD,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0003008	0.756	0.309	29	336	system process	BP	1	THRB,FAM107A,WASF3,CBR3,RNPEP,TPCN2,IRX5,SLIT2,ABL1,EMP2,KCNE3,CHRM1,DLL1,KLF15,CCBE1,F2RL1,PDE6D,FXN,CTNS,TBXA2R,SULF2,AGTR1,HOXC10,E2F4,DOP1B,NR2F6,ZFAND5,ACVRL1,JCHAIN	up_VSAP_EC
GO:0018130	0.756	0.314	27	1261	heterocycle biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,ACACB,PPARGC1A	up_AFEM_EC
GO:0009628	0.756	0.313	26	302	response to abiotic stimulus	BP	1	VEGFD,HTR2B,MFAP4,GJA1,HRH1,TLR3,LRRN4,TP53INP1,USP53,ITPR1,PLAC8B,ANKRD1,RBM4B,BNIP3,EGLN1,CDKN1A,PRKCE,APP,JUP,RAB11B,EDN1,XRRA1,DMC1,DDIT4,GNAQ,SLC8A1	up_ACOR_VSMC
GO:0009891	0.756	0.316	23	521	positive regulation of biosynthetic process	BP	1	DCN,LUM,LARP6,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,AKT2,TFE3,TEAD1,GLI3,PARK7,EEF2,MYDGF,CYBA,MAVS,MAPRE3,SHC1,PYM1,GREM1,SOAT1,THRB,ZBTB16	down_VCAV_EC
GO:0042493	0.756	0.341	13	178	response to drug	BP	1	PPP1R15B,RAD54L,TENT4A,CAV1,RAD51,TIMELESS,EZH2,CDK4,TFRC,PDXP,HMGB2,SIGMAR1,ARHGEF2	down_ACOR_VSMC
GO:0061564	0.756	0.362	9	119	axon development	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,STMN1,APOD,CREB1,SPTBN4	up_VCAV_EC
GO:0007517	0.756	0.369	8	100	muscle organ development	BP	1	FZD1,CDON,DLL1,SAV1,GTF3C5,SHOX2,FLOT1,CITED2	up_VSAP_EC
GO:0009267	0.756	0.422	4	60	cellular response to starvation	BP	1	SREBF1,SREBF2,RNF152,MIOS	down_ACOR_VSMC
GO:1905475	0.756	0.424	4	52	regulation of protein localization to membrane	BP	1	TCAF1,AR,DAG1,INPP5K	up_ACOR_VSMC
GO:0002040	0.756	0.452	3	46	sprouting angiogenesis	BP	1	GREM1,E2F8,JMJD6	down_ACOR_VSMC
GO:0031668	0.756	0.447	3	79	cellular response to extracellular stimulus	BP	1	KANK2,GABARAP,CLEC16A	down_VCAV_EC
GO:0001818	0.756	0.449	3	65	negative regulation of cytokine production	BP	1	NR1H4,SOCS5,BTK	down_VSAP_EC
GO:0030324	0.756	0.449	3	64	lung development	BP	1	ERRFI1,CTNNB1,PLOD3	down_VSAP_EC
GO:0042981	0.756	0.45	3	471	regulation of apoptotic process	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0016070	0.756	0.468	3	1479	RNA metabolic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0007272	0.756	0.499	2	31	ensheathment of neurons	BP	1	NAB2,PPARD	down_ACOR_VSMC
GO:0008366	0.756	0.499	2	31	axon ensheathment	BP	1	NAB2,PPARD	down_ACOR_VSMC
GO:0009062	0.756	0.499	2	31	fatty acid catabolic process	BP	1	PPARD,ACADL	down_ACOR_VSMC

GO:0007041	0.756	0.496	2	41	lysosomal transport	BP	1	HOOK3,TRAK1	down_VSAP_EC
GO:1902116	0.756	0.604	1	16	negative regulation of organelle assembly	BP	1	RBM14	down_ACOR_VSMC
GO:2001057	0.756	0.605	1	16	reactive nitrogen species metabolic process	BP	1	CAV1	down_ACOR_VSMC
GO:0007601	0.756	0.6	1	22	visual perception	BP	1	RPGR	down_VSAP_EC
GO:0048144	0.756	0.599	1	23	fibroblast proliferation	BP	1	CDKN1A	down_VSAP_EC
GO:0048145	0.756	0.599	1	23	regulation of fibroblast proliferation	BP	1	CDKN1A	down_VSAP_EC
GO:0050953	0.756	0.6	1	22	sensory perception of light stimulus	BP	1	RPGR	down_VSAP_EC
GO:0051642	0.756	0.608	1	13	centrosome localization	BP	1	SUN1	up_ACOR_VSMC
GO:0061842	0.756	0.608	1	13	microtubule organizing center localization	BP	1	SUN1	up_ACOR_VSMC
GO:0030858	0.756	0.603	1	17	positive regulation of epithelial cell	BP	1	PRKCH	up_VCAV_EC
GO:0060393	0.756	0.601	1	19	regulation of pathway-restricted SMAD protein	BP	1	BMP2	up_VCAV_EC
GO:0120163	0.756	0.604	1	17	negative regulation of cold-induced	BP	1	TLR4	up_VCAV_EC
GO:1903313	0.756	0.604	1	16	positive regulation of mRNA metabolic process	BP	1	CNOT7	up_VCAV_EC
GO:0006952	0.756	0.598	1	319	defense response	BP	1	CYP26B1	up_VFEM_EC
GO:0006974	0.756	0.597	1	333	cellular response to DNA damage stimulus	BP	1	EYA1	up_VFEM_EC
GO:0010941	0.756	0.602	1	524	regulation of cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0010660	0.756	0.607	1	14	regulation of muscle cell apoptotic process	BP	1	MFN2	up_VSAP_EC
GO:0010799	0.756	0.607	1	14	regulation of peptidyl-threonine	BP	1	TNKS1BP1	up_VSAP_EC
GO:0060512	0.756	0.607	1	14	prostate gland morphogenesis	BP	1	RARG	up_VSAP_EC
GO:0098661	0.756	0.606	1	14	inorganic anion transmembrane transport	BP	1	CLCN2	up_VSAP_EC
GO:0017144	0.757	0.331	16	199	drug metabolic process	BP	1	LIPT2,MAT2B,PCBD1,PPARGC1A,MAOA,FMO4,PTGDR,MOXD1,ENSCAFG00000018611,ALDOC,DDIT4,PTS,CAT,NT5C2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0006091	0.757	0.349	11	139	generation of precursor metabolites and energy	BP	1	LEP,PPARGC1A,BNIP3,PYGM,ALDOC,DDIT4,GAA,INPP5K,SLC25A12,NDUFA4L2,PARK7	up_ACOR_VSMC
GO:0010562	0.757	0.385	6	312	positive regulation of phosphorus metabolic	BP	1	LEP,GREM1,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0045937	0.757	0.385	6	312	positive regulation of phosphate metabolic	BP	1	LEP,GREM1,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0072006	0.757	0.421	4	59	nephron development	BP	1	GREM1,HOXB7,IQGAP1,SIX4	down_ACOR_VSMC
GO:0051234	0.757	0.513	2	1283	establishment of localization	BP	1	RAB11B,ERGIC1	down_VPOR_EC
GO:0140056	0.757	0.499	2	28	organelle localization by membrane tethering	BP	1	STX11,BVES	up_ACOR_VSMC
GO:0071840	0.757	0.535	2	2059	cellular component organization or biogenesis	BP	1	WNT7A,ESR1	up_AORT_VSMC
GO:0007166	0.757	0.499	2	686	cell surface receptor signaling pathway	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0009116	0.757	0.495	2	39	nucleoside metabolic process	BP	1	CDA,ACPP	up_VCAV_EC
GO:0016925	0.757	0.603	1	16	protein sumoylation	BP	1	UBA2	down_ACOR_VSMC
GO:0035136	0.757	0.603	1	16	forelimb morphogenesis	BP	1	HOXA9	down_ACOR_VSMC
GO:0071704	0.757	0.743	1	3535	organic substance metabolic process	BP	1	CST3	down_AORT_EC
GO:0021675	0.757	0.596	1	29	nerve development	BP	1	GLI3	down_VCAV_EC
GO:0000726	0.757	0.599	1	21	non-recombinational repair	BP	1	RBBP8	down_VSAP_EC
GO:0035272	0.757	0.599	1	21	exocrine system development	BP	1	NRP1	down_VSAP_EC
GO:0007131	0.757	0.605	1	14	reciprocal meiotic recombination	BP	1	DMC1	up_ACOR_VSMC
GO:0035825	0.757	0.605	1	14	homologous recombination	BP	1	DMC1	up_ACOR_VSMC
GO:0045913	0.757	0.604	1	15	positive regulation of carbohydrate metabolic	BP	1	PRKCE	up_ACOR_VSMC

GO:0043086	0.757	0.592	1	170	negative regulation of catalytic activity	BP	1	ASPN	up_VPOR_EC
GO:0003209	0.757	0.605	1	14	cardiac atrium morphogenesis	BP	1	SHOX2	up_VSAP_EC
GO:0003230	0.757	0.605	1	14	cardiac atrium development	BP	1	SHOX2	up_VSAP_EC
GO:1902751	0.757	0.606	1	14	positive regulation of cell cycle G2/M phase	BP	1	CDC25B	up_VSAP_EC
GO:0046888	0.757	0.606	1	14	negative regulation of hormone secretion	BP	1	KCNB1	up_VSAP_EC
GO:0045321	0.757525049	0.41663	4	191	leukocyte activation	BP	1	FZD5,NOD2,PTGER4,PRKCD	up_ACOR_EC
GO:0006357	0.758	0.293	48	547	regulation of transcription by RNA polymerase II	BP	1	FZD1,THRB,HOXA7,HOXA9,CDON,INSIG2,ZNF367,PPARGC1B,ZHX3,HOXD3,ABL1,PEX2,HDAC7,DLL1,OSR1,KLF15,ANXA4,RARG,CBX7,STAT6,F2RL1,RBL2,GLIS2,PIK3R1,BATF2,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,LRP4,TRERF1,NPAS2,CDK9,KDM2B,RAF1,NFIB,ABHD14B,ZNF205,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,HMOX1,CITED2	up_VSAP_EC
GO:0031328	0.758	0.294	46	512	positive regulation of cellular biosynthetic process	BP	1	TLR1,SMAD6,LBH,GATA5,GATA4,CDC7,PCGF5,HTR2B,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,FAM129A,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,NGRN,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0012501	0.758	0.296	43	561	programmed cell death	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,RNF152,DHCR24,NOC2L,EIF5A,B4GALT1,PPARD,CYCS,NUP62,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SGPL1,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0010941	0.758	0.297	40	524	regulation of cell death	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,DHCR24,NOC2L,EIF5A,B4GALT1,CYCS,NUP62,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0080135	0.758	0.324	18	240	regulation of cellular response to stress	BP	1	HMGB1,USP1,HMGA1,WDR76,PPP1R15B,PARPBP,INSIG1,RAD51,TIMELESS,MAP3K20,RNASEH2B,PCNA,ARG2,RSL1D1,DDX39B,EZR,TXNDC12,ARHGEF2	down_ACOR_VSMC
GO:0044770	0.758	0.365	8	161	cell cycle phase transition	BP	1	PLK3,ZPR1,EIF4EBP1,BACH1,RBBP8,CALM1,INHBA,CDKN1A	down_VSAP_EC
GO:0060271	0.758	0.376	7	89	cilium assembly	BP	1	FUZ,RILPL2,E2F4,KIF27,TMEM17,TTC8,CEP19	up_VSAP_EC
GO:0031647	0.758	0.417	4	87	regulation of protein stability	BP	1	CRYAB,CDC37,HTT,RAD23A	down_VSAP_EC
GO:0048469	0.758	0.496	2	31	cell maturation	BP	1	TRIP13,FBXO5	down_ACOR_VSMC
GO:0009101	0.758	0.49	2	113	glycoprotein biosynthetic process	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC
GO:0065003	0.758	0.497	2	616	protein-containing complex assembly	BP	1	TRIM9,CDC42EP5	up_VFEM_EC
GO:0060395	0.758	0.498	2	27	SMAD protein signal transduction	BP	1	HNF4A,NCEH1	up_VSAP_EC
GO:0043392	0.758	0.602	1	16	negative regulation of DNA binding	BP	1	NEK2	down_ACOR_VSMC
GO:0002376	0.758	0.603	1	622	immune system process	BP	1	GABPA	down_AFEM_EC
GO:0044773	0.758	0.595	1	28	mitotic DNA damage checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:0051492	0.758	0.595	1	28	regulation of stress fiber assembly	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0046928	0.758	0.597	1	23	regulation of neurotransmitter	BP	1	GSK3B	down_VSAP_EC
GO:0043583	0.758	0.591	1	59	ear development	BP	1	DLL1	up_AFEM_EC
GO:0045191	0.758	0.603	1	14	regulation of isotype switching	BP	1	THOC1	up_VCAV_EC
GO:0042698	0.758	0.603	1	14	ovulation cycle	BP	1	SLIT2	up_VSAP_EC
GO:0060043	0.758	0.603	1	14	regulation of cardiac muscle cell proliferation	BP	1	SAV1	up_VSAP_EC

GO:0007049	0.759	0.304	31	560	cell cycle	BP	1	ARHGEF2,ASNS,MYH9,PLK3,PTPN11,MZT1,PPP1R12A,TUBB,TNIK,NAA10,ZPR1,DDX39B,EIF4EBP1,CTNNB1,KPNB1,ANLN,SND1,CDK8,DDIT3,PDS5B,BACH1,CCNYL1,HTT,RBBP8,CALM1,RAD23A,PAK2,INHBA,NR4A1,CDKN1A,MADD	down_VSAP_EC
GO:0008150	0.759	0.395	24	5646	biological_process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,NETO1,GATM,SALL1,GALNT17,HOXC10,SLC16A12,IRX5,MAB21L1,PRR16,STIM1,TLR2,EMP1,CAV1,SHOX2,F5,HAPLN1,FGF5,GJB5	up_VSAP_VSMC
GO:0060548	0.759	0.315	22	294	negative regulation of cell death	BP	1	SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,FAM129B,AURKB,GREM1,PLK3,ARG2,DHCR24,NOC2L,NUP62,HMGB2,ENSCAFG00000000005299,CORO1A,TXNDC12,CTH,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0018107	0.759	0.447	3	45	peptidyl-threonine phosphorylation	BP	1	CDK1,HASPIN,TTK	down_ACOR_VSMC
GO:0001841	0.759	0.448	3	44	neural tube formation	BP	1	BCL10,HIF1A,LUZP1	up_VCAV_EC
GO:0009124	0.759	0.446	3	51	nucleoside monophosphate	BP	1	ADSS,ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0032270	0.759	0.445	3	479	positive regulation of cellular protein metabolic	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0045935	0.759	0.445	3	491	positive regulation of nucleobase-containing compound metabolic	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0031058	0.759	0.496	2	28	positive regulation of histone modification	BP	1	PHF1,CDK9	up_VSAP_EC
GO:0015909	0.759	0.6	1	16	long-chain fatty acid transport	BP	1	ACSL3	down_ACOR_VSMC
GO:0007166	0.759	0.603	1	686	cell surface receptor signaling pathway	BP	1	CITED2	down_VPOR_EC
GO:0045582	0.759	0.595	1	22	positive regulation of T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0010922	0.759	0.602	1	14	positive regulation of phosphatase activity	BP	1	NPNT	up_ACOR_VSMC
GO:2001236	0.759	0.59	1	59	regulation of extrinsic apoptotic signaling	BP	1	CYLD	up_AFEM_EC
GO:1903902	0.759	0.598	1	18	positive regulation of viral life cycle	BP	1	CNOT7	up_VCAV_EC
GO:0010922	0.759	0.602	1	14	positive regulation of phosphatase activity	BP	1	PPARGC1B	up_VSAP_EC
GO:0006903	0.759	0.603	1	14	vesicle targeting	BP	1	CEP19	up_VSAP_EC
GO:1903320	0.759666036	0.48744	2	102	regulation of protein modification by small protein conjugation or	BP	1	NOD2,PIAS1	up_ACOR_EC
GO:0051049	0.76	0.294	42	479	regulation of transport	BP	1	HNF4A,CD274,ARHGEF5,C5AR2,AMIGO1,SLC8B1,TBC1D10C,GABRE,TBC1D2B,CDH1,ABL1,KCNE3,CHRM1,DLL1,OSR1,IL17RC,CLIC5,KLF15,C1QTNF2,ANXA4,KLHL24,F2RL1,RAB11B,ICE1,PIK3R1,CRACR2B,GAS1,PASK,AZIN2,KCNB1,MAPKBP1,CYBA,ZNF205,FXYD1,STX4,VPS11,KCNC4,UBQLN2,FLOT1,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:0080134	0.76	0.3	34	386	regulation of response to stress	BP	1	TLR1,LEP,MID1,RASSF2,NACC2,COCH,TP53BP1,TLR3,SH3RF2,ZNF365,SASH1,ANKRD1,F2RL1,ENPP4,PTPN22,OS9,SESN3,SH3RF1,PRKCE,FUT8,PARP9,APP,DUSP22,EDN1,SESN1,OXR1,NOD2,SH3RF3,SERINC3,HERPUD1,MAP3K7,WFS1,PARK7,RREB1	up_ACOR_VSMC
GO:0048762	0.76	0.385	6	77	mesenchymal cell differentiation	BP	1	WNT11,AXIN2,OSR1,TIAM1,TGFBR2,CITED2	up_VSAP_EC
GO:0051234	0.76	0.427	4	1283	establishment of localization	BP	1	NR1H4,HOXA3,NPNT,NTRK2	up_APUL_EC
GO:0002449	0.76	0.419	4	53	lymphocyte mediated immunity	BP	1	EMP2,STAT6,MYD88,PPP3CB	up_VSAP_EC
GO:0002252	0.76	0.441	3	166	immune effector process	BP	1	LEP,DLL1,GPAM	up_AFEM_EC
GO:0031124	0.76	0.495	2	27	mRNA 3'-end processing	BP	1	CCNT1,APP	up_ACOR_VSMC
GO:0000187	0.76	0.495	2	28	activation of MAPK activity	BP	1	MAP3K5,C1QTNF2	up_VSAP_EC
GO:0009894	0.76	0.591	1	277	regulation of catabolic process	BP	1	NEDD4	down_ACOR_EC
GO:1903322	0.76	0.587	1	59	positive regulation of protein modification by small protein conjugation	BP	1	DCUN1D3	up_AFEM_EC
GO:0051253	0.76	0.592	1	359	negative regulation of RNA metabolic process	BP	1	NR1H4	up_APUL_EC

GO:0031663	0.76	0.598	1	17	lipopolysaccharide-mediated signaling	BP	1	TNFAIP3	up_VCAV_EC
GO:0034605	0.76	0.597	1	18	cellular response to heat	BP	1	CD34	up_VCAV_EC
GO:1902531	0.76	0.598	1	536	regulation of intracellular signal transduction	BP	1	ANKRD6	up_VPOR_VSMC
GO:0006928	0.76	0.597	1	557	movement of cell or subcellular component	BP	1	EMX2	up_VFEM_VSMC
GO:0042108	0.76	0.601	1	14	positive regulation of cytokine biosynthetic	BP	1	MYD88	up_VSAP_EC
GO:0030204	0.76	0.601	1	14	chondroitin sulfate metabolic process	BP	1	CHST7	up_VSAP_EC
GO:1902850	0.760528302	0.58785	1	52	microtubule cytoskeleton organization involved in	BP	1	CHMP4B	up_ACOR_EC
GO:0010629	0.761	0.312	22	502	negative regulation of gene expression	BP	1	NOTCH2,NAB2,KANK2,SAMD4B,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,PARK7,ZFP36L1,LOXL3,A2M,TSC22D3,GLIS2,SHC1,PYM1,GREM1,THRB,EIF4EBP1	down_VCAV_EC
GO:0044260	0.761	0.334	19	2593	cellular macromolecule metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,RSL24D1,RPL10L,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0009636	0.761	0.442	3	66	response to toxic substance	BP	1	CRYAB,KPNA4,SLC7A11	down_VSAP_EC
GO:0009145	0.761	0.446	3	40	purine nucleoside triphosphate biosynthetic	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0030705	0.761	0.487	2	56	cytoskeleton-dependent intracellular transport	BP	1	IFT57,MGARP	down_VCAV_EC
GO:0050803	0.761	0.487	2	55	regulation of synapse structure or activity	BP	1	PRNP,CDH2	down_VCAV_EC
GO:0050807	0.761	0.487	2	55	regulation of synapse organization	BP	1	PRNP,CDH2	down_VCAV_EC
GO:0048583	0.761	0.502	2	1095	regulation of response to stimulus	BP	1	DKK2,TAOK1	up_AORT_EC
GO:0071702	0.761	0.494	2	687	organic substance transport	BP	1	NR1H4,NTRK2	up_APUL_EC
GO:0010717	0.761	0.492	2	32	regulation of epithelial to mesenchymal transition	BP	1	MTOR,BMP2	up_VCAV_EC
GO:0010830	0.761	0.597	1	16	regulation of myotube differentiation	BP	1	MMP14	down_ACOR_VSMC
GO:0032434	0.761	0.587	1	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0012501	0.761	0.596	1	561	programmed cell death	BP	1	TAOK1	up_AORT_EC
GO:0051640	0.761	0.587	1	174	organelle localization	BP	1	HOOK3	up_VPOR_EC
GO:0000278	0.761	0.59	1	331	mitotic cell cycle	BP	1	MAP2K6	up_VFEM_EC
GO:0070098	0.761	0.6	1	14	chemokine-mediated signaling pathway	BP	1	SLIT2	up_VSAP_EC
GO:1904705	0.761	0.599	1	14	regulation of vascular smooth muscle cell	BP	1	MFN2	up_VSAP_EC
GO:1990874	0.761	0.599	1	14	vascular smooth muscle cell proliferation	BP	1	MFN2	up_VSAP_EC
GO:2001023	0.761	0.6	1	14	regulation of response to drug	BP	1	OSR1	up_VSAP_EC
GO:0006636	0.761	0.6	1	14	unsaturated fatty acid biosynthetic process	BP	1	PTGES	up_VSAP_EC
GO:2001239	0.761	0.6	1	14	regulation of extrinsic apoptotic signaling pathway in absence of	BP	1	HTRA2	up_VSAP_EC
GO:0051052	0.761333895	0.43914	3	145	regulation of DNA metabolic process	BP	1	PKIB,FIGNL1,PRKCD	up_ACOR_EC

GO:0008152	0.762	0.264	349	3714	metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,NAPEPLD,HOXA9,CDON,NECAB3,WNT11,HNF4A,ACSM3,DHDH,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,OSR2,INSIG2,ENPP2,PTGFR,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,RNPEP,TBC1D10C,PLBD1,ACAA1,MRPL37,CEP85,FOXRED2,ALDH3B1,ACACB,TPCN2,EEF2K,IL6R,IRX5,RETREG1,SLIT2,GDA,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,SLC6A4,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,EBF2,HDAC7,KLKB1,EMP2,DLL1,DLST,SESN1,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,GLUL,CTSS,GALNT15,DTX2,TENT5C,PGM2L1,ADHFE1,ENSCAFG00000013986,PDGFD,CERS4,HSD17B14,WARS2,VDR,DHRS4,NAA60,SAV1,ENSCAFG00000003792,KDELC2,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,ENSCAFG00000025332,PAFAH2,ABHD15,HSD3B7,ZNF688,ZBTB16,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,TRMT2A,VPS36,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,RECK,GATAD1,CISH,KLHL24,HSD17B8,PLPP3,ENSCAFG00000000071,SLC25A12,EXOSC7,CAMKK2,FAAH,APOL5,TNKS1BP1,KLHDC8B,PYM1,AMBRA1,F2RL1,RBL2,LMF1,PHKA2,RAB11B,NFE2L2,GLIS2,LPL,DFFB,PPIP5K1,MORC3,	up_VSAP_EC
GO:0048519	0.762	0.27	142	1554	negative regulation of biological process	BP	1	FZD1,THRB,HOXA7,TWIST2,HOXA9,ENSCAFG00000009113,WNT11,HNF4A,FAM107A,CD274,ACKR3,AXIN2,C5AR2,INSIG2,PTGFR,SLC8B1,PPARGC1B,SH2D4A,TBC1D10C,CEP85,LIMS2,GABRE,ACACB,SLIT2,CST3,CRADD,ZHX3,CDH1,SLC6A4,ABL1,PEX2,BTG1,HDAC7,KLKB1,KCNE3,DLL1,EPN2,SESN1,OSR1,TENT5C,FUZ,TRAFD1,SAV1,KLF15,ANXA4,ZBTB16,RARG,CBX7,STAT6,RECK,PLPP3,ENSCAFG00000000071,EXOSC7,PYM1,AMBRA1,F2RL1,RBL2,GLIS2,MORC3,MFN2,ZFP36L1,MT2A,FXN,PIK3R1,RBCK1,GAS1,MYC,PIK3IP1,PTGES,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,TMEM225B,H2AFJ,ZC3H10,HIC1,RTN4RL1,FBXO4,HOXC10,CREBRF,POLDIP2,MYD88,IKZF2,ATRIP,LRP4,PASK,ANKHD1,GDPD5,ZADH2,AZIN2,CASTOR1,PHF1,NPAS2,SMG9,FBXO7,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,PC,CDK9,CD83,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,HPGD,RAF1,MAPKBP1,NFIB,CYBA,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ARHGAP12,ACVRL1,TPRA1,UBQLN2,ARHGAP10,HTRA2,ASS1,TNRC6C,PPP3CB,NCK1,MAVS,ULK1,HMOX1,NPRL3,CITED2,BAG4,LBH,KEAP1,DPT,DDIT4,LATS2	up_VSAP_EC
GO:0044237	0.762	0.362	14	3491	cellular metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0000902	0.762	0.341	11	266	cell morphogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,THY1,TLX2,GLI3,ENSCAFG00000017708,UST,GREM1,BRSK1	down_VCAV_EC
GO:1902903	0.762	0.349	10	125	regulation of supramolecular fiber	BP	1	WNT11,ARHGEF5,SLIT2,ABL1,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,NCK1,BAG4	up_VSAP_EC
GO:0051098	0.762	0.354	9	129	regulation of binding	BP	1	HMGB1,HOXA3,CAV1,FAM129B,AURKB,STMN1,NEK2,GMNN,HMGB2	down_ACOR_VSMC
GO:0071840	0.762	0.401	6	2059	cellular component organization or biogenesis	BP	1	NR1H4,MYBPC2,CCL24,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0070646	0.762	0.397	5	63	protein modification by small protein removal	BP	1	ZRANB1,USP53,USP20,WDR48,PARK7	up_ACOR_VSMC
GO:0001764	0.762	0.444	3	45	neuron migration	BP	1	RAC1,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0010557	0.762	0.441	3	492	positive regulation of macromolecule biosynthetic process	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0031214	0.762	0.487	2	45	biomineral tissue development	BP	1	HIF1A,SLC20A1	down_VSAP_EC
GO:0042177	0.762	0.488	2	47	negative regulation of protein catabolic process	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0006354	0.762	0.491	2	30	DNA-templated transcription, elongation	BP	1	IWS1,THOC1	up_VCAV_EC
GO:0046660	0.762	0.589	1	28	female sex differentiation	BP	1	FOXO3	down_VCAV_EC

GO:0120034	0.762	0.59	1	28	positive regulation of plasma membrane bounded cell projection	BP	1	RAC2	down_VCAV_EC
GO:0006720	0.762	0.59	1	25	isoprenoid metabolic process	BP	1	RDH11	down_VSAP_EC
GO:0044380	0.762	0.598	1	14	protein localization to cytoskeleton	BP	1	MID1	up_ACOR_VSMC
GO:0061647	0.762	0.6	1	13	histone H3-K9 modification	BP	1	ATRX	up_ACOR_VSMC
GO:0007163	0.762	0.585	1	60	establishment or maintenance of cell	BP	1	KANK1	up_AFEM_EC
GO:0034329	0.762	0.585	1	60	cell junction assembly	BP	1	GREM1	up_AFEM_EC
GO:0006366	0.762	0.595	1	583	transcription by RNA polymerase II	BP	1	HOXA9	up_AORT_EC
GO:0043161	0.762	0.585	1	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	RNF6	up_VPOR_EC
GO:0051276	0.762	0.59	1	398	chromosome organization	BP	1	NR1H4	up_VPUL_EC
GO:0043687	0.762	0.598	1	14	post-translational protein modification	BP	1	TTL	up_VSAP_EC
GO:0061462	0.762	0.598	1	15	protein localization to lysosome	BP	1	NCOA4	up_VSAP_EC
GO:0097178	0.762	0.598	1	14	ruffle assembly	BP	1	BAG4	up_VSAP_EC
GO:0008152	0.763	0.36	15	3714	metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,HOXC10,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0001701	0.763	0.342	11	134	in utero embryonic development	BP	1	FGFR2,GJA1,LATS2,CITED2,SPINT1,EGLN1,ENSCAFG00000006238,SPINT2,CHD7,EDN1,INPP5K	up_ACOR_VSMC
GO:0019221	0.763	0.361	8	102	cytokine-mediated signaling pathway	BP	1	IFNGR1,LEP,F2RL1,CREBRF,CCDC3,PARP9,CCL5,LRRC4	up_ACOR_VSMC
GO:0061136	0.763	0.38	6	78	regulation of proteasomal protein catabolic process	BP	1	SH3RF2,OS9,RNF19A,PSEN1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0031325	0.763	0.383	6	914	positive regulation of cellular metabolic process	BP	1	ARHGEF2,ACVR2A,MTDH,ABHD5,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0032880	0.763	0.391	5	266	regulation of protein localization	BP	1	LEP,GPAM,CYLD,LRRC15,CCL5	up_AFEM_EC
GO:0060828	0.763	0.412	4	82	regulation of canonical Wnt signaling pathway	BP	1	PRICKLE1,ILK,APOE,DDIT3	down_VSAP_EC
GO:0010564	0.763	0.41	4	217	regulation of cell cycle process	BP	1	OVOL1,DCUN1D3,AXIN2,FAP	up_AFEM_EC
GO:0060491	0.763	0.413	4	62	regulation of cell projection assembly	BP	1	PODXL,MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0120032	0.763	0.413	4	62	regulation of plasma membrane bounded cell	BP	1	PODXL,MTOR,NCKAP1,FSCN1	up_VCAV_EC
GO:0061136	0.763	0.439	3	78	regulation of proteasomal protein catabolic process	BP	1	PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:1902275	0.763	0.439	3	60	regulation of chromatin organization	BP	1	IWS1,CTNNB1,KDM3A	down_VSAP_EC
GO:0006275	0.763	0.444	3	38	regulation of DNA replication	BP	1	CDC7,ATRX,ZNF365	up_ACOR_VSMC
GO:0030308	0.763	0.441	3	49	negative regulation of cell growth	BP	1	IFRD1,CDA,SMARCA4	up_VCAV_EC
GO:0006906	0.763	0.484	2	55	vesicle fusion	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0007611	0.763	0.485	2	54	learning or memory	BP	1	PRNP,BRSK1	down_VCAV_EC
GO:0048675	0.763	0.492	2	26	axon extension	BP	1	NRP1,ULK2	up_ACOR_VSMC
GO:0120162	0.763	0.489	2	31	positive regulation of cold-induced thermogenesis	BP	1	ADIPOR2,KDM3A	up_VCAV_EC
GO:0006513	0.763	0.491	2	28	protein monoubiquitination	BP	1	DDB2,KDM2B	up_VSAP_EC
GO:0001755	0.763	0.595	1	16	neural crest cell migration	BP	1	PHACTR4	down_ACOR_VSMC
GO:0051705	0.763	0.595	1	16	multi-organism behavior	BP	1	ANXA7	down_ACOR_VSMC
GO:0006814	0.763	0.587	1	28	sodium ion transport	BP	1	FXYD1	down_VCAV_EC
GO:0071621	0.763	0.588	1	27	granulocyte chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0051443	0.763	0.596	1	15	positive regulation of ubiquitin-protein	BP	1	DCUN1D4	up_ACOR_VSMC
GO:0042737	0.763	0.593	1	18	drug catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0044257	0.763	0.588	1	327	cellular protein catabolic process	BP	1	TRIM9	up_VFEM_EC

GO:0007632	0.763	0.596	1	14	visual behavior	BP	1	CTNS	up_VSAP_EC
GO:0034142	0.763	0.597	1	14	toll-like receptor 4 signaling pathway	BP	1	F2RL1	up_VSAP_EC
GO:1902742	0.763	0.597	1	14	apoptotic process involved in development	BP	1	SLIT2	up_VSAP_EC
GO:2000826	0.763	0.597	1	14	regulation of heart morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0051248	0.763	0.588	1	316	negative regulation of protein metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0006906	0.763022264	0.58404	1	55	vesicle fusion	BP	1	VPS16	up_ACOR_EC
GO:0051641	0.764	0.28	67	858	cellular localization	BP	1	ACSL3,SREBF1,RPA1,DDX39A,STXBP6,USP4,NEDD4,ZW10,CENPA,SLC29A1,NDC1,TIMM44,POLA2,CTDNEP1,HSPA9,RAN,HM13,BIRC5,INSIG1,CAV1,CDK1,RANBP1,NF2,AURKB,AAAS,MMP14,EZH2,PLK3,KIF22,CDCA8,ENSCAFG00000011598,PREB,TRAM1,NDC80,IPO4,YWHAB,RAC1,NUP62,EMP2,NUP188,HASPIN,TOMM34,SAMM50,GSTO1,TRAK1,DMAP1,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,RBM14,MIOS,CORO1A,CYC1,TTK,ASPM,TRAPPC6A,KNL1,PMPCA,TINF2,NUS1,CCT4,SIX4,CEP83,MTBP,ZWINT	down_ACOR_VSMC
GO:0045184	0.764	0.292	39	532	establishment of protein localization	BP	1	HCLS1,GBP5,TNFAIP3,TMEM173,IWS1,FERMT1,TLR4,GATA3,RAB11A,RAB27A,EXOC6,PPP3CA,ARG2,HHEX,SCAMP1,ABCA1,SNX2,MCC,THOC1,SH3GLB1,AKAP12,APOD,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,MCU,HIF1A,IPO11,LMTK2,ENSCAFG00000002015,RABGAP1,USP6NL	up_VCAV_EC
GO:0016032	0.764	0.378	6	94	viral process	BP	1	CXCL8,NECTIN2,PROX1,SMARCA4,CNOT7,USP6NL	up_VCAV_EC
GO:0009267	0.764	0.411	4	60	cellular response to starvation	BP	1	ATF3,RALB,MTOR,PMAIP1	up_VCAV_EC
GO:0021915	0.764	0.413	4	58	neural tube development	BP	1	BCL10,NUP133,HIF1A,LUZP1	up_VCAV_EC
GO:0051924	0.764	0.413	4	53	regulation of calcium ion transport	BP	1	SLC8B1,ABL1,CRACR2B,CYBA	up_VSAP_EC
GO:0051928	0.764	0.49	2	28	positive regulation of calcium ion transport	BP	1	PLCG2,WFS1	up_ACOR_VSMC
GO:0006950	0.764	0.498	2	1102	response to stress	BP	1	TAOK1,BPI	up_AORT_EC
GO:0006476	0.764	0.488	2	31	protein deacetylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0003008	0.764	0.483	2	336	system process	BP	1	HTR7,SEMA3A	up_VPOR_EC
GO:0071702	0.764	0.596	1	687	organic substance transport	BP	1	RAB11B	down_VPOR_EC
GO:0019068	0.764	0.594	1	15	virion assembly	BP	1	USP6NL	up_ACOR_VSMC
GO:0061028	0.764	0.596	1	14	establishment of endothelial barrier	BP	1	F2RL1	up_ACOR_VSMC
GO:0009267	0.764	0.582	1	60	cellular response to starvation	BP	1	CLEC16A	up_AFEM_EC
GO:0021575	0.764	0.595	1	15	hindbrain morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0021587	0.764	0.595	1	15	cerebellum morphogenesis	BP	1	PROX1	up_VCAV_EC
GO:0098930	0.764	0.591	1	17	axonal transport	BP	1	HIF1A	up_VCAV_EC
GO:0006468	0.764	0.592	1	544	protein phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0045746	0.764	0.595	1	14	negative regulation of Notch signaling pathway	BP	1	GDPD5	up_VSAP_EC
GO:0072507	0.764133865	0.48125	2	103	divalent inorganic cation homeostasis	BP	1	PTH1R,TMTC2	up_ACOR_EC
GO:0006352	0.764136585	0.58236	1	56	DNA-templated transcription, initiation	BP	1	CLSTN1	up_ACOR_EC
GO:0045934	0.764935996	0.34922	9	407	negative regulation of nucleobase-containing compound metabolic	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC

GO:0097659	0.765	0.272	98	1072	nucleic acid-templated transcription	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0007266	0.765	0.393	5	64	Rho protein signal transduction	BP	1	ABCA1,ARHGEF26,F2RL1,NRP1,SYNJ2BP	up_ACOR_VSMC
GO:0072507	0.765	0.407	4	103	divalent inorganic cation homeostasis	BP	1	PRNP,SLC39A6,THY1,CYBA	down_VCAV_EC
GO:0030323	0.765	0.437	3	65	respiratory tube development	BP	1	ERRFI1,CTNNB1,PLOD3	down_VSAP_EC
GO:0043067	0.765	0.437	3	479	regulation of programmed cell death	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0008637	0.765	0.486	2	35	apoptotic mitochondrial changes	BP	1	SLC25A5,PRELID1	down_ACOR_VSMC
GO:0097305	0.765	0.487	2	31	response to alcohol	BP	1	RAD51,CDK4	down_ACOR_VSMC
GO:0044087	0.765	0.482	2	339	regulation of cellular component biogenesis	BP	1	ENSCAFG00000002015,TWF1	up_VPOR_EC
GO:0099132	0.765	0.591	1	17	ATP hydrolysis coupled cation transmembrane	BP	1	ENSCAFG00000013366	down_ACOR_VSMC
GO:0021602	0.765	0.592	1	16	cranial nerve morphogenesis	BP	1	HOXA3	down_ACOR_VSMC
GO:0071310	0.765	0.593	1	634	cellular response to organic substance	BP	1	GABPA	down_AFEM_EC
GO:0050773	0.765	0.584	1	29	regulation of dendrite development	BP	1	TLX2	down_VCAV_EC
GO:0009566	0.765	0.586	1	24	fertilization	BP	1	SPINK2	down_VSAP_EC
GO:0031952	0.765	0.593	1	15	regulation of protein autophosphorylation	BP	1	RASSF2	up_ACOR_VSMC
GO:0032527	0.765	0.589	1	19	protein exit from endoplasmic reticulum	BP	1	GCC2	up_VCAV_EC
GO:0048146	0.765	0.589	1	18	positive regulation of fibroblast proliferation	BP	1	PDGFB	up_VCAV_EC
GO:0016226	0.765	0.594	1	14	iron-sulfur cluster assembly	BP	1	FXN	up_VSAP_EC
GO:0031163	0.765	0.594	1	14	metallo-sulfur cluster assembly	BP	1	FXN	up_VSAP_EC
GO:0014909	0.765	0.592	1	15	smooth muscle cell migration	BP	1	SLIT2	up_VSAP_EC
GO:0015696	0.765	0.594	1	14	ammonium transport	BP	1	SLC6A4	up_VSAP_EC

GO:0008152	0.766	0.269	181	3714	metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,GSTP1,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,MAOA,CFD,NAB2,NDN,ARSA,PRNP,LUM,UBA52,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,TRPV2,CLIP3,NUMBL,CHID1,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,RHBDL1,ENSCAFG00000025332,SAMD4B,EEF2K,TFE3,ACAA1,ME3,NR3C1,H6PD,HSD3B7,HR,SCP2,RPL23,RPL13,GLB1L,CLSTN1,PCSK7,PLCL1,DDOST,CSPG4,CYB5R3,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,THNSL2,PGLS,POFUT1,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,ASPN,POLDIP2,PIGS,ISOC2,HS3ST3B1,LRPAP1,EIF3K,THY1,GSTM4,NECAB3,RNF216,TEAD1,SUOX,CYP1B1,ADK,WDR45,AHCYL1,MRPL37,PEX5,CC2D1A,B4GALT1,RETSAT,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,ABHD15,CLEC16A,RETREG1,RNPEP,IDS,RPL27,COPS7A,CYBA,RBM38,ARL2BP,AMPD2,IFT57,BTD,MAVS,MRPS11,EMC6,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,ACSS2,TSC22D3,SLC3A2,MTFR1L,MAPRE3,GLIS2,CD	down_VCAV_EC
GO:1901576	0.766	0.273	89	1877	organic substance biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,ADCY6,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,LMO4,CLIP3,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,AKT2,LCAT,SAMD4B,TFE3,NR3C1,HSD3B7,HR,SCP2,RPL23,RPL13,CLSTN1,DDOST,CYB5R3,VDR,PRMT6,UROS,ENTPD3,THNSL2,ATP5MC1,CXXC5,GFPT2,PIGS,EIF3K,NECAB3,TEAD1,ADK,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,RPL27,AMPD2,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,RDH10,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,GLS2,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA,ACAT1	down_VCAV_EC
GO:0044093	0.766	0.312	19	437	positive regulation of molecular function	BP	1	PDGFRB,SNX18,LRP1,PRNP,LARP6,LMO4,AKT2,PLCL1,CSPG4,PARK7,SASH1,IFT57,MAVS,RAB7B,MAPRE3,DDR2,SHC1,GREM1,EVI5L	down_VCAV_EC
GO:0097190	0.766	0.406	4	217	apoptotic signaling pathway	BP	1	CD40,MLLT11,PLAGL2,CYLD	up_AFEM_EC
GO:0006403	0.766	0.435	3	64	RNA localization	BP	1	IWS1,SMG7,DDX39B	down_VSAP_EC
GO:0010717	0.766	0.485	2	32	regulation of epithelial to mesenchymal transition	BP	1	EZH2,GREM1	down_ACOR_VSMC
GO:0051701	0.766	0.482	2	45	interaction with host	BP	1	P4HB,DDX39B	down_VSAP_EC
GO:0070555	0.766	0.486	2	29	response to interleukin-1	BP	1	ANKRD1,CCL5	up_ACOR_VSMC
GO:0018105	0.766	0.479	2	116	peptidyl-serine phosphorylation	BP	1	CAMK2A,DMPK	up_AFEM_EC
GO:0032956	0.766	0.479	2	116	regulation of actin cytoskeleton organization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0071482	0.766	0.484	2	34	cellular response to light stimulus	BP	1	MAPK13,USP28	up_VCAV_EC
GO:0043436	0.766	0.583	1	303	oxoacid metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0015988	0.766	0.589	1	17	energy coupled proton transmembrane transport, against	BP	1	ENSCAFG00000013366	down_ACOR_VSMC
GO:0098930	0.766	0.589	1	17	axonal transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0035050	0.766	0.584	1	28	embryonic heart tube development	BP	1	IFT57	down_VCAV_EC
GO:1904029	0.766	0.584	1	28	regulation of cyclin-dependent protein kinase	BP	1	MAPRE3	down_VCAV_EC
GO:0072087	0.766	0.592	1	14	renal vesicle development	BP	1	BMP4	up_ACOR_VSMC
GO:0097009	0.766	0.594	1	13	energy homeostasis	BP	1	PPARGC1A	up_ACOR_VSMC
GO:1901617	0.766	0.579	1	60	organic hydroxy compound biosynthetic	BP	1	MOXD1	up_AFEM_EC
GO:0031577	0.766	0.589	1	17	spindle checkpoint	BP	1	ZW10	up_VCAV_EC

GO:0002712	0.766	0.592	1	15	regulation of B cell mediated immunity	BP	1	STAT6	up_VSAP_EC
GO:0002889	0.766	0.592	1	15	regulation of immunoglobulin	BP	1	STAT6	up_VSAP_EC
GO:1902108	0.766	0.592	1	14	regulation of mitochondrial membrane permeability involved in	BP	1	ZNF205	up_VSAP_EC
GO:0022402	0.767	0.294	31	407	cell cycle process	BP	1	PLK2,CXCL8,PDGFB,EDN1,RAB11A,FIGNL1,PPP3CA,CEP68,MZT1,UHRF2,STMN1,CENPC,ESCO1,TIMELESS,FES,SENP6,TAOK1,BLM,SMC5,RAD21,RAD17,SKIL,USP37,CUL4A,ZW10,ATRX,HAUS3,TOPBP1,TMOD3,FBXO5,SASS6	up_VCAV_EC
GO:0043170	0.767	0.377	9	2980	macromolecule metabolic process	BP	1	HOXA3,NR1H4,STK32B,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0031667	0.767	0.355	8	102	response to nutrient levels	BP	1	FAM107A,ACACB,SESN1,MAP3K5,PDK2,CASTOR1,BGLAP,NPRL3	up_VSAP_EC
GO:0006401	0.767	0.375	6	88	RNA catabolic process	BP	1	TENT2,CNOT6,PAN3,CNOT7,SMG7,DCP2	up_VCAV_EC
GO:0051346	0.767	0.375	6	78	negative regulation of hydrolase activity	BP	1	SH2D4A,CST3,ABL1,RECK,TMEM225B,BAG4	up_VSAP_EC
GO:0010821	0.767	0.436	3	49	regulation of mitochondrion	BP	1	SREBF1,SLC25A5,PRELID1	down_ACOR_VSMC
GO:0006694	0.767	0.437	3	42	steroid biosynthetic process	BP	1	LEP,SCP2,DKKL1	up_ACOR_VSMC
GO:0006575	0.767	0.48	2	53	cellular modified amino acid metabolic process	BP	1	PARK7,CRTAP	down_VCAV_EC
GO:0048193	0.767	0.477	2	116	Golgi vesicle transport	BP	1	TRAPPC3L,GAS1	up_AFEM_EC
GO:0050789	0.767	0.563	2	3295	regulation of biological process	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0006082	0.767	0.58	1	305	organic acid metabolic process	BP	1	CSGALNACT1	down_ACOR_EC
GO:0050715	0.767	0.582	1	29	positive regulation of cytokine secretion	BP	1	MAVS	down_VCAV_EC
GO:0007189	0.767	0.584	1	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	GNAQ	down_VSAP_EC
GO:0061035	0.767	0.583	1	24	regulation of cartilage development	BP	1	CTNNB1	down_VSAP_EC
GO:0000281	0.767	0.588	1	18	mitotic cytokinesis	BP	1	STMN1	up_VCAV_EC
GO:2000648	0.767	0.591	1	14	positive regulation of stem cell proliferation	BP	1	HIF1A	up_VCAV_EC
GO:0032774	0.768	0.268	98	1073	RNA biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0061448	0.768	0.363	7	89	connective tissue development	BP	1	LEP,BMP4,LNPK,PPARGC1A,FGF18,EDN1,ARID5B	up_ACOR_VSMC
GO:0034329	0.768	0.407	4	60	cell junction assembly	BP	1	FSCN1,CAV1,GREM1,RAC1	down_ACOR_VSMC
GO:0035107	0.768	0.407	4	60	appendage morphogenesis	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0035108	0.768	0.407	4	60	limb morphogenesis	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0006470	0.768	0.408	4	54	protein dephosphorylation	BP	1	NCEH1,SMPD1,DUSP26,RPRD1B	up_ACOR_VSMC
GO:0080090	0.768	0.456	3	1734	regulation of primary metabolic process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0097191	0.768	0.432	3	79	extrinsic apoptotic signaling pathway	BP	1	GABARAP,PARK7,FOXO3	down_VCAV_EC
GO:0045639	0.768	0.482	2	33	positive regulation of myeloid cell	BP	1	PRMT1,HMGB2	down_ACOR_VSMC

GO:0097553	0.768	0.482	2	32	calcium ion transmembrane import	BP	1	GSTO1,CORO1A	down_ACOR_VSMC
GO:0000724	0.768	0.478	2	57	double-strand break repair via homologous	BP	1	NABP2,FBH1	down_VCAV_EC
GO:0007127	0.768	0.484	2	28	meiosis I	BP	1	DMC1,SUN1	up_ACOR_VSMC
GO:0061982	0.768	0.484	2	28	meiosis I cell cycle process	BP	1	DMC1,SUN1	up_ACOR_VSMC
GO:0006754	0.768	0.481	2	36	ATP biosynthetic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:1905952	0.768	0.482	2	33	regulation of lipid localization	BP	1	ATP8A1,ABCA1	up_VCAV_EC
GO:0008219	0.768	0.483	2	611	cell death	BP	1	EMP1,CAV1	up_VSAP_VSMC
GO:1901698	0.768	0.579	1	266	response to nitrogen compound	BP	1	IGF1R	down_ACOR_EC
GO:0009303	0.768	0.587	1	16	rRNA transcription	BP	1	NCL	down_ACOR_VSMC
GO:0048641	0.768	0.587	1	16	regulation of skeletal muscle tissue	BP	1	SIX4	down_ACOR_VSMC
GO:1903727	0.768	0.588	1	16	positive regulation of phospholipid metabolic	BP	1	ACSL3	down_ACOR_VSMC
GO:0006029	0.768	0.58	1	29	proteoglycan metabolic process	BP	1	DCN	down_VCAV_EC
GO:0048167	0.768	0.581	1	28	regulation of synaptic plasticity	BP	1	BRSK1	down_VCAV_EC
GO:0070936	0.768	0.58	1	28	protein K48-linked ubiquitination	BP	1	RNF216	down_VCAV_EC
GO:0051438	0.768	0.582	1	24	regulation of ubiquitin-protein transferase	BP	1	TRIB3	down_VSAP_EC
GO:0005978	0.768	0.59	1	14	glycogen biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0009250	0.768	0.59	1	14	glucan biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0051321	0.768	0.576	1	61	meiotic cell cycle	BP	1	OVOL1	up_AFEM_EC
GO:0051965	0.768	0.586	1	17	positive regulation of synapse assembly	BP	1	EPHB1	up_VCAV_EC
GO:0098609	0.768	0.577	1	181	cell-cell adhesion	BP	1	SLC7A11	up_VPOR_EC
GO:0045934	0.768	0.583	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	NR1H4	up_VPUL_EC
GO:0006475	0.768009857	0.57694	1	54	internal protein amino acid acetylation	BP	1	PHF20	up_ACOR_EC
GO:0002521	0.768129133	0.42997	3	149	leukocyte differentiation	BP	1	FZD5,PTGER4,CLSTN1	up_ACOR_EC
GO:0090174	0.768700496	0.57577	1	56	organelle membrane fusion	BP	1	VPS16	up_ACOR_EC
GO:0032268	0.769	0.318	16	778	regulation of cellular protein metabolic process	BP	1	LEP,PRR16,GAS1,CRYAB,F3,GREM1,CLEC16A,CYLD,LRRC15,RECK,DCUN1D3,AXIN2,CCL5,CTIF,ADAM17,SAMD4B	up_AFEM_EC
GO:0008152	0.769	0.362	13	3714	metabolic process	BP	1	NR1H4,MAPK10,HOXA3,PLCL1,PCSK1N,GALNT17,LZTS1,ZDHHC16,NPNT,NTRK2,HOXA1,ENSCAFG00000002230,ENSCAFG00000028814	up_APUL_EC
GO:0016043	0.769	0.377	7	1973	cellular component organization	BP	1	EYA1,TRIM9,SIX1,RADIL,CYP26B1,CDC42EP5,MTSS1	up_VFEM_EC
GO:0051179	0.769	0.455	3	1747	localization	BP	1	ANKRD50,GPSM2,FSCN1	down_AFEM_EC
GO:0006473	0.769	0.432	3	66	protein acetylation	BP	1	IWS1,NAA10,MORF4L2	down_VSAP_EC
GO:0002181	0.769	0.48	2	35	cytoplasmic translation	BP	1	RBM14,EIF3M	down_ACOR_VSMC
GO:0050707	0.769	0.478	2	44	regulation of cytokine secretion	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0010467	0.769	0.509	2	1787	gene expression	BP	1	GATA5,C6	up_VCAV_VSMC
GO:0006140	0.769	0.58	1	28	regulation of nucleotide metabolic process	BP	1	PARK7	down_VCAV_EC
GO:0032206	0.769	0.582	1	23	positive regulation of telomere maintenance	BP	1	CTNNB1	down_VSAP_EC
GO:0051058	0.769	0.582	1	21	negative regulation of small GTPase mediated signal transduction	BP	1	TNFAIP1	down_VSAP_EC
GO:0060350	0.769	0.581	1	23	endochondral bone morphogenesis	BP	1	SERPINH1	down_VSAP_EC
GO:0034109	0.769	0.588	1	14	homotypic cell-cell adhesion	BP	1	JUP	up_ACOR_VSMC

GO:0046328	0.769	0.575	1	61	regulation of JNK cascade	BP	1	CYLD	up_AFEM_EC
GO:0010467	0.769	0.624	1	1787	gene expression	BP	1	HOXA3	up_APUL_VSMC
GO:0009896	0.77	0.345	9	127	positive regulation of catabolic process	BP	1	NEDD4,MTDH,ABHD5,PLK3,RNF152,DTL,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0031327	0.77	0.35	8	412	negative regulation of cellular biosynthetic	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1,SAMD4B	up_AFEM_EC
GO:0043062	0.77	0.361	7	99	extracellular structure organization	BP	1	ADAMTS9,LAMC2,FERMT1,ABCA1,SERAC1,OLFML2A,FSCN1	up_VCAV_EC
GO:2001242	0.77	0.404	4	62	regulation of intrinsic apoptotic signaling	BP	1	CAV1,NOC2L,TXNDC12,ARHGEF2	down_ACOR_VSMC
GO:0016043	0.77	0.427	4	1973	cellular component organization	BP	1	CHL1,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:2000112	0.77	0.441	3	1119	regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0120034	0.77	0.481	2	28	positive regulation of plasma membrane bounded cell projection	BP	1	F2RL1,NRP1	up_ACOR_VSMC
GO:0051591	0.77	0.584	1	16	response to cAMP	BP	1	EZR	down_ACOR_VSMC
GO:0016310	0.77	0.586	1	641	phosphorylation	BP	1	NDUFA10	down_AFEM_EC
GO:0010770	0.77	0.578	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	TRPV2	down_VCAV_EC
GO:2000573	0.77	0.578	1	28	positive regulation of DNA biosynthetic process	BP	1	GREM1	down_VCAV_EC
GO:0046782	0.77	0.583	1	17	regulation of viral transcription	BP	1	SMARCA4	up_VCAV_EC
GO:0030155	0.77	0.573	1	180	regulation of cell adhesion	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0031399	0.77	0.583	1	559	regulation of protein modification process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0043281	0.770240291	0.57344	1	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	IFI6	up_ACOR_EC
GO:1901575	0.771	0.323	13	643	organic substance catabolic process	BP	1	LEP,CTSS,TENT5C,CLEC16A,CYLD,MOXD1,RAB7A,AXIN2,ACACB,CTIF,FAP,SAMD4B,RNF181	up_AFEM_EC
GO:0045664	0.771	0.328	12	144	regulation of neuron differentiation	BP	1	ITM2C,BMP4,ZNF365,NRP1,ULK2,APP,PSEN1,SIPA1L1,SSH3,ASAP1,B2M,DISC1	up_ACOR_VSMC
GO:1905114	0.771	0.328	12	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	FZD1,WNT11,AXIN2,ABL1,RECK,PLPP3,FAM53B,SULF2,HIC1,LRP4,LIMD1,LATS2	up_VSAP_EC
GO:0031668	0.771	0.37	6	79	cellular response to extracellular stimulus	BP	1	FAM107A,SESN1,MAP3K5,PDK2,CASTOR1,NPRL3	up_VSAP_EC
GO:0045165	0.771	0.385	5	65	cell fate commitment	BP	1	BMP4,FGFR2,LATS2,LMO4,PSEN1	up_ACOR_VSMC
GO:0050679	0.771	0.402	4	62	positive regulation of epithelial cell proliferation	BP	1	HMGB1,B4GALT1,NRAS,HMGB2	down_ACOR_VSMC
GO:0016043	0.771	0.424	4	1973	cellular component organization	BP	1	EYA1,FBP1,SHOX2,ATP8B4	up_VFEM_VSMC
GO:0030072	0.771	0.43	3	48	peptide hormone secretion	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0051054	0.771	0.427	3	81	positive regulation of DNA metabolic process	BP	1	NABP2,TMEM161A,GREM1	down_VCAV_EC
GO:0019751	0.771	0.477	2	33	polyol metabolic process	BP	1	GK5,NUDT3	down_ACOR_VSMC
GO:0051784	0.771	0.48	2	28	negative regulation of nuclear division	BP	1	BMP4,ATRX	up_ACOR_VSMC
GO:0045787	0.771	0.471	2	117	positive regulation of cell cycle	BP	1	OVOL1,FAP	up_AFEM_EC
GO:0033554	0.771	0.479	2	708	cellular response to stress	BP	1	MAPK10,ZDHHC16	up_APUL_EC
GO:0016310	0.771	0.479	2	641	phosphorylation	BP	1	MAP2K6,CDC42EP5	up_VFEM_EC
GO:0006140	0.771	0.48	2	28	regulation of nucleotide metabolic process	BP	1	PDK2,DDIT4	up_VSAP_EC
GO:0051588	0.771	0.48	2	28	regulation of neurotransmitter	BP	1	KCNC4,FLOT1	up_VSAP_EC
GO:0015908	0.771	0.579	1	23	fatty acid transport	BP	1	APOE	down_VSAP_EC
GO:0030260	0.771	0.584	1	15	entry into host cell	BP	1	CTSB	up_ACOR_VSMC
GO:0044409	0.771	0.584	1	15	entry into host	BP	1	CTSB	up_ACOR_VSMC
GO:0051806	0.771	0.584	1	15	entry into cell of other organism involved in	BP	1	CTSB	up_ACOR_VSMC

GO:0051828	0.771	0.584	1	15	entry into other organism involved in symbiotic	BP	1	CTSB	up_ACOR_VSMC
GO:0008156	0.771	0.584	1	15	negative regulation of DNA replication	BP	1	RAD17	up_VCAV_EC
GO:1901564	0.772	0.258	155	2053	organonitrogen compound metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,NPR1,ST8SIA6,KIT,PRCP,PPP2R5A,PANK3,PRKCH,CDA,TNFAIP3,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,RELN,ST6GAL1,CTSC,PDE4D,IWS1,MEF2C,ATF3,KLKB1,TIPARP,RAPGEF1,WWP1,TLR4,QKI,LYVE1,TSPAN15,GATA3,USP33,EDN1,RALB,APLNR,CTTNBP2NL,SNCAIP,PIPOX,ZDHHC22,PSME4,NEDD9,PELI1,SERINC5,ADSS,YES1,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,SAMD8,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PREX2,SLK,BMP2K,SH3BP5,ST3GAL6,ENC1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,ENSCAFG00000010596,MADD,ARID4B,PAK2,GALNT18,PRKD2,SWAP70,CHST1,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,ESCO1,DPH5,VHL,OTUD4,SLC25A25,WSB1,PARP4,FES,NSD1,GUCY1B1,MRRF,PTGS2,MMD,TOP1,RAPGEF2,CREB1,BCL10,SENP6,USP28,TAOK1,CNOT7,GCH1,DCK,HMGB1,NOS2,PMAIP1,BLM,SPTBN4,RIPK1,USP13,USP38,PDGFD,USP37,BLVRA,C7H18orf25,CUL4A,BMX,UBE2D1,KDM5A,HIF1A,KDM3A,BCAT1,LMTK2,ATRX,RBBP6,ZDHHC6,TNFAIP1,IVNS1ABP,JCAD,PSMB9,PSMD12,TET	up_VCAV_EC
GO:0044271	0.772	0.26	137	1501	cellular nitrogen compound biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,ENSCAFG00000013986,CERS4,WARS2,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,ANKHD1,AZIN2,TRERF1,E2F4,NPAS2,FARS2,PCBD1,LIMD1,UBA52,RPUSD4,RPL15,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,PNPO,DCAKD,EIF3G,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,ASS1,TNRC6C,COA1,PPP3CB,NCK1,ZNF444,MRPL4,MAVS,HMOX1,ZNF662,LARS2,CITED2,B3GALT4,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:0007267	0.772	0.317	14	332	cell-cell signaling	BP	1	RECK,CLSTN1,PLCL1,CACNB3,THY1,ATP6V0C,GLI3,PARK7,CDH2,GREM1,NPHP4,FOXO3,BRSK1,CDK14	down_VCAV_EC
GO:0097190	0.772	0.341	9	217	apoptotic signaling pathway	BP	1	SLC35F6,GABARAP,ENSCAFG00000013404,TMEM161A,PARK7,ZMAT3,GSDME,FBH1,FOXO3	down_VCAV_EC
GO:0090596	0.772	0.399	4	84	sensory organ morphogenesis	BP	1	BCAR3,HIF1A,CTNNB1,SIX4	down_VSAP_EC
GO:0045833	0.772	0.478	2	29	negative regulation of lipid metabolic process	BP	1	ORMDL3,DKKL1	up_ACOR_VSMC
GO:0098876	0.772	0.477	2	29	vesicle-mediated transport to the plasma	BP	1	RAB11B,VPS26A	up_ACOR_VSMC
GO:2000573	0.772	0.478	2	28	positive regulation of DNA biosynthetic process	BP	1	MYC,FBXO4	up_VSAP_EC
GO:0001678	0.772	0.575	1	29	cellular glucose homeostasis	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0043255	0.772	0.574	1	29	regulation of carbohydrate biosynthetic	BP	1	AKT2	down_VCAV_EC
GO:0071347	0.772	0.576	1	25	cellular response to interleukin-1	BP	1	HIF1A	down_VSAP_EC
GO:0070266	0.772	0.583	1	14	necroptotic process	BP	1	TLR3	up_ACOR_VSMC
GO:0043903	0.772	0.57	1	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	RAB7A	up_AFEM_EC

GO:0031327	0.772	0.577	1	412	negative regulation of cellular biosynthetic	BP	1	NR1H4	up_VPUL_EC
GO:0043933	0.772	0.584	1	698	protein-containing complex subunit	BP	1	SLIT2	up_VPUL_VSMC
GO:0009057	0.773	0.283	36	473	macromolecule catabolic process	BP	1	RNPS1,USP1,USP4,EIF4A3,EDC3,HNRNPD,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,THRAP3,EDC4,FEN1,SMARCC1,RNASEH2B,PLK3,SMG9,DIS3,FASTKD3,UBE2J2,DTL,EZR,UBE2K,RAD23A,CDC20,BAP1,PSMC1,AIFM1,ENSCAFG00000015189,RNASEH2C,EXOSC5,UBE2C,AMER1	down_ACOR_VSMC
GO:0065007	0.773	0.314	26	3499	biological regulation	BP	1	C3AR1,BARX1,HTR7,CXHXorf57,HOOK3,HOXA3,ARHGEF2,TCEA1,ENSCAFG00000002015,SLC7A11,SEMA3A,ENSCAFG00000005494,ASPN,ACVR2A,FBP1,MTDH,GCC2,ABHD5,TWF1,PDE1C,PUM3,EIF5,CCAR1,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0002460	0.773	0.4	4	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	HMGB1,TFRC,FAM49B,EMP2	down_ACOR_VSMC
GO:0036503	0.773	0.428	3	47	ERAD pathway	BP	1	HM13,UBE2J2,PSMC1	down_ACOR_VSMC
GO:0002703	0.773	0.428	3	47	regulation of leukocyte mediated immunity	BP	1	HMGB1,TFRC,FAM49B	down_ACOR_VSMC
GO:0006139	0.773	0.452	3	1909	nucleobase-containing compound metabolic	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0010950	0.773	0.428	3	44	positive regulation of endopeptidase activity	BP	1	MBP,DAPK1,PERP	up_ACOR_VSMC
GO:0001837	0.773	0.427	3	48	epithelial to mesenchymal transition	BP	1	MTOR,BMP2,HIF1A	up_VCAV_EC
GO:0030518	0.773	0.43	3	42	intracellular steroid hormone receptor	BP	1	PPARGC1B,PRMT2,LBH	up_VSAP_EC
GO:0060401	0.773	0.428	3	42	cytosolic calcium ion transport	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0090174	0.773	0.471	2	56	organelle membrane fusion	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0045619	0.773	0.472	2	44	regulation of lymphocyte differentiation	BP	1	SOCS5,PTPN2	down_VSAP_EC
GO:0042770	0.773	0.474	2	35	signal transduction in response to DNA damage	BP	1	PMAIP1,ATRX	up_VCAV_EC
GO:0046148	0.773	0.579	1	17	pigment biosynthetic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0046825	0.773	0.581	1	16	regulation of protein export from nucleus	BP	1	RAN	down_ACOR_VSMC
GO:0046902	0.773	0.579	1	18	regulation of mitochondrial membrane	BP	1	SLC25A5	down_ACOR_VSMC
GO:0006112	0.773	0.573	1	30	energy reserve metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0006342	0.773	0.575	1	24	chromatin silencing	BP	1	MORF4L2	down_VSAP_EC
GO:0032760	0.773	0.576	1	22	positive regulation of tumor necrosis factor	BP	1	ARHGEF2	down_VSAP_EC
GO:1903557	0.773	0.576	1	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	down_VSAP_EC
GO:0007029	0.773	0.579	1	16	endoplasmic reticulum organization	BP	1	LNPK	up_ACOR_VSMC
GO:0002639	0.773	0.582	1	14	positive regulation of immunoglobulin	BP	1	TP53BP1	up_ACOR_VSMC
GO:0048247	0.773	0.58	1	16	lymphocyte chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:0051223	0.773	0.57	1	181	regulation of protein transport	BP	1	GCC2	up_VPOR_EC
GO:0007049	0.773	0.579	1	560	cell cycle	BP	1	CYP26B1	up_VPOR_VSMC
GO:0000060	0.773	0.581	1	15	protein import into nucleus, translocation	BP	1	MAVS	up_VSAP_EC
GO:0046622	0.773	0.581	1	15	positive regulation of organ growth	BP	1	ACACB	up_VSAP_EC
GO:0071897	0.773131749	0.56944	1	54	DNA biosynthetic process	BP	1	PKIB	up_ACOR_EC

GO:0031399	0.774	0.275	49	559	regulation of protein modification process	BP	1	FZD1,CDON,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,EMP2,MAP3K5,PDGFD,KLF15,C1QTNF2,CNPPD1,PLPP3,CAMKK2,TNKS1BP1,F2RL1,DDR2,TRAF7,MYC,RTN4RL1,SASH1,FBXO4,MYD88,LRP4,PHF1,FBXO7,CDK9,FBLN1,RAF1,QARS,ACVRL1,FLOT1,NCK1,MAVS,ZER1,MAP2K2,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0015980	0.774	0.355	7	106	energy derivation by oxidation of organic	BP	1	PRELID1,CDK1,FASTKD3,SUCLG1,CYCS,CYC1,PDHA1	down_ACOR_VSMC
GO:0030098	0.774	0.366	6	87	lymphocyte differentiation	BP	1	HMGB1,PRELID1,MMP14,HMGB3,TOX,JMJD6	down_ACOR_VSMC
GO:0032504	0.774	0.364	6	152	multicellular organism reproduction	BP	1	ADAMTS2,MEA1,B4GALT1,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0048609	0.774	0.364	6	152	multicellular organismal reproductive process	BP	1	ADAMTS2,MEA1,B4GALT1,FOXO3,THRB,ZBTB16	down_VCAV_EC
GO:0048284	0.774	0.38	5	66	organelle fusion	BP	1	TBC1D10C,TBC1D2B,MFN2,STX4,VPS11	up_VSAP_EC
GO:2001022	0.774	0.428	3	42	positive regulation of response to DNA damage	BP	1	NACC2,ANKRD1,PARP9	up_ACOR_VSMC
GO:0035196	0.774	0.578	1	16	production of miRNAs involved in gene silencing	BP	1	SRRT	down_ACOR_VSMC
GO:0098781	0.774	0.575	1	22	ncRNA transcription	BP	1	SMARCA4	down_VSAP_EC
GO:0032388	0.774	0.567	1	62	positive regulation of intracellular transport	BP	1	LEP	up_AFEM_EC
GO:0046717	0.774	0.577	1	17	acid secretion	BP	1	NOS2	up_VCAV_EC
GO:0006915	0.774	0.578	1	550	apoptotic process	BP	1	EYA1	up_VFEM_VSMC
GO:0070542	0.774	0.58	1	15	response to fatty acid	BP	1	PTGFR	up_VSAP_EC
GO:0044283	0.774156779	0.39474	4	201	small molecule biosynthetic process	BP	1	NR1H4,THNSL2,PTGDS,ALDOC	up_ACOR_EC
GO:0006732	0.774825047	0.46617	2	107	coenzyme metabolic process	BP	1	NMNAT2,ALDOC	up_ACOR_EC
GO:0043067	0.775	0.277	42	479	regulation of programmed cell death	BP	1	WNT11,CD274,ACKR3,MAP3K14,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,PTPMT1,ENSCAFG00000011993,PRMT2,KDM2B,RAF1,ZNF205,STX4,QARS,ARHGAP10,HTRA2,NCK1,HMOX1,MAP2K2,CITED2,DEDD2,LATS2	up_VSAP_EC
GO:0007059	0.775	0.338	9	127	chromosome segregation	BP	1	RAB11A,CENPC,ESCO1,TOP1,SMC5,RAD21,ZW10,ATRX,FBXO5	up_VCAV_EC
GO:0018205	0.775	0.363	6	122	peptidyl-lysine modification	BP	1	PLOD2,IWS1,MORF4L2,PLOD3,P3H4,KDM3A	down_VSAP_EC
GO:1901701	0.775	0.376	5	271	cellular response to oxygen-containing	BP	1	CHRM2,CAMK2A,NR3C1,KANK1,SOD1	up_AFEM_EC
GO:0046879	0.775	0.397	4	63	hormone secretion	BP	1	SREBF1,BIRC5,FAM129B,ENSCAFG00000005299	down_ACOR_VSMC
GO:0006665	0.775	0.425	3	48	sphingolipid metabolic process	BP	1	ELOVL1,ELOVL6,SGPL1	down_ACOR_VSMC
GO:0045333	0.775	0.423	3	74	cellular respiration	BP	1	ENSCAFG00000007260,HIF1A,BNIP3	down_VSAP_EC
GO:0048593	0.775	0.426	3	41	camera-type eye morphogenesis	BP	1	BMP4,CITED2,FRS2	up_ACOR_VSMC
GO:0043412	0.775	0.486	2	1225	macromolecule modification	BP	1	IVNS1ABP,USP33	down_AFEM_EC
GO:0017004	0.775	0.575	1	18	cytochrome complex assembly	BP	1	FASTKD3	down_ACOR_VSMC
GO:0030593	0.775	0.575	1	19	neutrophil chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:0034754	0.775	0.571	1	24	cellular hormone metabolic process	BP	1	REST	down_VSAP_EC
GO:0001937	0.775	0.579	1	15	negative regulation of endothelial cell	BP	1	SYNJ2BP	up_ACOR_VSMC
GO:0021602	0.775	0.578	1	16	cranial nerve morphogenesis	BP	1	EPHB1	up_VCAV_EC
GO:0032963	0.775	0.575	1	18	collagen metabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0071705	0.775	0.576	1	582	nitrogen compound transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0051130	0.775	0.57	1	342	positive regulation of cellular component	BP	1	CDC42EP5	up_VFEM_EC
GO:0045893	0.775	0.572	1	413	positive regulation of transcription, DNA-	BP	1	ARHGEF2	up_VPUL_EC

GO:0009141	0.775277709	0.46544	2	110	nucleoside triphosphate metabolic process	BP	1	AK7,ALDOC	up_ACOR_EC
GO:0034728	0.775314847	0.56605	1	56	nucleosome organization	BP	1	SOX9	up_ACOR_EC
GO:0072594	0.775861037	0.41937	3	155	establishment of protein localization to organelle	BP	1	MAVS,CHMP4B,PRKCD	up_ACOR_EC
GO:0031327	0.77599931	0.33559	9	412	negative regulation of cellular biosynthetic	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1, FOXC2,CLSTN1,RIOX2	up_ACOR_EC
GO:0051129	0.776	0.392	4	221	negative regulation of cellular component	BP	1	CRYAB,CLEC16A,FAP,KANK1	up_AFEM_EC
GO:0030324	0.776	0.395	4	64	lung development	BP	1	HHEX,PROX1,TIMELESS,CREB1	up_VCAV_EC
GO:1902107	0.776	0.424	3	47	positive regulation of leukocyte differentiation	BP	1	HMGB1,MMP14,TOX	down_ACOR_VSMC
GO:1901214	0.776	0.421	3	81	regulation of neuron death	BP	1	PRNP,PARK7,FOXO3	down_VCAV_EC
GO:0031398	0.776	0.423	3	51	positive regulation of protein ubiquitination	BP	1	PELI1,BCL10,UBE2D1	up_VCAV_EC
GO:0009201	0.776	0.426	3	41	ribonucleoside triphosphate biosynthetic	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0010628	0.776	0.47	2	527	positive regulation of gene expression	BP	1	ACVRL1,HOXA1	down_ACOR_EC
GO:0044272	0.776	0.47	2	35	sulfur compound biosynthetic process	BP	1	CHST7,ELOVL7	up_VCAV_EC
GO:0072524	0.776	0.469	2	37	pyridine-containing compound metabolic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0002682	0.776	0.467	2	343	regulation of immune system process	BP	1	C3AR1,ACVR2A	up_VPOR_EC
GO:0060675	0.776	0.472	2	29	ureteric bud morphogenesis	BP	1	HOXA11,WNT11	up_VSAP_EC
GO:0042181	0.776	0.575	1	17	ketone biosynthetic process	BP	1	PDSS1	down_ACOR_VSMC
GO:2001244	0.776	0.57	1	27	positive regulation of intrinsic apoptotic	BP	1	PTPN2	down_VSAP_EC
GO:0060147	0.776	0.578	1	14	regulation of posttranscriptional gene	BP	1	BMP4	up_ACOR_VSMC
GO:0060966	0.776	0.578	1	14	regulation of gene silencing by RNA	BP	1	BMP4	up_ACOR_VSMC
GO:0006623	0.776	0.576	1	16	protein targeting to vacuole	BP	1	GCC2	up_VCAV_EC
GO:0050732	0.776	0.574	1	18	negative regulation of peptidyl-tyrosine	BP	1	SH3BP5	up_VCAV_EC
GO:1902229	0.776	0.575	1	17	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	SKIL	up_VCAV_EC
GO:0006355	0.776	0.586	1	974	regulation of transcription, DNA-	BP	1	GATA5	up_VCAV_VSMC
GO:0006259	0.776	0.569	1	354	DNA metabolic process	BP	1	EYA1	up_VFEM_EC
GO:1902680	0.776	0.57	1	415	positive regulation of RNA biosynthetic process	BP	1	ARHGEF2	up_VPUL_EC
GO:1903508	0.776	0.57	1	415	positive regulation of nucleic acid-templated	BP	1	ARHGEF2	up_VPUL_EC
GO:0045620	0.776	0.576	1	15	negative regulation of lymphocyte	BP	1	FBXO7	up_VSAP_EC
GO:0050849	0.776	0.577	1	15	negative regulation of calcium-mediated	BP	1	TBC1D10C	up_VSAP_EC
GO:0018394	0.776076619	0.565	1	55	peptidyl-lysine acetylation	BP	1	PHF20	up_ACOR_EC
GO:0010001	0.776309829	0.56474	1	54	glial cell differentiation	BP	1	SH3TC2	up_ACOR_EC
GO:0071902	0.777	0.362	6	79	positive regulation of protein serine/threonine	BP	1	ARHGEF5,MAP3K5,PDGFD,C1QTNF2,TRAF7,S ASH1	up_VSAP_EC
GO:0061326	0.777	0.423	3	41	renal tubule development	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0072080	0.777	0.423	3	41	nephron tubule development	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0034645	0.777	0.44	3	1546	cellular macromolecule biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0000725	0.777	0.464	2	58	recombinational repair	BP	1	NABP2,FBH1	down_VCAV_EC
GO:0002685	0.777	0.465	2	55	regulation of leukocyte migration	BP	1	THY1,RAC2	down_VCAV_EC
GO:1901575	0.777	0.471	2	643	organic substance catabolic process	BP	1	TRIM9,CYP26B1	up_VFEM_EC
GO:0030216	0.777	0.567	1	29	keratinocyte differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0060688	0.777	0.567	1	29	regulation of morphogenesis of a	BP	1	GREM1	down_VCAV_EC

GO:0071322	0.777	0.568	1	29	cellular response to carbohydrate stimulus	BP	1	ZFP36L1	down_VCAV_EC
GO:0032435	0.777	0.575	1	15	negative regulation of proteasomal ubiquitin-dependent protein	BP	1	PARK7	up_ACOR_VSMC
GO:0060323	0.777	0.577	1	14	head morphogenesis	BP	1	ARID5B	up_ACOR_VSMC
GO:1904062	0.777	0.564	1	62	regulation of cation transmembrane transport	BP	1	FXYD1	up_AFEM_EC
GO:1903506	0.777	0.584	1	977	regulation of nucleic acid-templated transcription	BP	1	GATA5	up_VCAV_VSMC
GO:0021879	0.777	0.576	1	15	forebrain neuron differentiation	BP	1	SLIT2	up_VSAP_EC
GO:0044087	0.777	0.566	1	339	regulation of cellular component biogenesis	BP	1	CAV1	up_VSAP_VSMC
GO:0000723	0.77781215	0.5625	1	54	telomere maintenance	BP	1	PKIB	up_ACOR_EC
GO:0032200	0.77781215	0.5625	1	54	telomere organization	BP	1	PKIB	up_ACOR_EC
GO:0032147	0.778	0.362	6	77	activation of protein kinase activity	BP	1	LEP,MAP3K8,BMP4,FRS2,PSEN1,MAP3K7	up_ACOR_VSMC
GO:0010467	0.778	0.391	5	1787	gene expression	BP	1	HOXA3,NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0050890	0.778	0.375	5	67	cognition	BP	1	FAM107A,CBR3,CHRM1,CTNS,DOP1B	up_VSAP_EC
GO:0032543	0.778	0.467	2	34	mitochondrial translation	BP	1	TRUB2,FASTKD3	down_ACOR_VSMC
GO:0038127	0.778	0.468	2	32	ERBB signaling pathway	BP	1	NUP62,IQGAP1	down_ACOR_VSMC
GO:0044344	0.778	0.467	2	33	cellular response to fibroblast growth factor	BP	1	IQGAP1,FGF5	down_ACOR_VSMC
GO:0002688	0.778	0.467	2	34	regulation of leukocyte chemotaxis	BP	1	HMGB1,RAC1	down_ACOR_VSMC
GO:0071774	0.778	0.467	2	33	response to fibroblast growth factor	BP	1	IQGAP1,FGF5	down_ACOR_VSMC
GO:1901222	0.778	0.468	2	32	regulation of NIK/NF-kappaB signaling	BP	1	IRAK1,GREM1	down_ACOR_VSMC
GO:0009411	0.778	0.464	2	56	response to UV	BP	1	TMEM161A,BRSK1	down_VCAV_EC
GO:0050792	0.778	0.464	2	55	regulation of viral process	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0006513	0.778	0.47	2	28	protein monoubiquitination	BP	1	PCGF5,WDR48	up_ACOR_VSMC
GO:0050886	0.778	0.572	1	17	endocrine process	BP	1	FAM129B	down_ACOR_VSMC
GO:1900015	0.778	0.572	1	17	regulation of cytokine production involved in inflammatory response	BP	1	BAP1	down_ACOR_VSMC
GO:0120163	0.778	0.571	1	17	negative regulation of cold-induced	BP	1	HOXC10	down_ACOR_VSMC
GO:0032946	0.778	0.566	1	29	positive regulation of mononuclear cell	BP	1	GPAM	down_VCAV_EC
GO:0035304	0.778	0.565	1	29	regulation of protein dephosphorylation	BP	1	PDGFRB	down_VCAV_EC
GO:0046620	0.778	0.565	1	30	regulation of organ growth	BP	1	BMPR1A	down_VCAV_EC
GO:0050671	0.778	0.566	1	29	positive regulation of lymphocyte proliferation	BP	1	GPAM	down_VCAV_EC
GO:0072332	0.778	0.566	1	29	intrinsic apoptotic signaling pathway by p53	BP	1	ZMAT3	down_VCAV_EC
GO:0051193	0.778	0.574	1	15	regulation of cofactor metabolic process	BP	1	DDIT4	up_ACOR_VSMC
GO:0030224	0.778	0.572	1	18	monocyte differentiation	BP	1	MEF2C	up_VCAV_EC
GO:1903131	0.778	0.572	1	18	mononuclear cell differentiation	BP	1	MEF2C	up_VCAV_EC
GO:2001141	0.778	0.583	1	979	regulation of RNA biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0009890	0.778	0.567	1	420	negative regulation of biosynthetic process	BP	1	NR1H4	up_VPUL_EC
GO:0006509	0.778	0.574	1	15	membrane protein ectodomain proteolysis	BP	1	TIMP2	up_VSAP_EC
GO:0045022	0.778	0.574	1	15	early endosome to late endosome transport	BP	1	EMP2	up_VSAP_EC
GO:1903046	0.778166113	0.56188	1	55	meiotic cell cycle process	BP	1	FIGNL1	up_ACOR_EC
GO:1901991	0.778991875	0.56056	1	56	negative regulation of mitotic cell cycle phase	BP	1	BRSK1	up_ACOR_EC

GO:0032989	0.779	0.317	12	292	cellular component morphogenesis	BP	1	NDN,TRPV2,NUMBL,SEMA3C,POLDIP2,THY1,TLX2,GLI3,ENSCAFG00000017708,UST,GREM1,BRSK1	down_VCAV_EC
GO:0018193	0.779	0.347	7	368	peptidyl-amino acid modification	BP	1	LEP,HCK,GREM1,TPST2,CAMK2A,DMPK,ADAM17	up_AFEM_EC
GO:0007283	0.779	0.349	7	91	spermatogenesis	BP	1	HOXA11,HOXA9,ZNF449,HERPUD2,ZBTB16,PATZ1,KDM2B	up_VSAP_EC
GO:0031032	0.779	0.393	4	61	actomyosin structure organization	BP	1	NF2,STMN1,RAC1,SIX4	down_ACOR_VSMC
GO:0051716	0.779	0.413	4	2001	cellular response to stimulus	BP	1	EYA1,NETO1,FBP1,SHOX2	up_VFEM_VSMC
GO:0043401	0.779	0.42	3	46	steroid hormone mediated signaling	BP	1	SMARCA4,UFSP2,KDM3A	up_VCAV_EC
GO:0002822	0.779	0.421	3	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	CD274,STAT6,PPP3CB	up_VSAP_EC
GO:0098656	0.779	0.421	3	42	anion transmembrane transport	BP	1	OSR1,SLC25A12,CLCN2	up_VSAP_EC
GO:0015849	0.779	0.462	2	56	organic acid transport	BP	1	FOLR2,AKT2	down_VCAV_EC
GO:0046942	0.779	0.462	2	56	carboxylic acid transport	BP	1	FOLR2,AKT2	down_VCAV_EC
GO:0060688	0.779	0.468	2	29	regulation of morphogenesis of a	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0016050	0.779	0.46	2	119	vesicle organization	BP	1	RAB20,RAB7A	up_AFEM_EC
GO:0051881	0.779	0.569	1	19	regulation of mitochondrial membrane	BP	1	PRELID1	down_ACOR_VSMC
GO:0110111	0.779	0.571	1	17	negative regulation of animal organ	BP	1	GREM1	down_ACOR_VSMC
GO:0000018	0.779	0.564	1	31	regulation of DNA recombination	BP	1	FBH1	down_VCAV_EC
GO:0030183	0.779	0.564	1	30	B cell differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0045833	0.779	0.565	1	29	negative regulation of lipid metabolic process	BP	1	ORMDL3	down_VCAV_EC
GO:0098876	0.779	0.564	1	29	vesicle-mediated transport to the plasma	BP	1	RAB31	down_VCAV_EC
GO:0090630	0.779	0.567	1	23	activation of GTPase activity	BP	1	TAX1BP3	down_VSAP_EC
GO:0097306	0.779	0.567	1	22	cellular response to alcohol	BP	1	CTNNB1	down_VSAP_EC
GO:0006111	0.779	0.573	1	15	regulation of gluconeogenesis	BP	1	LEP	up_ACOR_VSMC
GO:0031638	0.779	0.573	1	15	zymogen activation	BP	1	PERP	up_ACOR_VSMC
GO:0043537	0.779	0.573	1	15	negative regulation of blood vessel endothelial	BP	1	JUP	up_ACOR_VSMC
GO:0050849	0.779	0.572	1	15	negative regulation of calcium-mediated	BP	1	ITPR1	up_ACOR_VSMC
GO:0002066	0.779	0.57	1	17	columnar/cuboidal epithelial cell	BP	1	HIF1A	up_VCAV_EC
GO:0045646	0.779	0.569	1	19	regulation of erythrocyte differentiation	BP	1	HIF1A	up_VCAV_EC
GO:0030855	0.779	0.561	1	183	epithelial cell differentiation	BP	1	BARX1	up_VPOR_EC
GO:0090087	0.779	0.561	1	185	regulation of peptide transport	BP	1	GCC2	up_VPOR_EC
GO:0034613	0.779	0.571	1	576	cellular protein localization	BP	1	LHFPL4	up_VPOR_VSMC
GO:0012501	0.779	0.569	1	561	programmed cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0010657	0.779	0.572	1	15	muscle cell apoptotic process	BP	1	MFN2	up_VSAP_EC
GO:0001937	0.779	0.573	1	15	negative regulation of endothelial cell	BP	1	ACVRL1	up_VSAP_EC
GO:0042304	0.779	0.572	1	15	regulation of fatty acid biosynthetic process	BP	1	INSIG2	up_VSAP_EC
GO:0034340	0.779	0.572	1	15	response to type I interferon	BP	1	MAVS	up_VSAP_EC
GO:0006898	0.77964915	0.55949	1	57	receptor-mediated endocytosis	BP	1	CALY	up_ACOR_EC
GO:0008150	0.78	0.424	13	5646	biological_process	BP	1	HOXC10,DKK2,ENSCAFG00000005494,HOXA9,HOXC6,LNPEP,SGCD,ERC1,TAOK1,DUSP2,BPI,CTNNAL1,GPR155	up_AORT_EC

GO:0051272	0.78	0.316	12	170	positive regulation of cellular component movement	BP	1	HMGB1,FBXO5,CAV1,MMP14,STMN1,RAC1,CORO1A,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0030036	0.78	0.33	9	223	actin cytoskeleton organization	BP	1	KIRREL1,RHOD,ENSCAFG00000014978,WIPF1,MYO1B,ACTR3B,SHC1,PLEKHH2,RAC2	down_VCAV_EC
GO:0032970	0.78	0.37	5	130	regulation of actin filament-based process	BP	1	KIRREL1,RHOD,ENSCAFG00000014978,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0072330	0.78	0.372	5	68	monocarboxylic acid biosynthetic process	BP	1	EDN1,ALDOC,DDIT4,PARK7,ELOVL7	up_ACOR_VSMC
GO:0006606	0.78	0.373	5	67	protein import into nucleus	BP	1	CDH1,PIK3R1,NUP98,SNUPN,MAVS	up_VSAP_EC
GO:0010556	0.78	0.427	3	1137	regulation of macromolecule	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0043534	0.78	0.46	2	57	blood vessel endothelial cell migration	BP	1	SPRED1,GREM1	down_VCAV_EC
GO:0043255	0.78	0.466	2	29	regulation of carbohydrate biosynthetic	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:1901222	0.78	0.465	2	32	regulation of NIK/NF-kappaB signaling	BP	1	TLR3,ENSCAFG00000002015	up_VCAV_EC
GO:0016310	0.78	0.466	2	641	phosphorylation	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0030148	0.78	0.563	1	28	sphingolipid biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:0048844	0.78	0.562	1	30	artery morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0006942	0.78	0.564	1	26	regulation of striated muscle contraction	BP	1	CALM1	down_VSAP_EC
GO:0070727	0.78	0.569	1	579	cellular macromolecule localization	BP	1	LHFPL4	up_VPOR_VSMC
GO:0006111	0.78	0.571	1	15	regulation of gluconeogenesis	BP	1	PDK2	up_VSAP_EC
GO:1900744	0.78	0.571	1	15	regulation of p38MAPK cascade	BP	1	SASH1	up_VSAP_EC
GO:0007623	0.7805286	0.55833	1	55	circadian rhythm	BP	1	PTGDS	up_ACOR_EC
GO:0006302	0.781	0.338	8	97	double-strand break repair	BP	1	CDC7,TP53BP1,ZNF365,MARF1,PARP9,DMC1,WDR48,FAN1	up_ACOR_VSMC
GO:0007409	0.781	0.337	8	109	axonogenesis	BP	1	EPHB1,IFRD1,RELN,GATA3,RAB11A,STMN1,CREB1,SPTBN4	up_VCAV_EC
GO:0070997	0.781	0.356	6	93	neuron death	BP	1	EPHB1,CD34,MEF2C,TLR4,GATA3,HIF1A	up_VCAV_EC
GO:0008544	0.781	0.37	5	75	epidermis development	BP	1	FLNB,NAB2,EZH2,HOXA7,GLI1	down_ACOR_VSMC
GO:0033673	0.781	0.37	5	84	negative regulation of kinase activity	BP	1	PPP2R5A,TNFAIP3,HHEX,PREX2,SH3BP5	up_VCAV_EC
GO:0002262	0.781	0.391	4	54	myeloid cell homeostasis	BP	1	ANKRD54,ZFP36L1,HMOX1,CITED2	up_VSAP_EC
GO:0035264	0.781	0.389	4	56	multicellular organism growth	BP	1	RARG,ZFP36L1,FXN,HTRA2	up_VSAP_EC
GO:0002366	0.781	0.414	3	65	leukocyte activation involved in immune	BP	1	SOCS5,TFRC,LYN	down_VSAP_EC
GO:0106106	0.781	0.417	3	48	cold-induced thermogenesis	BP	1	TLR4,ADIPOR2,KDM3A	up_VCAV_EC
GO:0120161	0.781	0.417	3	48	regulation of cold-induced thermogenesis	BP	1	TLR4,ADIPOR2,KDM3A	up_VCAV_EC
GO:0006352	0.781	0.459	2	56	DNA-templated transcription, initiation	BP	1	CLSTN1,CRCP	down_VCAV_EC
GO:0050821	0.781	0.46	2	48	protein stabilization	BP	1	CRYAB,CDC37	down_VSAP_EC
GO:2000106	0.781	0.464	2	29	regulation of leukocyte apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0002824	0.781	0.465	2	29	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	CD274,STAT6	up_VSAP_EC
GO:1905207	0.781	0.567	1	17	regulation of cardiocyte differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0044774	0.781	0.56	1	30	mitotic DNA integrity checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:0001578	0.781	0.563	1	23	microtubule bundle formation	BP	1	CCSER2	down_VSAP_EC
GO:0044786	0.781	0.564	1	23	cell cycle DNA replication	BP	1	ZPR1	down_VSAP_EC
GO:0032755	0.781	0.563	1	24	positive regulation of interleukin-6 production	BP	1	ARHGEF2	down_VSAP_EC
GO:0090224	0.781	0.568	1	16	regulation of spindle organization	BP	1	SENP6	up_VCAV_EC

GO:0045744	0.781	0.569	1	15	negative regulation of G protein-coupled receptor signaling pathway	BP	1	UBQLN2	up_VSAP_EC
GO:0003401	0.781	0.57	1	15	axis elongation	BP	1	WNT11	up_VSAP_EC
GO:0019076	0.781	0.569	1	15	viral release from host cell	BP	1	PC	up_VSAP_EC
GO:0035890	0.781	0.569	1	15	exit from host	BP	1	PC	up_VSAP_EC
GO:0035891	0.781	0.569	1	15	exit from host cell	BP	1	PC	up_VSAP_EC
GO:0052126	0.781	0.569	1	15	movement in host environment	BP	1	PC	up_VSAP_EC
GO:0052192	0.781	0.569	1	15	movement in environment of other organism involved in	BP	1	PC	up_VSAP_EC
GO:0007167	0.782	0.287	23	274	enzyme linked receptor protein signaling pathway	BP	1	FZD1,HNF4A,FGF7,ABL1,DLL1,EPN2,PDGFD,CCBE1,STAT5A,PDK2,PIK3R1,ZEB1,SULF2,LRP4,NCEH1,HPGD,IGFBP6,RAF1,ZFAND5,ACVRL1,NCK1,TGFBR2,CITED2	up_VSAP_EC
GO:0071704	0.782	0.338	14	3535	organic substance metabolic process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,GATM,SALL1,GALNT17,IRX5,PRR16,TLR2,CAV1,SHOX2	up_VSAP_VSMC
GO:0031328	0.782	0.323	10	512	positive regulation of cellular biosynthetic	BP	1	HOXA9,LBH,PRR16,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0098660	0.782	0.329	9	141	inorganic ion transmembrane transport	BP	1	PDE4D,CHD7,APLNR,SLC39A8,KCNJ3,KCNJ2,SLC25A25,PLCG2,MCU	up_VCAV_EC
GO:0002263	0.782	0.37	5	68	cell activation involved in immune response	BP	1	ABL1,DLL1,STAT6,F2RL1,STX4	up_VSAP_EC
GO:0016051	0.782	0.387	4	63	carbohydrate biosynthetic process	BP	1	MPDU1,B3GNT2,B4GALT1,PGD	down_ACOR_VSMC
GO:1903364	0.782	0.389	4	61	positive regulation of cellular protein catabolic	BP	1	PLK3,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0006352	0.782	0.389	4	56	DNA-templated transcription, initiation	BP	1	MED14,GTF3C1,CLSTN1,GTF2A1L	up_ACOR_VSMC
GO:1901575	0.782	0.388	4	643	organic substance catabolic process	BP	1	FBP1,ABHD5,USP33,RNF6	up_VPOR_EC
GO:0001837	0.782	0.416	3	48	epithelial to mesenchymal transition	BP	1	EZH2,GREM1,NOLC1	down_ACOR_VSMC
GO:0015711	0.782	0.412	3	81	organic anion transport	BP	1	FOLR2,AKT2,SCP2	down_VCAV_EC
GO:0044260	0.782	0.457	3	2593	cellular macromolecule metabolic process	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0051592	0.782	0.462	2	33	response to calcium ion	BP	1	CAV1,IQGAP1	down_ACOR_VSMC
GO:0007156	0.782	0.464	2	26	homophilic cell adhesion via plasma membrane adhesion molecules	BP	1	CDH18,CELSR2	up_ACOR_VSMC
GO:0035304	0.782	0.464	2	29	regulation of protein dephosphorylation	BP	1	SMPD1,DUSP26	up_ACOR_VSMC
GO:0034620	0.782	0.461	2	38	cellular response to unfolded protein	BP	1	ATF3,NCK1	up_VCAV_EC
GO:0071479	0.782	0.463	2	29	cellular response to ionizing radiation	BP	1	TNKS1BP1,FBXO4	up_VSAP_EC
GO:0043647	0.782	0.567	1	17	inositol phosphate metabolic process	BP	1	NUDT3	down_ACOR_VSMC
GO:0008152	0.782	0.716	1	3714	metabolic process	BP	1	CST3	down_AORT_EC
GO:0010389	0.782	0.559	1	30	regulation of G2/M transition of mitotic cell	BP	1	BRSK1	down_VCAV_EC
GO:0010923	0.782	0.559	1	30	negative regulation of phosphatase activity	BP	1	SPRED1	down_VCAV_EC
GO:0019079	0.782	0.56	1	29	viral genome replication	BP	1	MAVS	down_VCAV_EC
GO:0030500	0.782	0.562	1	25	regulation of bone mineralization	BP	1	HIF1A	down_VSAP_EC
GO:0046634	0.782	0.561	1	24	regulation of alpha-beta T cell activation	BP	1	SOCS5	down_VSAP_EC
GO:0048278	0.782	0.562	1	25	vesicle docking	BP	1	EXOC5	down_VSAP_EC
GO:0048519	0.782	0.597	1	1554	negative regulation of biological process	BP	1	GATA5	down_VSAP_VSMC
GO:0031016	0.782	0.568	1	15	pancreas development	BP	1	BMP4	up_ACOR_VSMC
GO:0002053	0.782	0.567	1	15	positive regulation of mesenchymal cell	BP	1	FGFR2	up_ACOR_VSMC
GO:0045191	0.782	0.569	1	14	regulation of isotype switching	BP	1	TP53BP1	up_ACOR_VSMC
GO:0055021	0.782	0.568	1	15	regulation of cardiac muscle tissue growth	BP	1	SAV1	up_VSAP_EC

GO:0015849	0.782503324	0.55526	1	56	organic acid transport	BP	1	CFI	up_ACOR_EC
GO:0046942	0.782503324	0.55526	1	56	carboxylic acid transport	BP	1	CFI	up_ACOR_EC
GO:0031324	0.783	0.258	65	735	negative regulation of cellular metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,INSIG2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,SLIT2,CST3,ZHX3,ABL1,PEX2,HDAC7,OSR1,TENT5C,KLF15,RARG,CBX7,STAT6,RECK,PLPP3,ENSCAFG00000000071,F2RL1,GLIS2,ZFP36L1,GAS1,MYC,PIK3IP1,SHOX2,TMEM225B,H2AFJ,ZC3H10,RTN4RL1,POLDIP2,IKZF2,PASK,ANKHD1,PHF1,FBXO7,LIMD1,CDK9,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ACVRL1,UBQLN2,HTRA2,TNRC6C,NCK1,HMOX1,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0016311	0.783	0.366	5	106	dephosphorylation	BP	1	NUAK1,PPP1R12A,HTT,ARFGEF3,CALM1	down_VSAP_EC
GO:0046883	0.783	0.414	3	49	regulation of hormone secretion	BP	1	SREBF1,BIRC5,ENSCAFG00000005299	down_ACOR_VSMC
GO:0072331	0.783	0.457	2	49	signal transduction by p53 class mediator	BP	1	SESN2,CDKN1A	down_VSAP_EC
GO:0007492	0.783	0.463	2	27	endoderm development	BP	1	BMP4,LAMA3	up_ACOR_VSMC
GO:1903305	0.783	0.459	2	36	regulation of regulated secretory pathway	BP	1	RAB27A,FES	up_VCAV_EC
GO:0019637	0.783	0.456	2	342	organophosphate metabolic process	BP	1	AK5,FBP1	up_VPOR_EC
GO:0032611	0.783	0.564	1	17	interleukin-1 beta production	BP	1	ARG2	down_ACOR_VSMC
GO:0043299	0.783	0.563	1	18	leukocyte degranulation	BP	1	CORO1A	down_ACOR_VSMC
GO:0097305	0.783	0.558	1	31	response to alcohol	BP	1	ADCY6	down_VCAV_EC
GO:2001257	0.783	0.557	1	30	regulation of cation channel activity	BP	1	CACNB3	down_VCAV_EC
GO:0002200	0.783	0.56	1	23	somatic diversification of immune receptors	BP	1	TFRC	down_VSAP_EC
GO:0002562	0.783	0.56	1	23	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	TFRC	down_VSAP_EC
GO:0016444	0.783	0.56	1	23	somatic cell DNA recombination	BP	1	TFRC	down_VSAP_EC
GO:0042255	0.783	0.558	1	29	ribosome assembly	BP	1	RSL24D1	down_VSAP_EC
GO:0016051	0.783	0.554	1	63	carbohydrate biosynthetic process	BP	1	LEP	up_AFEM_EC
GO:0006414	0.783	0.566	1	15	translational elongation	BP	1	EEF2	up_VSAP_EC
GO:0097193	0.783268079	0.45405	2	109	intrinsic apoptotic signaling pathway	BP	1	FIGNL1,CLU	up_ACOR_EC
GO:0009893	0.784	0.252	90	995	positive regulation of metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MBP,LIPT2,SKP2,PRKAA2,MLLT3,BMP4,FGFR2,TP53BP1,GJA1,ATRX,MED14,TLR3,SH3RF2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,AR,SASH1,LMO4,FGF18,PLAC8B,F2RL1,FAM129A,DAPK1,RBM4B,BNIP3,EGLN1,CDKN1A,CRLF3,NRP1,PTPN22,NPNT,ATP7A,SMARCD3,SMPD1,CCDC3,PRKCE,CCNT1,FRS2,RNF19A,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,CCL5,DDR2,PERP,DUSP22,EDN1,AKTIP,DUSP26,NOD2,FAM107A,DISC1,SH3RF3,DCUN1D4,HERPUD1,RPRD1B,MAP3K7,INPP5K,WFS1,ZKSCAN1,SH3BP4,ENSCAFG00000029553,PARK7,TEAD1,NGRN,HMBOX1,SSBP2,BVES,CRKL	up_ACOR_VSMC

GO:0034645	0.784	0.257	72	1546	cellular macromolecule biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,LMO4,CLIP3,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,AKT2,LCAT,SAMD4B,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,DDOST,VDR,PRMT6,CXXC5,GFPT2,PIGS,EIF3K,NECAB3,TEAD1,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,ZFP36L1,MYDGF,RPL27,MAVS,MRPS11,LOXL3,RPS27,FUT8,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0051246	0.784	0.297	17	832	regulation of protein metabolic process	BP	1	LEP,PRR16,GAS1,CRYAB,F3,GREM1,CLEC16A,CYLD,LRRC15,RECK,DCUN1D3,RAB7A,AXIN2,CCL5,CTIF,ADAM17,SAMD4B	up_AFEM_EC
GO:0043170	0.784	0.348	10	2980	macromolecule metabolic process	BP	1	NR1H4,MAPK10,HOXA3,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0044403	0.784	0.328	9	116	symbiont process	BP	1	USP6NL,MX1,ISG15,F2RL1,CTSB,ULK2,DAG1,ATG16L2,INPP5K	up_ACOR_VSMC
GO:0048732	0.784	0.333	8	116	gland development	BP	1	HOXA3,CAV1,EZH2,E2F8,B4GALT1,HOXA9,GLI1,SIX4	down_ACOR_VSMC
GO:0046777	0.784	0.343	7	86	protein autophosphorylation	BP	1	RASSF2,FGFR2,GRK7,DAPK1,ULK2,DDR2,LMTK2	up_ACOR_VSMC
GO:0045927	0.784	0.385	4	61	positive regulation of growth	BP	1	MMP14,PPARD,EZR,GLI1	down_ACOR_VSMC
GO:0007623	0.784	0.386	4	55	circadian rhythm	BP	1	CHRM1,NR2F6,NCOA2,ASS1	up_VSAP_EC
GO:0019222	0.784	0.437	3	1934	regulation of metabolic process	BP	1	CST3,HDAC7,CITED2	down_VPOR_EC
GO:0009059	0.784	0.431	3	1563	macromolecule biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0010646	0.784	0.417	3	945	regulation of cell communication	BP	1	EYA1,TIAM1,CYP26B1	up_VFEM_EC
GO:0007612	0.784	0.459	2	33	learning	BP	1	HMGCR,AAAS	down_ACOR_VSMC
GO:0002758	0.784	0.456	2	46	innate immune response-activating signal	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0018107	0.784	0.456	2	45	peptidyl-threonine phosphorylation	BP	1	GSK3B,CAMK2D	down_VSAP_EC
GO:0002221	0.784	0.456	2	46	pattern recognition receptor signaling	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0043123	0.784	0.456	2	46	positive regulation of I-kappaB kinase/NF-kappaB	BP	1	MTDH,CTNNB1	down_VSAP_EC
GO:0009953	0.784	0.459	2	34	dorsal/ventral pattern formation	BP	1	DLL4,EDN1	up_VCAV_EC
GO:1900182	0.784	0.46	2	33	positive regulation of protein localization to	BP	1	HCLS1,TMEM173	up_VCAV_EC
GO:0042058	0.784	0.562	1	17	regulation of epidermal growth factor receptor	BP	1	NUP62	down_ACOR_VSMC
GO:0034502	0.784	0.556	1	30	protein localization to chromosome	BP	1	NABP2	down_VCAV_EC
GO:1903670	0.784	0.556	1	30	regulation of sprouting angiogenesis	BP	1	SPRED1	down_VCAV_EC
GO:0042307	0.784	0.558	1	23	positive regulation of protein import into	BP	1	ZPR1	down_VSAP_EC
GO:0043388	0.784	0.563	1	16	positive regulation of DNA binding	BP	1	PARK7	up_ACOR_VSMC
GO:0055081	0.784	0.563	1	17	anion homeostasis	BP	1	ABCA1	up_VCAV_EC
GO:0070201	0.784	0.553	1	187	regulation of establishment of protein	BP	1	GCC2	up_VPOR_EC
GO:0019637	0.784	0.556	1	342	organophosphate metabolic process	BP	1	ADCY3	up_VFEM_EC
GO:1902235	0.784	0.565	1	15	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic	BP	1	NCK1	up_VSAP_EC
GO:0019068	0.784	0.565	1	15	virion assembly	BP	1	PC	up_VSAP_EC
GO:0050654	0.784	0.565	1	15	chondroitin sulfate proteoglycan metabolic	BP	1	CHST7	up_VSAP_EC
GO:0070374	0.784440469	0.55224	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	NRP1	up_ACOR_EC
GO:0001838	0.784478223	0.55226	1	56	embryonic epithelial tube formation	BP	1	SOX9	up_ACOR_EC
GO:0043112	0.784639232	0.55193	1	57	receptor metabolic process	BP	1	CALY	up_ACOR_EC
GO:0030705	0.784860054	0.55168	1	56	cytoskeleton-dependent intracellular transport	BP	1	DYNC1I1	up_ACOR_EC

GO:0060255	0.785	0.244	164	1782	regulation of macromolecule metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MEIS2,MBP,FBXL20,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,ZNF331,FGFR2,TP53BP1,EIF4A2,GJA1,ELF1,ATRX,MED14,TRPS1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,ISG15,ZNF782,ZNF365,AR,ZNF484,SASH1,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,CDKN2B,CST3,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,PTPN22,LRPAP1,NPNT,OS9,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,MARF1,FRS2,RNF19A,CCPG1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,MXI1,CHD7,JUP,TLE4,SPINK2,ZNF432,CCL5,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,OXR1,RNF141,AKTIP,DUSP26,CBX7,NOD2,LRRC4,ARID5B,FAM107A,ZNF629,PRKAG3,ZFP3,ENSCAFG00000018360,DISC1,SH3RF3,DCUN1D4,KLF11,HERPUD1,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,LHX9,WFS1,AZIN2,WDR48,CTIF,ZKSCAN1,ZN	up_ACOR_VSMC
GO:0051604	0.785	0.333	8	102	protein maturation	BP	1	KLKB1,NAA60,CCBE1,LMF1,GAS1,FKRP,TSPAN5,LONP2	up_VSAP_EC
GO:0019538	0.785	0.365	6	1713	protein metabolic process	BP	1	EYA1,MAP2K6,MME,TRIM9,CDC42EP5,CHST7	up_VFEM_EC
GO:0051146	0.785	0.365	5	76	striated muscle cell differentiation	BP	1	SDC1,MMP14,EZH2,GREM1,SIX4	down_ACOR_VSMC
GO:0009144	0.785	0.381	4	103	purine nucleoside triphosphate metabolic	BP	1	ATP5MC1,UQCR10,ADK,PARK7	down_VCAV_EC
GO:0000724	0.785	0.385	4	57	double-strand break repair via homologous	BP	1	FIGNL1,BLM,SMC5,GINS4	up_VCAV_EC
GO:0030323	0.785	0.383	4	65	respiratory tube development	BP	1	HHEX,PROX1,TIMELESS,CREB1	up_VCAV_EC
GO:0030902	0.785	0.413	3	41	hindbrain development	BP	1	SEC24B,ZNF365,ATRN	up_ACOR_VSMC
GO:0048588	0.785	0.413	3	44	developmental cell growth	BP	1	IFRD1,EDN1,RAB11A	up_VCAV_EC
GO:0048731	0.785	0.472	2	1247	system development	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0009612	0.785	0.454	2	47	response to mechanical stimulus	BP	1	BNIP3,HTT	down_VSAP_EC
GO:0007265	0.785	0.452	2	121	Ras protein signal transduction	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0090101	0.785	0.458	2	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CTDSPL2,SKIL	up_VCAV_EC
GO:0098876	0.785	0.459	2	29	vesicle-mediated transport to the plasma	BP	1	RAB11B,CCDC93	up_VSAP_EC
GO:0030224	0.785	0.561	1	18	monocyte differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:0051965	0.785	0.561	1	17	positive regulation of synapse assembly	BP	1	TPBG	down_ACOR_VSMC
GO:1903131	0.785	0.561	1	18	mononuclear cell differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:0055081	0.785	0.562	1	17	anion homeostasis	BP	1	HOXA3	down_ACOR_VSMC
GO:0006638	0.785	0.555	1	30	neutral lipid metabolic process	BP	1	GPAM	down_VCAV_EC
GO:0006639	0.785	0.555	1	30	acylglycerol metabolic process	BP	1	GPAM	down_VCAV_EC
GO:0048525	0.785	0.557	1	25	negative regulation of viral process	BP	1	REST	down_VSAP_EC
GO:0034340	0.785	0.564	1	15	response to type I interferon	BP	1	ISG15	up_ACOR_VSMC
GO:0045910	0.785	0.564	1	14	negative regulation of DNA recombination	BP	1	TP53BP1	up_ACOR_VSMC
GO:0080134	0.785	0.556	1	386	regulation of response to stress	BP	1	NR1H4	up_APUL_EC
GO:2000113	0.785	0.556	1	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0009725	0.785	0.551	1	188	response to hormone	BP	1	RNF6	up_VPOR_EC

GO:0034508	0.785	0.564	1	15	centromere complex assembly	BP	1	CENPP	up_VSAP_EC
GO:0045806	0.785	0.563	1	15	negative regulation of endocytosis	BP	1	UBQLN2	up_VSAP_EC
GO:0032729	0.785	0.563	1	15	positive regulation of interferon-gamma	BP	1	ABL1	up_VSAP_EC
GO:0051591	0.785	0.562	1	16	response to cAMP	BP	1	ZFP36L1	up_VSAP_EC
GO:0006323	0.785687823	0.55025	1	58	DNA packaging	BP	1	SOX9	up_ACOR_EC
GO:0006950	0.786	0.248	100	1102	response to stress	BP	1	VEGFD,TLR1,SMAD6,LGR6,LEP,DCBLD2,MAP3K8,MID1,CD83,CDC7,RASSF2,FBXL20,NACC2,COCH,PRKAA2,LNPK,TM7SF3,TP53BP1,MX1,ABCA1,GJA1,ATRX,HRH1,TLR3,SH3RF2,PPARGC1A,TP53INP1,ZBTB40,ISG15,ZNF365,SASH1,TMX3,ZBTB4,POLK,ITPR1,PLAC8B,ANKRD1,F2RL1,FAM129A,ENPP4,GABARAPL1,DAPK1,BNIP3,EGLN1,CDKN1A,C1S,CLSTN1,CREBRF,PTPN22,CHD2,ULK2,OS9,STT3B,EVL,PTGDR,SESN3,SH3RF1,PRKCE,MARF1,FUT8,PARP9,CHD6,APP,PSEN1,SHPRH,PIK3C3,LAMP2,CCL5,CLN8,DUSP22,EDN1,SESN1,OXR1,NOD2,DMC1,DDIT4,JAM3,SH3RF3,SERINC3,JKAMP,SCAMP5,TNFRSF11B,HERPUD1,TXNDC5,MAP3K7,FAF2,BMT2,WFS1,RPAIN,WDR48,CAT,DZIP3,ENSCAFG00000029553,NMNAT1,PARK7,STC2,ZFYVE1,BVES,RREB1,FAN1	up_ACOR_VSMC
GO:0008104	0.786	0.271	34	763	protein localization	BP	1	GPAM,SNX18,LRP1,PRNP,FBN1,TLN2,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SNUPN,SSR2,TRIM8,SCAMP4,CLTB,SSR3,WDR45,PEX5,SCAMP2,GLI3,PARK7,ARL2BP,MAVS,CDH2,TOM1,SEC61B,GLIS2,RAB31,HM13,ARHGAP1,EVI5L,LONP2,SEC61A1	down_VCAV_EC
GO:0051336	0.786	0.291	18	251	regulation of hydrolase activity	BP	1	HMGB1,SLC29A1,PRELID1,BIRC5,ABHD5,EZH2,PCNA,PDCD2,DHCR24,CYCS,IQGAP1,IQGAP2,HMGB2,ENSCAFG00000005299,AIFM1,TRAPPC6A,KNL1,DELE1	down_ACOR_VSMC
GO:0031347	0.786	0.318	10	144	regulation of defense response	BP	1	HMGB1,IRAK1,SLC29A1,CAV1,ARG2,CACTIN,HMGB2,RBM14,POLR3F,BAP1	down_ACOR_VSMC
GO:0015980	0.786	0.332	8	106	energy derivation by oxidation of organic	BP	1	LEP,PPARGC1A,BNIP3,PYGM,GAA,INPP5K,SLC25A12,PARK7	up_ACOR_VSMC
GO:0006631	0.786	0.341	7	93	fatty acid metabolic process	BP	1	LEP,PPARGC1A,ACAD11,CYP2J2,EDN1,HPGD,ELOVL7	up_ACOR_VSMC
GO:0009152	0.786	0.351	6	80	purine ribonucleotide biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,ELOVL7	up_ACOR_VSMC
GO:0001934	0.786	0.361	5	274	positive regulation of protein phosphorylation	BP	1	LEP,GREM1,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0009914	0.786	0.383	4	64	hormone transport	BP	1	SREBF1,BIRC5,FAM129B,ENSCAFG00000005299	down_ACOR_VSMC
GO:0016070	0.786	0.395	4	1479	RNA metabolic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0006906	0.786	0.383	4	55	vesicle fusion	BP	1	TBC1D10C,TBC1D2B,STX4,VPS11	up_VSAP_EC
GO:0050776	0.786	0.406	3	173	regulation of immune response	BP	1	LEP,CD40,CYLD	up_AFEM_EC
GO:0031328	0.786	0.409	3	512	positive regulation of cellular biosynthetic	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0030218	0.786	0.411	3	42	erythrocyte differentiation	BP	1	ANKRD54,ZFP36L1,CITED2	up_VSAP_EC
GO:1904375	0.786	0.455	2	35	regulation of protein localization to cell	BP	1	PPP2R5A,EPB41	up_VCAV_EC
GO:1903146	0.786	0.559	1	17	regulation of autophagy of mitochondrion	BP	1	SREBF1	down_ACOR_VSMC
GO:0015718	0.786	0.554	1	30	monocarboxylic acid transport	BP	1	AKT2	down_VCAV_EC
GO:0042133	0.786	0.553	1	30	neurotransmitter metabolic process	BP	1	MAOA	down_VCAV_EC
GO:0065009	0.786	0.563	1	735	regulation of molecular function	BP	1	CST3	down_VPOR_EC
GO:0106027	0.786	0.556	1	24	neuron projection organization	BP	1	APOE	down_VSAP_EC
GO:0015991	0.786	0.561	1	16	ATP hydrolysis coupled proton transport	BP	1	ATP6V0E1	up_ACOR_VSMC
GO:0090311	0.786	0.562	1	15	regulation of protein deacetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0090662	0.786	0.561	1	16	ATP hydrolysis coupled transmembrane transport	BP	1	ATP6V0E1	up_ACOR_VSMC
GO:0099131	0.786	0.561	1	16	ATP hydrolysis coupled ion transmembrane	BP	1	ATP6V0E1	up_ACOR_VSMC

GO:0042594	0.786	0.55	1	64	response to starvation	BP	1	CLEC16A	up_AFEM_EC
GO:0005975	0.786	0.55	1	183	carbohydrate metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0031638	0.786	0.562	1	15	zymogen activation	BP	1	KLKB1	up_VSAP_EC
GO:0018105	0.787	0.323	9	116	peptidyl-serine phosphorylation	BP	1	CAMKK2,TNKS1BP1,MORC3,RAF1,NCK1,ULK1,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0055080	0.787	0.336	7	176	cation homeostasis	BP	1	PRNP,SLC39A6,THY1,ATP6V0C,SCARA5,CYBA,ATOX1	down_VCAV_EC
GO:0042254	0.787	0.36	5	128	ribosome biogenesis	BP	1	RPS10,RPL27,MRPS11,RPS27,RPLP0	down_VCAV_EC
GO:0043122	0.787	0.381	4	62	regulation of I-kappaB kinase/NF-kappaB	BP	1	IRAK1,MTDH,NUP62,CTH	down_ACOR_VSMC
GO:0060255	0.787	0.43	3	1782	regulation of macromolecule metabolic	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0046483	0.787	0.433	3	1948	heterocycle metabolic process	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0009855	0.787	0.409	3	42	determination of bilateral symmetry	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:1901292	0.787	0.454	2	34	nucleoside phosphate catabolic process	BP	1	NUDT1,NUDT3	down_ACOR_VSMC
GO:0043473	0.787	0.457	2	28	pigmentation	BP	1	ATRN,RAB11B	up_ACOR_VSMC
GO:1990542	0.787	0.455	2	32	mitochondrial transmembrane transport	BP	1	MICU2,SLC25A12	up_ACOR_VSMC
GO:0007043	0.787	0.457	2	28	cell-cell junction assembly	BP	1	PKP4,JUP	up_ACOR_VSMC
GO:0007040	0.787	0.455	2	33	lysosome organization	BP	1	HOOK3,ABCA1	up_VCAV_EC
GO:0044264	0.787	0.456	2	32	cellular polysaccharide metabolic process	BP	1	PCDH12,PPP1CB	up_VCAV_EC
GO:0080171	0.787	0.455	2	33	lytic vacuole organization	BP	1	HOOK3,ABCA1	up_VCAV_EC
GO:0090501	0.787	0.456	2	29	RNA phosphodiester bond hydrolysis	BP	1	EXOSC7,RCL1	up_VSAP_EC
GO:0044281	0.787	0.456	2	622	small molecule metabolic process	BP	1	GATM,CAV1	up_VSAP_VSMC
GO:1901983	0.787	0.554	1	24	regulation of protein acetylation	BP	1	IWS1	down_VSAP_EC
GO:1990868	0.787	0.559	1	16	response to chemokine	BP	1	CCL5	up_ACOR_VSMC
GO:1990869	0.787	0.559	1	16	cellular response to chemokine	BP	1	CCL5	up_ACOR_VSMC
GO:0030324	0.787	0.548	1	64	lung development	BP	1	THRB	up_AFEM_EC
GO:0016126	0.787	0.555	1	20	sterol biosynthetic process	BP	1	LBR	up_VCAV_EC
GO:0042149	0.787	0.558	1	17	cellular response to glucose starvation	BP	1	PMAIP1	up_VCAV_EC
GO:0031128	0.787	0.56	1	15	developmental induction	BP	1	HOXA11	up_VSAP_EC
GO:0019538	0.788	0.241	155	1713	protein metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,SKP2,PRKAA2,ITM2C,BMP4,CPXM1,LCAT,B3GNT7,FGFR2,CCDC126,ABCA1,EIF4A2,ATRX,TARSL2,TLR3,SH3RF2,LATS2,PIGN,PDE5A,PIGS,ISG15,ZNRF3,SASH1,CTSS,PTPN3,FGF18,NDRG2,TMX3,CDKN2B,USP53,GRK7,CST3,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,PSEN2,ERO1B,DAPK1,APOL6,CTSB,RBM4B,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,C1S,NRP1,UBR1,PTPN22,ULK2,DMPK,NPNT,OS9,STT3B,SMPD1,FUT11,C7,UBE2H,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,FRS2,RNF19A,LYPLAL1,SCG5,DAG1,FUT8,POMK,PARP9,APP,PSEN1,PCSK6,SYNJ2BP,SHPRH,PIK3C3,LAMP2,SPINK2,CCL5,DDR2,CLN8,PERP,PSKH1,DUSP22,SIAH1,EDN1,OXR1,RNF141,PHF20,AKTIP,CTSF,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PCYOX1,PRKAG3,DISC1,SH3RF3,EOGT,DCUN1D4,RNF181,USP20,HERPUD1,RPRD1B,MAP3K7,INPP5K,FAF2,CNOT4,NCSTN,KLHDC8B,WFS1,AZIN2,UBA52,KLHL36,WDR48,CTIF,DZIP3,ERAP1,ENSCAFG00000029553,PARK7,NGRN,ZDHHC21,LMF1,CRKL,CDKL2	up_ACOR_VSMC

GO:1901698	0.788	0.282	22	266	response to nitrogen compound	BP	1	FOXRED2,SLIT2,CDH1,GOT1,CHRM1,MAP3K5,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,ABAT,MYD88,CASTOR1,PQBP1,UBQLN2,FLOT1,NCK1,MAVS,BGLAP	up_VSAP_EC
GO:0016050	0.788	0.328	8	119	vesicle organization	BP	1	STXBP6,SDC1,FBXO5,INSIG1,CAV1,PREB,CORO1A,TRAPPC6A	down_ACOR_VSMC
GO:0009890	0.788	0.327	8	420	negative regulation of biosynthetic process	BP	1	LEP,CRY2,HOXA7,LMCD1,THRB,GREM1,NR3C1,SAMD4B	up_AFEM_EC
GO:1901987	0.788	0.377	4	107	regulation of cell cycle phase transition	BP	1	KANK2,ZFP36L1,LSM10,BRSK1	down_VCAV_EC
GO:1990778	0.788	0.377	4	91	protein localization to cell periphery	BP	1	EXOC5,KIF5B,TNIK,BLZF1	down_VSAP_EC
GO:0031323	0.788	0.429	3	1788	regulation of cellular metabolic process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0030217	0.788	0.406	3	65	T cell differentiation	BP	1	SOCS5,PTPN2,CTNNB1	down_VSAP_EC
GO:0007050	0.788	0.406	3	53	cell cycle arrest	BP	1	CXCL8,UHRF2,SKIL	up_VCAV_EC
GO:0051247	0.788	0.406	3	502	positive regulation of protein metabolic process	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731	up_VPOR_EC
GO:0019219	0.788	0.417	3	1151	regulation of nucleobase-containing compound metabolic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0007259	0.788	0.408	3	42	JAK-STAT cascade	BP	1	IL6R,STAT5A,RTN4RL1	up_VSAP_EC
GO:0051028	0.788	0.453	2	33	mRNA transport	BP	1	DDX39A,DDX39B	down_ACOR_VSMC
GO:0000187	0.788	0.455	2	28	activation of MAPK activity	BP	1	FRS2,MAP3K7	up_ACOR_VSMC
GO:0002042	0.788	0.455	2	29	cell migration involved in sprouting angiogenesis	BP	1	NRP1,PIK3C2A	up_ACOR_VSMC
GO:0031397	0.788	0.55	1	30	negative regulation of protein ubiquitination	BP	1	PARK7	down_VCAV_EC
GO:0002286	0.788	0.552	1	24	T cell activation involved in immune response	BP	1	SOCS5	down_VSAP_EC
GO:0018023	0.788	0.553	1	23	peptidyl-lysine trimethylation	BP	1	IWS1	down_VSAP_EC
GO:0042221	0.788	0.568	1	1012	response to chemical	BP	1	TLR2	up_AFEM_VSMC
GO:0051276	0.788	0.551	1	398	chromosome organization	BP	1	NR1H4	up_APUL_EC
GO:1903901	0.788	0.555	1	19	negative regulation of viral life cycle	BP	1	PROX1	up_VCAV_EC
GO:0065003	0.788	0.557	1	616	protein-containing complex assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0019222	0.789	0.239	178	1934	regulation of metabolic process	BP	1	ADRA1B,TLR1,SMAD6,PLCG2,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MEIS2,MBP,FBXL20,RECK,LIPT2,FEZ1,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,ZNF331,FGFR2,TP53BP1,MFAP4,EIF4A2,GJA1,ELF1,ATRX,MED14,TRPS1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,ISG15,ZNF782,ZNF365,AR,ZNF484,SASH1,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,CDKN2B,CST3,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,BNIP3,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,PTPN22,LRPAP1,NPNT,OS9,ATP7A,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,SH3RF1,CCDC3,PRKCE,CCNT1,MARF1,DKKL1,FRS2,RNF19A,CCPG1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,FUT8,PPP1R26,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,MXI1,CHD7,JUP,TLE4,SPINK2,ZNF432,CCL5,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,OXR1,RNF141,AKTIP,DUSP26,CBX7,NOD2,LRRC4,ARID5B,FAM107A,ZNF629,PRKAG3,ZFP3,DDIT4,ENSCAFG00000018360,DISC1,SH3RF3,DCUN1D4,KLF11,HERPUD1,RPRD1B,ZNF461,ZNF252,FEZ2,ENSCAFG0000003	up_ACOR_VSMC
GO:0009987	0.789	0.339	21	5086	cellular process	BP	1	HOXA11,TBX15,HOXA10,HOXA9,PITX1,EMX2,NETO1,GATM,SALL1,GALNT17,HOXC10,IRX5,MAB21L1,PRR16,STIM1,TLR2,EMP1,CAV1,SHOX2,FGF5,GJB5	up_VSAP_VSMC
GO:0045859	0.789	0.288	18	219	regulation of protein kinase activity	BP	1	MAP3K14,ARHGEF5,CEP85,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,CAMKK2,DDR2,TRAF7,RTN4RL1,SASH1,FBXO7,MAP2K2,TGFBR2,LATS2	up_VSAP_EC

GO:0006163	0.789	0.31	11	174	purine nucleotide metabolic process	BP	1	NPR1,PANK3,PIPOX,ADSS,GUCY1A1,ELOVL7, ENSCAFG00000024323,SLC25A25,GUCY1B1, NOS2,HIF1A	up_VCAV_EC
GO:0032496	0.789	0.359	5	77	response to lipopolysaccharide	BP	1	IRAK1,MTDH,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:1901360	0.789	0.401	4	2016	organic cyclic compound metabolic process	BP	1	BARX1,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0033002	0.789	0.379	4	55	muscle cell proliferation	BP	1	IL6R,SAV1,MFN2,HMOX1	up_VSAP_EC
GO:0072089	0.789	0.406	3	43	stem cell proliferation	BP	1	ZFP36L1,DAGLB,FBLN1	up_VSAP_EC
GO:0007187	0.789	0.406	3	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	GPR1,ADGRD1,CHRM1	up_VSAP_EC
GO:1905897	0.789	0.451	2	34	regulation of response to endoplasmic reticulum	BP	1	PPP1R15B,TXNDC12	down_ACOR_VSMC
GO:0008033	0.789	0.448	2	52	tRNA processing	BP	1	AARS,RTCB	down_VSAP_EC
GO:0055072	0.789	0.453	2	30	iron ion homeostasis	BP	1	EGLN1,B2M	up_ACOR_VSMC
GO:0009749	0.789	0.451	2	34	response to glucose	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0044249	0.789	0.48	2	1851	cellular biosynthetic process	BP	1	CYP1A1,GATA5	up_VCAV_VSMC
GO:0051172	0.789	0.454	2	663	negative regulation of nitrogen compound	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0070647	0.789	0.547	1	311	protein modification by small protein conjugation	BP	1	USP28	down_ACOR_EC
GO:1901264	0.789	0.555	1	18	carbohydrate derivative transport	BP	1	SLC35C2	down_ACOR_VSMC
GO:0055072	0.789	0.549	1	30	iron ion homeostasis	BP	1	SCARA5	down_VCAV_EC
GO:0000288	0.789	0.551	1	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	CNOT7	down_VSAP_EC
GO:0008585	0.789	0.551	1	24	female gonad development	BP	1	INHBA	down_VSAP_EC
GO:0046545	0.789	0.551	1	24	development of primary female sexual	BP	1	INHBA	down_VSAP_EC
GO:0048701	0.789	0.55	1	25	embryonic cranial skeleton morphogenesis	BP	1	SIX4	down_VSAP_EC
GO:0071230	0.789	0.552	1	23	cellular response to amino acid stimulus	BP	1	SESN2	down_VSAP_EC
GO:0035307	0.789	0.555	1	18	positive regulation of protein	BP	1	PPP2R5A	up_VCAV_EC
GO:0051254	0.789	0.551	1	431	positive regulation of RNA metabolic process	BP	1	ARHGEF2	up_VPUL_EC
GO:0045913	0.789	0.558	1	15	positive regulation of carbohydrate metabolic	BP	1	C1QTNF2	up_VSAP_EC
GO:1901616	0.789	0.557	1	15	organic hydroxy compound catabolic	BP	1	INPP5E	up_VSAP_EC
GO:0044242	0.789850051	0.54391	1	57	cellular lipid catabolic process	BP	1	PRKCD	up_ACOR_EC
GO:0035264	0.789902877	0.54391	1	56	multicellular organism growth	BP	1	PLS1	up_ACOR_EC
GO:0006351	0.79	0.245	97	1069	transcription, DNA-templated	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2 ,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2, TP53BP1,ELF1,ATRX,MED14,TRPS1,TLR3,ELL 2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF5 50,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF57 2,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,H KR1,EGLN1,JMY,CRLF3,ENSCAFG0000000623 8,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CC NT1,CCPG1,ENSCAFG00000030568,ZNF175,Z NF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1, CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2, DUSP22,MED23,EDN1,RNF141,GTF2A1L,DUS P26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSC AFG00000018360,KLF11,RPRD1B,ZNF461,ZN F252,ENSCAFG00000030317,MAP3K7,INPP5 K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG000 00029553,YEATS2,ID3,PARK7,TEAD1,ZNF454 ,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC

GO:0042981	0.79	0.261	41	471	regulation of apoptotic process	BP	1	WNT11,CD274,ACKR3,MAP3K14,PTGFR,PLEKHF1,LIMS2,SLIT2,CRADD,ABL1,BTG1,DLL1,OSR1,MAP3K5,ADAMTSL4,SAV1,ZBTB16,RARG,AMBRA1,MFN2,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,MYC,PTPMT1,PRMT2,KDM2B,RAF1,ZNF205,STX4,QARS,ARHGAP10,HTRA2,NCK1,HMOX1,MAP2K2,CITED2,DEDD2,LATS2	up_VSAP_EC
GO:0008202	0.79	0.358	5	80	steroid metabolic process	BP	1	TIPARP,BMP2,ABCA1,PROX1,LBR	up_VCAV_EC
GO:0002062	0.79	0.405	3	48	chondrocyte differentiation	BP	1	GREM1,POC1A,SERPINH1	down_ACOR_VSMC
GO:0006725	0.79	0.429	3	1956	cellular aromatic compound metabolic	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0009913	0.79	0.404	3	47	epidermal cell differentiation	BP	1	PRKCH,FLNB,JAG1	up_VCAV_EC
GO:0023051	0.79	0.409	3	954	regulation of signaling	BP	1	EYA1,TIAM1,CYP26B1	up_VFEM_EC
GO:0044281	0.79	0.45	2	622	small molecule metabolic process	BP	1	CSGALNACT1,TNRC6B	down_ACOR_EC
GO:0051983	0.79	0.447	2	47	regulation of chromosome segregation	BP	1	NAA10,CTNNB1	down_VSAP_EC
GO:2001257	0.79	0.451	2	30	regulation of cation channel activity	BP	1	KCNE3,KLHL24	up_VSAP_EC
GO:0002294	0.79	0.554	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	HMGB1	down_ACOR_VSMC
GO:0007528	0.79	0.554	1	17	neuromuscular junction development	BP	1	SIX4	down_ACOR_VSMC
GO:0002287	0.79	0.554	1	17	alpha-beta T cell activation involved in	BP	1	HMGB1	down_ACOR_VSMC
GO:0002292	0.79	0.554	1	17	T cell differentiation involved in immune	BP	1	HMGB1	down_ACOR_VSMC
GO:0002293	0.79	0.554	1	17	alpha-beta T cell differentiation involved in	BP	1	HMGB1	down_ACOR_VSMC
GO:0042093	0.79	0.554	1	17	T-helper cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0070169	0.79	0.553	1	18	positive regulation of biomineral tissue	BP	1	FBXO5	down_ACOR_VSMC
GO:0050848	0.79	0.547	1	30	regulation of calcium-mediated signaling	BP	1	PRNP	down_VCAV_EC
GO:0055007	0.79	0.547	1	31	cardiac muscle cell differentiation	BP	1	GREM1	down_VCAV_EC
GO:0003281	0.79	0.547	1	30	ventricular septum development	BP	1	LMO4	down_VCAV_EC
GO:0110020	0.79	0.546	1	31	regulation of actomyosin structure organization	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0098693	0.79	0.549	1	25	regulation of synaptic vesicle cycle	BP	1	GSK3B	down_VSAP_EC
GO:0010390	0.79	0.555	1	15	histone monoubiquitination	BP	1	PCGF5	up_ACOR_VSMC
GO:0016180	0.79	0.556	1	15	snRNA processing	BP	1	INTS9	up_ACOR_VSMC
GO:0019233	0.79	0.554	1	16	sensory perception of pain	BP	1	POMK	up_ACOR_VSMC
GO:0030516	0.79	0.556	1	15	regulation of axon extension	BP	1	NRP1	up_ACOR_VSMC
GO:0090150	0.79	0.543	1	64	establishment of protein localization to membrane	BP	1	REEP2	up_AFEM_EC
GO:0009968	0.79	0.548	1	392	negative regulation of signal transduction	BP	1	NR1H4	up_APUL_EC
GO:0010558	0.79	0.549	1	392	negative regulation of macromolecule biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0000724	0.790415692	0.54303	1	57	double-strand break repair via homologous	BP	1	FIGNL1	up_ACOR_EC
GO:0051186	0.79057763	0.39892	3	159	cofactor metabolic process	BP	1	NMNAT2,ENSCAFG00000028814,ALDOC	up_ACOR_EC

GO:0009058	0.791	0.247	90	1910	biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,ADCY6,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,LMO4,CLIP3,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,AKT2,LCAT,SAMD4B,TFE3,NR3C1,HSD3B7,HR,SCP2,RPL23,RPL13,CLSTN1,DDOST,CYB5R3,VDR,PRMT6,UROS,ENTPD3,THNSL2,ATP5MC1,CXXC5,GFPT2,PIGS,EIF3K,NECAB3,TEAD1,ADK,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,RPL27,CYBA,AMPD2,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,RDH10,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,GLS2,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA,ACAT1	down_VCAV_EC
GO:0044419	0.791	0.319	9	117	interspecies interaction between organisms	BP	1	USP6NL,MX1,ISG15,F2RL1,CTSB,ULK2,DAG1,ATG16L2,INPP5K	up_ACOR_VSMC
GO:0034655	0.791	0.318	9	135	nucleobase-containing compound catabolic	BP	1	CDA,TENT2,CNOT6,ENSCAFG00000024323,PAN3,CNOT7,SMG7,HIF1A,DCP2	up_VCAV_EC
GO:0001655	0.791	0.325	8	116	urogenital system development	BP	1	GREM1,ARG2,HOXB7,IQGAP1,SGPL1,JMJD6,SIX4,AMER1	down_ACOR_VSMC
GO:0051346	0.791	0.357	5	78	negative regulation of hydrolase activity	BP	1	AMOT,PAK2,PTGS2,KDM5A,FKBP15	up_VCAV_EC
GO:0034404	0.791	0.403	3	50	nucleobase-containing small molecule	BP	1	NUDT1,CTPS1,NUDT3	down_ACOR_VSMC
GO:0018210	0.791	0.403	3	48	peptidyl-threonine modification	BP	1	MTOR,PRKD2,LMTK2	up_VCAV_EC
GO:0006986	0.791	0.403	3	42	response to unfolded protein	BP	1	PIK3R1,CREBRF,NCK1	up_VSAP_EC
GO:0009953	0.791	0.448	2	34	dorsal/ventral pattern formation	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0098742	0.791	0.446	2	44	cell-cell adhesion via plasma-membrane	BP	1	PVR,CDH11	down_VSAP_EC
GO:0032507	0.791	0.552	1	18	maintenance of protein location in cell	BP	1	INSIG1	down_ACOR_VSMC
GO:0043507	0.791	0.548	1	23	positive regulation of JUN kinase activity	BP	1	TNIK	down_VSAP_EC
GO:0051303	0.791	0.547	1	26	establishment of chromosome localization	BP	1	KPNB1	down_VSAP_EC
GO:0010657	0.791	0.554	1	15	muscle cell apoptotic process	BP	1	DMPK	up_ACOR_VSMC
GO:0034308	0.791	0.553	1	16	primary alcohol metabolic process	BP	1	PARK7	up_ACOR_VSMC
GO:0045620	0.791	0.554	1	15	negative regulation of lymphocyte	BP	1	BMP4	up_ACOR_VSMC
GO:0071277	0.791	0.554	1	15	cellular response to calcium ion	BP	1	PRKAA2	up_ACOR_VSMC
GO:0035303	0.791	0.542	1	65	regulation of dephosphorylation	BP	1	MYO1D	up_AFEM_EC
GO:0002366	0.791	0.542	1	65	leukocyte activation involved in immune	BP	1	DLL1	up_AFEM_EC
GO:0008219	0.791	0.551	1	611	cell death	BP	1	TAOK1	up_AORT_EC
GO:0044281	0.791	0.552	1	622	small molecule metabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0031401	0.791	0.546	1	358	positive regulation of protein modification	BP	1	MAP2K6	up_VFEM_EC
GO:0031324	0.791	0.555	1	735	negative regulation of cellular metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0065009	0.791	0.555	1	735	regulation of molecular function	BP	1	HOXA3	up_VPUL_VSMC
GO:0006333	0.79166444	0.54093	1	59	chromatin assembly or disassembly	BP	1	SOX9	up_ACOR_EC
GO:0006163	0.792	0.322	8	174	purine nucleotide metabolic process	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1,AK5	down_VSAP_EC
GO:0048762	0.792	0.356	5	77	mesenchymal cell differentiation	BP	1	EZH2,GREM1,NOLC1,PHACTR4,AMER1	down_ACOR_VSMC
GO:0010035	0.792	0.372	4	107	response to inorganic substance	BP	1	PRNP,MT2A,ANXA11,PARK7	down_VCAV_EC
GO:0000725	0.792	0.375	4	58	recombinational repair	BP	1	FIGNL1,BLM,SMC5,GINS4	up_VCAV_EC
GO:0045807	0.792	0.447	2	35	positive regulation of endocytosis	BP	1	GREM1,HIST1H1A	down_ACOR_VSMC
GO:0050851	0.792	0.447	2	34	antigen receptor-mediated signaling	BP	1	MNDA,EZR	down_ACOR_VSMC
GO:0090101	0.792	0.447	2	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	CAV1,GREM1	down_ACOR_VSMC

GO:1902107	0.792	0.444	2	47	positive regulation of leukocyte differentiation	BP	1	SOCS5,EVI2B	down_VSAP_EC
GO:1900076	0.792	0.449	2	29	regulation of cellular response to insulin	BP	1	SESN3,INPP5K	up_ACOR_VSMC
GO:1905269	0.792	0.447	2	32	positive regulation of chromatin organization	BP	1	GATA3,PRKD2	up_VCAV_EC
GO:0042552	0.792	0.448	2	30	myelination	BP	1	WASF3,AMIGO1	up_VSAP_EC
GO:0031050	0.792	0.55	1	17	dsRNA processing	BP	1	SRRT	down_ACOR_VSMC
GO:0045661	0.792	0.549	1	18	regulation of myoblast differentiation	BP	1	PPARD	down_ACOR_VSMC
GO:0070918	0.792	0.55	1	17	production of small RNA involved in gene silencing	BP	1	SRRT	down_ACOR_VSMC
GO:0120162	0.792	0.544	1	31	positive regulation of cold-induced thermogenesis	BP	1	TRPV2	down_VCAV_EC
GO:0006635	0.792	0.546	1	25	fatty acid beta-oxidation	BP	1	SESN2	down_VSAP_EC
GO:0045844	0.792	0.546	1	24	positive regulation of striated muscle tissue	BP	1	CTNNB1	down_VSAP_EC
GO:0048636	0.792	0.546	1	24	positive regulation of muscle organ	BP	1	CTNNB1	down_VSAP_EC
GO:0060324	0.792	0.546	1	24	face development	BP	1	PTPN11	down_VSAP_EC
GO:0061515	0.792	0.546	1	24	myeloid cell development	BP	1	PTPN11	down_VSAP_EC
GO:0050795	0.792	0.552	1	15	regulation of behavior	BP	1	HTR2B	up_ACOR_VSMC
GO:0090114	0.792	0.553	1	15	COPII-coated vesicle budding	BP	1	SEC24B	up_ACOR_VSMC
GO:0030323	0.792	0.539	1	65	respiratory tube development	BP	1	THRB	up_AFEM_EC
GO:0071495	0.792	0.544	1	365	cellular response to endogenous stimulus	BP	1	AVPR1A	up_VFEM_EC
GO:0035196	0.792	0.552	1	16	production of miRNAs involved in gene silencing	BP	1	ZC3H10	up_VSAP_EC
GO:1903727	0.792	0.552	1	16	positive regulation of phospholipid metabolic	BP	1	AMBRA1	up_VSAP_EC
GO:0048706	0.792705431	0.53931	1	59	embryonic skeletal system development	BP	1	FOXC2	up_ACOR_EC
GO:0042110	0.792860579	0.44007	2	109	T cell activation	BP	1	FZD5,PTGER4	up_ACOR_EC
GO:0050789	0.793	0.231	306	3295	regulation of biological process	BP	1	GPR1,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,NAPEPLD,TWIST2,HOXA9,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,NECAB3,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,SLC8B1,RADIL,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,TBC1D10C,MAB21L1,CEP85,LIMS2,GABRE,ARHGEF6,ACACB,TPCN2,EEF2K,DDHD1,IL6R,IRX5,SLIT2,CST3,CRADD,CRIP2,LRRC28,ZHX3,TBC1D2B,ABTB1,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,GOT1,EBF2,BTG1,HDAC7,KLKB1,EMP2,KCNE3,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,DTX2,TENT5C,CLIC5,FUZ,ADAMTSL4,PDGFD,TRAFD1,SAV1,RHPN1,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,ZNF688,ZBTB16,TOX,CNPPD1,RARG,CCBE1,PTGES2,CBX7,STAT5A,STAT6,RECK,GATAD1,CISH,KLHL24,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,TNKS1BP1,RASD2,PYM1,AMBRA1,F2RL1,RBL2,LMF1,RAB11B,GLIS2,MORC3,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,MT2A,FXN,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,CRACR2B,GAS1,BATF2,OMD,MYC,PIK3IP1,PTGES,SSBP2,IRX3,ZEB1,DLC1,FBXW4,DLD,TBXA2	up_VSAP_EC
GO:0007010	0.793	0.259	39	441	cytoskeleton organization	BP	1	SYNPO2L,PDLIM3,FGF13,EPB41L4A,ARHGAP28,ACTN2,MID1,ZRANB1,PRKAA2,SYNPO2,TUBB4A,ATRX,XIRP1,WASF3,NEBL,ZMYM2,F2RL1,JMY,NRP1,EVL,DES,PRKCE,MYO1B,TTC17,RND1,DAG1,SIPA1L1,CLN8,SSH3,EDN1,FAM107A,JAM3,DISC1,TACC1,SUN1,INPP5K,WASL,ATP2C1,MYOZ2	up_ACOR_VSMC

GO:0016477	0.793	0.264	32	426	cell migration	BP	1	FSCN1,HMGB1,ANLN,FMNL3,RACGAP1,SDC1,FBXO5,CAV1,MMP14,GREM1,HOXA7,B4GALT1,PRCP,PPARD,RAP2C,RAC1,EMP2,NUP188,HMGB2,CORO1A,SGPL1,PHACTR4,ASPM,ENSCAFG00000010224,ITGA2,ARHGEF2,TWIST2,NUS1,AMOTL1,SIX4,DEPDC1B,PIK3CD	down_ACOR_VSMC
GO:0031328	0.793	0.275	22	512	positive regulation of cellular biosynthetic process	BP	1	DCN,LUM,LARP6,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,AKT2,TFE3,TEAD1,GLI3,PARK7,EEF2,MYDGF,MAVS,MAPRE3,SHC1,PYM1,GREM1,SOAT1,THRB,ZBTB16	down_VCAV_EC
GO:0071900	0.793	0.315	9	131	regulation of protein serine/threonine kinase	BP	1	IRAK1,HMGCR,CAV1,CDKN2C,EZH2,MAP3K20,CKS2,NUP62,CCNB3	down_ACOR_VSMC
GO:0006469	0.793	0.354	5	78	negative regulation of protein kinase activity	BP	1	HMGCR,CAV1,NF2,CDKN2C,NUP62	down_ACOR_VSMC
GO:2000116	0.793	0.355	5	67	regulation of cysteine-type endopeptidase	BP	1	CST3,CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0044271	0.793	0.385	4	1501	cellular nitrogen compound biosynthetic	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0009266	0.793	0.401	3	43	response to temperature stimulus	BP	1	HTR2B,TP53INP1,PLAC8B	up_ACOR_VSMC
GO:1900182	0.793	0.447	2	33	positive regulation of protein localization to	BP	1	CDK1,DMAP1	down_ACOR_VSMC
GO:2001237	0.793	0.447	2	33	negative regulation of extrinsic apoptotic	BP	1	HMGB2,ARHGEF2	down_ACOR_VSMC
GO:0051234	0.793	0.46	2	1283	establishment of localization	BP	1	ANKRD50,GPSM2	down_AFEM_EC
GO:0060047	0.793	0.441	2	57	heart contraction	BP	1	IRX5,THRB	down_VCAV_EC
GO:0051092	0.793	0.443	2	47	positive regulation of NF-kappaB transcription	BP	1	ARHGEF2,MTDH	down_VSAP_EC
GO:0050848	0.793	0.448	2	30	regulation of calcium-mediated signaling	BP	1	TBC1D10C,PDK2	up_VSAP_EC
GO:0007017	0.793	0.542	1	273	microtubule-based process	BP	1	SPG11	down_ACOR_EC
GO:0042737	0.793	0.549	1	18	drug catabolic process	BP	1	PDXP	down_ACOR_VSMC
GO:0006476	0.793	0.543	1	31	protein deacetylation	BP	1	SPRED1	down_VCAV_EC
GO:0001836	0.793	0.548	1	18	release of cytochrome c from mitochondria	BP	1	BNIP3	up_ACOR_VSMC
GO:0043330	0.793	0.551	1	16	response to exogenous dsRNA	BP	1	TLR3	up_ACOR_VSMC
GO:1901135	0.793	0.543	1	390	carbohydrate derivative metabolic process	BP	1	GALNT17	up_APUL_EC
GO:0006984	0.793	0.547	1	19	ER-nucleus signaling pathway	BP	1	NCK1	up_VCAV_EC
GO:0061462	0.793	0.551	1	15	protein localization to lysosome	BP	1	GCC2	up_VCAV_EC
GO:0006623	0.793	0.55	1	16	protein targeting to vacuole	BP	1	NCOA4	up_VSAP_EC
GO:0071383	0.79370108	0.53782	1	58	cellular response to steroid hormone stimulus	BP	1	AQP1	up_ACOR_EC
GO:0080090	0.794	0.234	158	1734	regulation of primary metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,HNF4A,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,TBC1D10C,CEP85,ACACB,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,CBX7,STAT6,RECK,GATAD1,PLPP3,ENSCAFG00000000071,CAMKK2,TNKS1BP1,PYM1,AMBRA1,F2RL1,RBL2,LMF1,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,BATF2,MYC,PIK3IP1,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,PHF1,E2F4,NPAS2,FBXO7,LIMD1,RNF166,RPUSD4,LONP2,CDK9,PRMT2,KDM2B,FBLN1,OSBPL7,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,PQBP1,TIMP2,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,UBQLN2,ZNF517,HTRA2,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,ZER1,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,KEAP1,DDIT4,ZNF772,SOAT1,LATS2	up_VSAP_EC

GO:0006796	0.794	0.245	73	938	phosphate-containing compound metabolic process	BP	1	ACSL3,PRPSAP1,HMGB1,ACLY,IRAK1,MCM7,ILF3,HMGCR,NNT,RRM1,SLC29A1,PPM1G,PPP1R15B,RAN,BIRC5,CAV1,CDK1,RAD51,NF2,PFAS,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,CDK4,RNASEH2B,DHX33,CKS2,TKT,MVD,ELOVL1,RAP2C,YWHAB,CYCS,RAC1,NUP62,EMP2,PDXP,VAC14,IQGAP1,HASPIN,CACTIN,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,ELOVL6,FDFT1,CYC1,TTK,ATP5F1A,MAST2,MELK,DCK,PRPS1,ENSCAFG00000013366,ARHGEF2,KNL1,PDHA1,TADA2A,NUDT1,PGD,CCNB3,NUS1,GK5,CTPS1,ATP5F1D,NUDT3,PIK3CD	down_ACOR_VSMC
GO:0006811	0.794	0.272	24	330	ion transport	BP	1	ACSL3,NNT,NEDD4,HOXA3,SLC35C2,PRELID1,CAV1,SLC30A1,CLIC1,NKAIN1,SLC17A9,TFRC,PPARD,GSTO1,CDK2,NIPA2,CORO1A,CYC1,SLC20A1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0070647	0.794	0.274	22	311	protein modification by small protein conjugation or removal	BP	1	TNFAIP3,TNIP1,USP33,PELI1,ENSCAFG00000010893,ASB9,HMG20A,ENC1,UHRF2,VHL,OTUD4,WSB1,BCL10,SENP6,USP28,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,IVNS1ABP	up_VCAV_EC
GO:1901565	0.794	0.279	19	442	organonitrogen compound catabolic process	BP	1	LRP1,MAOA,CHID1,TIMP2,PSMF1,THNSL2,RNF216,PARK7,CLEC16A,RNPEP,ENSCAFG00000002977,ENSCAFG00000017708,SEC61B,HM13,LONP2,GLS2,PACSIN3,BCKDHB,ACAT1	down_VCAV_EC
GO:0010638	0.794	0.284	17	207	positive regulation of organelle organization	BP	1	SYNPO2L,ACTN2,LNPK,SYNPO2,ATRX,PPARGC1A,F2RL1,MARCH5,BNIP3,JMY,NRP1,EVL,PRKCE,EDN1,ASAP1,WASL,HMBOX1	up_ACOR_VSMC
GO:0050808	0.794	0.33	7	93	synapse organization	BP	1	FZD1,SEZ6L,WASF3,AMIGO1,LRRN3,ABL1,LRP4	up_VSAP_EC
GO:0031503	0.794	0.341	6	79	protein-containing complex localization	BP	1	NACC2,IFT43,DAG1,AP2B1,WASL,ENSCAFG00000013536	up_ACOR_VSMC
GO:0006796	0.794	0.343	6	938	phosphate-containing compound metabolic	BP	1	ARHGEF2,AK5,ASPN,ACVR2A,FBP1,ENSCAFG00000032731	up_VPOR_EC
GO:0043433	0.794	0.399	3	49	negative regulation of DNA-binding transcription factor activity	BP	1	IRAK1,EZH2,CACTIN	down_ACOR_VSMC
GO:0090316	0.794	0.399	3	48	positive regulation of intracellular protein	BP	1	RAN,PLK3,DMAP1	down_ACOR_VSMC
GO:0051252	0.794	0.405	3	1051	regulation of RNA metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0022406	0.794	0.443	2	35	membrane docking	BP	1	EZR,CEP83	down_ACOR_VSMC
GO:0008625	0.794	0.445	2	30	extrinsic apoptotic signaling pathway via death domain receptors	BP	1	DAPK1,PARK7	up_ACOR_VSMC
GO:0016999	0.794	0.446	2	30	antibiotic metabolic process	BP	1	CAT,PARK7	up_ACOR_VSMC
GO:0050848	0.794	0.445	2	30	regulation of calcium-mediated signaling	BP	1	C28H10orf71,ITPR1	up_ACOR_VSMC
GO:0051253	0.794	0.44	2	359	negative regulation of RNA metabolic process	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0030038	0.794	0.54	1	31	contractile actin filament bundle assembly	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0030307	0.794	0.541	1	31	positive regulation of cell growth	BP	1	TRPV2	down_VCAV_EC
GO:0043149	0.794	0.54	1	31	stress fiber assembly	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0035329	0.794	0.549	1	16	hippo signaling	BP	1	AMOT	up_VCAV_EC
GO:0051973	0.794	0.545	1	19	positive regulation of telomerase activity	BP	1	HMBOX1	up_VCAV_EC
GO:0009890	0.794404933	0.31254	9	420	negative regulation of biosynthetic process	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,RIOX2	up_ACOR_EC

GO:0009058	0.795	0.232	175	1910	biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,HOXA9,CDON,NECAB3,WNT11,ACSM3,ARHGEF5,LIPC,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,GOT1,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,GLUL,GALNT15,ENSCAFG00000013986,CERS4,WARS2,VDR,SAV1,ENSCAFG00000003792,KLF15,C1QTNF2,ANXA4,HSD3B7,ZNF688,ZBTB16,COQ9,RARG,CBX7,STAT5A,STAT6,GATAD1,HSD17B8,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,PPIP5K1,DDR2,PDK2,ICE1,ZFP36L1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,PLA2G6,MYC,PTGES,SSBP2,IRX3,ZEB1,FKRP,HACD4,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,ENSCAFG00000016140,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,GALNT11,DAGLB,E2F4,NPAS2,MOCOS,ZDHHC8,FARS2,LCAT,PCBD1,LIMD1,UBA52,RPUSD4,RPL15,ACSS2,PC,CDK9,DHRS9,NR2F6,PRMT2,KDM2B,MVK,PNPO,DCAKD,FAXDC2,EIF3G,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MPST,TAF8,NFIB,ABHD14B,CYBA,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,CYB5	up_VSAP_EC
GO:0051171	0.795	0.244	79	1697	regulation of nitrogen compound metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,PRNP,LUM,FBN1,GLIPR2,BGN,LARP6,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,TFE3,NR3C1,HR,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,CXXC5,ASPN,EIF3K,THY1,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,SPRED1,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0032989	0.795	0.27	24	292	cellular component morphogenesis	BP	1	WASF3,ENPP2,RADIL,SLIT2,ABL1,CDC42EP5,PLXNA4,RILPL2,CDC42EP2,SHOX2,POLDIP2,LRP4,DPYSL2,FRMD6,LIMD1,FBLN1,NFIB,PQBP1,TTL,FLOT1,ULK1,MAP2K2,OGN,LATS2	up_VSAP_EC
GO:0001944	0.795	0.279	19	263	vasculature development	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,ADAMTS6,NCL,EMP2,FOSL1,SGPL1,CTH,JMJD6,NUS1	down_ACOR_VSMC
GO:0032504	0.795	0.299	12	152	multicellular organism reproduction	BP	1	HOXA11,THRB,HOXA9,SLIT2,ZNF449,HERPUD2,ZBTB16,PATZ1,CREBRF,KDM2B,HPGD,CITED2	up_VSAP_EC
GO:0048609	0.795	0.299	12	152	multicellular organismal reproductive process	BP	1	HOXA11,THRB,HOXA9,SLIT2,ZNF449,HERPUD2,ZBTB16,PATZ1,CREBRF,KDM2B,HPGD,CITED2	up_VSAP_EC
GO:0006913	0.795	0.308	10	124	nucleocytoplasmic transport	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,RPAIN,PARK7,PTPN14	up_ACOR_VSMC
GO:0051169	0.795	0.308	10	124	nuclear transport	BP	1	LEP,FERMT1,BMP4,CDKN1A,PTPN22,PSEN1,JUP,RPAIN,PARK7,PTPN14	up_ACOR_VSMC
GO:0051301	0.795	0.314	9	117	cell division	BP	1	LBH,HTR2B,FGFR2,PKP4,PRKCE,PIK3C3,SPECC1L,MITD1,CAT	up_ACOR_VSMC
GO:0018105	0.795	0.32	8	116	peptidyl-serine phosphorylation	BP	1	SLC29A1,CAV1,CDK1,AURKB,CDK2,CLSPN,TTK,MAST2	down_ACOR_VSMC
GO:1901652	0.795	0.32	8	105	response to peptide	BP	1	GOT1,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,NCK1,BGLAP	up_VSAP_EC
GO:0010720	0.795	0.367	4	110	positive regulation of cell development	BP	1	TRPV2,NUMBL,SEMA3C,GLI3	down_VCAV_EC
GO:0015980	0.795	0.367	4	106	energy derivation by oxidation of organic	BP	1	AKT2,UQCR10,PARK7,MTFR1L	down_VCAV_EC
GO:0000819	0.795	0.368	4	87	sister chromatid segregation	BP	1	NAA10,CTNNB1,KPNB1,PDS5B	down_VSAP_EC
GO:0051188	0.795	0.393	3	81	cofactor biosynthetic process	BP	1	UROS,ACSS2,ACAT1	down_VCAV_EC
GO:0060993	0.795	0.398	3	42	kidney morphogenesis	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0062014	0.795	0.443	2	35	negative regulation of small molecule metabolic	BP	1	INSIG1,BRCA1	down_ACOR_VSMC
GO:0043281	0.795	0.439	2	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	PARK7,IFT57	down_VCAV_EC

GO:0050684	0.795	0.44	2	46	regulation of mRNA processing	BP	1	IWS1,REST	down_VSAP_EC
GO:0043487	0.795	0.444	2	33	regulation of RNA stability	BP	1	TENT2,SMG7	up_VCAV_EC
GO:1901700	0.795	0.439	2	364	response to oxygen-containing compound	BP	1	ARHGEF2,MTDH	up_VPOR_EC
GO:0035987	0.795	0.546	1	17	endodermal cell differentiation	BP	1	MMP14	down_ACOR_VSMC
GO:0045839	0.795	0.541	1	25	negative regulation of mitotic nuclear division	BP	1	NAA10	down_VSAP_EC
GO:0016079	0.795	0.54	1	27	synaptic vesicle exocytosis	BP	1	GSK3B	down_VSAP_EC
GO:0016925	0.795	0.547	1	16	protein sumoylation	BP	1	PARK7	up_ACOR_VSMC
GO:0006890	0.795	0.545	1	18	retrograde vesicle-mediated transport, Golgi	BP	1	RAB6A	up_VCAV_EC
GO:0000725	0.795568733	0.53488	1	58	recombinational repair	BP	1	FIGNL1	up_ACOR_EC
GO:0051179	0.796	0.232	159	1747	localization	BP	1	SLC43A1,EMX2,HOXA7,PEX7,TWIST2,WNT11,HNF4A,FAM107A,DNM1,CD274,ACKR3,ARHGEF5,AXIN2,C5AR2,LIPC,AMIGO1,ENPP2,CALHM2,SLC8B1,PLEKHF1,TBC1D10C,SLC43A3,GABARE,MFSD3,ACACB,TPCN2,SLIT2,NIPAL3,TBC1D2B,CDH1,SLC6A4,FGF7,ABL1,PEX2,HDAC7,SLC16A12,EMP2,KCNE3,CHRM1,DLL1,EPN2,OSR1,IL17RC,SCAMP4,CLIC5,FUZ,PDGFD,KLF15,C1QTNF2,ANXA4,PLXNA4,RILPL2,ANKRD54,HSD3B7,ABCB11,CCS,CCBE1,VPS36,STAT5A,AP5B1,RECK,KLHL24,SLC25A12,APOL5,TOM1,F2RL1,LMF1,RAB11B,GLIS2,MORC3,DDR2,MFN2,ICE1,ZFP36L1,PIK3R1,SLC25A28,TIAM1,CRACR2B,GAS1,SLC27A6,CTNS,SCARA5,TBXA2R,SLC10A6,CIZ1,CFAP69,SASH1,FBXO4,NIPAL1,MYD88,ERGIC1,LRP4,PASK,MON1B,NUP98,SCFD2,TSPAN5,AZIN2,HPS4,FRMD6,CCDC93,ABCA9,CLCN2,STEAP3,FBXO7,KCNB1,LCAT,LIMD1,LONP2,BORCS6,SNUPN,DOP1B,DENND5A,FBLN1,AP5Z1,OSBPL7,FTL,MYO1B,SCAMP2,ENSCAFG00000013366,RAF1,PNP,MAPKBP1,TAF8,ZFYVE21,ZNF580,CYBA,ZNF205,XKR8,FXYD1,STX4,ZFAND5,TTL,VPS11,KCNC4,ARHGAP12,ACVRL1,UBQLN2,FLOT1,PPP3CB,PEX6,NCK1,STK11IP,SLC25A40,MAVS,ULK1,CEP19,HMOX1,MAP2K2,TGFBR2,SAA1,BAG4,N	up_VSAP_EC
GO:0051253	0.796	0.286	15	359	negative regulation of RNA metabolic process	BP	1	NAB2,KANK2,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,LOXL3,TSC22D3,GLIS2,SHC1,GREM1,THRB	down_VCAV_EC
GO:0040008	0.796	0.325	7	179	regulation of growth	BP	1	GPAM,NOTCH2,MT2A,BMPR1A,IGFBP6,TRPV2,PEX5	down_VCAV_EC
GO:0043087	0.796	0.338	6	83	regulation of GTPase activity	BP	1	ARHGEF5,TBC1D10C,TBC1D2B,F2RL1,TIAM1,SBF2	up_VSAP_EC
GO:0007034	0.796	0.369	4	55	vacuolar transport	BP	1	SCARB2,LAMP2,ENSCAFG00000001846,AKTIP	up_ACOR_VSMC
GO:1905330	0.796	0.396	3	48	regulation of morphogenesis of an	BP	1	GREM1,HOXB7,SIX4	down_ACOR_VSMC
GO:0007030	0.796	0.395	3	49	Golgi organization	BP	1	ZW10,PLK3,PRMT5	down_ACOR_VSMC
GO:0034764	0.796	0.395	3	50	positive regulation of transmembrane transport	BP	1	RELN,APLNR,PLCG2	up_VCAV_EC
GO:0015031	0.796	0.394	3	510	protein transport	BP	1	XPOT,GCC2,SRP54	up_VPOR_EC
GO:0010468	0.796	0.456	2	1270	regulation of gene expression	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:1901136	0.796	0.44	2	38	carbohydrate derivative catabolic process	BP	1	CDA,LYVE1	up_VCAV_EC
GO:0006890	0.796	0.544	1	18	retrograde vesicle-mediated transport, Golgi	BP	1	ARCN1	down_ACOR_VSMC
GO:1901989	0.796	0.538	1	31	positive regulation of cell cycle phase transition	BP	1	LSM10	down_VCAV_EC
GO:0072665	0.796	0.539	1	25	protein localization to vacuole	BP	1	SH3GLB1	down_VSAP_EC
GO:0031401	0.796	0.537	1	358	positive regulation of protein modification	BP	1	CAV1	up_VSAP_VSMC
GO:0007093	0.796767185	0.5329	1	59	mitotic cell cycle checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0033554	0.796975791	0.28331	16	708	cellular response to stress	BP	1	BRSK1,AQP1,EDEM2,FZD5,NOD2,RGMA,PAK3,GUCY1B1,TNFRSF19,MAPK8IP2,FIGNL1,SH3RF3,CLU,PRKACA,HM13,PRKCD	up_ACOR_EC

GO:0032880	0.797	0.271	22	266	regulation of protein localization	BP	1	HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,CDH1,ABL1,IL17RC,ANXA4,F2RL1,RAB11B,GLIS2,ICE1,PIK3R1,FBXO4,LRP4,KCNB1,MAPKBP1,STX4,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:0030099	0.797	0.31	9	133	myeloid cell differentiation	BP	1	HSPA9,PRMT1,HMGB3,HOXA7,HOXB7,TFRC,HMGB2,HOXA9,JMJD6	down_ACOR_VSMC
GO:0044257	0.797	0.333	6	327	cellular protein catabolic process	BP	1	CTSS,CLEC16A,CYLD,RAB7A,FAP,RNF181	up_AFEM_EC
GO:0097191	0.797	0.349	5	79	extrinsic apoptotic signaling pathway	BP	1	CAV1,CASP2,HMGB2,ARHGEF2,DELE1	down_ACOR_VSMC
GO:0008033	0.797	0.394	3	52	tRNA processing	BP	1	THUMPD2,OSGEP,RTCB	down_ACOR_VSMC
GO:0018210	0.797	0.395	3	48	peptidyl-threonine modification	BP	1	CDK1,HASPIN,TTK	down_ACOR_VSMC
GO:0009891	0.797	0.393	3	521	positive regulation of biosynthetic process	BP	1	ARHGEF2,ACVR2A,RNF6	up_VPOR_EC
GO:0046916	0.797	0.439	2	35	cellular transition metal ion homeostasis	BP	1	SLC30A1,TFRC	down_ACOR_VSMC
GO:0007163	0.797	0.436	2	60	establishment or maintenance of cell	BP	1	UST,BRSK1	down_VCAV_EC
GO:0006913	0.797	0.434	2	124	nucleocytoplasmic transport	BP	1	LEP,CRY2	up_AFEM_EC
GO:0051169	0.797	0.434	2	124	nuclear transport	BP	1	LEP,CRY2	up_AFEM_EC
GO:0006464	0.797	0.45	2	1162	cellular protein modification process	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0036211	0.797	0.45	2	1162	protein modification process	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0002821	0.797	0.441	2	30	positive regulation of adaptive immune	BP	1	CD274,STAT6	up_VSAP_EC
GO:1903038	0.797	0.442	2	30	negative regulation of leukocyte cell-cell	BP	1	CD274,ASS1	up_VSAP_EC
GO:0002534	0.797	0.542	1	18	cytokine production involved in inflammatory	BP	1	BAP1	down_ACOR_VSMC
GO:0045747	0.797	0.542	1	18	positive regulation of Notch signaling pathway	BP	1	SLC35C2	down_ACOR_VSMC
GO:0042542	0.797	0.536	1	31	response to hydrogen peroxide	BP	1	PARK7	down_VCAV_EC
GO:0007064	0.797	0.545	1	15	mitotic sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0010501	0.797	0.545	1	15	RNA secondary structure unwinding	BP	1	EIF4A2	up_ACOR_VSMC
GO:0002548	0.797	0.542	1	17	monocyte chemotaxis	BP	1	CCL5	up_ACOR_VSMC
GO:1903573	0.797	0.541	1	20	negative regulation of response to endoplasmic	BP	1	NCK1	up_VCAV_EC
GO:0043065	0.797	0.532	1	188	positive regulation of apoptotic process	BP	1	STK17B	up_VPOR_EC
GO:0120036	0.797	0.536	1	373	plasma membrane bounded cell projection	BP	1	CDC42EP5	up_VFEM_EC
GO:0042176	0.798	0.299	11	140	regulation of protein catabolic process	BP	1	FBXL20,SH3RF2,PTPN3,EGLN1,OS9,RNF19A,PSEN1,DISC1,HERPUD1,AZIN2,PARK7	up_ACOR_VSMC
GO:0046605	0.798	0.44	2	30	regulation of centrosome cycle	BP	1	CEP85,FBXW5	up_VSAP_EC
GO:0048644	0.798	0.534	1	31	muscle organ morphogenesis	BP	1	BMPR1A	down_VCAV_EC
GO:0008104	0.798	0.545	1	763	protein localization	BP	1	RAB11B	down_VPOR_EC
GO:0021575	0.798	0.543	1	15	hindbrain morphogenesis	BP	1	ZNF365	up_ACOR_VSMC
GO:0021587	0.798	0.543	1	15	cerebellum morphogenesis	BP	1	ZNF365	up_ACOR_VSMC
GO:0070884	0.798	0.542	1	16	regulation of calcineurin-NFAT signaling cascade	BP	1	C28H10orf71	up_ACOR_VSMC
GO:0106056	0.798	0.542	1	16	regulation of calcineurin-mediated signaling	BP	1	C28H10orf71	up_ACOR_VSMC
GO:1903146	0.798	0.542	1	17	regulation of autophagy of mitochondrion	BP	1	HIF1A	up_VCAV_EC
GO:0070884	0.798	0.542	1	16	regulation of calcineurin-NFAT signaling cascade	BP	1	TBC1D10C	up_VSAP_EC
GO:0106056	0.798	0.542	1	16	regulation of calcineurin-mediated signaling	BP	1	TBC1D10C	up_VSAP_EC
GO:0034613	0.799	0.249	43	576	cellular protein localization	BP	1	HCLS1,GBP5,PPP2R5A,TNFAIP3,AMOT,TMEM173,EXOC3L2,RELN,IWS1,FERMT1,TSPAN15,RAB11A,RAB27A,ZDHHC22,PPP3CA,HOOK3,TSPAN14,HHEX,CEP68,MZT1,EPB41,SNX2,THOC1,SH3GLB1,AKAP12,APOD,EXOC5,RAPGEF2,CTDSPL2,PAN3,GCC2,CTNNA1,STX11,SMG7,TBC1D1,NUP133,SPTBN4,RAD21,ZW10,IPO11,ATRX,RABGAP1,USP6NL	up_VCAV_EC

GO:0031327	0.799	0.255	35	412	negative regulation of cellular biosynthetic process	BP	1	FZD1,THRB,HOXA7,WNT11,INSIG2,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,ENSCAFG00000000071,GLIS2,ZFP36L1,SHOX2,H2AFJ,IKZF2,PASK,ANKHD1,LIMD1,PRMT2,KDM2B,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1,DDIT4	up_VSAP_EC
GO:0044238	0.799	0.283	25	3383	primary metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,ABHD5,FAM135A,RRP15,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0007346	0.799	0.278	17	210	regulation of mitotic cell cycle	BP	1	FAM107A,MAP3K14,CEP85,CRADD,ABL1,ZFP36L1,GAS1,POLDIP2,FBXW5,FBXO7,TTC28,ZFP36L2,TTL,TPRA1,CDC26,LSM10,MAP2K2	up_VSAP_EC
GO:0055086	0.799	0.283	15	237	nucleobase-containing small molecule metabolic process	BP	1	NPR1,PANK3,CDA,PIPOX,ADSS,GUCY1A1,MTOR,ACPP,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,DCK,NOS2,HIF1A	up_VCAV_EC
GO:0033157	0.799	0.333	6	82	regulation of intracellular protein transport	BP	1	CDH1,ICE1,PIK3R1,KCNB1,MAVS,BAG4	up_VSAP_EC
GO:0042594	0.799	0.364	4	64	response to starvation	BP	1	SREBF1,SREBF2,RNF152,MIOS	down_ACOR_VSMC
GO:0043270	0.799	0.365	4	56	positive regulation of ion transport	BP	1	AMIGO1,ABL1,CHRM1,FXYD1	up_VSAP_EC
GO:0090174	0.799	0.366	4	56	organelle membrane fusion	BP	1	TBC1D10C,TBC1D2B,STX4,VPS11	up_VSAP_EC
GO:0007041	0.799	0.393	3	41	lysosomal transport	BP	1	SCARB2,LAMP2,AKTIP	up_ACOR_VSMC
GO:0043467	0.799	0.437	2	35	regulation of generation of precursor metabolites	BP	1	PRELID1,CDK1	down_ACOR_VSMC
GO:0017157	0.799	0.433	2	58	regulation of exocytosis	BP	1	SDC4,RAC2	down_VCAV_EC
GO:0010605	0.799	0.439	2	745	negative regulation of macromolecule metabolic	BP	1	NR1H4,PCSK1N	up_APUL_EC
GO:0071804	0.799	0.533	1	31	cellular potassium ion transport	BP	1	PRNP	down_VCAV_EC
GO:0071805	0.799	0.533	1	31	potassium ion transmembrane transport	BP	1	PRNP	down_VCAV_EC
GO:1902117	0.799	0.532	1	32	positive regulation of organelle assembly	BP	1	SDC4	down_VCAV_EC
GO:0003208	0.799	0.535	1	24	cardiac ventricle morphogenesis	BP	1	HIF1A	down_VSAP_EC
GO:0030148	0.799	0.534	1	28	sphingolipid biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0022402	0.799	0.534	1	407	cell cycle process	BP	1	LZTS1	up_APUL_EC
GO:0007422	0.799	0.538	1	18	peripheral nervous system development	BP	1	EDNRB	up_VCAV_EC
GO:0031648	0.799	0.538	1	19	protein destabilization	BP	1	BMP2	up_VCAV_EC
GO:0048538	0.799	0.537	1	20	thymus development	BP	1	GATA3	up_VCAV_EC
GO:0060389	0.799	0.536	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	BMP2	up_VCAV_EC
GO:0018193	0.799	0.533	1	368	peptidyl-amino acid modification	BP	1	EYA1	up_VFEM_EC
GO:0061337	0.799	0.541	1	16	cardiac conduction	BP	1	KCNE3	up_VSAP_EC
GO:0038083	0.799	0.541	1	16	peptidyl-tyrosine autophosphorylation	BP	1	ABL1	up_VSAP_EC
GO:0010468	0.799223684	0.26105	30	1270	regulation of gene expression	BP	1	CDH3,NR1H4,GATA4,TRPS1,SOX9,PKNOX2,ENSCAFG00000004331,FZD5,DUSP26,RASL11A,NOD2,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0043583	0.79923056	0.52898	1	59	ear development	BP	1	SOX9	up_ACOR_EC

GO:0071704	0.799756139	0.2448	88	3535	organic substance metabolic process	BP	1	C7,CDH3,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,CALY,THNSL2,SOX9,NMNAT2,PKNOX2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,SARDH,EDEM2,PI3,FZD5,CCDC3,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,ENSCAFG00000028814,SMAD6,B3GNT7,KLHL25,PLCE1,ZMYND8,NIT2,PTGDS,PAK3,CFI,GUCY1B1,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,CHPT1,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,AK7,LRRC4,RBM38,CLU,SFMBT2,ALDOC,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,AGPAT2,HM13,PRKCD,PM20D1,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC
GO:0015931	0.799994049	0.52776	1	59	nucleobase-containing compound transport	BP	1	SLC25A42	up_ACOR_EC
GO:0051252	0.8	0.234	95	1051	regulation of RNA metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0006351	0.8	0.235	84	1069	transcription, DNA-templated	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,POLR3F,HOXA10,ERF,TCERG1,SMARCAL1,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103,POLR1C	down_ACOR_VSMC
GO:0006464	0.8	0.245	53	1162	cellular protein modification process	BP	1	NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,GLIPR2,BGN,BMPR1A,KRTCAP2,VKORC1,CLIP3,AKT1S1,AKT2,EEF2K,HR,PLCL1,DDOST,CSPG4,PRMT6,GFPT2,ASPN,PIGS,HS3ST3B1,THY1,RNF216,WDR45,B4GALT1,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,COPS7A,ARL2BP,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,SPRED1,MAPRE3,CDKL2,DDR2,SHC1,CRTAP,FBH1,GREM1,RPN2,KLHL29,BRSK1,CDK14	down_VCAV_EC
GO:0036211	0.8	0.245	53	1162	protein modification process	BP	1	NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,GLIPR2,BGN,BMPR1A,KRTCAP2,VKORC1,CLIP3,AKT1S1,AKT2,EEF2K,HR,PLCL1,DDOST,CSPG4,PRMT6,GFPT2,ASPN,PIGS,HS3ST3B1,THY1,RNF216,WDR45,B4GALT1,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,COPS7A,ARL2BP,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,SPRED1,MAPRE3,CDKL2,DDR2,SHC1,CRTAP,FBH1,GREM1,RPN2,KLHL29,BRSK1,CDK14	down_VCAV_EC
GO:0009891	0.8	0.3	10	521	positive regulation of biosynthetic process	BP	1	HOXA9,LBH,PRR16,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0016032	0.8	0.322	7	94	viral process	BP	1	USP6NL,MX1,ISG15,CTSB,DAG1,ATG16L2,INPP5K	up_ACOR_VSMC
GO:0006401	0.8	0.361	4	88	RNA catabolic process	BP	1	ZPR1,SMG7,CNOT7,SND1	down_VSAP_EC
GO:0000956	0.8	0.364	4	55	nuclear-transcribed mRNA catabolic process	BP	1	PNRC1,DCP1B,CNOT4,CTIF	up_ACOR_VSMC

GO:0071840	0.8	0.386	4	2059	cellular component organization or biogenesis	BP	1	CHL1,NKX2-5,BAMBI,CYP26B1	up_VPOR_VSMC
GO:0010952	0.8	0.39	3	46	positive regulation of peptidase activity	BP	1	MBP,DAPK1,PERP	up_ACOR_VSMC
GO:0031326	0.8	0.399	3	1176	regulation of cellular biosynthetic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0014902	0.8	0.436	2	34	myotube differentiation	BP	1	MMP14,SIX4	down_ACOR_VSMC
GO:0001892	0.8	0.435	2	35	embryonic placenta development	BP	1	E2F8,PLK4	down_ACOR_VSMC
GO:0072329	0.8	0.436	2	34	monocarboxylic acid catabolic process	BP	1	PPARD,ACADL	down_ACOR_VSMC
GO:0032675	0.8	0.436	2	34	regulation of interleukin-6 production	BP	1	HMGB1,ARHGEF2	down_ACOR_VSMC
GO:0015931	0.8	0.432	2	59	nucleobase-containing compound transport	BP	1	SNUPN,ZFP36L1	down_VCAV_EC
GO:0030595	0.8	0.432	2	57	leukocyte chemotaxis	BP	1	HSD3B7,RAC2	down_VCAV_EC
GO:0071478	0.8	0.432	2	58	cellular response to radiation	BP	1	AKT2,TMEM161A	down_VCAV_EC
GO:1903522	0.8	0.431	2	58	regulation of blood circulation	BP	1	IRX5,THRB	down_VCAV_EC
GO:0031099	0.8	0.437	2	30	regeneration	BP	1	LGR6,GJA1	up_ACOR_VSMC
GO:0071901	0.8	0.434	2	37	negative regulation of protein serine/threonine	BP	1	TNFAIP3,HHEX	up_VCAV_EC
GO:1904427	0.8	0.537	1	18	positive regulation of calcium ion	BP	1	GSTO1	down_ACOR_VSMC
GO:0007292	0.8	0.531	1	32	female gamete generation	BP	1	FOXO3	down_VCAV_EC
GO:2000107	0.8	0.539	1	16	negative regulation of leukocyte apoptotic	BP	1	BMP4	up_ACOR_VSMC
GO:0030030	0.8	0.531	1	377	cell projection organization	BP	1	CDC42EP5	up_VFEM_EC
GO:1990868	0.8	0.54	1	16	response to chemokine	BP	1	SLIT2	up_VSAP_EC
GO:1990869	0.8	0.54	1	16	cellular response to chemokine	BP	1	SLIT2	up_VSAP_EC
GO:0042771	0.8	0.539	1	16	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	DDIT4	up_VSAP_EC
GO:0044265	0.800434162	0.30489	9	423	cellular macromolecule catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,HM13	up_ACOR_EC
GO:0071840	0.801	0.235	96	2059	cellular component organization or biogenesis	BP	1	ADAMTS2,SLC35F6,KIRREL1,SNX18,FBLN2,LRP1,DCN,NDN,PRNP,LUM,SDC4,ATP8B2,COA1,LOX,TLN2,NABP2,LMO4,RECK,IGFBP6,RPS10,TRPV2,COL6A1,CLIP3,NUMBL,NAGLU,RHOD,ENSCAFG00000014978,GABARAP,AKT1S1,AKT2,TTC8,LCAT,CHCHD10,SYDE1,HR,SCP2,CLSTN1,CACNB3,PRMT6,CABIN1,WIPF1,RASSF8,SEMA3C,POLDIP2,CRISPLD2,LRPAP1,EIF3K,THY1,WDR45,PEX5,ARHGAP10,TLX2,ATP6V0C,MYO1B,B4GALT1,GLI3,PARK7,ADAMTSL4,MAST2,SCARA5,CLEC16A,NCDN,RETREG1,RPL27,CYBA,IFT57,MAVS,MRPS11,EMC6,CDH2,LOXL3,MPV17,ORMDL3,RPS27,NCLN,ENSCAFG00000017708,MGARP,ACTR3B,UST,MTFR1L,RAB31,PRKCSH,DDR2,SHC1,PYM1,GREM1,PLEKHH2,RPLP0,EVI5L,LONP2,RAC2,SOAT1,PACSIN3,RGMA,ECM2,BRSK1	down_VCAV_EC
GO:0007369	0.801	0.362	4	63	gastrulation	BP	1	NF2,MMP14,UGDH,ITGA2	down_ACOR_VSMC
GO:0006473	0.801	0.361	4	66	protein acetylation	BP	1	IWS1,GATA3,ESCO1,TAOK1	up_VCAV_EC
GO:0051047	0.801	0.385	3	84	positive regulation of secretion	BP	1	SDC4,CYBA,MAVS	down_VCAV_EC
GO:0007411	0.801	0.389	3	45	axon guidance	BP	1	EPHB1,RELN,GATA3	up_VCAV_EC
GO:0097485	0.801	0.389	3	45	neuron projection guidance	BP	1	EPHB1,RELN,GATA3	up_VCAV_EC
GO:0009799	0.801	0.39	3	43	specification of symmetry	BP	1	DLL1,TGFBR2,CITED2	up_VSAP_EC
GO:0042471	0.801	0.434	2	34	ear morphogenesis	BP	1	INSIG1,SIX4	down_ACOR_VSMC
GO:0007093	0.801	0.43	2	59	mitotic cell cycle checkpoint	BP	1	NABP2,BRSK1	down_VCAV_EC
GO:0042133	0.801	0.435	2	30	neurotransmitter metabolic process	BP	1	MAOA,MOXD1	up_ACOR_VSMC

GO:0018209	0.801	0.428	2	125	peptidyl-serine modification	BP	1	CAMK2A,DMPK	up_AFEM_EC
GO:0009746	0.801	0.433	2	35	response to hexose	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0034284	0.801	0.433	2	35	response to monosaccharide	BP	1	SMARCA4,HIF1A	up_VCAV_EC
GO:0097305	0.801	0.435	2	31	response to alcohol	BP	1	CTNNA1,BLM	up_VCAV_EC
GO:0007422	0.801	0.535	1	18	peripheral nervous system development	BP	1	NAB2	down_ACOR_VSMC
GO:0010822	0.801	0.529	1	31	positive regulation of mitochondrion	BP	1	DCN	down_VCAV_EC
GO:0032231	0.801	0.53	1	32	regulation of actin filament bundle assembly	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:0044264	0.801	0.53	1	32	cellular polysaccharide metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0051865	0.801	0.529	1	31	protein autoubiquitination	BP	1	SASH1	down_VCAV_EC
GO:0070665	0.801	0.53	1	31	positive regulation of leukocyte proliferation	BP	1	GPAM	down_VCAV_EC
GO:0090100	0.801	0.53	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	BMPR1A	down_VCAV_EC
GO:1901568	0.801	0.532	1	26	fatty acid derivative metabolic process	BP	1	PTGS2	down_VSAP_EC
GO:0032212	0.801	0.538	1	16	positive regulation of telomere maintenance via	BP	1	HMBOX1	up_ACOR_VSMC
GO:0047496	0.801	0.539	1	15	vesicle transport along microtubule	BP	1	DYNC1I1	up_ACOR_VSMC
GO:1904358	0.801	0.538	1	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	HMBOX1	up_ACOR_VSMC
GO:0003205	0.801	0.526	1	67	cardiac chamber development	BP	1	LUZP1	up_AFEM_EC
GO:0002028	0.801	0.534	1	19	regulation of sodium ion transport	BP	1	SPTBN4	up_VCAV_EC
GO:0043068	0.801	0.527	1	190	positive regulation of programmed cell death	BP	1	STK17B	up_VPOR_EC
GO:0030163	0.801	0.53	1	365	protein catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:0034976	0.801116835	0.42771	2	112	response to endoplasmic reticulum stress	BP	1	EDEM2,HM13	up_ACOR_EC
GO:0032943	0.80127301	0.52563	1	60	mononuclear cell proliferation	BP	1	PRKCD	up_ACOR_EC
GO:0046651	0.80127301	0.52563	1	60	lymphocyte proliferation	BP	1	PRKCD	up_ACOR_EC
GO:1901564	0.802	0.223	189	2053	organonitrogen compound metabolic process	BP	1	FZD1,PRR16,NAPEPLD,CDON,NECAB3,WNT11,HNF4A,ACSM3,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,RNPEP,TBC1D10C,MRPL37,CEP85,FOXRED2,ACACB,EEF2K,IL6R,SLIT2,GDA,CST3,CRADD,ABTB1,NADK,FGF7,ABL1,KLHL36,SULT1A1,GOT1,KLKB1,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,GLUL,CTSS,GALNT15,DTX2,ADHFE1,ENSCAFG00000013986,PDGFD,CERS4,WARS2,NAA60,DDB2,KLF15,C1QTNF2,HPSE,CNPPD1,COQ9,ALDH6A1,CCBE1,VPS36,NDUFS1,ENSCAFG00000004260,RECK,CISH,KLHL24,PLPP3,ENSCAFG00000000071,CAMKK2,APOL5,TNKS1BP1,KLHDC8B,PYM1,F2RL1,LMF1,PHKA2,MORC3,DDR2,PDK2,ZFP36L1,TRAF7,FXN,GALK1,PIK3R1,RBCK1,KBTBD12,GAS1,MYC,RNF24,FKRP,FBXW4,CTNS,DLD,HACD4,SULF2,CAPN5,ABAT,EEF2,RTN4RL1,SASH1,BCKDHB,FBXO4,RMND5A,ENSCAFG00000016140,CLYBL,LARP6,MYD88,NDUFS2,RPL13,LRP4,PASK,ANKHD1,TSPAN5,NT5C2,AZIN2,GALNT11,STK16,NCEH1,PHF1,CFD,FBXW5,FBXO7,MOCOS,ZDHHC8,ASB8,UBA7,EHHADH,FARS2,LCAT,PCBD1,UBA52,RNF166,RPUSD4,LONP2,RPL15,ACSS2,CDK9,KDM2B,FBLN1,MVK,RNF216,PNPO,DCAKD,EIF3G,OSBPL7,ENSCAFG00000002977,SAMD4B,ZFP36L	up_VSAP_EC

GO:0006807	0.802	0.228	184	3221	nitrogen compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,ENSCAFG00000028814,TRIB3,PGAM1,PUM3,UGCG,PM20D2,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,HIF1A,FOXP4,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,AK5,GTF2H1,ARMCX3,CUL2,MYO1E,HTT,REST,RBBP8,ZMYND8,MAPK10,EIF2S1,PRMT1,P3H4,NR4A2,EXT1,SPOP,CALM1,RAB11FIP1,GLO1,DISC1,ENSCAFG0000	down_VSAP_EC
GO:0032880	0.802	0.27	19	266	regulation of protein localization	BP	1	HCLS1,PPP2R5A,TMEM173,IWS1,FERMT1,TLR4,GATA3,ARG2,EPB41,SH3GLB1,SWAP70,APOD,CD200,MMD,CTDSPL2,GCC2,HMGB1,MCU,HIF1A	up_VCAV_EC
GO:0008285	0.802	0.282	14	201	negative regulation of cell proliferation	BP	1	HMGA1,MNDA,CAV1,FAM129B,NF2,CDKN2C,GREM1,ARG2,B4GALT1,PPARD,NUP62,SMARCB1,TINF2,MTBP	down_ACOR_VSMC
GO:0042060	0.802	0.312	8	103	wound healing	BP	1	LGR6,DCBLD2,LNPK,GJA1,F2RL1,ENPP4,PRKCE,RREB1	up_ACOR_VSMC
GO:0042692	0.802	0.319	7	105	muscle cell differentiation	BP	1	SDC1,MMP14,EZH2,GREM1,RBM14,CTH,SIX4	down_ACOR_VSMC
GO:0051170	0.802	0.344	5	69	import into nucleus	BP	1	CDH1,PIK3R1,NUP98,SNUPN,MAVS	up_VSAP_EC
GO:0000723	0.802	0.361	4	54	telomere maintenance	BP	1	ATRX,ZNF365,STN1,HMBOX1	up_ACOR_VSMC
GO:0032200	0.802	0.361	4	54	telomere organization	BP	1	ATRX,ZNF365,STN1,HMBOX1	up_ACOR_VSMC
GO:0006733	0.802	0.388	3	45	oxidoreduction coenzyme metabolic process	BP	1	ALDOC,DDIT4,NMNAT1	up_ACOR_VSMC
GO:0097696	0.802	0.388	3	43	STAT cascade	BP	1	IL6R,STAT5A,RTN4RL1	up_VSAP_EC
GO:0003015	0.802	0.429	2	58	heart process	BP	1	IRX5,THRB	down_VCAV_EC
GO:1901657	0.802	0.431	2	43	glycosyl compound metabolic process	BP	1	CDA,ACPP	up_VCAV_EC
GO:0010171	0.802	0.533	1	18	body morphogenesis	BP	1	SGPL1	down_ACOR_VSMC
GO:0019933	0.802	0.528	1	32	cAMP-mediated signaling	BP	1	ADCY6	down_VCAV_EC
GO:0051817	0.802	0.528	1	31	modification of morphology or physiology of other organism	BP	1	NAPEPLD	down_VCAV_EC
GO:0097327	0.802	0.53	1	25	response to antineoplastic agent	BP	1	CTNNB1	down_VSAP_EC
GO:0045934	0.802	0.529	1	407	negative regulation of nucleobase-containing compound metabolic	BP	1	NR1H4	up_APUL_EC
GO:0000381	0.802	0.533	1	19	regulation of alternative mRNA splicing, via	BP	1	WTAP	up_VCAV_EC
GO:0051653	0.802	0.537	1	15	spindle localization	BP	1	ZW10	up_VCAV_EC
GO:1901216	0.802	0.533	1	19	positive regulation of neuron death	BP	1	TLR4	up_VCAV_EC
GO:0050701	0.802	0.536	1	16	interleukin-1 secretion	BP	1	F2RL1	up_VSAP_EC
GO:0006753	0.802025875	0.35685	4	211	nucleoside phosphate metabolic process	BP	1	NMNAT2,GUCY1B1,AK7,ALDOC	up_ACOR_EC
GO:0010638	0.802302337	0.3565	4	207	positive regulation of organelle organization	BP	1	PKIB,SYNPO2,ACTN2,NRP1	up_ACOR_EC

GO:0044260	0.803	0.223	202	2593	cellular macromolecule metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,ST8SIA6,KIT,SELE,LYZ,PPP2R5A,CXCL8,PRKCH,CALCRL,FLI1,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,RELN,ST6GAL1,CTSC,PDE4D,IWS1,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,TCF4,SMAD1,CTTNBP2NL,FOXN2,MEOX1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,ENSCAFG00000010893,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,TENT2,ELF4,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PREX2,SLK,BMP2K,SH3BP5,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,PAK2,GALNT18,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,MFNG,NCK1,ESCO1,DPH5,VHL,TIMELESS,OTUD4,LDB2,CD200,WSB1,PARP4,FES,JAG1,NSD1,MRRF,PTGS2,MMD,TOP1,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,SENP6,BASP1,PAN3,USP28,TAOK1,CNOT7,SMG7,ENSCAFG00000002897,PPP1CB,ASF1A,HMGB1,AHR,NOS2,PMAIP1,BDP1,ZNF789,BLM,NUP133,NR4A2,SPTBN4,RIPK1,	up_VCAV_EC
GO:0009887	0.803	0.262	23	314	animal organ morphogenesis	BP	1	EIF4A3,HOXA3,NAB2,INSIG1,CAV1,NF2,MMP14,GREM1,SMARCC1,HOXA7,HOXB7,GMNN,POC1A,B4GALT1,HOXB5,HOXC4,SGPL1,PHACTR4,TBX15,SERPINH1,GLI1,HMGN1,SIX4	down_ACOR_VSMC
GO:0043254	0.803	0.285	13	164	regulation of protein complex assembly	BP	1	ARHGEF5,SLIT2,ABL1,CDC42EP5,CDC42EP2,ICE1,LCAT,RAF1,VPS11,NCK1,ULK1,BAG4,JCHAIN	up_VSAP_EC
GO:0051223	0.803	0.316	7	181	regulation of protein transport	BP	1	GPAM,PRNP,ENSCAFG00000014978,AKT2,GLI3,PARK7,MAVS	down_VCAV_EC
GO:0052548	0.803	0.328	6	80	regulation of endopeptidase activity	BP	1	CST3,CRADD,MAP3K5,RECK,MYC,HTRA2	up_VSAP_EC
GO:0030324	0.803	0.359	4	64	lung development	BP	1	TIMELESS,MMP14,GLI1,JMJD6	down_ACOR_VSMC
GO:0007623	0.803	0.36	4	55	circadian rhythm	BP	1	PRKAA2,PPARGC1A,RBM4B,GNAQ	up_ACOR_VSMC
GO:0044238	0.803	0.413	4	3383	primary metabolic process	BP	1	CYP1A1,LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0006351	0.803	0.392	3	1069	transcription, DNA-templated	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0007030	0.803	0.386	3	49	Golgi organization	BP	1	GCC2,ZW10,USP6NL	up_VCAV_EC
GO:0022607	0.803	0.391	3	969	cellular component assembly	BP	1	TRIM9,SIX1,CDC42EP5	up_VFEM_EC
GO:0046632	0.803	0.433	2	29	alpha-beta T cell differentiation	BP	1	CD83,IL18R1	up_ACOR_VSMC
GO:0120036	0.803	0.428	2	373	plasma membrane bounded cell projection	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:1903432	0.803	0.533	1	18	regulation of TORC1 signaling	BP	1	RNF152	down_ACOR_VSMC
GO:0050728	0.803	0.527	1	31	negative regulation of inflammatory response	BP	1	CHID1	down_VCAV_EC
GO:0002712	0.803	0.536	1	15	regulation of B cell mediated immunity	BP	1	TP53BP1	up_ACOR_VSMC
GO:0002889	0.803	0.536	1	15	regulation of immunoglobulin	BP	1	TP53BP1	up_ACOR_VSMC
GO:0032102	0.803	0.523	1	67	negative regulation of response to external	BP	1	LEP	up_AFEM_EC
GO:0010648	0.803	0.528	1	407	negative regulation of cell communication	BP	1	NR1H4	up_APUL_EC
GO:0046128	0.803	0.529	1	23	purine ribonucleoside metabolic process	BP	1	ACPP	up_VCAV_EC
GO:0003156	0.803	0.53	1	20	regulation of animal organ formation	BP	1	BMP2	up_VCAV_EC
GO:0051252	0.803	0.544	1	1051	regulation of RNA metabolic process	BP	1	GATA5	up_VCAV_VSMC
GO:0042180	0.803493368	0.52198	1	61	cellular ketone metabolic process	BP	1	NR1H4	up_ACOR_EC

GO:0051246	0.804	0.236	64	832	regulation of protein metabolic process	BP	1	HMGB1,SREBF1,IRAK1,ILF3,USP4,EIF4A3,HMGCR,HNRNPD,UBE2S,NEDD4,U2AF2,PSMD3,SLC29A1,PPP1R15B,PRELID1,BIRC5,CAV1,RAD51,FANCI,TRUB2,NF2,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,SMARCC1,PLK3,DHX33,CKS2,PDCD2,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,RAP2C,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,DTL,CACTIN,ENSCAFG00000005299,EZR,CLSPN,RBM14,RAD23A,NOLC1,CDC20,PUM3,MAST2,AIFM1,ARHGEF2,TADA2A,TINF2,DELE1,CCNB3,MTBP,NECAB3,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0001568	0.804	0.269	18	252	blood vessel development	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,ADAMTS6,NCL,EMP2,FOSL1,SGPL1,JMJD6,NUS1	down_ACOR_VSMC
GO:0009150	0.804	0.295	10	161	purine ribonucleotide metabolic process	BP	1	NPR1,PANK3,PIPOX,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,HIF1A	up_VCAV_EC
GO:0051258	0.804	0.317	7	94	protein polymerization	BP	1	FAM107A,SLIT2,ABL1,CDC42EP5,CDC42EP2,NCK1,BAG4	up_VSAP_EC
GO:0050896	0.804	0.386	4	2346	response to stimulus	BP	1	GPSM2,IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0060326	0.804	0.381	3	84	cell chemotaxis	BP	1	PDGFRB,HSD3B7,RAC2	down_VCAV_EC
GO:0006813	0.804	0.429	2	37	potassium ion transport	BP	1	KCNJ3,KCNJ2	up_VCAV_EC
GO:0090303	0.804	0.53	1	18	positive regulation of wound healing	BP	1	PPARD	down_ACOR_VSMC
GO:0009166	0.804	0.525	1	31	nucleotide catabolic process	BP	1	ACAT1	down_VCAV_EC
GO:0097581	0.804	0.526	1	26	lamellipodium organization	BP	1	FSCN1	down_VSAP_EC
GO:0003338	0.804	0.533	1	15	metanephros morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0032655	0.804	0.532	1	16	regulation of interleukin-12 production	BP	1	TLR3	up_ACOR_VSMC
GO:0099132	0.804	0.531	1	17	ATP hydrolysis coupled cation transmembrane	BP	1	ATP6V0E1	up_ACOR_VSMC
GO:0023057	0.804	0.525	1	409	negative regulation of signaling	BP	1	NR1H4	up_APUL_EC
GO:0009308	0.804	0.53	1	20	amine metabolic process	BP	1	ODC1	up_VCAV_EC
GO:0031529	0.804	0.529	1	20	ruffle organization	BP	1	MTOR	up_VCAV_EC
GO:0010498	0.804	0.521	1	194	proteasomal protein catabolic process	BP	1	RNF6	up_VPOR_EC
GO:0009101	0.804212649	0.42302	2	113	glycoprotein biosynthetic process	BP	1	GALNT5,B3GNT7	up_ACOR_EC
GO:0010038	0.80422099	0.52073	1	62	response to metal ion	BP	1	AQP1	up_ACOR_EC
GO:0010212	0.80475874	0.51999	1	60	response to ionizing radiation	BP	1	FIGNL1	up_ACOR_EC
GO:0048856	0.805	0.225	122	1533	anatomical structure development	BP	1	ELK3,FSCN1,HMGB1,FLNB,USP1,ANLN,FMNL3,ACSL4,EIF4A3,HINFP,NEDD4,SLC29A1,MTDH,HEY1,HOXA3,TRIP13,SF1,SRRT,GINS4,SDC1,CTDNEP1,RAD54L,FBXO5,HSPA9,NAB2,HNRNPH3,B3GNT2,CFAP298,PRELID1,INSIG1,PRMT1,CAV1,CDK1,CASP2,XYLT1,TIMELESS,NF2,ANPEP,PFAS,MMP14,EZH2,STMN1,SLC30A1,GREM1,MAP3K20,NEK2,ADIPOR2,CDK4,SMARCC1,RNASEH2B,HMGB3,PCNA,HOXA7,SMG9,ARG2,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,POC1A,BRCA1,WDR62,E2F8,B4GALT1,NAV2,PRCP,TFRC,ADAMTS6,PPARD,RAP2C,NCL,RAC1,UGDH,EMP2,FOSL1,PLK4,IQGAP1,HOXC6,HMGB2,CDC42EP4,ARCN1,CDK2,SMARCB1,RAB35,HOXB5,RBBP8,EZR,TOX,HOXC4,RBM14,CORO1A,SGPL1,NOLC1,BEND6,PHACTR4,CDC20,SLC20A1,ASPM,PRPS1,TBX15,ENSCAFG00000010224,RADIL,ITGA2,CTH,ARHGEF2,HOXA9,SERPINH1,GLI1,JMJD6,MSC,EMG1,RTTN,RTCB,NUS1,HMGN1,TBCC,SIX4,TTLL1,TPBG,AMER1,ANXA7	down_ACOR_VSMC
GO:0051254	0.805	0.268	18	431	positive regulation of RNA metabolic process	BP	1	DCN,LUM,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,ZFP36L1,MYDGF,MAVS,MAPRE3,SHC1,GREM1,THRB,ZBTB16	down_VCAV_EC

GO:0045596	0.805	0.276	15	186	negative regulation of cell differentiation	BP	1	TMEM176B,TMEM176A,SMAD6,LBH,ITM2C,BMP4,TP53INP1,ZNF365,NRP1,ULK2,FRS2,APP,PSEN1,ASAP1,B2M	up_ACOR_VSMC
GO:0003006	0.805	0.313	7	180	developmental process involved in reproduction	BP	1	BMPR1A,B4GALT1,ZFP36L1,IRX5,RDH10,FOXO3,ZBTB16	down_VCAV_EC
GO:0001701	0.805	0.336	5	134	in utero embryonic development	BP	1	BMPR1A,GLI3,ZFP36L1,PRKCSH,RDH10	down_VCAV_EC
GO:0006631	0.805	0.354	4	93	fatty acid metabolic process	BP	1	TRIB3,SESN2,PTGS2,SLC45A3	down_VSAP_EC
GO:0042594	0.805	0.357	4	64	response to starvation	BP	1	ATF3,RALB,MTOR,PMAIP1	up_VCAV_EC
GO:0071840	0.805	0.377	4	2059	cellular component organization or biogenesis	BP	1	EYA1,FBP1,SHOX2,ATP8B4	up_VFEM_VSMC
GO:0048518	0.805	0.4	3	1676	positive regulation of biological process	BP	1	DKK2,HOXA9,TAOK1	up_AORT_EC
GO:0032774	0.805	0.389	3	1073	RNA biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0097659	0.805	0.39	3	1072	nucleic acid-templated transcription	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0046488	0.805	0.384	3	44	phosphatidylinositol metabolic process	BP	1	INPP5E,PIK3R1,ZFYVE21	up_VSAP_EC
GO:0002429	0.805	0.427	2	35	immune response-activating cell surface receptor signaling	BP	1	MNDA,EZR	down_ACOR_VSMC
GO:0009267	0.805	0.423	2	60	cellular response to starvation	BP	1	GABARAP,CLEC16A	down_VCAV_EC
GO:0050000	0.805	0.525	1	27	chromosome localization	BP	1	KPNB1	down_VSAP_EC
GO:0010830	0.805	0.53	1	16	regulation of myotube differentiation	BP	1	DMPK	up_ACOR_VSMC
GO:0035019	0.805	0.531	1	16	somatic stem cell population maintenance	BP	1	LBH	up_ACOR_VSMC
GO:0002263	0.805	0.52	1	68	cell activation involved in immune response	BP	1	DLL1	up_AFEM_EC
GO:1901575	0.805	0.531	1	643	organic substance catabolic process	BP	1	LNPEP	up_AORT_EC
GO:0090317	0.805	0.531	1	16	negative regulation of intracellular protein	BP	1	BAG4	up_VSAP_EC
GO:0046427	0.805	0.532	1	16	positive regulation of JAK-STAT cascade	BP	1	IL6R	up_VSAP_EC
GO:0018193	0.805	0.522	1	368	peptidyl-amino acid modification	BP	1	CAV1	up_VSAP_VSMC
GO:0007281	0.805686561	0.51848	1	60	germ cell development	BP	1	PYGO2	up_ACOR_EC
GO:0008150	0.806	0.224	534	5646	biological_process	BP	1	GPR1,TBX15,HOXA11,FZD1,PRR16,SLC43A1,THRB,EMX2,ENOX1,HOXA7,HOXA10,PEX7,NAPEPLD,PCDH19,TWIST2,HOXA9,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,NECAB3,WNT11,HNF4A,ACSM3,DHDH,SERPINB8,FAM107A,DNM1,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,ACKR2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,CALHM2,LRRN3,PTGFR,SLC8B1,RADIL,ZNF367,PPARGC1B,PLEKHF1,CBR3,SH2D4A,RNPEP,TBC1D10C,PLBD1,MAB21L1,ACAA1,SLC43A3,MRPL37,CEP85,GJB5,LIMS2,LRIG3,FOXRED2,GABRE,ARHGEF6,ALDH3B1,MFSD3,ACACB,TPCN2,EEF2K,DDHD1,IL6R,IRX5,RETREG1,SLIT2,GDA,CST3,NIPAL3,CRADD,CRIP2,LRRC28,ZHX3,TBC1D2B,NDUFS7,ABTB1,HOXD3,CDH1,SLC6A4,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,EBF2,BTG1,HDAC7,KLKB1,SLC16A12,EMP2,KCNE3,CHRM1,DLL1,EPN2,DLST,HOXA6,SESN1,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,IL17RC,GLUL,CTSS,GALNT15,DTX2,SCAMP4,TENT5C,CLIC5,PGM2L1,FUZ,CORO2B,ADHFE1,ADAMTSL4,ENSCAFG00000013986,PDGFD,TRAFD1,CERS4,HSD17B14,WARS2,VDR,DHRS4,NAA60,SAV1,RHPN1,SMARCD2,HERPUD2,ENSCAFG00000003792,KDELC2,TNFSF13,DDB2,KLF15,C1	up_VSAP_EC
GO:0055086	0.806	0.287	11	237	nucleobase-containing small molecule metabolic	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ENTPD4,ALDOC,PAPSS1,AK5,CMPK1	down_VSAP_EC
GO:1901214	0.806	0.325	6	81	regulation of neuron death	BP	1	FZD1,ABL1,MAP3K5,AMBRA1,FBXO7,KDM2B	up_VSAP_EC
GO:0090316	0.806	0.381	3	48	positive regulation of intracellular protein	BP	1	HCLS1,TMEM173,CTDSPL2	up_VCAV_EC
GO:0002819	0.806	0.383	3	44	regulation of adaptive immune response	BP	1	CD274,STAT6,PPP3CB	up_VSAP_EC
GO:0043484	0.806	0.383	3	43	regulation of RNA splicing	BP	1	PIK3R1,NUP98,PQBP1	up_VSAP_EC

GO:0009058	0.806	0.455	2	1910	biosynthetic process	BP	1	CYP1A1,GATA5	up_VCAV_VSMC
GO:0046637	0.806	0.527	1	18	regulation of alpha-beta T cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0071260	0.806	0.527	1	19	cellular response to mechanical stimulus	BP	1	CASP2	down_ACOR_VSMC
GO:0038127	0.806	0.522	1	32	ERBB signaling pathway	BP	1	SHC1	down_VCAV_EC
GO:1901863	0.806	0.523	1	25	positive regulation of muscle tissue	BP	1	CTNNB1	down_VSAP_EC
GO:1904591	0.806	0.523	1	25	positive regulation of protein import	BP	1	ZPR1	down_VSAP_EC
GO:0010823	0.806	0.528	1	17	negative regulation of mitochondrion	BP	1	BNIP3	up_ACOR_VSMC
GO:0015988	0.806	0.528	1	17	energy coupled proton transmembrane transport, against	BP	1	ATP6V0E1	up_ACOR_VSMC
GO:0045666	0.806	0.518	1	68	positive regulation of neuron differentiation	BP	1	IRX3	up_AFEM_EC
GO:0031327	0.806	0.523	1	412	negative regulation of cellular biosynthetic	BP	1	NR1H4	up_APUL_EC
GO:0032212	0.806	0.53	1	16	positive regulation of telomere maintenance via	BP	1	FBXO4	up_VSAP_EC
GO:1901570	0.806	0.53	1	16	fatty acid derivative biosynthetic process	BP	1	PTGES	up_VSAP_EC
GO:1904358	0.806	0.53	1	16	positive regulation of telomere maintenance via telomere lengthening	BP	1	FBXO4	up_VSAP_EC
GO:0072175	0.806511441	0.51714	1	60	epithelial tube formation	BP	1	SOX9	up_ACOR_EC
GO:1901135	0.806995857	0.30281	8	390	carbohydrate derivative metabolic process	BP	1	GALNT5,PORCN,EDEM2,B3GNT7,GUCY1B1,PIGS,ALDOC,PRKCD	up_ACOR_EC
GO:0016311	0.807	0.312	7	106	dephosphorylation	BP	1	SLC29A1,PPM1G,PPP1R15B,PPP2R5D,YWHAB,IQGAP1,KNL1	down_ACOR_VSMC
GO:0070997	0.807	0.313	7	93	neuron death	BP	1	FZD1,THRB,ABL1,MAP3K5,AMBRA1,FBXO7,KDM2B	up_VSAP_EC
GO:0097529	0.807	0.38	3	52	myeloid leukocyte migration	BP	1	HMGB1,MMP14,RAC1	down_ACOR_VSMC
GO:0044249	0.807	0.402	3	1851	cellular biosynthetic process	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC
GO:0010506	0.807	0.377	3	86	regulation of autophagy	BP	1	DCN,POLDIP2,CLEC16A	down_VCAV_EC
GO:0015833	0.807	0.379	3	521	peptide transport	BP	1	XPOT,GCC2,SRP54	up_VPOR_EC
GO:0009889	0.807	0.389	3	1190	regulation of biosynthetic process	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0006941	0.807	0.425	2	36	striated muscle contraction	BP	1	CAV1,ARG2	down_ACOR_VSMC
GO:0003231	0.807	0.422	2	48	cardiac ventricle development	BP	1	LTBP1,HIF1A	down_VSAP_EC
GO:1901989	0.807	0.426	2	31	positive regulation of cell cycle phase transition	BP	1	CDC7,APP	up_ACOR_VSMC
GO:0009056	0.807	0.427	2	755	catabolic process	BP	1	PLCL1,LZTS1	up_APUL_EC
GO:0065007	0.807	0.509	2	3499	biological regulation	BP	1	HOXA3,TBX5	up_APUL_VSMC
GO:0055088	0.807	0.424	2	37	lipid homeostasis	BP	1	ABCA1,NR1D2	up_VCAV_EC
GO:0030163	0.807	0.421	2	365	protein catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0031532	0.807	0.426	2	31	actin cytoskeleton reorganization	BP	1	FGF7,ABL1	up_VSAP_EC
GO:0014896	0.807	0.526	1	18	muscle hypertrophy	BP	1	EZH2	down_ACOR_VSMC
GO:0014897	0.807	0.526	1	18	striated muscle hypertrophy	BP	1	EZH2	down_ACOR_VSMC
GO:0045599	0.807	0.525	1	19	negative regulation of fat cell differentiation	BP	1	INSIG1	down_ACOR_VSMC
GO:0060393	0.807	0.525	1	19	regulation of pathway-restricted SMAD protein	BP	1	GREM1	down_ACOR_VSMC
GO:0003300	0.807	0.526	1	18	cardiac muscle hypertrophy	BP	1	EZH2	down_ACOR_VSMC
GO:0032268	0.807	0.531	1	778	regulation of cellular protein metabolic process	BP	1	CST3	down_VPOR_EC
GO:0002312	0.807	0.523	1	24	B cell activation involved in immune response	BP	1	TFRC	down_VSAP_EC
GO:0007035	0.807	0.527	1	16	vacuolar acidification	BP	1	DMXL1	up_ACOR_VSMC
GO:0042509	0.807	0.526	1	17	regulation of tyrosine phosphorylation of STAT	BP	1	PARP9	up_ACOR_VSMC

GO:0072593	0.807	0.515	1	68	reactive oxygen species metabolic process	BP	1	SOD1	up_AFEM_EC
GO:2000058	0.807	0.515	1	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0006024	0.807	0.528	1	16	glycosaminoglycan biosynthetic process	BP	1	CHST7	up_VSAP_EC
GO:0051130	0.807128914	0.31036	7	342	positive regulation of cellular component	BP	1	PKIB,CALY,SYNPO2,ACTN2,LRP4,NRP1,PRKCD	up_ACOR_EC
GO:0044839	0.807616129	0.51525	1	61	cell cycle G2/M phase transition	BP	1	BRSK1	up_ACOR_EC
GO:0000077	0.807650337	0.51527	1	60	DNA damage checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0048869	0.808	0.226	88	1119	cellular developmental process	BP	1	ELK3,HMGB1,SREBF1,FLNB,ANLN,FMNL3,ACSL4,HMGA1,HINFP,NEDD4,SLC29A1,TRIP13,SF1,SRRT,SDC1,FBXO5,HSPA9,NAB2,HNRNPH3,B3GNT2,CFAP298,PRELID1,INSIG1,PRMT1,CAV1,CDK1,CASP2,NF2,ANPEP,MMP14,EZH2,STMN1,GREM1,HMGB3,PCNA,HOXA7,ARG2,PDCD2,HOXC10,HOXB7,POC1A,WDR62,E2F8,B4GALT1,NAV2,TFRC,PPARD,RAP2C,RAC1,NUP62,EMP2,PLK4,IQGAP1,RSL1D1,HMGB2,CDC42EP4,SMARCB1,RAB35,HOXB5,EZR,SMC6,TOX,RBM14,CORO1A,SGPL1,NOLC1,BEND6,PHACTR4,ERF,ASPM,ENSCAFG00000010224,ELF4,TXNDC12,RADIL,ITGA2,CTH,ARHGEF2,TWIST2,HOXA9,SERPINH1,GLI1,JMJD6,CDC5L,TBCC,SIX4,TTLL1,AMER1,ANXA7	down_ACOR_VSMC
GO:0097659	0.808	0.226	84	1072	nucleic acid-templated transcription	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,POLR3F,HOXA10,ERF,TCERG1,SMARCAL1,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103,POLR1C	down_ACOR_VSMC
GO:0070727	0.808	0.239	43	579	cellular macromolecule localization	BP	1	HCLS1,GBP5,PPP2R5A,TNFAIP3,AMOT,TMEM173,EXOC3L2,RELN,IWS1,FERMT1,TSPAN15,RAB11A,RAB27A,ZDHHC22,PPP3CA,HOOK3,TSPAN14,HHEX,CEP68,MZT1,EPB41,SNX2,THOC1,SH3GLB1,AKAP12,APOD,EXOC5,RAPGEF2,CTDSPL2,PAN3,GCC2,CTNNA1,STX11,SMG7,TBC1D1,NUP133,SPTBN4,RAD21,ZW10,IPO11,ATRX,RABGAP1,USP6NL	up_VCAV_EC
GO:0009894	0.808	0.256	23	277	regulation of catabolic process	BP	1	LEP,HTR2B,FBXL20,FEZ1,PRKAA2,SH3RF2,TP53INP1,PTPN3,DAPK1,BNIP3,EGLN1,OS9,PRKCE,RNF19A,PSEN1,DDIT4,DISC1,HERPUD1,FEZ2,AZIN2,SH3BP4,ENSCAFG00000029553,PARK7	up_ACOR_VSMC
GO:0006139	0.808	0.287	13	1909	nucleobase-containing compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RRP15,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0017144	0.808	0.295	9	199	drug metabolic process	BP	1	PGK1,TPI1,PGAM1,HIF1A,ALDH18A1,ALDOC,AK5,REST,KDM3A	down_VSAP_EC
GO:1902532	0.808	0.301	8	204	negative regulation of intracellular signal	BP	1	DCN,PRNP,BGN,AKT1S1,TMEM161A,ASPN,PARK7,SPRED1	down_VCAV_EC
GO:1901652	0.808	0.311	7	105	response to peptide	BP	1	SREBF1,CAV1,TIMELESS,CDK4,SMARCC1,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:1902105	0.808	0.322	6	80	regulation of leukocyte differentiation	BP	1	TMEM176B,TMEM176A,CD83,RASSF2,BMP4,CLSTN1	up_ACOR_VSMC
GO:0030098	0.808	0.35	4	87	lymphocyte differentiation	BP	1	SOCS5,PTPN2,CTNNB1,BTK	down_VSAP_EC
GO:0034728	0.808	0.352	4	56	nucleosome organization	BP	1	ATRX,TSPYL5,SMARCD3,SHPRH	up_ACOR_VSMC
GO:0048754	0.808	0.353	4	57	branching morphogenesis of an epithelial tube	BP	1	HOXA11,SLIT2,ABL1,TGFBR2	up_VSAP_EC
GO:0006334	0.808	0.379	3	45	nucleosome assembly	BP	1	ATRX,TSPYL5,SHPRH	up_ACOR_VSMC
GO:0007049	0.808	0.423	2	560	cell cycle	BP	1	USP28,ATRIP	down_ACOR_EC

GO:0038061	0.808	0.424	2	34	NIK/NF-kappaB signaling	BP	1	IRAK1,GREM1	down_ACOR_VSMC
GO:0032434	0.808	0.419	2	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	PARK7,CLEC16A	down_VCAV_EC
GO:0010389	0.808	0.425	2	30	regulation of G2/M transition of mitotic cell	BP	1	CDC7,APP	up_ACOR_VSMC
GO:0010833	0.808	0.425	2	30	telomere maintenance via telomere lengthening	BP	1	STN1,HMBOX1	up_ACOR_VSMC
GO:0009206	0.808	0.422	2	39	purine ribonucleoside triphosphate biosynthetic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0030030	0.808	0.42	2	377	cell projection organization	BP	1	SEMA3A,RNF6	up_VPOR_EC
GO:0007272	0.808	0.425	2	31	ensheathment of neurons	BP	1	WASF3,AMIGO1	up_VSAP_EC
GO:0008366	0.808	0.425	2	31	axon ensheathment	BP	1	WASF3,AMIGO1	up_VSAP_EC
GO:0002204	0.808	0.525	1	18	somatic recombination of immunoglobulin genes involved in immune	BP	1	TFRC	down_ACOR_VSMC
GO:0032387	0.808	0.523	1	20	negative regulation of intracellular transport	BP	1	INSIG1	down_ACOR_VSMC
GO:0002208	0.808	0.525	1	18	somatic diversification of immunoglobulins involved in immune response	BP	1	TFRC	down_ACOR_VSMC
GO:0043367	0.808	0.525	1	18	CD4-positive, alpha-beta T cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0045190	0.808	0.525	1	18	isotype switching	BP	1	TFRC	down_ACOR_VSMC
GO:0060038	0.808	0.525	1	18	cardiac muscle cell proliferation	BP	1	GLI1	down_ACOR_VSMC
GO:0060420	0.808	0.524	1	18	regulation of heart growth	BP	1	GLI1	down_ACOR_VSMC
GO:0034644	0.808	0.517	1	32	cellular response to UV	BP	1	TMEM161A	down_VCAV_EC
GO:2001237	0.808	0.518	1	33	negative regulation of extrinsic apoptotic	BP	1	PARK7	down_VCAV_EC
GO:0060395	0.808	0.52	1	27	SMAD protein signal transduction	BP	1	INHBA	down_VSAP_EC
GO:0090501	0.808	0.518	1	29	RNA phosphodiester bond hydrolysis	BP	1	MRPL1	down_VSAP_EC
GO:0072330	0.808	0.515	1	68	monocarboxylic acid biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0006281	0.808	0.514	1	208	DNA repair	BP	1	CXHXorf57	up_VPOR_EC
GO:0015991	0.808	0.527	1	16	ATP hydrolysis coupled proton transport	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0090662	0.808	0.527	1	16	ATP hydrolysis coupled transmembrane transport	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0099131	0.808	0.527	1	16	ATP hydrolysis coupled ion transmembrane	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0019233	0.808	0.527	1	16	sensory perception of pain	BP	1	NR2F6	up_VSAP_EC
GO:0045597	0.80864569	0.3305	5	253	positive regulation of cell differentiation	BP	1	SOX9,CCDC3,TBX5,CLSTN1,NRP1	up_ACOR_EC
GO:0009987	0.809	0.279	39	5086	cellular process	BP	1	C3AR1,BARX1,HTR7,OSTC,CXHXorf57,OGA,MZT1,HOOK3,HOXA3,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,SLC7A11,SEMA3A,ENSCAFG00000005494,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,GCC2,SV2C,RPL10L,ABHD5,TWF1,PDE1C,FAM135A,RRP15,SRP54,KLHL28,PUM3,EIF5,CCAR1,STK17B,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0060070	0.809	0.31	7	105	canonical Wnt signaling pathway	BP	1	SDC1,CTDNEP1,CAV1,GREM1,ASPM,GLI1,AMER1	down_ACOR_VSMC
GO:0016570	0.809	0.308	7	143	histone modification	BP	1	NR1H4,IWS1,MORF4L2,REST,ZMYND8,PRMT1,KDM3A	down_VSAP_EC
GO:0006643	0.809	0.333	5	68	membrane lipid metabolic process	BP	1	CERS4,KDELC2,ENSCAFG00000000071,HACD4,B3GALT4	up_VSAP_EC
GO:0051223	0.809	0.372	3	181	regulation of protein transport	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:0001656	0.809	0.421	2	35	metanephros development	BP	1	GREM1,SIX4	down_ACOR_VSMC
GO:0035270	0.809	0.421	2	35	endocrine system development	BP	1	HOXA3,GLI1	down_ACOR_VSMC
GO:0009896	0.809	0.415	2	127	positive regulation of catabolic process	BP	1	CLEC16A,RAB7A	up_AFEM_EC
GO:0010812	0.809	0.521	1	19	negative regulation of cell-substrate adhesion	BP	1	HOXA7	down_ACOR_VSMC

GO:0042116	0.809	0.523	1	18	macrophage activation	BP	1	JMJD6	down_ACOR_VSMC
GO:0034968	0.809	0.517	1	34	histone lysine methylation	BP	1	PRMT6	down_VCAV_EC
GO:1904035	0.809	0.524	1	16	regulation of epithelial cell apoptotic process	BP	1	WFS1	up_ACOR_VSMC
GO:0009108	0.809	0.513	1	68	coenzyme biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0060038	0.809	0.523	1	18	cardiac muscle cell proliferation	BP	1	MEF2C	up_VCAV_EC
GO:0006351	0.809	0.535	1	1069	transcription, DNA-templated	BP	1	GATA5	up_VCAV_VSMC
GO:0008219	0.809	0.522	1	611	cell death	BP	1	EYA1	up_VFEM_VSMC
GO:0007528	0.809	0.524	1	17	neuromuscular junction development	BP	1	LRP4	up_VSAP_EC
GO:0061951	0.809	0.525	1	16	establishment of protein localization to plasma	BP	1	RILPL2	up_VSAP_EC
GO:0034248	0.81	0.3	8	125	regulation of cellular amide metabolic process	BP	1	QKI,MTOR,SAMD8,ENC1,SECISBP2L,NCK1,DPH5,CNOT7	up_VCAV_EC
GO:0070997	0.81	0.318	6	93	neuron death	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIGMAR1,AIFM1,SIX4	down_ACOR_VSMC
GO:0060485	0.81	0.318	6	93	mesenchyme development	BP	1	EZH2,GREM1,NOLC1,PHACTR4,SIX4,AMER1	down_ACOR_VSMC
GO:1903046	0.81	0.35	4	55	meiotic cell cycle process	BP	1	ATRX,MARF1,DMC1,SUN1	up_ACOR_VSMC
GO:0006898	0.81	0.35	4	57	receptor-mediated endocytosis	BP	1	DNM1,ACKR3,UBQLN2,FLOT1	up_VSAP_EC
GO:0007254	0.81	0.374	3	67	JNK cascade	BP	1	TNIK,MAPK10,SH3RF3	down_VSAP_EC
GO:0002695	0.81	0.377	3	44	negative regulation of leukocyte activation	BP	1	CD274,TBC1D10C,FBXO7	up_VSAP_EC
GO:0071695	0.81	0.376	3	45	anatomical structure maturation	BP	1	IRX5,RECK,NTN4	up_VSAP_EC
GO:0007281	0.81	0.416	2	60	germ cell development	BP	1	FOXO3,ZBTB16	down_VCAV_EC
GO:1904888	0.81	0.421	2	31	cranial skeletal system development	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0008104	0.81	0.423	2	763	protein localization	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0044248	0.81	0.422	2	691	cellular catabolic process	BP	1	TRIM9,CYP26B1	up_VFEM_EC
GO:0048644	0.81	0.421	2	31	muscle organ morphogenesis	BP	1	FZD1,SHOX2	up_VSAP_EC
GO:0043085	0.81	0.514	1	323	positive regulation of catalytic activity	BP	1	LYN	down_ACOR_EC
GO:0035296	0.81	0.514	1	32	regulation of tube diameter	BP	1	ADCY6	down_VCAV_EC
GO:0097746	0.81	0.514	1	32	regulation of blood vessel diameter	BP	1	ADCY6	down_VCAV_EC
GO:0032088	0.81	0.516	1	26	negative regulation of NF-kappaB transcription	BP	1	NR1H4	down_VSAP_EC
GO:1902600	0.81	0.515	1	31	proton transmembrane transport	BP	1	NDUFA4L2	down_VSAP_EC
GO:1903426	0.81	0.522	1	17	regulation of reactive oxygen species	BP	1	PARK7	up_ACOR_VSMC
GO:0019083	0.81	0.52	1	19	viral transcription	BP	1	SMARCA4	up_VCAV_EC
GO:0097006	0.81	0.521	1	19	regulation of plasma lipoprotein particle levels	BP	1	ABCA1	up_VCAV_EC
GO:0032774	0.81	0.533	1	1073	RNA biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0097659	0.81	0.534	1	1072	nucleic acid-templated transcription	BP	1	GATA5	up_VCAV_VSMC
GO:0002376	0.81	0.522	1	622	immune system process	BP	1	HOXA9	up_VFEM_VSMC
GO:0032268	0.81	0.525	1	778	regulation of cellular protein metabolic process	BP	1	SLIT2	up_VPUL_VSMC

GO:0032774	0.811	0.223	84	1073	RNA biosynthetic process	BP	1	ELK3,HMGB1,SREBF1,IRAK1,ILF3,CBX5,PPRC1,ATAD2,HMGA1,SREBF2,HINFP,NEDD4,MED17,MTDH,HEY1,SRRT,NAB2,CDCA7L,FUS,BIRC5,MYBBP1A,INSIG1,PRMT1,CAV1,TIMELESS,THRAP3,FAM129B,TCEA1,AURKB,NONO,EZH2,GREM1,SMARCC1,PLK3,DHX33,HOXA7,UHRF1,CKS2,GMNN,BRCA1,NOC2L,E2F8,PPARD,YBX3,NCL,NUP62,FOSL1,SUV39H1,ZNF367,CACTIN,HMGB2,DMAP1,CDK2,SMARCB1,DDX39B,CCNA2,ENSCAFG00000005299,EZR,RBM14,POLR3F,HOXA10,ERF,TCERG1,SMARCAL1,TBX15,ELF4,PRMT5,PSMC1,CTH,ARHGEF2,SUPT16H,TADA2A,HAT1,HIST2H2AC,HOXA9,GLI1,JMJD6,H2AFX,CDC5L,HMGN1,SIX4,MED16,ENSCAFG00000017103,POLR1C	down_ACOR_VSMC
GO:0031323	0.811	0.226	83	1788	regulation of cellular metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,PRNP,LUM,FBN1,GLIPR2,BGN,LARP6,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,TFE3,NR3C1,HR,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,CXXC5,ASPN,POLDIP2,LRPAP1,EIF3K,THY1,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,SPRED1,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,LONP2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0072657	0.811	0.282	11	144	protein localization to membrane	BP	1	FGF13,ACTN2,TCAF1,GLRB,AR,AGRN,DAG1,JUP,RAB11B,LRRC4,INPP5K	up_ACOR_VSMC
GO:0007268	0.811	0.287	10	130	chemical synaptic transmission	BP	1	GPR1,FAM107A,SLC6A4,ABL1,CHRM1,SLC12A6,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0098916	0.811	0.287	10	130	anterograde trans-synaptic signaling	BP	1	GPR1,FAM107A,SLC6A4,ABL1,CHRM1,SLC12A6,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0045785	0.811	0.306	7	107	positive regulation of cell adhesion	BP	1	HMGB1,CAV1,TFRC,FAM49B,RAC1,EMP2,CORO1A	down_ACOR_VSMC
GO:0031668	0.811	0.33	5	79	cellular response to extracellular stimulus	BP	1	ATF3,RALB,MTOR,PMAIP1,ITGA6	up_VCAV_EC
GO:1901137	0.811	0.344	4	232	carbohydrate derivative biosynthetic process	BP	1	XYLT1,ACACB,PPARGC1A,CSGALNACT2	up_AFEM_EC
GO:0051321	0.811	0.348	4	61	meiotic cell cycle	BP	1	FIGNL1,CENPC,ATRX,FBXO5	up_VCAV_EC
GO:0043112	0.811	0.348	4	57	receptor metabolic process	BP	1	ACKR3,RAB11B,UBQLN2,FLOT1	up_VSAP_EC
GO:1901215	0.811	0.348	4	57	negative regulation of neuron death	BP	1	FZD1,AMBRA1,FBXO7,KDM2B	up_VSAP_EC
GO:0002263	0.811	0.373	3	68	cell activation involved in immune response	BP	1	SOCS5,TFRC,LYN	down_VSAP_EC
GO:0046330	0.811	0.416	2	47	positive regulation of JNK cascade	BP	1	TNIK,SH3RF3	down_VSAP_EC
GO:0048489	0.811	0.418	2	38	synaptic vesicle transport	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0097480	0.811	0.418	2	38	establishment of synaptic vesicle localization	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0033619	0.811	0.519	1	19	membrane protein proteolysis	BP	1	HM13	down_ACOR_VSMC
GO:0008150	0.811	1	1	5646	biological_process	BP	1	GATA5	down_AFEM_VSMC
GO:0006367	0.811	0.513	1	32	transcription initiation from RNA polymerase II	BP	1	CLSTN1	down_VCAV_EC
GO:0009060	0.811	0.513	1	31	aerobic respiration	BP	1	MTFR1L	down_VCAV_EC
GO:0051028	0.811	0.512	1	33	mRNA transport	BP	1	ZFP36L1	down_VCAV_EC
GO:0009410	0.811	0.515	1	27	response to xenobiotic stimulus	BP	1	HOMER1	down_VSAP_EC
GO:0008333	0.811	0.518	1	19	endosome to lysosome transport	BP	1	HOOK3	up_VCAV_EC
GO:0035137	0.811	0.519	1	18	hindlimb morphogenesis	BP	1	CHD7	up_VCAV_EC
GO:0072210	0.811	0.518	1	19	metanephric nephron development	BP	1	PDGFB	up_VCAV_EC
GO:1902275	0.811983099	0.50811	1	60	regulation of chromatin organization	BP	1	PYGO2	up_ACOR_EC

GO:0006511	0.812	0.259	18	253	ubiquitin-dependent protein catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C	down_ACOR_VSMC
GO:0043408	0.812	0.262	17	211	regulation of MAPK cascade	BP	1	CDON,ACKR3,ARHGEF5,C5AR2,TBC1D10C,ABL1,MAP3K5,PDGFD,C1QTNF2,F2RL1,TRAF7,MYC,SASH1,MYD88,FBLN1,RAF1,QARS	up_VSAP_EC
GO:0080134	0.812	0.264	16	386	regulation of response to stress	BP	1	BMPR1A,CHID1,TMEM161A,THY1,RNF216,PARK7,SASH1,CYBA,MAVS,FUT8,SPRED1,RAB7B,A2M,FBH1,NAPEPLD,RGMA	down_VCAV_EC
GO:0072657	0.812	0.29	9	144	protein localization to membrane	BP	1	PPP2R5A,RELN,TSPAN15,RAB11A,ZDHHC22,TSPAN14,SH3GLB1,EXOC5,RAPGEF2	up_VCAV_EC
GO:0071840	0.812	0.32	7	2059	cellular component organization or biogenesis	BP	1	EYA1,TRIM9,SIX1,RADIL,CYP26B1,CDC42EP5,MTSS1	up_VFEM_EC
GO:0007264	0.812	0.313	6	164	small GTPase mediated signal transduction	BP	1	NOTCH2,ARHGEF25,RHOD,DOCK10,ARHGAP1,RAC2	down_VCAV_EC
GO:0051179	0.812	0.329	6	1747	localization	BP	1	EMX2,NETO1,SLC16A12,STIM1,TLR2,CAV1	up_VSAP_VSMC
GO:0051188	0.812	0.328	5	81	cofactor biosynthetic process	BP	1	ACLY,ELOVL1,ELOVL6,PDHA1,PDSS1	down_ACOR_VSMC
GO:0043534	0.812	0.347	4	57	blood vessel endothelial cell migration	BP	1	FGF18,NRP1,JUP,PIK3C2A	up_ACOR_VSMC
GO:0007417	0.812	0.343	4	235	central nervous system development	BP	1	HOXC10,LEP,DLL1,PLXNA4	up_AFEM_EC
GO:0071216	0.812	0.413	2	61	cellular response to biotic stimulus	BP	1	SASH1,FBH1	down_VCAV_EC
GO:0010639	0.812	0.411	2	128	negative regulation of organelle organization	BP	1	CLEC16A,KANK1	up_AFEM_EC
GO:0001656	0.812	0.417	2	35	metanephros development	BP	1	PDGFB,GATA3	up_VCAV_EC
GO:0031648	0.812	0.516	1	19	protein destabilization	BP	1	RAD23A	down_ACOR_VSMC
GO:0072210	0.812	0.516	1	19	metanephric nephron development	BP	1	GREM1	down_ACOR_VSMC
GO:0008150	0.812	1	1	5646	biological_process	BP	1	MXRA5	down_AORT_VSMC
GO:0051261	0.812	0.511	1	33	protein depolymerization	BP	1	PLEKHH2	down_VCAV_EC
GO:0045814	0.812	0.512	1	27	negative regulation of gene expression,	BP	1	MORF4L2	down_VSAP_EC
GO:0042181	0.812	0.518	1	17	ketone biosynthetic process	BP	1	DKKL1	up_ACOR_VSMC
GO:0002763	0.812	0.519	1	17	positive regulation of myeloid leukocyte	BP	1	CLSTN1	up_ACOR_VSMC
GO:0009890	0.812	0.512	1	420	negative regulation of biosynthetic process	BP	1	NR1H4	up_APUL_EC
GO:0010092	0.812	0.517	1	19	specification of animal organ identity	BP	1	MEF2C	up_VCAV_EC
GO:0051972	0.812	0.517	1	20	regulation of telomerase activity	BP	1	HMBOX1	up_VCAV_EC
GO:0031050	0.812	0.518	1	17	dsRNA processing	BP	1	ZC3H10	up_VSAP_EC
GO:0070918	0.812	0.518	1	17	production of small RNA involved in gene silencing	BP	1	ZC3H10	up_VSAP_EC
GO:0051568	0.812	0.518	1	17	histone H3-K4 methylation	BP	1	WDR82	up_VSAP_EC
GO:2001252	0.812330791	0.50745	1	61	positive regulation of chromosome organization	BP	1	PKIB	up_ACOR_EC
GO:0031570	0.812952619	0.50642	1	61	DNA integrity checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0006355	0.813	0.229	54	974	regulation of transcription, DNA-templated	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0048232	0.813	0.305	7	95	male gamete generation	BP	1	HOXA11,HOXA9,ZNF449,HERPUD2,ZBTB16,PATZ1,KDM2B	up_VSAP_EC
GO:0030323	0.813	0.345	4	65	respiratory tube development	BP	1	TIMELESS,MMP14,GLI1,JMJD6	down_ACOR_VSMC
GO:1900180	0.813	0.37	3	50	regulation of protein localization to nucleus	BP	1	CDK1,NF2,DMAP1	down_ACOR_VSMC
GO:0034250	0.813	0.371	3	45	positive regulation of cellular amide metabolic	BP	1	FAM129A,APP,NGRN	up_ACOR_VSMC
GO:0042542	0.813	0.416	2	31	response to hydrogen peroxide	BP	1	CAT,PARK7	up_ACOR_VSMC

GO:1901989	0.813	0.416	2	31	positive regulation of cell cycle phase transition	BP	1	CDC25B,LSM10	up_VSAP_EC
GO:0048469	0.813	0.416	2	31	cell maturation	BP	1	IRX5,NTN4	up_VSAP_EC
GO:0090559	0.813	0.514	1	20	regulation of membrane permeability	BP	1	SLC25A5	down_ACOR_VSMC
GO:0035821	0.813	0.51	1	32	modification of morphology or physiology	BP	1	NAPEPLD	down_VCAV_EC
GO:0015918	0.813	0.511	1	27	sterol transport	BP	1	APOE	down_VSAP_EC
GO:0030301	0.813	0.511	1	27	cholesterol transport	BP	1	APOE	down_VSAP_EC
GO:0043506	0.813	0.513	1	25	regulation of JUN kinase activity	BP	1	TNIK	down_VSAP_EC
GO:0010569	0.813	0.518	1	17	regulation of double-strand break repair via homologous	BP	1	FIGNL1	up_VCAV_EC
GO:0048477	0.813	0.516	1	19	oogenesis	BP	1	FBXO5	up_VCAV_EC
GO:0080134	0.813	0.509	1	386	regulation of response to stress	BP	1	EYA1	up_VFEM_EC
GO:0002526	0.813	0.516	1	17	acute inflammatory response	BP	1	SAA1	up_VSAP_EC
GO:0051321	0.813163975	0.50606	1	61	meiotic cell cycle	BP	1	FIGNL1	up_ACOR_EC
GO:0051641	0.814	0.222	76	858	cellular localization	BP	1	EXPH5,SH3TC2,FGF13,RHOT1,DNAJC6,ACTN2,PLCG2,LEP,MID1,HTR2B,TCAF1,USP6NL,FBXL20,NACC2,PRKAA2,FERMT1,BMP4,EVI5L,ABCA1,SCARB2,ATRX,SEC24B,LATS2,GLRB,AR,STX11,TMEM108,IFT43,ITPR1,KLHL20,MARCH5,CDKN1A,NRP1,PTPN22,OS9,SCP2,PRKCE,AGRN,SCG5,POLR2M,DAG1,PARP9,APP,PSEN1,SGSM2,SYNJ2BP,CHD7,PIK3C3,LAMP2,JUP,CLN8,RAB11B,DYNC1I2,AKTIP,KCNC4,LRRC4,LMTK2,DISC1,AP2B1,SAR1B,HERPUD1,GAA,SUN1,VPS26A,INPP5K,FAF2,PREPL,RPAIN,WASL,SH3BP4,DYNC1I1,PARK7,ENSCAFG00000013536,BVES,LMF1,PTPN14	up_ACOR_VSMC
GO:1901575	0.814	0.243	28	643	organic substance catabolic process	BP	1	LRP1,MAOA,CHID1,TIMP2,AKT2,PSMF1,SAMD4B,ACAA1,PLCL1,ENTPD3,THNSL2,RNF216,PEX5,PARK7,ZFP36L1,CLEC16A,RNPEP,ENSCAFG00000002977,ENSCAFG00000017708,SEC61B,HM13,PYM1,FBH1,LONP2,GLS2,PACSIN3,BCKDHB,ACAT1	down_VCAV_EC
GO:0051090	0.814	0.289	9	134	regulation of DNA-binding transcription factor	BP	1	IRAK1,PPRC1,MTDH,EZH2,GREM1,DHX33,CACTIN,CTH,ARHGEF2	down_ACOR_VSMC
GO:0048705	0.814	0.303	7	95	skeletal system morphogenesis	BP	1	BMP4,FGFR2,CITED2,FGF18,PSEN1,ARID5B,WDR48	up_ACOR_VSMC
GO:0048869	0.814	0.308	7	1119	cellular developmental process	BP	1	BARX1,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,ACVR2A,RNF6	up_VPOR_EC
GO:0009142	0.814	0.371	3	46	nucleoside triphosphate biosynthetic process	BP	1	PPARGC1A,ALDOC,DDIT4	up_ACOR_VSMC
GO:0042886	0.814	0.369	3	527	amide transport	BP	1	XPOT,GCC2,SRP54	up_VPOR_EC
GO:0007368	0.814	0.413	2	37	determination of left/right symmetry	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0046483	0.814	0.443	2	1948	heterocycle metabolic process	BP	1	CYP1A1,GATA5	up_VCAV_VSMC
GO:0043933	0.814	0.415	2	698	protein-containing complex subunit	BP	1	TRIM9,CDC42EP5	up_VFEM_EC
GO:0038066	0.814	0.514	1	19	p38MAPK cascade	BP	1	EZR	down_ACOR_VSMC
GO:0051588	0.814	0.508	1	28	regulation of neurotransmitter	BP	1	GSK3B	down_VSAP_EC
GO:2000142	0.814	0.515	1	17	regulation of DNA-templated transcription,	BP	1	CLSTN1	up_ACOR_VSMC
GO:0045604	0.814	0.515	1	17	regulation of epidermal cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0034622	0.814	0.509	1	421	cellular protein-containing complex assembly	BP	1	TUBB4A	up_APUL_EC
GO:0070534	0.814	0.514	1	19	protein K63-linked ubiquitination	BP	1	PELI1	up_VCAV_EC
GO:1901575	0.814	0.514	1	643	organic substance catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0065003	0.814	0.515	1	616	protein-containing complex assembly	BP	1	FBP1	up_VFEM_VSMC
GO:0042149	0.814	0.515	1	17	cellular response to glucose starvation	BP	1	SESN1	up_VSAP_EC

GO:0048709	0.814	0.515	1	17	oligodendrocyte differentiation	BP	1	WASF3	up_VSAP_EC
GO:0006355	0.815	0.218	86	974	regulation of transcription, DNA-templated	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,F2RL1,RBL2,GLIS2,DDR2,ICE1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0002682	0.815	0.245	25	343	regulation of immune system process	BP	1	HMGB1,IRAK1,MNDA,SLC29A1,HSPA9,PRELID1,PRMT1,CAV1,MMP14,HMGB3,HOXA7,ARG2,PDCD2,TFRC,FAM49B,RAC1,CACTIN,HMGB2,EZR,TOX,RBM14,CORO1A,POLR3F,HOXA9,PIK3CD	down_ACOR_VSMC
GO:0007169	0.815	0.266	14	178	transmembrane receptor protein tyrosine kinase signaling pathway	BP	1	FGF7,ABL1,DLL1,EPN2,PDGFD,CCBE1,STAT5A,PDK2,PIK3R1,SULF2,IGFBP6,RAF1,ZFAND5,NCK1	up_VSAP_EC
GO:0006417	0.815	0.301	7	109	regulation of translation	BP	1	QKI,MTOR,ENC1,SECISBP2L,NCK1,DPH5,CNOT7	up_VCAV_EC
GO:0009260	0.815	0.312	6	83	ribonucleotide biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,ELOVL7	up_ACOR_VSMC
GO:0046390	0.815	0.312	6	83	ribose phosphate biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,ELOVL7	up_ACOR_VSMC
GO:0034645	0.815	0.355	4	1546	cellular macromolecule biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:1901576	0.815	0.39	3	1877	organic substance biosynthetic process	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC
GO:0070646	0.815	0.409	2	63	protein modification by small protein removal	BP	1	PARK7,COPS7A	down_VCAV_EC
GO:0006400	0.815	0.412	2	33	tRNA modification	BP	1	TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0009062	0.815	0.414	2	31	fatty acid catabolic process	BP	1	LEP,ACAD11	up_ACOR_VSMC
GO:0030307	0.815	0.413	2	31	positive regulation of cell growth	BP	1	NRP1,EDN1	up_ACOR_VSMC
GO:0038061	0.815	0.412	2	34	NIK/NF-kappaB signaling	BP	1	TLR3,ENSCAFG00000002015	up_VCAV_EC
GO:0008333	0.815	0.511	1	19	endosome to lysosome transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0043331	0.815	0.512	1	20	response to dsRNA	BP	1	CAV1	down_ACOR_VSMC
GO:0044344	0.815	0.506	1	33	cellular response to fibroblast growth factor	BP	1	ZFP36L1	down_VCAV_EC
GO:0051453	0.815	0.506	1	33	regulation of intracellular pH	BP	1	ATP6V0C	down_VCAV_EC
GO:0071774	0.815	0.506	1	33	response to fibroblast growth factor	BP	1	ZFP36L1	down_VCAV_EC
GO:0017004	0.815	0.513	1	18	cytochrome complex assembly	BP	1	TTC19	up_ACOR_VSMC
GO:0032984	0.815	0.502	1	70	protein-containing complex disassembly	BP	1	CLEC16A	up_AFEM_EC
GO:0000184	0.815	0.513	1	18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BP	1	SMG7	up_VCAV_EC
GO:0051276	0.815	0.507	1	398	chromosome organization	BP	1	EYA1	up_VFEM_EC
GO:0070661	0.815182473	0.50254	1	63	leukocyte proliferation	BP	1	PRKCD	up_ACOR_EC
GO:0051301	0.815884737	0.40503	2	117	cell division	BP	1	DIXDC1,CHMP4B	up_ACOR_EC
GO:0034613	0.816	0.227	50	576	cellular protein localization	BP	1	EXPH5,SH3TC2,FGF13,ACTN2,LEP,MID1,TCAF1,USP6NL,NACC2,PRKAA2,FERMT1,BMP4,EVI5L,SCARB2,ATRX,SEC24B,LATS2,GLRB,AR,STX11,MARCH5,CDKN1A,NRP1,PTPN22,OS9,AGRN,SCG5,DAG1,PARP9,PSEN1,SGSM2,SYNJ2BP,PIK3C3,LAMP2,JUP,RAB11B,LRRC4,DISC1,AP2B1,SAR1B,HERPUD1,SUN1,VPS26A,INPP5K,FAF2,RPAIN,WASL,SH3BP4,PARK7,PTPN14	up_ACOR_VSMC

GO:0050794	0.816	0.264	22	3075	regulation of cellular process	BP	1	C3AR1,BARX1,CXHXorf57,HOOK3,HOXA3,ARHGEF2,TCEA1,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,ABHD5,TWF1,PDE1C,PUM3,EIF5,CCAR1,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0045893	0.816	0.257	17	413	positive regulation of transcription, DNA-templated	BP	1	DCN,LUM,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,MYDGF,MAVS,MAPRE3,SHC1,GREM1,THRB,ZBTB16	down_VCAV_EC
GO:0071900	0.816	0.281	10	131	regulation of protein serine/threonine kinase	BP	1	ARHGEF5,ABL1,MAP3K5,PDGFD,C1QTNF2,CNPPD1,TRAF7,SASH1,FBXO7,LATS2	up_VSAP_EC
GO:0016569	0.816	0.299	7	144	covalent chromatin modification	BP	1	NR1H4,IWS1,MORF4L2,REST,ZMYND8,PRMT1,KDM3A	down_VSAP_EC
GO:0045944	0.816	0.321	5	287	positive regulation of transcription by RNA polymerase II	BP	1	HOXA9,DLL1,THRB,GREM1,PPARGC1A	up_AFEM_EC
GO:0006457	0.816	0.339	4	77	protein folding	BP	1	PPIE,SH3GLB1,PPIG,PDIA5	up_VCAV_EC
GO:0016579	0.816	0.366	3	49	protein deubiquitination	BP	1	USP1,USP4,BAP1	down_ACOR_VSMC
GO:0043902	0.816	0.367	3	45	positive regulation of multi-organism process	BP	1	PDE5A,SASH1,F2RL1	up_ACOR_VSMC
GO:0051716	0.816	0.391	3	2001	cellular response to stimulus	BP	1	GATA5,IL22RA1,SLIT2	up_VPUL_VSMC
GO:1901617	0.816	0.407	2	60	organic hydroxy compound biosynthetic	BP	1	CYB5R3,PARK7	down_VCAV_EC
GO:0010256	0.816	0.405	2	129	endomembrane system organization	BP	1	REEP2,DMPK	up_AFEM_EC
GO:0030858	0.816	0.512	1	17	positive regulation of epithelial cell	BP	1	BMP4	up_ACOR_VSMC
GO:0048194	0.816	0.51	1	18	Golgi vesicle budding	BP	1	ATP8A1	up_VCAV_EC
GO:0010942	0.816	0.502	1	200	positive regulation of cell death	BP	1	STK17B	up_VPOR_EC
GO:0043603	0.816	0.506	1	372	cellular amide metabolic process	BP	1	MME	up_VFEM_EC
GO:0016310	0.816	0.512	1	641	phosphorylation	BP	1	FBP1	up_VFEM_VSMC
GO:0051128	0.816	0.515	1	790	regulation of cellular component organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0009057	0.816485819	0.27907	10	473	macromolecule catabolic process	BP	1	EDEM2,KLHL25,PIAS1,CLU,CHMP4B,TP53INP2,RNF114,UBE2H,AZIN2,HM13	up_ACOR_EC
GO:0008104	0.817	0.22	67	763	protein localization	BP	1	EXPH5,SH3TC2,FGF13,TLR1,ACTN2,LEP,MID1,HTR2B,TCAF1,USP6NL,MBP,NACC2,PRKAA2,FERMT1,BMP4,EVI5L,TM7SF3,ABCA1,SCARB2,ATRX,SEC24B,LATS2,GLRB,CD274,AR,STX11,ANKRD1,F2RL1,MARCH5,CDKN1A,NRP1,PTPN22,NPNT,OS9,PRKCE,AGRN,SCG5,DAG1,PARP9,PSEN1,SGSM2,SYNJ2BP,PIK3C3,LAMP2,JUP,CCL5,RAB11B,NOD2,LRRC4,LMTK2,DISC1,AP2B1,SCAMP5,SAR1B,HERPUD1,SUN1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,WASL,SH3BP4,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0051345	0.817	0.279	10	151	positive regulation of hydrolase activity	BP	1	HMGB1,SLC29A1,PRELID1,ABHD5,EZH2,PCNA,PDCD2,CYCS,HMGB2,AIFM1	down_ACOR_VSMC
GO:0010256	0.817	0.28	10	129	endomembrane system organization	BP	1	SH3TC2,USP6NL,LNPK,ABCA1,AR,DMPK,AKTIP,ASAP1,SUN1,WASL	up_ACOR_VSMC
GO:0099537	0.817	0.279	10	131	trans-synaptic signaling	BP	1	GPR1,FAM107A,SLC6A4,ABL1,CHRM1,SLC12A6,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0008610	0.817	0.29	8	177	lipid biosynthetic process	BP	1	NR1H4,TRIB3,UGCG,PTGS2,SLC45A3,APOE,SH3GLB1,REST	down_VSAP_EC
GO:0051054	0.817	0.31	6	81	positive regulation of DNA metabolic process	BP	1	CDC7,TP53BP1,ATRX,PPARGC1A,PARP9,HMBOX1	up_ACOR_VSMC
GO:0043281	0.817	0.34	4	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	CRADD,MAP3K5,MYC,HTRA2	up_VSAP_EC
GO:0071356	0.817	0.34	4	57	cellular response to tumor necrosis factor	BP	1	F2RL1,ZFP36L1,ZFP36L2,BAG4	up_VSAP_EC
GO:0010941	0.817	0.365	3	524	regulation of cell death	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0097164	0.817	0.367	3	44	ammonium ion metabolic process	BP	1	ENPP2,AZIN2,LCAT	up_VSAP_EC
GO:0044839	0.817	0.405	2	61	cell cycle G2/M phase transition	BP	1	BRSK1,CDK14	down_VCAV_EC
GO:0051656	0.817	0.403	2	129	establishment of organelle localization	BP	1	CHRM2,CAMK2A	up_AFEM_EC
GO:0051098	0.817	0.403	2	129	regulation of binding	BP	1	GREM2,CYLD	up_AFEM_EC

GO:0090100	0.817	0.41	2	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	ACVRL1,CITED2	up_VSAP_EC
GO:0032008	0.817	0.509	1	19	positive regulation of TOR signaling	BP	1	MIOS	down_ACOR_VSMC
GO:1903036	0.817	0.509	1	19	positive regulation of response to wounding	BP	1	PPARD	down_ACOR_VSMC
GO:0098930	0.817	0.51	1	17	axonal transport	BP	1	TMEM108	up_ACOR_VSMC
GO:1903727	0.817	0.511	1	16	positive regulation of phospholipid metabolic	BP	1	HTR2B	up_ACOR_VSMC
GO:0061912	0.817	0.509	1	18	selective autophagy	BP	1	SPTLC2	up_VCAV_EC
GO:0016310	0.817	0.51	1	641	phosphorylation	BP	1	ANKRD6	up_VPOR_VSMC
GO:0009719	0.817	0.503	1	395	response to endogenous stimulus	BP	1	AVPR1A	up_VFEM_EC
GO:0002287	0.817	0.511	1	17	alpha-beta T cell activation involved in	BP	1	STAT6	up_VSAP_EC
GO:0002292	0.817	0.511	1	17	T cell differentiation involved in immune	BP	1	STAT6	up_VSAP_EC
GO:0002293	0.817	0.511	1	17	alpha-beta T cell differentiation involved in	BP	1	STAT6	up_VSAP_EC
GO:0002294	0.817	0.511	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	STAT6	up_VSAP_EC
GO:0042093	0.817	0.511	1	17	T-helper cell differentiation	BP	1	STAT6	up_VSAP_EC
GO:0043406	0.817285165	0.49906	1	62	positive regulation of MAP kinase activity	BP	1	FZD5	up_ACOR_EC
GO:1901988	0.817351529	0.49888	1	63	negative regulation of cell cycle phase transition	BP	1	BRSK1	up_ACOR_EC
GO:0010628	0.818	0.227	46	527	positive regulation of gene expression	BP	1	SMAD6,LBH,GATA5,GATA4,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,GJA1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,FAM129A,RBM4B,EGLN1,CRLF3,PTPN22,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,NGRN,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0071704	0.818	0.261	26	3535	organic substance metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,HOXA3,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,ABHD5,FAM135A,RRP15,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0048871	0.818	0.29	8	120	multicellular organismal homeostasis	BP	1	CAV1,STMN1,ADIPOR2,HOXC10,PRCP,TFRC,ELOVL6,CORO1A	down_ACOR_VSMC
GO:0010035	0.818	0.29	8	107	response to inorganic substance	BP	1	ENSCAFG00000009113,CDH1,ABL1,MAP3K5,SLC25A12,MT2A,ZNF580,HMOX1	up_VSAP_EC
GO:0022618	0.818	0.335	4	111	ribonucleoprotein complex assembly	BP	1	RPS10,EIF3K,MRPS11,RPS27	down_VCAV_EC
GO:0006401	0.818	0.361	3	88	RNA catabolic process	BP	1	SAMD4B,ZFP36L1,PYM1	down_VCAV_EC
GO:2001020	0.818	0.36	3	88	regulation of response to DNA damage stimulus	BP	1	TMEM161A,SPRED1,FBH1	down_VCAV_EC
GO:0007224	0.818	0.404	2	50	smoothened signaling pathway	BP	1	PRKACB,CHSY1	down_VSAP_EC
GO:0051716	0.818	0.436	2	2001	cellular response to stimulus	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0009145	0.818	0.406	2	40	purine nucleoside triphosphate biosynthetic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0060349	0.818	0.407	2	38	bone morphogenesis	BP	1	MEF2C,STC1	up_VCAV_EC
GO:0032663	0.818	0.507	1	19	regulation of interleukin-2 production	BP	1	EZR	down_ACOR_VSMC
GO:0051592	0.818	0.502	1	33	response to calcium ion	BP	1	ANXA11	down_VCAV_EC
GO:0016073	0.818	0.503	1	26	snRNA metabolic process	BP	1	MRPL1	down_VSAP_EC
GO:0072332	0.818	0.502	1	29	intrinsic apoptotic signaling pathway by p53	BP	1	CDKN1A	down_VSAP_EC
GO:0033173	0.818	0.508	1	17	calcineurin-NFAT signaling cascade	BP	1	C28H10orf71	up_ACOR_VSMC
GO:0097720	0.818	0.508	1	17	calcineurin-mediated signaling	BP	1	C28H10orf71	up_ACOR_VSMC
GO:1904377	0.818	0.505	1	21	positive regulation of protein localization to cell	BP	1	EPB41	up_VCAV_EC

GO:0031057	0.818	0.507	1	18	negative regulation of histone modification	BP	1	PHF1	up_VSAP_EC
GO:0007088	0.818277066	0.49724	1	64	regulation of mitotic nuclear division	BP	1	CHMP4B	up_ACOR_EC
GO:0048878	0.819	0.248	20	283	chemical homeostasis	BP	1	HMGB1,SREBF2,RALY,HOXA3,BIRC5,INSIG1,CAV1,STMN1,SLC30A1,ADIPOR2,PRCP,TFRC,GSTO1,ENSCAFG00000005299,CORO1A,NCOA5,LIPC,NUS1,THADA,ANXA7	down_ACOR_VSMC
GO:0043170	0.819	0.339	6	2980	macromolecule metabolic process	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0014706	0.819	0.333	4	112	striated muscle tissue development	BP	1	BMPR1A,SEMA3C,TSC22D3,GREM1	down_VCAV_EC
GO:0000165	0.819	0.334	4	236	MAPK cascade	BP	1	LEP,CYLD,CCL5,CDC42EP5	up_AFEM_EC
GO:0016458	0.819	0.337	4	59	gene silencing	BP	1	H2AFJ,ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0007051	0.819	0.36	3	70	spindle organization	BP	1	MZT1,TUBB,KPNB1	down_VSAP_EC
GO:1902905	0.819	0.36	3	72	positive regulation of supramolecular fiber	BP	1	WDR1,ACTR3,NRP1	down_VSAP_EC
GO:0043523	0.819	0.361	3	52	regulation of neuron apoptotic process	BP	1	MEF2C,GATA3,HIF1A	up_VCAV_EC
GO:0045580	0.819	0.406	2	35	regulation of T cell differentiation	BP	1	HMGB1,PRELID1	down_ACOR_VSMC
GO:0006006	0.819	0.402	2	61	glucose metabolic process	BP	1	AKT2,H6PD	down_VCAV_EC
GO:0032970	0.819	0.4	2	130	regulation of actin filament-based process	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0035601	0.819	0.406	2	36	protein deacylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0098732	0.819	0.406	2	36	macromolecule deacylation	BP	1	PRKD2,KDM5A	up_VCAV_EC
GO:0009166	0.819	0.408	2	31	nucleotide catabolic process	BP	1	GALK1,DDIT4	up_VSAP_EC
GO:0071702	0.819	0.408	2	687	organic substance transport	BP	1	SLC16A12,TLR2	up_VSAP_VSMC
GO:0001959	0.819	0.499	1	33	regulation of cytokine-mediated signaling	BP	1	MAVS	down_VCAV_EC
GO:0007612	0.819	0.499	1	33	learning	BP	1	BRSK1	down_VCAV_EC
GO:0046847	0.819	0.506	1	17	filopodium assembly	BP	1	NRP1	up_ACOR_VSMC
GO:1901796	0.819	0.507	1	18	regulation of signal transduction by p53 class	BP	1	ANKRD1	up_ACOR_VSMC
GO:0006950	0.819	0.518	1	1102	response to stress	BP	1	C6	up_VCAV_VSMC
GO:0044283	0.819	0.496	1	201	small molecule biosynthetic process	BP	1	FBP1	up_VPOR_EC
GO:0006629	0.819	0.501	1	382	lipid metabolic process	BP	1	CYP26B1	up_VFEM_EC
GO:0051726	0.819	0.5	1	393	regulation of cell cycle	BP	1	MAP2K6	up_VFEM_EC
GO:1902229	0.819	0.507	1	17	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	ACKR3	up_VSAP_EC
GO:1903506	0.82	0.222	54	977	regulation of nucleic acid-templated transcription	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0051603	0.82	0.245	21	305	proteolysis involved in cellular protein catabolic process	BP	1	TNFAIP3,CTSC,WWP1,USP33,PSME4,PELI1,CASP8,ENC1,USP28,PMAIP1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0090087	0.82	0.294	7	185	regulation of peptide transport	BP	1	GPAM,PRNP,ENSCAFG00000014978,AKT2,GLI3,PARK7,MAVS	down_VCAV_EC
GO:0044782	0.82	0.295	7	96	cilium organization	BP	1	FUZ,RILPL2,E2F4,KIF27,TMEM17,TTC8,CEP19	up_VSAP_EC
GO:0045087	0.82	0.303	6	161	innate immune response	BP	1	CFD,TRIM8,CYBA,MAVS,RAB7B,A2M	down_VCAV_EC
GO:0030278	0.82	0.334	4	66	regulation of ossification	BP	1	FBXO5,GREM1,TWIST2,GLI1	down_ACOR_VSMC
GO:1905475	0.82	0.361	3	52	regulation of protein localization to membrane	BP	1	ACSL3,MMP14,EZR	down_ACOR_VSMC

GO:0010811	0.82	0.405	2	36	positive regulation of cell-substrate adhesion	BP	1	RAC1,EMP2	down_ACOR_VSMC
GO:0016573	0.82	0.402	2	50	histone acetylation	BP	1	IWS1,MORF4L2	down_VSAP_EC
GO:1903321	0.82	0.498	1	33	negative regulation of protein modification by small protein conjugation	BP	1	PARK7	down_VCAV_EC
GO:0070555	0.82	0.498	1	29	response to interleukin-1	BP	1	HIF1A	down_VSAP_EC
GO:0001756	0.82	0.505	1	17	somitogenesis	BP	1	PSEN1	up_ACOR_VSMC
GO:0002443	0.82	0.494	1	71	leukocyte mediated immunity	BP	1	LEP	up_AFEM_EC
GO:0030042	0.82	0.505	1	17	actin filament depolymerization	BP	1	F2RL1	up_VSAP_EC
GO:0030834	0.82	0.505	1	17	regulation of actin filament depolymerization	BP	1	F2RL1	up_VSAP_EC
GO:0032611	0.82	0.504	1	17	interleukin-1 beta production	BP	1	F2RL1	up_VSAP_EC
GO:0032945	0.82	0.505	1	17	negative regulation of mononuclear cell	BP	1	CD274	up_VSAP_EC
GO:0050672	0.82	0.505	1	17	negative regulation of lymphocyte proliferation	BP	1	CD274	up_VSAP_EC
GO:0098927	0.82	0.505	1	17	vesicle-mediated transport between endosomal compartments	BP	1	EMP2	up_VSAP_EC
GO:0048284	0.820736763	0.49291	1	66	organelle fusion	BP	1	VPS16	up_ACOR_EC
GO:0018193	0.821	0.237	27	368	peptidyl-amino acid modification	BP	1	POLE3,SLC29A1,PRMT1,CAV1,CDK1,NF2,AURKB,EZH2,GREM1,BRCA1,NOC2L,RAP2C,HASPIN,DMAP1,CDK2,CLSPN,TTK,MAST2,MELK,PRMT5,CTH,ARHGEF2,TADA2A,JMJD6,UBA2,TTLL1,PPIB	down_ACOR_VSMC
GO:0072358	0.821	0.247	19	268	cardiovascular system development	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,ADAMTS6,NCL,EMP2,FOSL1,SGPL1,CTH,JMJD6,NUS1	down_ACOR_VSMC
GO:0030111	0.821	0.293	7	108	regulation of Wnt signaling pathway	BP	1	CTDNEP1,CAV1,GREM1,ASPM,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0031331	0.821	0.293	7	110	positive regulation of cellular catabolic process	BP	1	PLK2,TNFAIP3,RALB,SPTLC2,SH3GLB1,CNOT7,HIF1A	up_VCAV_EC
GO:0050673	0.821	0.314	5	135	epithelial cell proliferation	BP	1	BMPR1A,B4GALT1,ZFP36L1,MYDGF,IFT57	down_VCAV_EC
GO:0051338	0.821	0.313	5	288	regulation of transferase activity	BP	1	LEP,GREM1,LRRC15,DCUN1D3,ADAM17	up_AFEM_EC
GO:0009892	0.821	0.318	5	835	negative regulation of metabolic process	BP	1	CXHXorf57,ENSCAFG00000002015,ASPN,FBP1,MTDH	up_VPOR_EC
GO:0001666	0.821	0.333	4	67	response to hypoxia	BP	1	CAV1,PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:0036293	0.821	0.333	4	67	response to decreased oxygen levels	BP	1	CAV1,PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:0002285	0.821	0.359	3	50	lymphocyte activation involved in immune	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0090087	0.821	0.356	3	185	regulation of peptide transport	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:1905269	0.821	0.404	2	32	positive regulation of chromatin organization	BP	1	PHF1,CDK9	up_VSAP_EC
GO:1902893	0.821	0.501	1	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	PPARD	down_ACOR_VSMC
GO:0042733	0.821	0.498	1	27	embryonic digit morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0031400	0.821	0.493	1	205	negative regulation of protein modification	BP	1	ASPN	up_VPOR_EC
GO:1901575	0.821	0.502	1	643	organic substance catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0046530	0.821	0.504	1	17	photoreceptor cell differentiation	BP	1	THRB	up_VSAP_EC
GO:0046717	0.821	0.504	1	17	acid secretion	BP	1	ABCB11	up_VSAP_EC

GO:0006793	0.822	0.214	73	948	phosphorus metabolic process	BP	1	ACSL3,PRPSAP1,HMGB1,ACLY,IRAK1,MCM7,ILF3,HMGCR,NNT,RRM1,SLC29A1,PPM1G,PPP1R15B,RAN,BIRC5,CAV1,CDK1,RAD51,NF2,PFAS,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,CDK4,RNASEH2B,DHX33,CKS2,TKT,MVD,ELOVL1,RAP2C,YWHAB,CYCS,RAC1,NUP62,EMP2,PDXP,VAC14,IQGAP1,HASPIN,CACTIN,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,ELOVL6,FDFT1,CYC1,TTK,ATP5F1A,MAST2,MELK,DCK,PRPS1,ENSCAFG00000013366,ARHGEF2,KNL1,PDHA1,TADA2A,NUDT1,PGD,CCNB3,NUS1,GK5,CTPS1,ATP5F1D,NUDT3,PIK3CD	down_ACOR_VSMC
GO:0010556	0.822	0.221	51	1137	regulation of macromolecule biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,AKT2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,EIF3K,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,MAVS,LOXL3,ORMDL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:1902680	0.822	0.249	17	415	positive regulation of RNA biosynthetic process	BP	1	DCN,LUM,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,MYDGF,MAVS,MAPRE3,SHC1,GREM1,THRB,ZBTB16	down_VCAV_EC
GO:1903508	0.822	0.249	17	415	positive regulation of nucleic acid-templated transcription	BP	1	DCN,LUM,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,MYDGF,MAVS,MAPRE3,SHC1,GREM1,THRB,ZBTB16	down_VCAV_EC
GO:0071396	0.822	0.278	9	134	cellular response to lipid	BP	1	IRAK1,TFPI,NEDD4,MTDH,INSIG1,THRAP3,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0009126	0.822	0.292	7	100	purine nucleoside monophosphate metabolic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0009167	0.822	0.292	7	100	purine ribonucleoside monophosphate metabolic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0052547	0.822	0.302	6	82	regulation of peptidase activity	BP	1	CST3,CRADD,MAP3K5,RECK,MYC,HTRA2	up_VSAP_EC
GO:0009059	0.822	0.345	4	1563	macromolecule biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0035967	0.822	0.399	2	42	cellular response to topologically incorrect	BP	1	ATF3,NCK1	up_VCAV_EC
GO:0043603	0.822	0.494	1	372	cellular amide metabolic process	BP	1	RPSA	down_ACOR_EC
GO:0042035	0.822	0.499	1	20	regulation of cytokine biosynthetic process	BP	1	MAST2	down_ACOR_VSMC
GO:0005976	0.822	0.495	1	34	polysaccharide metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0009303	0.822	0.503	1	16	rRNA transcription	BP	1	GTF3C1	up_ACOR_VSMC
GO:0006508	0.822	0.497	1	483	proteolysis	BP	1	PTGER2	up_VPUL_EC
GO:0043170	0.822584874	0.21977	73	2980	macromolecule metabolic process	BP	1	C7,CDH3,NR1H4,GATA4,BRSK1,TRPS1,TBX18,PLCL1,PKIB,CALY,SOX9,PKNOX2,GALNT5,PCSK1N,PHF20,NDRG2,PORCN,ENSCAFG00000004331,EDEM2,PI3,FZD5,IFI6,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PAK3,GRK7,TNFRSF19,CST3,PIAS1,DCLK2,USP53,MAPK8IP2,MAVS,FOXC2,FIGNL1,LRRC15,KLHDC8B,PIGS,LRP4,CLSTN1,SH3RF3,LRRC4,RBM38,CLU,SFMBT2,ZNF229,CHMP4B,TP53INP2,RARRES2,GMEB2,AGBL5,RIOX2,RNF114,UBE2H,STK32C,NRP1,AZIN2,HM13,PRKCD,PYGO2,DBNDD2,EFEMP1,CCNYL1,TLE2	up_ACOR_EC

GO:0080090	0.823	0.212	80	1734	regulation of primary metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,PRNP,LUM,FBN1,GLIPR2,BGN,LARP6,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,TFE3,NR3C1,HR,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,CXXC5,ASPN,EIF3K,THY1,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,SPRED1,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,LONP2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0046907	0.823	0.224	39	536	intracellular transport	BP	1	HCLS1,KIT,MX2,TMEM173,IWS1,FERMT1,RAB11A,KIF3C,RAB27A,PPP3CA,HOOK3,SNAP23,HHEX,RAB6A,ANKRD50,ABCA1,SNX2,THOC1,AKAP12,APOD,FES,EHD4,CTDSPL2,PAN3,GCC2,STX11,SMG7,VPS54,TBC1D1,NUP133,DNAJC13,ZW10,HIF1A,IPO11,ALS2,LMTK2,DOP1B,RABGAP1,USP6NL	up_VCAV_EC
GO:0090066	0.823	0.266	11	162	regulation of anatomical structure size	BP	1	CAPG,CAV1,LIMA1,RAC1,PDXP,IQGAP2,CDC42EP4,EZR,CORO1A,ARPC1B,ANXA7	down_ACOR_VSMC
GO:0031347	0.823	0.267	11	144	regulation of defense response	BP	1	TLR1,LEP,COCH,TLR3,F2RL1,PTPN22,PRKCE,PARP9,APP,NOD2,PARK7	up_ACOR_VSMC
GO:0044770	0.823	0.299	6	161	cell cycle phase transition	BP	1	KANK2,ZFP36L1,LSM10,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0046034	0.823	0.301	6	88	ATP metabolic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,PARK7	up_ACOR_VSMC
GO:0044087	0.823	0.299	6	339	regulation of cellular component biogenesis	BP	1	CRYAB,GREM1,CYLD,RAB7A,CDC42EP5,KANK1	up_AFEM_EC
GO:0034330	0.823	0.313	5	80	cell junction organization	BP	1	FSCN1,CAV1,NF2,GREM1,RAC1	down_ACOR_VSMC
GO:0042327	0.823	0.311	5	289	positive regulation of phosphorylation	BP	1	LEP,GREM1,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0007162	0.823	0.33	4	66	negative regulation of cell adhesion	BP	1	HMGB1,NF2,HOXA7,ARG2	down_ACOR_VSMC
GO:0051403	0.823	0.329	4	89	stress-activated MAPK cascade	BP	1	TNIK,MAPK10,SH3RF3,MID1	down_VSAP_EC
GO:1990138	0.823	0.399	2	35	neuron projection extension	BP	1	SLC29A1,IQGAP1	down_ACOR_VSMC
GO:0060491	0.823	0.395	2	62	regulation of cell projection assembly	BP	1	EVI5L,RAC2	down_VCAV_EC
GO:0120032	0.823	0.395	2	62	regulation of plasma membrane bounded cell	BP	1	EVI5L,RAC2	down_VCAV_EC
GO:0021872	0.823	0.499	1	19	forebrain generation of neurons	BP	1	ASPM	down_ACOR_VSMC
GO:0014902	0.823	0.491	1	34	myotube differentiation	BP	1	RBM38	down_VCAV_EC
GO:0042471	0.823	0.492	1	34	ear morphogenesis	BP	1	NAGLU	down_VCAV_EC
GO:0010463	0.823	0.493	1	28	mesenchymal cell proliferation	BP	1	CTNNB1	down_VSAP_EC
GO:2000573	0.823	0.494	1	28	positive regulation of DNA biosynthetic process	BP	1	CTNNB1	down_VSAP_EC
GO:0006471	0.823	0.5	1	17	protein ADP-ribosylation	BP	1	PARP9	up_ACOR_VSMC
GO:0046782	0.823	0.499	1	17	regulation of viral transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0051653	0.823	0.503	1	15	spindle localization	BP	1	WASL	up_ACOR_VSMC
GO:0051881	0.823	0.499	1	19	regulation of mitochondrial membrane	BP	1	PARK7	up_ACOR_VSMC
GO:0032008	0.823	0.498	1	19	positive regulation of TOR signaling	BP	1	RELN	up_VCAV_EC
GO:0060113	0.823	0.499	1	18	inner ear receptor cell differentiation	BP	1	JAG1	up_VCAV_EC
GO:0071156	0.823	0.498	1	21	regulation of cell cycle arrest	BP	1	UHRF2	up_VCAV_EC
GO:0034660	0.823	0.49	1	211	ncRNA metabolic process	BP	1	RRP15	up_VPOR_EC
GO:0050810	0.823	0.501	1	17	regulation of steroid biosynthetic process	BP	1	INSIG2	up_VSAP_EC
GO:0007369	0.823054801	0.48912	1	63	gastrulation	BP	1	FOXC2	up_ACOR_EC
GO:0070646	0.823175043	0.48891	1	63	protein modification by small protein removal	BP	1	USP53	up_ACOR_EC

GO:1903506	0.824	0.208	86	977	regulation of nucleic acid-templated transcription	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,F2RL1,RBL2,GLIS2,DDR2,ICE1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:2001141	0.824	0.217	54	979	regulation of RNA biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0006914	0.824	0.275	9	141	autophagy	BP	1	PLK2,RALB,SPTLC2,MTOR,DEPP1,SH3GLB1,HMGB1,USP13,HIF1A	up_VCAV_EC
GO:0061919	0.824	0.275	9	141	process utilizing autophagic mechanism	BP	1	PLK2,RALB,SPTLC2,MTOR,DEPP1,SH3GLB1,HMGB1,USP13,HIF1A	up_VCAV_EC
GO:0006732	0.824	0.298	6	107	coenzyme metabolic process	BP	1	PANK3,PIPOX,ELOVL7,ENSCAFG00000024323,GCH1,HIF1A	up_VCAV_EC
GO:0071702	0.824	0.329	4	687	organic substance transport	BP	1	XPOT,SLC7A11,GCC2,SRP54	up_VPOR_EC
GO:0046434	0.824	0.354	3	52	organophosphate catabolic process	BP	1	PDXP,NUDT1,NUDT3	down_ACOR_VSMC
GO:1990845	0.824	0.355	3	51	adaptive thermogenesis	BP	1	TLR4,ADIPOR2,KDM3A	up_VCAV_EC
GO:0043412	0.824	0.41	2	1225	macromolecule modification	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0006303	0.824	0.496	1	19	double-strand break repair via nonhomologous	BP	1	POLA1	down_ACOR_VSMC
GO:0030521	0.824	0.497	1	19	androgen receptor signaling pathway	BP	1	THRAP3	down_ACOR_VSMC
GO:0055017	0.824	0.496	1	19	cardiac muscle tissue growth	BP	1	GLI1	down_ACOR_VSMC
GO:0009749	0.824	0.491	1	34	response to glucose	BP	1	GPAM	down_VCAV_EC
GO:0051298	0.824	0.491	1	35	centrosome duplication	BP	1	BRSK1	down_VCAV_EC
GO:0035196	0.824	0.5	1	16	production of miRNAs involved in gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:0051965	0.824	0.498	1	17	positive regulation of synapse assembly	BP	1	SLITRK5	up_ACOR_VSMC
GO:1902229	0.824	0.498	1	17	regulation of intrinsic apoptotic signaling pathway in response to	BP	1	NACC2	up_ACOR_VSMC
GO:1902905	0.824	0.487	1	72	positive regulation of supramolecular fiber	BP	1	CDC42EP5	up_AFEM_EC
GO:2000112	0.824	0.51	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0046148	0.824	0.498	1	17	pigment biosynthetic process	BP	1	CPOX	up_VSAP_EC
GO:0120163	0.824	0.498	1	17	negative regulation of cold-induced	BP	1	HOXC10	up_VSAP_EC
GO:1904894	0.824	0.498	1	17	positive regulation of STAT cascade	BP	1	IL6R	up_VSAP_EC
GO:0009968	0.824	0.491	1	392	negative regulation of signal transduction	BP	1	CAV1	up_VSAP_VSMC

GO:0044249	0.825	0.209	86	1851	cellular biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,ADCY6,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,LMO4,CLIP3,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,AKT2,LCAT,SAMD4B,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,DDOST,VDR,PRMT6,UROS,ENTPD3,THNSL2,ATP5MC1,CXXC5,GFPT2,PIGS,EIF3K,NECAB3,TEAD1,ADK,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,RPL27,AMPD2,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,RDH10,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,GLS2,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA,ACAT1	down_VCAV_EC
GO:0034097	0.825	0.243	19	238	response to cytokine	BP	1	IFNGR1,LEP,AFF3,EIF4A2,ISG15,CD274,KLHL20,ANKRD1,F2RL1,DAPK1,CREBRF,NPNT,EVL,CCDC3,PARP9,CCL5,LRRC4,ARID5B,INPP5K	up_ACOR_VSMC
GO:1901652	0.825	0.281	8	105	response to peptide	BP	1	ACTN2,LEP,PTPN22,SESN3,APP,PSEN1,NOD2,INPP5K	up_ACOR_VSMC
GO:0055086	0.825	0.325	4	237	nucleobase-containing small molecule metabolic	BP	1	GPAM,ATP6V1B2,ACACB,PPARGC1A	up_AFEM_EC
GO:0071478	0.825	0.329	4	58	cellular response to radiation	BP	1	DDB2,TNKS1BP1,PIK3R1,FBXO4	up_VSAP_EC
GO:0031647	0.825	0.35	3	87	regulation of protein stability	BP	1	PRNP,PARK7,NCLN	down_VCAV_EC
GO:0060271	0.825	0.35	3	89	cilium assembly	BP	1	TTC8,IFT57,EVI5L	down_VCAV_EC
GO:0009451	0.825	0.352	3	59	RNA modification	BP	1	TRMT9B,WTAP,ZC3H13	up_VCAV_EC
GO:0140013	0.825	0.353	3	50	meiotic nuclear division	BP	1	FIGNL1,CENPC,FBXO5	up_VCAV_EC
GO:0045860	0.825	0.39	2	132	positive regulation of protein kinase activity	BP	1	LEP,ADAM17	up_AFEM_EC
GO:0080134	0.825	0.392	2	386	regulation of response to stress	BP	1	CXHXorf57,ARHGEF2	up_VPOR_EC
GO:0032330	0.825	0.495	1	20	regulation of chondrocyte differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0002381	0.825	0.496	1	19	immunoglobulin production involved in immunoglobulin	BP	1	TFRC	down_ACOR_VSMC
GO:0030641	0.825	0.489	1	34	regulation of cellular pH	BP	1	ATP6V0C	down_VCAV_EC
GO:0043280	0.825	0.49	1	33	positive regulation of cysteine-type endopeptidase activity	BP	1	IFT57	down_VCAV_EC
GO:0043200	0.825	0.49	1	26	response to amino acid	BP	1	SESN2	down_VSAP_EC
GO:0002444	0.825	0.496	1	18	myeloid leukocyte mediated immunity	BP	1	F2RL1	up_ACOR_VSMC
GO:0043299	0.825	0.496	1	18	leukocyte degranulation	BP	1	F2RL1	up_ACOR_VSMC
GO:0090342	0.825	0.496	1	17	regulation of cell aging	BP	1	MARCH5	up_ACOR_VSMC
GO:0042278	0.825	0.492	1	25	purine nucleoside metabolic process	BP	1	ACPP	up_VCAV_EC
GO:0043408	0.825	0.486	1	211	regulation of MAPK cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0050886	0.825	0.496	1	17	endocrine process	BP	1	F2RL1	up_VSAP_EC
GO:0090303	0.825	0.495	1	18	positive regulation of wound healing	BP	1	HPSE	up_VSAP_EC
GO:1905207	0.825	0.496	1	17	regulation of cardiocyte differentiation	BP	1	DLL1	up_VSAP_EC
GO:0070727	0.826	0.215	50	579	cellular macromolecule localization	BP	1	EXPH5,SH3TC2,FGF13,ACTN2,LEP,MID1,TCAF1,USP6NL,NACC2,PRKAA2,FERMT1,BMP4,EVI5L,SCARB2,ATRX,SEC24B,LATS2,GLRB,AR,STX11,MARCH5,CDKN1A,NRP1,PTPN22,OS9,AGRN,SCG5,DAG1,PARP9,PSEN1,SGSM2,SYNJ2BP,PIK3C3,LAMP2,JUP,RAB11B,LRRC4,DISC1,AP2B1,SAR1B,HERPUD1,SUN1,VPS26A,INPP5K,FAF2,RPAIN,WASL,SH3BP4,PARK7,PTPN14	up_ACOR_VSMC
GO:0006333	0.826	0.326	4	59	chromatin assembly or disassembly	BP	1	NAA60,SMARCD2,GATAD1,CENPP	up_VSAP_EC
GO:0009058	0.826	0.373	3	1910	biosynthetic process	BP	1	DARS,EIF3M,GABPA	down_AFEM_EC

GO:0070201	0.826	0.347	3	187	regulation of establishment of protein	BP	1	LEP,GPAM,CCL5	up_AFEM_EC
GO:0042221	0.826	0.356	3	1012	response to chemical	BP	1	MME,AVPR1A,CYP26B1	up_VFEM_EC
GO:0043903	0.826	0.391	2	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:2000113	0.826	0.392	2	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0010332	0.826	0.493	1	20	response to gamma radiation	BP	1	MAP3K20	down_ACOR_VSMC
GO:0030166	0.826	0.494	1	19	proteoglycan biosynthetic process	BP	1	XYLT1	down_ACOR_VSMC
GO:0008104	0.826	0.497	1	763	protein localization	BP	1	GPSM2	down_AFEM_EC
GO:0021537	0.826	0.484	1	73	telencephalon development	BP	1	PLXNA4	up_AFEM_EC
GO:0010171	0.826	0.493	1	18	body morphogenesis	BP	1	CDON	up_VSAP_EC
GO:0006023	0.826	0.495	1	17	aminoglycan biosynthetic process	BP	1	CHST7	up_VSAP_EC
GO:1903708	0.826901827	0.4823	1	65	positive regulation of hemopoiesis	BP	1	CLSTN1	up_ACOR_EC
GO:0051247	0.827	0.221	37	502	positive regulation of protein metabolic process	BP	1	HMGB1,SREBF1,IRAK1,EIF4A3,HNRNPD,UBE2S,NEDD4,SLC29A1,PRELID1,CAV1,FANCI,TRUB2,EZH2,PPP2R5D,GREM1,MAP3K20,PLK3,DHX33,CKS2,PDCD2,BRCA1,FASTKD3,EIF5A,RAP2C,CYCS,RAC1,EMP2,DTL,EZR,CLSPN,RAD23A,CDC20,AIFM1,ARHGEF2,TADA2A,AMER1,DCUN1D5	down_ACOR_VSMC
GO:1904951	0.827	0.286	7	108	positive regulation of establishment of protein localization	BP	1	ACSL3,HMGB1,RAN,PLK3,DMAP1,EZR,CCT4	down_ACOR_VSMC
GO:0051493	0.827	0.283	7	188	regulation of cytoskeleton organization	BP	1	KIRREL1,CLIP3,RHOD,ENSCAFG00000014978,SYDE1,ACTR3B,PLEKHH2	down_VCAV_EC
GO:0043434	0.827	0.307	5	80	response to peptide hormone	BP	1	SREBF1,CAV1,CDK4,SMARCC1,NCOA5	down_ACOR_VSMC
GO:0072593	0.827	0.324	4	68	reactive oxygen species metabolic process	BP	1	NNT,CAV1,ARG2,PRCP	down_ACOR_VSMC
GO:0032868	0.827	0.324	4	66	response to insulin	BP	1	PPARG,BAIAP2L1,MTOR,NCK1	up_VCAV_EC
GO:0009416	0.827	0.347	3	88	response to light stimulus	BP	1	AKT2,TMEM161A,BRSK1	down_VCAV_EC
GO:0019538	0.827	0.367	3	1713	protein metabolic process	BP	1	LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0007165	0.827	0.41	2	1496	signal transduction	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0048522	0.827	0.41	2	1484	positive regulation of cellular process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:1903076	0.827	0.394	2	32	regulation of protein localization to plasma	BP	1	PIK3R1,STX4	up_VSAP_EC
GO:0097530	0.827	0.486	1	33	granulocyte migration	BP	1	RAC2	down_VCAV_EC
GO:0000281	0.827	0.492	1	18	mitotic cytokinesis	BP	1	MITD1	up_ACOR_VSMC
GO:0051172	0.827	0.492	1	663	negative regulation of nitrogen compound	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002204	0.827	0.493	1	18	somatic recombination of immunoglobulin genes involved in immune	BP	1	STAT6	up_VSAP_EC
GO:0002208	0.827	0.493	1	18	somatic diversification of immunoglobulins involved in immune response	BP	1	STAT6	up_VSAP_EC
GO:0006919	0.827	0.493	1	17	activation of cysteine-type endopeptidase activity involved in apoptotic	BP	1	CRADD	up_VSAP_EC
GO:0015988	0.827	0.494	1	17	energy coupled proton transmembrane transport, against	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0042181	0.827	0.493	1	17	ketone biosynthetic process	BP	1	COQ9	up_VSAP_EC
GO:0045190	0.827	0.493	1	18	isotype switching	BP	1	STAT6	up_VSAP_EC
GO:0099132	0.827	0.494	1	17	ATP hydrolysis coupled cation transmembrane	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:0032418	0.827	0.494	1	17	lysosome localization	BP	1	BORCS6	up_VSAP_EC
GO:0042509	0.827	0.493	1	17	regulation of tyrosine phosphorylation of STAT	BP	1	IL6R	up_VSAP_EC

GO:0009889	0.828	0.209	66	1190	regulation of biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,AARS,TRIB3,PGAM1,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,HIF1A,SLC45A3,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0010948	0.828	0.285	7	96	negative regulation of cell cycle process	BP	1	FAM107A,CRADD,ZFP36L1,FBXO7,CDK9,ZFP36L2,TPRA1	up_VSAP_EC
GO:0070838	0.828	0.285	7	96	divalent metal ion transport	BP	1	SLC8B1,TPCN2,NIPAL3,ABL1,CRACR2B,NIPAL1,CYBA	up_VSAP_EC
GO:0051348	0.828	0.306	5	90	negative regulation of transferase activity	BP	1	PPP2R5A,TNFAIP3,HHEX,PREX2,SH3BP5	up_VCAV_EC
GO:0010595	0.828	0.347	3	52	positive regulation of endothelial cell migration	BP	1	HMGB1,NUS1,AMOTL1	down_ACOR_VSMC
GO:0051493	0.828	0.344	3	188	regulation of cytoskeleton organization	BP	1	CYLD,CDC42EP5,KANK1	up_AFEM_EC
GO:0008643	0.828	0.349	3	45	carbohydrate transport	BP	1	KLF15,C1QTNF2,PIK3R1	up_VSAP_EC
GO:0030282	0.828	0.392	2	37	bone mineralization	BP	1	HOXA3,GREM1	down_ACOR_VSMC
GO:0018393	0.828	0.389	2	51	internal peptidyl-lysine acetylation	BP	1	IWS1,MORF4L2	down_VSAP_EC
GO:0032879	0.828	0.494	1	767	regulation of localization	BP	1	GPSM2	down_AFEM_EC
GO:0018022	0.828	0.482	1	36	peptidyl-lysine methylation	BP	1	PRMT6	down_VCAV_EC
GO:0070167	0.828	0.485	1	29	regulation of biomineral tissue development	BP	1	HIF1A	down_VSAP_EC
GO:0045670	0.828	0.492	1	16	regulation of osteoclast differentiation	BP	1	RASSF2	up_ACOR_VSMC
GO:0031346	0.828	0.481	1	73	positive regulation of cell projection organization	BP	1	CDC42EP5	up_AFEM_EC
GO:0061138	0.828	0.48	1	73	morphogenesis of a branching epithelium	BP	1	GREM1	up_AFEM_EC
GO:0070507	0.828	0.48	1	73	regulation of microtubule cytoskeleton organization	BP	1	CYLD	up_AFEM_EC
GO:0044248	0.828	0.492	1	691	cellular catabolic process	BP	1	LNPEP	up_AORT_EC
GO:0030166	0.828	0.489	1	19	proteoglycan biosynthetic process	BP	1	CHST7	up_VCAV_EC
GO:0072132	0.828	0.487	1	23	mesenchyme morphogenesis	BP	1	BMP2	up_VCAV_EC
GO:0022402	0.828	0.485	1	407	cell cycle process	BP	1	CYP26B1	up_VFEM_EC
GO:0044249	0.829	0.196	168	1851	cellular biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,HOXA9,CDON,NECAB3,WNT11,ACSM3,ARHGEF5,LIPC,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,GOT1,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,GLUL,GALNT15,ENSCAFG00000013986,CERS4,WARS2,VDR,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,COQ9,RARG,CBX7,STAT5A,STAT6,GATAD1,HSD17B8,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,PLA2G6,MYC,PTGES,SSBP2,IRX3,ZEB1,FKRP,HACD4,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,ENSCAFG00000016140,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,GALNT11,DAGLB,E2F4,NPAS2,MOCOS,ZDHHC8,FARS2,LCAT,PCBD1,LIMD1,UBA52,RPUSD4,RPL15,ACSS2,CDK9,DHRS9,NR2F6,PRMT2,KDM2B,MVK,PNPO,DCAKD,EIF3G,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MPST,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,ALDH9A1,ZNF517,ASS1,TNRC6C,COA1,PPP3CB,NCK1,ZNF444,	up_VSAP_EC
GO:0051649	0.829	0.256	12	630	establishment of localization in cell	BP	1	LEP,KCNC4,CRY2,VPS26C,GAS1,CRYAB,CHRM2,MYO1D,CAMK2A,REEP2,BVES,RAB7A	up_AFEM_EC

GO:0009991	0.829	0.283	7	110	response to extracellular stimulus	BP	1	SREBF1,SREBF2,RNF152,PDXP,FOSL1,MIOS,NUDT1	down_ACOR_VSMC
GO:0070201	0.829	0.281	7	187	regulation of establishment of protein	BP	1	GPAM,PRNP,ENSCAFG00000014978,AKT2,GLI3,PARK7,MAVS	down_VCAV_EC
GO:0008150	0.829	0.452	6	5646	biological_process	BP	1	HOXC10,SLC20A2,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:1901214	0.829	0.305	5	81	regulation of neuron death	BP	1	BIRC5,ENSCAFG00000005299,CORO1A,SIGMAR1,SIX4	down_ACOR_VSMC
GO:0032868	0.829	0.322	4	66	response to insulin	BP	1	SREBF1,CDK4,SMARCC1,NCOA5	down_ACOR_VSMC
GO:0008654	0.829	0.323	4	58	phospholipid biosynthetic process	BP	1	PLA2G6,LCAT,MVK,IDH1	up_VSAP_EC
GO:0006575	0.829	0.347	3	53	cellular modified amino acid metabolic process	BP	1	GSTO1,ENSCAFG00000006478,GGH	down_ACOR_VSMC
GO:2000112	0.829	0.354	3	1119	regulation of cellular macromolecule biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:2001251	0.829	0.388	2	49	negative regulation of chromosome organization	BP	1	NAA10,KDM3A	down_VSAP_EC
GO:0008593	0.829	0.39	2	33	regulation of Notch signaling pathway	BP	1	GATA5,SYNJ2BP	up_ACOR_VSMC
GO:0008286	0.829	0.39	2	36	insulin receptor signaling pathway	BP	1	BAIAP2L1,NCK1	up_VCAV_EC
GO:0051298	0.829	0.391	2	35	centrosome duplication	BP	1	PLK2,SASS6	up_VCAV_EC
GO:0034644	0.829	0.391	2	32	cellular response to UV	BP	1	DDB2,PIK3R1	up_VSAP_EC
GO:0021766	0.829	0.487	1	20	hippocampus development	BP	1	NF2	down_ACOR_VSMC
GO:0055117	0.829	0.486	1	21	regulation of cardiac muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0035556	0.829	0.494	1	845	intracellular signal transduction	BP	1	HDAC7	down_VPOR_EC
GO:0051246	0.829	0.493	1	832	regulation of protein metabolic process	BP	1	CST3	down_VPOR_EC
GO:0042472	0.829	0.484	1	27	inner ear morphogenesis	BP	1	SIX4	down_VSAP_EC
GO:0055081	0.829	0.49	1	17	anion homeostasis	BP	1	ABCA1	up_ACOR_VSMC
GO:0060541	0.829	0.479	1	73	respiratory system development	BP	1	THRB	up_AFEM_EC
GO:0033554	0.829	0.49	1	708	cellular response to stress	BP	1	TAOK1	up_AORT_EC
GO:1903578	0.829	0.485	1	22	regulation of ATP metabolic process	BP	1	HIF1A	up_VCAV_EC
GO:0046580	0.829	0.489	1	18	negative regulation of Ras protein signal	BP	1	MFN2	up_VSAP_EC
GO:0006629	0.829	0.483	1	382	lipid metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:2001141	0.83	0.202	86	979	regulation of RNA biosynthetic process	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,F2RL1,RBL2,GLIS2,DDR2,ICE1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0060255	0.83	0.204	82	1782	regulation of macromolecule metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,NDN,PRNP,LUM,FBN1,GLIPR2,BGN,LARP6,KANK2,BMPR1A,NABP2,LMO4,RECK,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,TFE3,NR3C1,HR,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,CXXC5,ASPN,LRPAP1,EIF3K,THY1,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,FUT8,SPRED1,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC

GO:0051130	0.83	0.289	6	342	positive regulation of cellular component	BP	1	DLL1,MLLT11,GREM1,CLEC16A,PPARGC1A,CDC42EP5	up_AFEM_EC
GO:0015711	0.83	0.304	5	81	organic anion transport	BP	1	ACSL3,SLC35C2,PRELID1,PPARD,SLC25A19	down_ACOR_VSMC
GO:0048736	0.83	0.32	4	66	appendage development	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0060173	0.83	0.32	4	66	limb development	BP	1	GREM1,MAP3K20,HOXC10,HOXA9	down_ACOR_VSMC
GO:0006333	0.83	0.32	4	59	chromatin assembly or disassembly	BP	1	ATRX,TSPYL5,SMARCD3,SHPRH	up_ACOR_VSMC
GO:0048545	0.83	0.32	4	68	response to steroid hormone	BP	1	TFPI,SMARCA4,UFSP2,KDM3A	up_VCAV_EC
GO:1903050	0.83	0.343	3	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	PSMF1,PARK7,CLEC16A	down_VCAV_EC
GO:0031345	0.83	0.345	3	46	negative regulation of cell projection organization	BP	1	SLIT2,RTN4RL1,LRP4	up_VSAP_EC
GO:0060048	0.83	0.481	1	30	cardiac muscle contraction	BP	1	CALM1	down_VSAP_EC
GO:0033043	0.83	0.482	1	446	regulation of organelle organization	BP	1	TUBB4A	up_APUL_EC
GO:0010556	0.83	0.5	1	1137	regulation of macromolecule	BP	1	GATA5	up_VCAV_VSMC
GO:0060113	0.83	0.488	1	18	inner ear receptor cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0031297	0.83	0.486	1	18	replication fork processing	BP	1	CDK9	up_VSAP_EC
GO:0043603	0.83	0.481	1	372	cellular amide metabolic process	BP	1	PRR16	up_VSAP_VSMC
GO:0002366	0.830882173	0.47529	1	65	leukocyte activation involved in immune	BP	1	PTGER4	up_ACOR_EC
GO:0006810	0.831	0.198	111	1244	transport	BP	1	SLC43A1,PEX7,HNF4A,DNM1,CD274,ACKR3,ARHGEF5,C5AR2,LIPC,AMIGO1,CALHM2,SLC8B1,TBC1D10C,SLC43A3,GABRE,MFSD3,TPCN2,NIPAL3,TBC1D2B,CDH1,SLC6A4,FGF7,ABL1,PEX2,SLC16A12,EMP2,KCNE3,CHRM1,DLL1,EPN2,OSR1,IL17RC,SCAMP4,CLIC5,KLF15,C1QTNF2,ANXA4,RILPL2,ANKRD54,ABCB11,CCS,VPS36,AP5B1,KLHL24,SLC25A12,APOL5,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,ZFP36L1,PIK3R1,SLC25A28,CRACR2B,GAS1,SLC27A6,CTNS,SCARA5,SLC10A6,NIPAL1,ERGIC1,PASK,MON1B,NUP98,SCFD2,AZIN2,HPS4,CCDC93,ABCA9,CLCN2,STEAP3,FBXO7,KCNB1,LCAT,LONP2,SNUPN,DOP1B,DENND5A,AP5Z1,OSBPL7,FTL,MYO1B,SCAMP2,ENSCAFG00000013366,RAF1,PNP,MAPKBP1,ZFYVE21,CYBA,ZNF205,XKR8,FXYD1,STX4,VPS11,KCNC4,ARHGAP12,UBQLN2,FLOT1,PPP3CB,PEX6,SLC25A40,MAVS,CEP19,TGFBR2,BAG4,NCOA4,NAGPA,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0009314	0.831	0.266	9	143	response to radiation	BP	1	KIT,GATA3,FIGNL1,MAPK13,ENSCAFG00000010596,USP28,BLM,HIF1A,TOPBP1	up_VCAV_EC
GO:1901564	0.831	0.294	7	2053	organonitrogen compound metabolic	BP	1	EYA1,MAP2K6,MME,TRIM9,CDC42EP5,ADCY3,CHST7	up_VFEM_EC
GO:0044262	0.831	0.341	3	89	cellular carbohydrate metabolic process	BP	1	AKT2,ADK,B4GALT1	down_VCAV_EC
GO:0002699	0.831	0.344	3	46	positive regulation of immune effector process	BP	1	STAT6,F2RL1,STX4	up_VSAP_EC
GO:0050684	0.831	0.345	3	46	regulation of mRNA processing	BP	1	ZFP36L1,NUP98,CDK9	up_VSAP_EC
GO:0002768	0.831	0.386	2	37	immune response-regulating cell surface receptor signaling	BP	1	MNDA,EZR	down_ACOR_VSMC
GO:0007275	0.831	0.402	2	1370	multicellular organism development	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:1901360	0.831	0.415	2	2016	organic cyclic compound metabolic process	BP	1	CYP1A1,GATA5	up_VCAV_VSMC
GO:0006629	0.831	0.383	2	382	lipid metabolic process	BP	1	ABHD5,FAM135A	up_VPOR_EC
GO:0010558	0.831	0.383	2	392	negative regulation of macromolecule biosynthetic process	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0010466	0.831	0.388	2	32	negative regulation of peptidase activity	BP	1	CST3,RECK	up_VSAP_EC
GO:0010951	0.831	0.388	2	32	negative regulation of endopeptidase activity	BP	1	CST3,RECK	up_VSAP_EC
GO:0098739	0.831	0.483	1	20	import across plasma membrane	BP	1	SLC30A1	down_ACOR_VSMC

GO:0010033	0.831	0.488	1	772	response to organic substance	BP	1	GABPA	down_AFEM_EC
GO:0051784	0.831	0.48	1	28	negative regulation of nuclear division	BP	1	NAA10	down_VSAP_EC
GO:2000045	0.831	0.48	1	29	regulation of G1/S transition of mitotic cell	BP	1	CDKN1A	down_VSAP_EC
GO:0051291	0.831	0.482	1	21	protein heterooligomerization	BP	1	RIPK1	up_VCAV_EC
GO:0010557	0.831	0.481	1	492	positive regulation of macromolecule biosynthetic process	BP	1	ARHGEF2	up_VPUL_EC
GO:0045935	0.831	0.481	1	491	positive regulation of nucleobase-containing compound metabolic	BP	1	ARHGEF2	up_VPUL_EC
GO:0006473	0.831255299	0.47457	1	66	protein acetylation	BP	1	PHF20	up_ACOR_EC
GO:0010498	0.832	0.242	15	194	proteasomal protein catabolic process	BP	1	SH3RF2,KLHL20,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,RNF181,HERPUD1,FAF2,WFS1,DZIP3,PARK7	up_ACOR_VSMC
GO:0030335	0.832	0.255	11	165	positive regulation of cell migration	BP	1	HMGB1,FBXO5,CAV1,MMP14,RAC1,CORO1A,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0099536	0.832	0.26	10	133	synaptic signaling	BP	1	GPR1,FAM107A,SLC6A4,ABL1,CHRM1,SLC12A6,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0045935	0.832	0.264	9	491	positive regulation of nucleobase-containing compound metabolic	BP	1	HOXA9,LBH,DLL1,MLLT11,THRB,GREM1,NFE2L1,MYBL1,PPARGC1A	up_AFEM_EC
GO:0045862	0.832	0.279	7	112	positive regulation of proteolysis	BP	1	HMGB1,PRELID1,PLK3,PDCD2,CYCS,RAD23A,AIFM1	down_ACOR_VSMC
GO:0006820	0.832	0.279	7	109	anion transport	BP	1	ACSL3,SLC35C2,PRELID1,SLC17A9,PPARD,SLC20A1,SLC25A19	down_ACOR_VSMC
GO:0051726	0.832	0.277	7	393	regulation of cell cycle	BP	1	LEP,GAS1,OVOL1,CYLD,DCUN1D3,AXIN2,FAP	up_AFEM_EC
GO:0060326	0.832	0.3	5	84	cell chemotaxis	BP	1	HMGB1,RAC1,HMGB2,CORO1A,PIK3CD	down_ACOR_VSMC
GO:0070925	0.832	0.298	5	293	organelle assembly	BP	1	RAB20,CYLD,DNAL1,RAB7A,SPATA6	up_AFEM_EC
GO:0071375	0.832	0.317	4	68	cellular response to peptide hormone stimulus	BP	1	PPARG,BAIAP2L1,NCK1,NR4A1	up_VCAV_EC
GO:0030177	0.832	0.343	3	51	positive regulation of Wnt signaling pathway	BP	1	BMP2,HHEX,SMARCA4	up_VCAV_EC
GO:0071222	0.832	0.343	3	46	cellular response to lipopolysaccharide	BP	1	ABL1,SASH1,MYD88	up_VSAP_EC
GO:0006810	0.832	0.396	2	1244	transport	BP	1	ENSCAFG00000005494,GPR155	up_AORT_EC
GO:0006986	0.832	0.384	2	42	response to unfolded protein	BP	1	ATF3,NCK1	up_VCAV_EC
GO:0015850	0.832	0.385	2	37	organic hydroxy compound transport	BP	1	RALBP1,ABCA1	up_VCAV_EC
GO:0017148	0.832	0.386	2	36	negative regulation of translation	BP	1	ENC1,CNOT7	up_VCAV_EC
GO:0035305	0.832	0.386	2	37	negative regulation of dephosphorylation	BP	1	SWAP70,FKBP15	up_VCAV_EC
GO:0034968	0.832	0.386	2	34	histone lysine methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:2001237	0.832	0.385	2	33	negative regulation of extrinsic apoptotic	BP	1	RAF1,HMOX1	up_VSAP_EC
GO:0033692	0.832	0.481	1	20	cellular polysaccharide biosynthetic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:0070887	0.832	0.486	1	775	cellular response to chemical stimulus	BP	1	GABPA	down_AFEM_EC
GO:0097300	0.832	0.485	1	17	programmed necrotic cell death	BP	1	TLR3	up_ACOR_VSMC
GO:0043933	0.832	0.484	1	698	protein-containing complex subunit	BP	1	TAOK1	up_AORT_EC
GO:0006720	0.832	0.479	1	25	isoprenoid metabolic process	BP	1	ALDH1A3	up_VCAV_EC
GO:0021695	0.832	0.481	1	20	cerebellar cortex development	BP	1	PROX1	up_VCAV_EC
GO:0001775	0.832	0.474	1	219	cell activation	BP	1	SLC7A11	up_VPOR_EC
GO:0051246	0.832	0.487	1	832	regulation of protein metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0045935	0.833	0.223	26	491	positive regulation of nucleobase-containing compound metabolic process	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,TFRC,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0046483	0.833	0.255	13	1948	heterocycle metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RRP15,CCAR1,GNPNAT1,RNF6	up_VPOR_EC

GO:0019637	0.833	0.285	6	342	organophosphate metabolic process	BP	1	GPAM,ATP6V1B2,ACACB,NAPEPLD,PPARGC1A,AGPAT2	up_AFEM_EC
GO:0050663	0.833	0.34	3	52	cytokine secretion	BP	1	HMGB1,ARG2,EZR	down_ACOR_VSMC
GO:1901564	0.833	0.365	3	2053	organonitrogen compound metabolic	BP	1	CST3,MGAT4B,GBGT1	down_VPOR_EC
GO:0031333	0.833	0.342	3	46	negative regulation of protein complex assembly	BP	1	SLIT2,RAF1,ULK1	up_VSAP_EC
GO:0007416	0.833	0.383	2	36	synapse assembly	BP	1	EPHB1,MEF2C	up_VCAV_EC
GO:0009201	0.833	0.382	2	41	ribonucleoside triphosphate biosynthetic	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0017156	0.833	0.385	2	32	calcium ion regulated exocytosis	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0090263	0.833	0.384	2	33	positive regulation of canonical Wnt signaling	BP	1	FAM53B,SULF2	up_VSAP_EC
GO:0006493	0.833	0.48	1	20	protein O-linked glycosylation	BP	1	SLC35C2	down_ACOR_VSMC
GO:0032268	0.833	0.484	1	778	regulation of cellular protein metabolic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0002244	0.833	0.475	1	35	hematopoietic progenitor cell differentiation	BP	1	EEF2	down_VCAV_EC
GO:0009746	0.833	0.475	1	35	response to hexose	BP	1	GPAM	down_VCAV_EC
GO:0001938	0.833	0.475	1	34	positive regulation of endothelial cell	BP	1	MYDGF	down_VCAV_EC
GO:0034284	0.833	0.475	1	35	response to monosaccharide	BP	1	GPAM	down_VCAV_EC
GO:1905897	0.833	0.475	1	34	regulation of response to endoplasmic reticulum	BP	1	PARK7	down_VCAV_EC
GO:0007586	0.833	0.481	1	20	digestion	BP	1	TLR4	up_VCAV_EC
GO:0022600	0.833	0.481	1	20	digestive system process	BP	1	TLR4	up_VCAV_EC
GO:0043933	0.833	0.483	1	698	protein-containing complex subunit	BP	1	NKX2-5	up_VPOR_VSMC
GO:0071702	0.833	0.482	1	687	organic substance transport	BP	1	TRPC4	up_VPOR_VSMC
GO:0001666	0.83370092	0.47015	1	67	response to hypoxia	BP	1	AQP1	up_ACOR_EC
GO:0036293	0.83370092	0.47015	1	67	response to decreased oxygen levels	BP	1	AQP1	up_ACOR_EC
GO:0009890	0.834	0.215	35	420	negative regulation of biosynthetic process	BP	1	FZD1,THRB,HOXA7,WNT11,INSIG2,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,ENSCAFG00000000071,GLIS2,ZFP36L1,SHOX2,H2AFJ,IKZF2,PASK,ANKHD1,LIMD1,PRMT2,KDM2B,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1,DDIT4	up_VSAP_EC
GO:0019941	0.834	0.233	18	258	modification-dependent protein catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C	down_ACOR_VSMC
GO:0009259	0.834	0.256	10	166	ribonucleotide metabolic process	BP	1	NPR1,PANK3,PIPOX,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,HIF1A	up_VCAV_EC
GO:0009991	0.834	0.269	8	110	response to extracellular stimulus	BP	1	FAM107A,ACACB,SESN1,MAP3K5,PDK2,CASTOR1,BGLAP,NPRL3	up_VSAP_EC
GO:0006310	0.834	0.277	7	93	DNA recombination	BP	1	CDC7,TP53BP1,ZNF365,DMC1,RPAIN,WDR48,FAN1	up_ACOR_VSMC
GO:0015980	0.834	0.284	6	106	energy derivation by oxidation of organic	BP	1	PCDH12,ADGRF5,MTOR,SLC25A25,PPP1CB,HIF1A	up_VCAV_EC
GO:0007416	0.834	0.382	2	36	synapse assembly	BP	1	SIX4,TPBG	down_ACOR_VSMC
GO:0006403	0.834	0.377	2	64	RNA localization	BP	1	SNUPN,ZFP36L1	down_VCAV_EC
GO:0042594	0.834	0.378	2	64	response to starvation	BP	1	GABARAP,CLEC16A	down_VCAV_EC
GO:0048738	0.834	0.378	2	64	cardiac muscle tissue development	BP	1	BMPR1A,GREM1	down_VCAV_EC
GO:0045017	0.834	0.379	2	52	glycerolipid biosynthetic process	BP	1	NR1H4,SH3GLB1	down_VSAP_EC
GO:0044087	0.834	0.473	1	339	regulation of cellular component biogenesis	BP	1	ACVRL1	down_ACOR_EC
GO:1901655	0.834	0.478	1	20	cellular response to ketone	BP	1	CDK4	down_ACOR_VSMC
GO:0030490	0.834	0.472	1	35	maturation of SSU-rRNA	BP	1	MRPS11	down_VCAV_EC
GO:0032204	0.834	0.473	1	35	regulation of telomere maintenance	BP	1	NABP2	down_VCAV_EC

GO:0033036	0.834	0.484	1	852	macromolecule localization	BP	1	RAB11B	down_VPOR_EC
GO:0002011	0.834	0.474	1	28	morphogenesis of an epithelial sheet	BP	1	ADAM17	down_VSAP_EC
GO:0046660	0.834	0.475	1	28	female sex differentiation	BP	1	INHBA	down_VSAP_EC
GO:0002287	0.834	0.48	1	17	alpha-beta T cell activation involved in	BP	1	IL18R1	up_ACOR_VSMC
GO:0002293	0.834	0.48	1	17	alpha-beta T cell differentiation involved in	BP	1	IL18R1	up_ACOR_VSMC
GO:0002294	0.834	0.48	1	17	CD4-positive, alpha-beta T cell differentiation involved in immune	BP	1	IL18R1	up_ACOR_VSMC
GO:0032652	0.834	0.479	1	18	regulation of interleukin-1 production	BP	1	NOD2	up_ACOR_VSMC
GO:0002292	0.834	0.48	1	17	T cell differentiation involved in immune	BP	1	IL18R1	up_ACOR_VSMC
GO:0042093	0.834	0.48	1	17	T-helper cell differentiation	BP	1	IL18R1	up_ACOR_VSMC
GO:0019219	0.834	0.493	1	1151	regulation of nucleobase-containing compound metabolic process	BP	1	GATA5	up_VCAV_VSMC
GO:1904427	0.834	0.481	1	18	positive regulation of calcium ion	BP	1	ABL1	up_VSAP_EC
GO:0032272	0.834	0.479	1	18	negative regulation of protein polymerization	BP	1	SLIT2	up_VSAP_EC
GO:0035148	0.834765396	0.4683	1	66	tube formation	BP	1	SOX9	up_ACOR_EC
GO:0016331	0.834797285	0.46824	1	66	morphogenesis of embryonic epithelium	BP	1	SOX9	up_ACOR_EC
GO:2000113	0.835	0.215	32	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	FZD1,THRB,HOXA7,WNT11,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,ZFP36L1,SHOX2,H2AFJ,IKZF2,PASK,ANKHD1,LIMD1,PRMT2,KDM2B,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1	up_VSAP_EC
GO:0060548	0.835	0.222	24	294	negative regulation of cell death	BP	1	FZD1,WNT11,ACKR3,PTGFR,LIMS2,ABL1,DLL1,OSR1,RARG,AMBRA1,PIK3R1,RBCK1,MYC,NPAS2,FBXO7,WISP2,ENSCAFG00000011993,KDM2B,RAF1,QARS,ARHGAP10,NCK1,HMOX1,CITED2	up_VSAP_EC
GO:0008360	0.835	0.338	3	46	regulation of cell shape	BP	1	CDC7,WASF3,BVES	up_ACOR_VSMC
GO:0051983	0.835	0.338	3	47	regulation of chromosome segregation	BP	1	AXIN2,TTL,CDC26	up_VSAP_EC
GO:0042445	0.835	0.338	3	46	hormone metabolic process	BP	1	HSD17B8,RETSAT,DHRS9	up_VSAP_EC
GO:0002366	0.835	0.376	2	65	leukocyte activation involved in immune	BP	1	LOXL3,RAC2	down_VCAV_EC
GO:0031324	0.835	0.381	2	735	negative regulation of cellular metabolic process	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0002637	0.835	0.477	1	20	regulation of immunoglobulin	BP	1	TFRC	down_ACOR_VSMC
GO:1901184	0.835	0.476	1	20	regulation of ERBB signaling pathway	BP	1	NUP62	down_ACOR_VSMC
GO:0050864	0.835	0.471	1	36	regulation of B cell activation	BP	1	ZFP36L1	down_VCAV_EC
GO:0009119	0.835	0.472	1	32	ribonucleoside metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0051492	0.835	0.473	1	28	regulation of stress fiber assembly	BP	1	NRP1	down_VSAP_EC
GO:0045661	0.835	0.479	1	18	regulation of myoblast differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0000122	0.835	0.468	1	218	negative regulation of transcription by RNA polymerase II	BP	1	MTDH	up_VPOR_EC
GO:0045859	0.835	0.468	1	219	regulation of protein kinase activity	BP	1	ASPN	up_VPOR_EC
GO:0010648	0.835	0.471	1	407	negative regulation of cell communication	BP	1	CAV1	up_VSAP_VSMC
GO:0009057	0.836	0.208	40	473	macromolecule catabolic process	BP	1	ZRANB1,FBXL20,SKP2,PNRC1,SH3RF2,ISG15,ZNRF3,CTSS,PTPN3,KLHL20,CTSB,BNIP3,EGLN1,DCP1B,UBR1,OS9,STT3B,UBE2H,PYGM,RNF24,RNF19A,LYPLAL1,PSEN1,LAMP2,CLN8,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,GAA,FAF2,CNOT4,WFS1,AZIN2,CTIF,DZIP3,PARK7	up_ACOR_VSMC

GO:0032270	0.836	0.212	35	479	positive regulation of cellular protein metabolic process	BP	1	HMGB1,SREBF1,IRAK1,EIF4A3,HNRNPD,UBE2S,SLC29A1,PRELID1,CAV1,FANCI,TRUB2,EZH2,PPP2R5D,GREM1,MAP3K20,PLK3,DHX33,CKS2,PDCD2,BRCA1,FASTKD3,EIF5A,RAP2C,CYCS,RAC1,EMP2,EZR,CLSPN,RAD23A,CDC20,AIFM1,ARHGEF2,TADA2A,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0031325	0.836	0.232	18	914	positive regulation of cellular metabolic process	BP	1	HOXA9,LEP,LBH,PRR16,DLL1,F3,MLLT11,THRB,GREM1,NFE2L1,CLEC16A,MYBL1,DCUN1D3,BVES,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0071826	0.836	0.273	7	117	ribonucleoprotein complex subunit	BP	1	SCAF11,CNOT6,MRRF,PAN3,PRPF39,CNOT7,LSM14A	up_VCAV_EC
GO:0072511	0.836	0.274	7	97	divalent inorganic cation transport	BP	1	SLC8B1,TPCN2,NIPAL3,ABL1,CRACR2B,NIPAL1,CYBA	up_VSAP_EC
GO:0050808	0.836	0.283	6	93	synapse organization	BP	1	EPHB1,ARHGEF15,RELN,MEF2C,ALS2,P2RX2	up_VCAV_EC
GO:0010976	0.836	0.337	3	47	positive regulation of neuron projection	BP	1	SHOX2,NCK1,MAP2K2	up_VSAP_EC
GO:0045727	0.836	0.377	2	40	positive regulation of translation	BP	1	MTOR,NCK1	up_VCAV_EC
GO:0065009	0.836	0.38	2	735	regulation of molecular function	BP	1	MAP2K6,TIAM1	up_VFEM_EC
GO:0009119	0.836	0.38	2	32	ribonucleoside metabolic process	BP	1	NT5C2,PNP	up_VSAP_EC
GO:0001708	0.836	0.474	1	20	cell fate specification	BP	1	HOXC10	down_ACOR_VSMC
GO:0042440	0.836	0.475	1	21	pigment metabolic process	BP	1	PRPS1	down_ACOR_VSMC
GO:0002688	0.836	0.47	1	34	regulation of leukocyte chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0045747	0.836	0.476	1	18	positive regulation of Notch signaling pathway	BP	1	GATA5	up_ACOR_VSMC
GO:0045333	0.836	0.465	1	74	cellular respiration	BP	1	PPARGC1A	up_AFEM_EC
GO:0042490	0.836	0.476	1	19	mechanoreceptor differentiation	BP	1	JAG1	up_VCAV_EC
GO:0044248	0.836	0.477	1	691	cellular catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:0003300	0.836	0.476	1	18	cardiac muscle hypertrophy	BP	1	KLF15	up_VSAP_EC
GO:0014896	0.836	0.476	1	18	muscle hypertrophy	BP	1	KLF15	up_VSAP_EC
GO:0014897	0.836	0.476	1	18	striated muscle hypertrophy	BP	1	KLF15	up_VSAP_EC
GO:0030100	0.836295646	0.46531	1	70	regulation of endocytosis	BP	1	CALY	up_ACOR_EC
GO:0072593	0.836571972	0.46492	1	68	reactive oxygen species metabolic process	BP	1	PRKCD	up_ACOR_EC
GO:1901362	0.837	0.19	115	1293	organic cyclic compound biosynthetic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,ENSCAFG00000013986,VDR,SAV1,KLF15,ANXA4,HSD3B7,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,HSD17B8,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,PDK2,ICE1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,FBXO4,ENSCAFG00000016140,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,MOCOS,PCBD1,LIMD1,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,MVK,PNPO,DCAKD,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,CYB5R3,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:0001558	0.837	0.281	6	101	regulation of cell growth	BP	1	IFRD1,CDA,EDN1,RAB11A,MTOR,SMARCA4	up_VCAV_EC
GO:0090092	0.837	0.294	5	72	regulation of transmembrane receptor protein serine/threonine	BP	1	FZD1,ABL1,ZEB1,ACVRL1,CITED2	up_VSAP_EC
GO:0048519	0.837	0.303	5	1554	negative regulation of biological process	BP	1	HOXA9,PITX1,HOXC10,CAV1,SHOX2	up_VSAP_VSMC
GO:0019222	0.837	0.357	3	1934	regulation of metabolic process	BP	1	IVNS1ABP,SRSF6,GABPA	down_AFEM_EC
GO:0017157	0.837	0.334	3	58	regulation of exocytosis	BP	1	RAB27A,RSC1A1,FES	up_VCAV_EC

GO:1901136	0.837	0.377	2	38	carbohydrate derivative catabolic process	BP	1	NUDT1,NUDT3	down_ACOR_VSMC
GO:2000241	0.837	0.376	2	40	regulation of reproductive process	BP	1	ARHGDIB,FBXO5	up_VCAV_EC
GO:0021795	0.837	0.473	1	20	cerebral cortex cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0035637	0.837	0.473	1	21	multicellular organismal signaling	BP	1	CAV1	down_ACOR_VSMC
GO:0070509	0.837	0.473	1	21	calcium ion import	BP	1	SLC30A1	down_ACOR_VSMC
GO:0002702	0.837	0.469	1	28	positive regulation of production of molecular mediator of immune	BP	1	TFRC	down_VSAP_EC
GO:0044773	0.837	0.469	1	28	mitotic DNA damage checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0010629	0.837	0.471	1	502	negative regulation of gene expression	BP	1	NR1H4	up_VPUL_EC
GO:0070231	0.837	0.474	1	18	T cell apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0060038	0.837	0.475	1	18	cardiac muscle cell proliferation	BP	1	SAV1	up_VSAP_EC
GO:0023057	0.837	0.468	1	409	negative regulation of signaling	BP	1	CAV1	up_VSAP_VSMC
GO:0006351	0.838	0.192	94	1069	transcription, DNA-templated	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,ICE1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,NR2F6,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0031326	0.838	0.198	65	1176	regulation of cellular biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,AARS,TRIB3,PGAM1,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,HIF1A,SLC45A3,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0015833	0.838	0.208	37	521	peptide transport	BP	1	HCLS1,GBP5,TMEM173,IWS1,FERMT1,CHD7,TLR4,GATA3,EDN1,RAB11A,RAB27A,EXOC6,PPP3CA,ARG2,HHEX,SCAMP1,ABCA1,SNX2,THOC1,AKAP12,APOD,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,MCU,HIF1A,IPO11,LMTK2,RABGAP1,USP6NL	up_VCAV_EC
GO:0048870	0.838	0.21	33	451	cell motility	BP	1	FSCN1,HMGB1,ANLN,FMNL3,RACGAP1,SDC1,FBXO5,CAV1,MMP14,GREM1,HOXA7,B4GALT1,PRCP,PPARD,RAP2C,RAC1,EMP2,NUP188,HMGB2,CORO1A,SGPL1,PHACTR4,ASPM,ENSCAFG00000010224,ITGA2,ARHGEF2,TWIST2,NUS1,AMOTL1,SIX4,DEPDC1B,TTLL1,PIK3CD	down_ACOR_VSMC
GO:0051674	0.838	0.21	33	451	localization of cell	BP	1	FSCN1,HMGB1,ANLN,FMNL3,RACGAP1,SDC1,FBXO5,CAV1,MMP14,GREM1,HOXA7,B4GALT1,PRCP,PPARD,RAP2C,RAC1,EMP2,NUP188,HMGB2,CORO1A,SGPL1,PHACTR4,ASPM,ENSCAFG00000010224,ITGA2,ARHGEF2,TWIST2,NUS1,AMOTL1,SIX4,DEPDC1B,TTLL1,PIK3CD	down_ACOR_VSMC
GO:0006725	0.838	0.249	13	1956	cellular aromatic compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RRP15,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0045862	0.838	0.264	8	112	positive regulation of proteolysis	BP	1	MBP,SH3RF2,DAPK1,RNF19A,PSEN1,PERP,DISC1,HERPUD1	up_ACOR_VSMC
GO:0044782	0.838	0.279	6	96	cilium organization	BP	1	CFAP298,POC1A,RTTN,CEP83,TTLL1,KIF24	down_ACOR_VSMC

GO:0043405	0.838	0.28	6	85	regulation of MAP kinase activity	BP	1	ARHGEF5,MAP3K5,PDGFD,C1QTNF2,TRAF7,SASH1	up_VSAP_EC
GO:0030833	0.838	0.31	4	59	regulation of actin filament polymerization	BP	1	JMY,EVL,PRKCE,WASL	up_ACOR_VSMC
GO:0043903	0.838	0.309	4	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	MX1,ISG15,F2RL1,INPP5K	up_ACOR_VSMC
GO:0030509	0.838	0.333	3	47	BMP signaling pathway	BP	1	SMAD6,BMP4,ENSCAFG00000018360	up_ACOR_VSMC
GO:0010556	0.838	0.341	3	1137	regulation of macromolecule	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0016051	0.838	0.372	2	63	carbohydrate biosynthetic process	BP	1	AKT2,B4GALT1	down_VCAV_EC
GO:0002285	0.838	0.373	2	50	lymphocyte activation involved in immune	BP	1	SOCS5,TFRC	down_VSAP_EC
GO:0032414	0.838	0.47	1	21	positive regulation of ion transmembrane transporter activity	BP	1	GSTO1	down_ACOR_VSMC
GO:0031109	0.838	0.465	1	36	microtubule polymerization or	BP	1	CLIP3	down_VCAV_EC
GO:0006464	0.838	0.485	1	1162	cellular protein modification process	BP	1	LIMK1	up_VCAV_VSMC
GO:0036211	0.838	0.485	1	1162	protein modification process	BP	1	LIMK1	up_VCAV_VSMC
GO:0097190	0.838	0.463	1	217	apoptotic signaling pathway	BP	1	ARHGEF2	up_VPOR_EC
GO:0035556	0.838	0.477	1	845	intracellular signal transduction	BP	1	SLIT2	up_VPUL_VSMC
GO:0070664	0.838	0.473	1	18	negative regulation of leukocyte proliferation	BP	1	CD274	up_VSAP_EC
GO:0061025	0.838402361	0.46155	1	69	membrane fusion	BP	1	VPS16	up_ACOR_EC
GO:0017144	0.839	0.238	13	199	drug metabolic process	BP	1	ACLY,CAV1,CDK1,SUCLG1,CYCS,PDXP,CYC1,ATP5F1A,ENSCAFG00000013366,CTH,ENSCAFG00000005637,PDHA1,ATP5F1D	down_ACOR_VSMC
GO:0001701	0.839	0.251	10	134	in utero embryonic development	BP	1	GJB5,MFN2,ZFP36L1,TAF8,ZFAND5,ACVRL1,TGFBR2,CITED2,KEAP1,LATS2	up_VSAP_EC
GO:0072521	0.839	0.26	8	185	purine-containing compound metabolic	BP	1	ENPP1,PGK1,TPI1,PGAM1,HIF1A,ALDOC,PAPSS1,AK5	down_VSAP_EC
GO:0042063	0.839	0.307	4	67	gliogenesis	BP	1	NAB2,NF2,EZH2,ENSCAFG00000010224	down_ACOR_VSMC
GO:0046034	0.839	0.328	3	88	ATP metabolic process	BP	1	ATP5MC1,UQCR10,PARK7	down_VCAV_EC
GO:1903311	0.839	0.329	3	72	regulation of mRNA metabolic process	BP	1	IWS1,CNOT7,REST	down_VSAP_EC
GO:0009142	0.839	0.332	3	46	nucleoside triphosphate biosynthetic process	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0032635	0.839	0.374	2	37	interleukin-6 production	BP	1	HMGB1,ARHGEF2	down_ACOR_VSMC
GO:0035303	0.839	0.369	2	65	regulation of dephosphorylation	BP	1	PDGFRB,SPRED1	down_VCAV_EC
GO:0002440	0.839	0.371	2	51	production of molecular mediator of immune	BP	1	TFRC,BTK	down_VSAP_EC
GO:0010605	0.839	0.375	2	745	negative regulation of macromolecule metabolic	BP	1	HOXA7,SIX1	up_VFEM_EC
GO:0016445	0.839	0.469	1	20	somatic diversification of immunoglobulins	BP	1	TFRC	down_ACOR_VSMC
GO:0016447	0.839	0.469	1	20	somatic recombination of immunoglobulin gene	BP	1	TFRC	down_ACOR_VSMC
GO:0042089	0.839	0.469	1	21	cytokine biosynthetic process	BP	1	MAST2	down_ACOR_VSMC
GO:0061383	0.839	0.469	1	20	trabecula morphogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:0007416	0.839	0.463	1	36	synapse assembly	BP	1	CDH2	down_VCAV_EC
GO:0031050	0.839	0.472	1	17	dsRNA processing	BP	1	BMP4	up_ACOR_VSMC
GO:0070918	0.839	0.472	1	17	production of small RNA involved in gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:0010464	0.839	0.468	1	21	regulation of mesenchymal cell	BP	1	ZEB1	up_VCAV_EC
GO:0045921	0.839	0.466	1	24	positive regulation of exocytosis	BP	1	RAB27A	up_VCAV_EC
GO:0001932	0.839	0.465	1	416	regulation of protein phosphorylation	BP	1	MAP2K6	up_VFEM_EC
GO:0015031	0.839	0.466	1	510	protein transport	BP	1	NR1H4	up_VPUL_EC

GO:0044271	0.84	0.213	31	1501	cellular nitrogen compound biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0033673	0.84	0.278	6	84	negative regulation of kinase activity	BP	1	CEP85,ABL1,PIK3IP1,RTN4RL1,FBXO7,LATS2	up_VSAP_EC
GO:0030198	0.84	0.288	5	81	extracellular matrix organization	BP	1	FSCN1,COLGALT1,GREM1,B4GALT1,SERPINH1	down_ACOR_VSMC
GO:2000058	0.84	0.305	4	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	SLC29A1,SMARCC1,PLK3,RAD23A	down_ACOR_VSMC
GO:0042180	0.84	0.306	4	61	cellular ketone metabolic process	BP	1	PPARGC1A,PRKCE,DKKL1,PARK7	up_ACOR_VSMC
GO:1901800	0.84	0.332	3	46	positive regulation of proteasomal protein catabolic process	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:1901575	0.84	0.372	2	643	organic substance catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0035924	0.84	0.468	1	21	cellular response to vascular endothelial growth factor stimulus	BP	1	NUS1	down_ACOR_VSMC
GO:0060389	0.84	0.467	1	21	pathway-restricted SMAD protein phosphorylation	BP	1	GREM1	down_ACOR_VSMC
GO:1903533	0.84	0.466	1	21	regulation of protein targeting	BP	1	SREBF1	down_ACOR_VSMC
GO:0001892	0.84	0.462	1	35	embryonic placenta development	BP	1	ZFP36L1	down_VCAV_EC
GO:0045621	0.84	0.463	1	28	positive regulation of lymphocyte	BP	1	SOCS5	down_VSAP_EC
GO:0046578	0.84	0.458	1	77	regulation of Ras protein signal transduction	BP	1	KANK1	up_AFEM_EC
GO:1901606	0.84	0.466	1	22	alpha-amino acid catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:1903902	0.84	0.47	1	18	positive regulation of viral life cycle	BP	1	PC	up_VSAP_EC
GO:0045666	0.840367841	0.45802	1	68	positive regulation of neuron differentiation	BP	1	NRP1	up_ACOR_EC
GO:0048545	0.84085875	0.45712	1	68	response to steroid hormone	BP	1	AQP1	up_ACOR_EC
GO:1901576	0.841	0.183	170	1877	organic substance biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,HOXA9,CDON,NECAB3,WNT11,ACSM3,ARHGEF5,LIPC,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,GOT1,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,GLUL,GALNT15,ENSCAFG00000013986,CERS4,WARS2,VDR,SAV1,KLF15,C1QTNF2,ANXA4,HSD3B7,ZNF688,ZBTB16,COQ9,RARG,CBX7,STAT5A,STAT6,GATAD1,HSD17B8,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,PPIP5K1,DDR2,PDK2,ICE1,ZFP36L1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,PLA2G6,MYC,PTGES,SSBP2,IRX3,ZEB1,FKRP,HACD4,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,ENSCAFG00000016140,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,GALNT11,E2F4,NPAS2,MOCOS,ZDHHC8,FARS2,LCAT,PCBD1,LIMD1,UBA52,RPUSD4,RPL15,ACSS2,PC,CDK9,DHRS9,NR2F6,PRMT2,KDM2B,MVK,PNPO,DCAKD,FAXDC2,EIF3G,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,CYB5R3,ZNF517,ASS1,TNRC6C,COA1,PPP3CB,NC	up_VSAP_EC
GO:0015833	0.841	0.201	44	521	peptide transport	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,TBC1D10C,TBC1D2B,CDH1,ABL1,PEX2,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,PASK,NUP98,HPS4,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,STX4,VPS11,PPP3CB,PEX6,MAVS,BAG4,NCOA4,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0034097	0.841	0.222	19	238	response to cytokine	BP	1	CD274,SLIT2,TRAFD1,CDC42EP2,RARG,STAT6,F2RL1,ZFP36L1,RTN4RL1,CREBRF,CDK9,ZFP36L2,STX4,TIMP2,HTRA2,PPP3CB,MAVS,BAG4,KEAP1	up_VSAP_EC

GO:0051347	0.841	0.233	14	182	positive regulation of transferase activity	BP	1	MAP3K14,ARHGEF5,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CAMKK2,AMBRA1,DDR2,TRAF7,SASH1,MAP2K2,TGFBR2	up_VSAP_EC
GO:0040017	0.841	0.24	12	180	positive regulation of locomotion	BP	1	HMGB1,FBXO5,CAV1,MMP14,RAC1,SMC3,CORO1A,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0009987	0.841	0.314	11	5086	cellular process	BP	1	HOXC10,DKK2,ENSCAFG00000005494,HOXA9,LNPEP,SGCD,ERC1,TAOK1,BPI,CTNNAL1,GPR155	up_AORT_EC
GO:0009896	0.841	0.258	8	127	positive regulation of catabolic process	BP	1	PLK2,TNFAIP3,TIPARP,RALB,SPTLC2,SH3GLB1,CNOT7,HIF1A	up_VCAV_EC
GO:0006164	0.841	0.276	6	86	purine nucleotide biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,ELOVL7	up_ACOR_VSMC
GO:0033157	0.841	0.287	5	82	regulation of intracellular protein transport	BP	1	SREBF1,RAN,INSIG1,PLK3,DMAP1	down_ACOR_VSMC
GO:0030522	0.841	0.303	4	67	intracellular receptor signaling pathway	BP	1	NEDD4,THRAP3,EZH2,PRCP	down_ACOR_VSMC
GO:0045787	0.841	0.301	4	117	positive regulation of cell cycle	BP	1	POLDIP2,LSM10,MAPRE3,EIF4EBP1	down_VCAV_EC
GO:0019725	0.841	0.301	4	245	cellular homeostasis	BP	1	RAB20,RAB7A,ATP6V0B,DMPK	up_AFEM_EC
GO:0006874	0.841	0.326	3	91	cellular calcium ion homeostasis	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0000070	0.841	0.325	3	75	mitotic sister chromatid segregation	BP	1	NAA10,KPNB1,PDS5B	down_VSAP_EC
GO:0090304	0.841	0.345	3	1694	nucleic acid metabolic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0008088	0.841	0.465	1	21	axo-dendritic transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0072666	0.841	0.465	1	21	establishment of protein localization to vacuole	BP	1	NEDD4	down_ACOR_VSMC
GO:0035270	0.841	0.461	1	35	endocrine system development	BP	1	BMPR1A	down_VCAV_EC
GO:0051173	0.841	0.471	1	874	positive regulation of nitrogen compound	BP	1	CITED2	down_VPOR_EC
GO:0050793	0.841	0.468	1	731	regulation of developmental process	BP	1	HOXA9	up_AORT_EC
GO:0031326	0.841	0.481	1	1176	regulation of cellular biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:1901135	0.841	0.462	1	390	carbohydrate derivative metabolic process	BP	1	GALNT17	up_VSAP_VSMC
GO:0034654	0.842	0.192	68	1236	nucleobase-containing compound biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,PGK1,TPI1,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A,CMPK1	down_VSAP_EC
GO:1901566	0.842	0.2	43	598	organonitrogen compound biosynthetic process	BP	1	ACSL3,ACLY,ILF3,BCAT1,EIF4A3,HNRNPD,VARS,RRBP1,PPP1R15B,MPDU1,SLC35C2,MRPS18B,B3GNT2,XYLT1,TRUB2,PFAS,DHX33,ARG2,FASTKD3,EIF5A,B4GALT1,ELOVL1,FARSA,NCL,UGDH,MRPL37,ELOVL6,RBM14,CYC1,NOLC1,RARS,ATP5F1A,PUM3,PRPS1,ENSCAFG00000013366,CTH,PDHA1,MRPL18,NUS1,CTPS1,NECAB3,EIF3M,ATP5F1D	down_ACOR_VSMC
GO:0010629	0.842	0.201	43	502	negative regulation of gene expression	BP	1	LEP,GATA5,NACC2,PRKAA2,FERMT1,BMP4,PNRC1,FGFR2,GJA1,ATRX,TRPS1,TP53INP1,ZNF174,DAPK1,CDKN1A,ENSCAFG00000006238,DCP1B,CLSTN1,PTPN22,TBX20,CCNT1,PARP9,APP,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,CNOT4,WFS1,CTIF,ENSCAFG00000029553,ID3,PARK7,STC2,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0080134	0.842	0.21	28	386	regulation of response to stress	BP	1	HMGB1,USP1,IRAK1,HMGA1,TFPI,WDR76,SLC29A1,PPP1R15B,PARPBP,INSIG1,CAV1,RAD51,TIMELESS,MAP3K20,RNASEH2B,PCNA,ARG2,PPARD,RSL1D1,CACTIN,HMGB2,DDX39B,EZR,RBM14,POLR3F,BAP1,TXNDC12,ARHGEF2	down_ACOR_VSMC
GO:0031331	0.842	0.264	7	110	positive regulation of cellular catabolic process	BP	1	MTDH,ABHD5,PLK3,RNF152,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0051179	0.842	0.299	5	1747	localization	BP	1	NR1H4,TBX5,HOXA3,NPNT,NTRK2	up_APUL_EC

GO:0007283	0.842	0.324	3	91	spermatogenesis	BP	1	ADAMTS2,MEA1,ZBTB16	down_VCAV_EC
GO:0006915	0.842	0.326	3	550	apoptotic process	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0030433	0.842	0.368	2	38	ubiquitin-dependent ERAD pathway	BP	1	UBE2J2,PSMC1	down_ACOR_VSMC
GO:0032092	0.842	0.368	2	38	positive regulation of protein binding	BP	1	HOXA3,CAV1	down_ACOR_VSMC
GO:0006885	0.842	0.368	2	39	regulation of pH	BP	1	EDNRB,EDN1	up_VCAV_EC
GO:0001706	0.842	0.464	1	20	endoderm formation	BP	1	MMP14	down_ACOR_VSMC
GO:0038034	0.842	0.464	1	21	signal transduction in absence of ligand	BP	1	CASP2	down_ACOR_VSMC
GO:0051899	0.842	0.463	1	22	membrane depolarization	BP	1	CAV1	down_ACOR_VSMC
GO:0097192	0.842	0.464	1	21	extrinsic apoptotic signaling pathway in	BP	1	CASP2	down_ACOR_VSMC
GO:0030004	0.842	0.459	1	36	cellular monovalent inorganic cation	BP	1	ATP6V0C	down_VCAV_EC
GO:0097530	0.842	0.459	1	33	granulocyte migration	BP	1	WDR1	down_VSAP_EC
GO:0099518	0.842	0.467	1	17	vesicle cytoskeletal trafficking	BP	1	DYNC1I1	up_ACOR_VSMC
GO:0043967	0.842	0.463	1	21	histone H4 acetylation	BP	1	IWS1	up_VCAV_EC
GO:0051851	0.842	0.462	1	23	modification by host of symbiont morphology or	BP	1	SMARCA4	up_VCAV_EC
GO:0071702	0.842	0.466	1	687	organic substance transport	BP	1	SLC16A12	up_VFEM_VSMC
GO:0044271	0.843	0.189	82	1501	cellular nitrogen compound biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,PGAM1,PUM3,UGCG,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,KDM3A,CMPK1	down_VSAP_EC
GO:0015031	0.843	0.199	43	510	protein transport	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,TBC1D10C,TBC1D2B,CDH1,ABL1,PEX2,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,NUP98,HPS4,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,STX4,VPS11,PPP3CB,PEX6,MAVS,BAG4,NCOA4,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0043170	0.843	0.232	21	2980	macromolecule metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,HOXA3,ARHGEF2,TCEA1,ENSCAFG00000002015,ASPN,ACVR2A,MTDH,RSL24D1,RPL10L,RRP15,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0009101	0.843	0.264	7	113	glycoprotein biosynthetic process	BP	1	MPDU1,SLC35C2,B3GNT2,XYLT1,B4GALT1,NUS1,NECAB3	down_ACOR_VSMC
GO:0033673	0.843	0.285	5	84	negative regulation of kinase activity	BP	1	HMGCR,CAV1,NF2,CDKN2C,NUP62	down_ACOR_VSMC
GO:0016236	0.843	0.284	5	88	macroautophagy	BP	1	RALB,SPTLC2,MTOR,SH3GLB1,HIF1A	up_VCAV_EC
GO:0050808	0.843	0.322	3	93	synapse organization	BP	1	PRNP,CACNB3,CDH2	down_VCAV_EC
GO:0050921	0.843	0.366	2	39	positive regulation of chemotaxis	BP	1	HMGB1,RAC1	down_ACOR_VSMC
GO:0006378	0.843	0.462	1	20	mRNA polyadenylation	BP	1	WDR33	down_ACOR_VSMC
GO:0010596	0.843	0.461	1	21	negative regulation of endothelial cell migration	BP	1	HMGB1	down_ACOR_VSMC
GO:0042310	0.843	0.46	1	21	vasoconstriction	BP	1	CAV1	down_ACOR_VSMC
GO:0097756	0.843	0.46	1	21	negative regulation of blood vessel diameter	BP	1	CAV1	down_ACOR_VSMC
GO:0002181	0.843	0.456	1	35	cytoplasmic translation	BP	1	EIF3K	down_VCAV_EC
GO:0006275	0.843	0.455	1	38	regulation of DNA replication	BP	1	FBH1	down_VCAV_EC

GO:0035601	0.843	0.457	1	36	protein deacylation	BP	1	SPRED1	down_VCAV_EC
GO:0098732	0.843	0.457	1	36	macromolecule deacylation	BP	1	SPRED1	down_VCAV_EC
GO:0031099	0.843	0.457	1	30	regeneration	BP	1	IFRD1	down_VSAP_EC
GO:0032272	0.843	0.463	1	18	negative regulation of protein polymerization	BP	1	TUBB4A	up_ACOR_VSMC
GO:1902115	0.843	0.453	1	77	regulation of organelle assembly	BP	1	CYLD	up_AFEM_EC
GO:0061640	0.843	0.459	1	23	cytoskeleton-dependent cytokinesis	BP	1	STMN1	up_VCAV_EC
GO:0033554	0.843	0.464	1	708	cellular response to stress	BP	1	EYA1	up_VFEM_VSMC
GO:0044248	0.843	0.463	1	691	cellular catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0002381	0.843	0.462	1	19	immunoglobulin production involved in immunoglobulin	BP	1	STAT6	up_VSAP_EC
GO:0021872	0.843	0.463	1	19	forebrain generation of neurons	BP	1	SLIT2	up_VSAP_EC
GO:1903036	0.843	0.463	1	19	positive regulation of response to wounding	BP	1	HPSE	up_VSAP_EC
GO:0014070	0.843380266	0.32071	3	172	response to organic cyclic compound	BP	1	AQP1,PAK3,MAVS	up_ACOR_EC
GO:0042063	0.843406932	0.45248	1	67	gliogenesis	BP	1	SH3TC2	up_ACOR_EC
GO:0030163	0.844	0.211	25	365	protein catabolic process	BP	1	PLK2,TNFAIP3,CTSC,TIPARP,WWP1,USP33,PSME4,PELI1,ODC1,CASP8,ENC1,USP28,PMAIP1,RIPK1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0051173	0.844	0.224	17	874	positive regulation of nitrogen compound metabolic process	BP	1	HOXA9,LEP,LBH,PRR16,DLL1,F3,MLLT11,THRB,GREM1,NFE2L1,MYBL1,DCUN1D3,RAB7A,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0006897	0.844	0.236	12	158	endocytosis	BP	1	DNM1,ACKR3,ABL1,DLL1,EPN2,F2RL1,CYBA,XKR8,ARHGAP12,UBQLN2,FLOT1,PPP3CB	up_VSAP_EC
GO:0016569	0.844	0.243	10	144	covalent chromatin modification	BP	1	IWS1,GATA3,UHRF2,ARID4B,PRKD2,NSD1,KDM5A,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0030029	0.844	0.247	9	239	actin filament-based process	BP	1	KIRREL1,RHOD,ENSCAFG00000014978,WIPF1,MYO1B,ACTR3B,SHC1,PLEKHH2,RAC2	down_VCAV_EC
GO:0044782	0.844	0.263	7	96	cilium organization	BP	1	EVI5L,IFT43,TTC17,ASAP1,DISC1,ATXN10,ENSCAFG00000013536	up_ACOR_VSMC
GO:0006935	0.844	0.281	5	143	chemotaxis	BP	1	PDGFRB,HSD3B7,SEMA3C,GLI3,RAC2	down_VCAV_EC
GO:0042330	0.844	0.281	5	143	taxis	BP	1	PDGFRB,HSD3B7,SEMA3C,GLI3,RAC2	down_VCAV_EC
GO:0050727	0.844	0.284	5	74	regulation of inflammatory response	BP	1	LEP,TLR3,APP,NOD2,PARK7	up_ACOR_VSMC
GO:0060537	0.844	0.297	4	117	muscle tissue development	BP	1	BMPR1A,SEMA3C,TSC22D3,GREM1	down_VCAV_EC
GO:0019219	0.844	0.33	3	1151	regulation of nucleobase-containing compound metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0010468	0.844	0.334	3	1270	regulation of gene expression	BP	1	NR1H4,ARHGEF2,NEO1	up_VPUL_EC
GO:0042742	0.844	0.365	2	39	defense response to bacterium	BP	1	ARG2,HMGB2	down_ACOR_VSMC
GO:0051453	0.844	0.366	2	33	regulation of intracellular pH	BP	1	SLC26A7,DMXL1	up_ACOR_VSMC
GO:0046467	0.844	0.363	2	45	membrane lipid biosynthetic process	BP	1	SPTLC2,SAMD8	up_VCAV_EC
GO:0008306	0.844	0.46	1	21	associative learning	BP	1	HMGCR	down_ACOR_VSMC
GO:0008637	0.844	0.454	1	35	apoptotic mitochondrial changes	BP	1	SLC35F6	down_VCAV_EC
GO:1903305	0.844	0.454	1	36	regulation of regulated secretory pathway	BP	1	RAC2	down_VCAV_EC
GO:0051865	0.844	0.455	1	31	protein autoubiquitination	BP	1	SH3RF3	down_VSAP_EC
GO:0032147	0.844	0.451	1	77	activation of protein kinase activity	BP	1	LEP	up_AFEM_EC
GO:0048144	0.844	0.458	1	23	fibroblast proliferation	BP	1	PDGFB	up_VCAV_EC
GO:0048145	0.844	0.458	1	23	regulation of fibroblast proliferation	BP	1	PDGFB	up_VCAV_EC
GO:0032922	0.844	0.461	1	19	circadian regulation of gene expression	BP	1	NCOA2	up_VSAP_EC
GO:0006687	0.844	0.462	1	18	glycosphingolipid metabolic process	BP	1	B3GALT4	up_VSAP_EC

GO:0032963	0.844	0.462	1	18	collagen metabolic process	BP	1	LARP6	up_VSAP_EC
GO:0001775	0.844863084	0.29509	4	219	cell activation	BP	1	FZD5,NOD2,PTGER4,PRKCD	up_ACOR_EC
GO:0016070	0.845	0.182	114	1479	RNA metabolic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,TARSL2,MTOR,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TRMT9B,TIMELESS,LDB2,CD200,JAG1,NSD1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,WTAP,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0010629	0.845	0.197	42	502	negative regulation of gene expression	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,PPARGC1B,ACACB,ZHX3,PEX2,HDAC7,OSR1,TENT5C,RARG,CBX7,STAT6,EXOSC7,PYM1,RBL2,GLIS2,ZFP36L1,GAS1,SHOX2,H2AFJ,ZC3H10,IKZF2,ANKHD1,SMG9,LIMD1,PC,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1	up_VSAP_EC
GO:0034622	0.845	0.215	20	421	cellular protein-containing complex assembly	BP	1	CELF1,SEC24D,MZT1,SRP54,PRPF3,DDX39B,BRD2,CNOT7,ACTR3,CRYAB,STRAP,TWF1,PLEKHG2,GBP5,EIF2S1,CLTC,CAPG,RSL24D1,SEC13,MYBPC2	down_VSAP_EC
GO:0009161	0.845	0.261	7	103	ribonucleoside monophosphate	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0043543	0.845	0.281	5	84	protein acylation	BP	1	POLE3,BRCA1,NOC2L,DMAP1,TADA2A	down_ACOR_VSMC
GO:0006091	0.845	0.28	5	139	generation of precursor metabolites and energy	BP	1	AKT2,UQCR10,PARK7,MTFR1L,ACAT1	down_VCAV_EC
GO:0016485	0.845	0.282	5	73	protein processing	BP	1	KLKB1,CCBE1,GAS1,FKRP,LONP2	up_VSAP_EC
GO:0031929	0.845	0.298	4	62	TOR signaling	BP	1	SESN1,CASTOR1,NPRL3,DDIT4	up_VSAP_EC
GO:0016197	0.845	0.32	3	78	endosomal transport	BP	1	ANKRD50,TMEM87B,RAB6A	down_VSAP_EC
GO:0006282	0.845	0.323	3	48	regulation of DNA repair	BP	1	AXIN2,NPAS2,CDK9	up_VSAP_EC
GO:0044743	0.845	0.456	1	23	protein transmembrane import into intracellular	BP	1	TIMM44	down_ACOR_VSMC
GO:0046605	0.845	0.454	1	30	regulation of centrosome cycle	BP	1	CTNNB1	down_VSAP_EC
GO:0060563	0.845	0.459	1	18	neuroepithelial cell differentiation	BP	1	SEC24B	up_ACOR_VSMC
GO:1904427	0.845	0.459	1	18	positive regulation of calcium ion	BP	1	PLCG2	up_ACOR_VSMC
GO:0009889	0.845	0.473	1	1190	regulation of biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0044265	0.845	0.454	1	423	cellular macromolecule catabolic process	BP	1	TRIM9	up_VFEM_EC
GO:1901264	0.845	0.46	1	18	carbohydrate derivative transport	BP	1	CYBA	up_VSAP_EC
GO:0001932	0.845	0.454	1	416	regulation of protein phosphorylation	BP	1	CAV1	up_VSAP_VSMC

GO:0065007	0.846	0.174	323	3499	biological regulation	BP	1	GPR1,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,NAPEPLD,TWIST2,HOXA9,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,NECAB3,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,SLC8B1,RADIL,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,RNPEP,TBC1D10C,MAB21L1,CEP85,LIMS2,GABRE,ARHGEF6,ACACB,TPCN2,EEF2K,DDHD1,IL6R,IRX5,SLIT2,CST3,CRADD,CRIP2,LRRC28,ZHX3,TBC1D2B,ABTB1,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,GOT1,EBF2,BTG1,HDAC7,KLKB1,EMP2,KCNE3,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,DTX2,TENT5C,CLIC5,FUZ,ADAMTSL4,PDGFD,TRAFD1,SAV1,RHPN1,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CLDN1,CDC42EP2,ZNF688,ZBTB16,TOX,CNPPD1,RARG,CCBE1,PTGES2,CBX7,STAT5A,STAT6,RECK,GATAD1,CISH,KLHL24,HSD17B8,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,TNKS1BP1,RASD2,PYM1,AMBRA1,F2RL1,RBL2,LMF1,RAB11B,GLIS2,MORC3,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,MT2A,FXN,RGL1,RETSAT,PIK3R1,RBCK1,SLC25A28,FAM53B,TIAM1,CRACR2B,GAS1,BATF2,OMD,MYC,PIK3IP1,PTGE	up_VSAP_EC
GO:0097659	0.846	0.183	94	1072	nucleic acid-templated transcription	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,ICE1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,NR2F6,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0010604	0.846	0.198	40	919	positive regulation of macromolecule metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,DCN,PRNP,LUM,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,CLIP3,ENSCAFG00000014978,SSBP2,AKT2,TFE3,CSPG4,TMEM161A,TEAD1,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,SASH1,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,SOAT1,THRB,PACSIN3,ZBTB16	down_VCAV_EC
GO:0006807	0.846	0.227	23	3221	nitrogen compound metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,RRP15,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0033043	0.846	0.217	18	446	regulation of organelle organization	BP	1	SLC35F6,KIRREL1,DCN,SDC4,NABP2,CLIP3,RHOD,ENSCAFG00000014978,AKT2,SYDE1,PRMT6,CLEC16A,MAVS,CDH2,MGARP,ACTR3B,PLEKHH2,EVI5L	down_VCAV_EC
GO:0043086	0.846	0.23	13	170	negative regulation of catalytic activity	BP	1	SH2D4A,CEP85,ACACB,CST3,ABL1,RECK,PIK3IP1,TMEM225B,RTN4RL1,FBXO7,TIMP2,BAG4,LATS2	up_VSAP_EC
GO:0016071	0.846	0.293	4	248	mRNA metabolic process	BP	1	TENT5C,AXIN2,CTIF,SAMD4B	up_AFEM_EC
GO:0070588	0.846	0.32	3	54	calcium ion transmembrane transport	BP	1	GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0009127	0.846	0.321	3	47	purine nucleoside monophosphate biosynthetic process	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0009168	0.846	0.321	3	47	purine ribonucleoside monophosphate biosynthetic process	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0006892	0.846	0.361	2	39	post-Golgi vesicle-mediated transport	BP	1	ACSL3,STXBP6	down_ACOR_VSMC
GO:0002218	0.846	0.359	2	53	activation of innate immune response	BP	1	NR1H4,LYN	down_VSAP_EC
GO:0031056	0.846	0.36	2	50	regulation of histone modification	BP	1	IWS1,KDM3A	down_VSAP_EC
GO:0000018	0.846	0.363	2	31	regulation of DNA recombination	BP	1	TP53BP1,ZNF365	up_ACOR_VSMC

GO:1901564	0.846	0.391	2	2053	organonitrogen compound metabolic	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0051234	0.846	0.373	2	1283	establishment of localization	BP	1	ENSCAFG00000005494,GPR155	up_AORT_EC
GO:0030968	0.846	0.362	2	33	endoplasmic reticulum unfolded protein	BP	1	PIK3R1,NCK1	up_VSAP_EC
GO:0042107	0.846	0.455	1	22	cytokine metabolic process	BP	1	MAST2	down_ACOR_VSMC
GO:0051145	0.846	0.455	1	21	smooth muscle cell differentiation	BP	1	CTH	down_ACOR_VSMC
GO:0045454	0.846	0.451	1	35	cell redox homeostasis	BP	1	PDIA4	down_VCAV_EC
GO:0006400	0.846	0.451	1	33	tRNA modification	BP	1	AARS	down_VSAP_EC
GO:0016999	0.846	0.453	1	30	antibiotic metabolic process	BP	1	KDM3A	down_VSAP_EC
GO:0046637	0.846	0.458	1	18	regulation of alpha-beta T cell differentiation	BP	1	CD83	up_ACOR_VSMC
GO:0015833	0.846	0.454	1	521	peptide transport	BP	1	NR1H4	up_VPUL_EC
GO:0030521	0.846	0.457	1	19	androgen receptor signaling pathway	BP	1	PRMT2	up_VSAP_EC
GO:0042490	0.846	0.456	1	19	mechanoreceptor differentiation	BP	1	DLL1	up_VSAP_EC
GO:0046902	0.846	0.458	1	18	regulation of mitochondrial membrane	BP	1	ZNF205	up_VSAP_EC
GO:0048814	0.846	0.458	1	19	regulation of dendrite morphogenesis	BP	1	PQBP1	up_VSAP_EC
GO:0002263	0.8468391	0.44603	1	68	cell activation involved in immune response	BP	1	PTGER4	up_ACOR_EC
GO:0032501	0.847	0.178	141	1782	multicellular organismal process	BP	1	ELK3,ACSL3,HMGB1,SREBF1,FLNB,USP1,IRAK1,ANLN,ACSL4,EIF4A3,HMGCR,TFPI,HNRNPD,SMC1A,TFPI2,HINFP,NEDD4,MED17,SLC29A1,MTDH,HEY1,HOXA3,NDC1,TRIP13,SF1,SRRT,GINS4,CTDNEP1,RAD54L,FBXO5,HSPA9,NAB2,B3GNT2,PRELID1,INSIG1,PRMT1,CAV1,XYLT1,TIMELESS,LIMA1,FAM129B,NF2,ANPEP,AAAS,MMP14,EZH2,STMN1,SLC30A1,GREM1,MAP3K20,NEK2,ADIPOR2,CDK4,SMARCC1,RNASEH2B,HMGB3,DHX33,HOXA7,SMG9,ARG2,ANXA5,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,NCAPH,POC1A,TRPV4,BRCA1,WDR62,E2F8,B4GALT1,NAV2,PRCP,TFRC,ADAMTS6,PPARD,ITGB3,HIST1H1A,FAM49B,NCL,RAC1,UGDH,EMP2,NUP188,FOSL1,PLK4,IQGAP1,HOXC6,CACTIN,HMGB2,ARCN1,SMC3,CDK2,SMARCB1,RAB35,HOXB5,RBBP8,EZR,TOX,HOXC4,ELOVL6,CORO1A,SGPL1,NOLC1,BEND6,POLR3F,PHACTR4,CDC20,TTK,SLC20A1,BAP1,ASPM,MAST2,PRPS1,TBX15,ENSCAFG00000010224,ITGA2,CTH,ARHGEF2,TWIST2,HOXA9,SERPINH1,GLI1,JMJD6,H2AFX,MSC,LIPC,EMG1,RTTN,RTCB,NUS1,HMGN1,AMOTL1,SIX4,TTLL1,TPBG,NOB1,AMER1,PIK3CD	down_ACOR_VSMC
GO:0048511	0.847	0.279	5	72	rhythmic process	BP	1	PRKAA2,PPARGC1A,RBM4B,GNAQ,ID3	up_ACOR_VSMC
GO:0071826	0.847	0.292	4	117	ribonucleoprotein complex subunit	BP	1	RPS10,EIF3K,MRPS11,RPS27	down_VCAV_EC
GO:0023014	0.847	0.292	4	248	signal transduction by protein phosphorylation	BP	1	LEP,CYLD,CCL5,CDC42EP5	up_AFEM_EC
GO:0006338	0.847	0.32	3	45	chromatin remodeling	BP	1	ATRX,SMARCD3,CHD7	up_ACOR_VSMC
GO:0019058	0.847	0.357	2	64	viral life cycle	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0048284	0.847	0.356	2	66	organelle fusion	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0010718	0.847	0.453	1	21	positive regulation of epithelial to mesenchymal	BP	1	EZH2	down_ACOR_VSMC
GO:0021536	0.847	0.454	1	21	diencephalon development	BP	1	GLI1	down_ACOR_VSMC
GO:0006754	0.847	0.448	1	36	ATP biosynthetic process	BP	1	ATP5MC1	down_VCAV_EC
GO:0035150	0.847	0.448	1	36	regulation of tube size	BP	1	ADCY6	down_VCAV_EC
GO:0050880	0.847	0.448	1	36	regulation of blood vessel size	BP	1	ADCY6	down_VCAV_EC
GO:0003281	0.847	0.449	1	30	ventricular septum development	BP	1	LTBP1	down_VSAP_EC

GO:0006457	0.847	0.445	1	77	protein folding	BP	1	UNC45B	up_AFEM_EC
GO:0000380	0.847	0.453	1	22	alternative mRNA splicing, via spliceosome	BP	1	WTAP	up_VCAV_EC
GO:0003179	0.847	0.455	1	19	heart valve morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0048483	0.847	0.456	1	19	autonomic nervous system development	BP	1	PLXNA4	up_VSAP_EC
GO:0051251	0.847273974	0.44516	1	69	positive regulation of lymphocyte activation	BP	1	NOD2	up_ACOR_EC
GO:0043603	0.847311021	0.25594	7	372	cellular amide metabolic process	BP	1	NR1H4,PCSK1N,ENSCAFG00000028814,KLHL25,NIT2,PRKCD,PM20D1	up_ACOR_EC
GO:0035239	0.848	0.211	21	299	tube morphogenesis	BP	1	ELK3,MTDH,HOXA3,CAV1,TIMELESS,ANPEP,MMP14,GREM1,ADIPOR2,HOXA7,HOXB7,E2F8,B4GALT1,PRCP,NCL,EMP2,SGPL1,PHACTR4,JMJD6,NUS1,SIX4	down_ACOR_VSMC
GO:0044703	0.848	0.228	13	172	multi-organism reproductive process	BP	1	HOXA11,THRB,HOXA9,EMP2,ZNF449,HERPUD2,ZBTB16,RECK,PATZ1,CFAP69,KDM2B,HPGD,CITED2	up_VSAP_EC
GO:0042176	0.848	0.243	9	140	regulation of protein catabolic process	BP	1	NEDD4,PSMD3,SLC29A1,SMARCC1,PLK3,DTL,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0080135	0.848	0.242	9	240	regulation of cellular response to stress	BP	1	BMPR1A,TMEM161A,THY1,PARK7,SASH1,FUT8,SPRED1,FBH1,RGMA	down_VCAV_EC
GO:0051260	0.848	0.265	6	100	protein homooligomerization	BP	1	PRMT1,CAV1,TK1,B4GALT1,SIGMAR1,CTH	down_ACOR_VSMC
GO:0032271	0.848	0.278	5	73	regulation of protein polymerization	BP	1	TUBB4A,JMY,EVL,PRKCE,WASL	up_ACOR_VSMC
GO:0051301	0.848	0.291	4	117	cell division	BP	1	SNX18,NUMBL,ANXA11,ZBTB16	down_VCAV_EC
GO:0009953	0.848	0.359	2	34	dorsal/ventral pattern formation	BP	1	HOXA11,LRP4	up_VSAP_EC
GO:0042136	0.848	0.451	1	21	neurotransmitter biosynthetic process	BP	1	CAV1	down_ACOR_VSMC
GO:0032623	0.848	0.452	1	21	interleukin-2 production	BP	1	EZR	down_ACOR_VSMC
GO:0001763	0.848	0.444	1	78	morphogenesis of a branching structure	BP	1	GREM1	up_AFEM_EC
GO:0045732	0.848	0.443	1	78	positive regulation of protein catabolic process	BP	1	RAB7A	up_AFEM_EC
GO:0090068	0.848	0.444	1	78	positive regulation of cell cycle process	BP	1	FAP	up_AFEM_EC
GO:1905954	0.848	0.454	1	19	positive regulation of lipid localization	BP	1	ACACB	up_VSAP_EC
GO:0032774	0.849	0.18	94	1073	RNA biosynthetic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,ICE1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,CDK9,NR2F6,PRMT2,KDM2B,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:1902679	0.849	0.203	27	329	negative regulation of RNA biosynthetic process	BP	1	LEP,NACC2,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,ZNF174,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:1903507	0.849	0.203	27	329	negative regulation of nucleic acid-templated transcription	BP	1	LEP,NACC2,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,ZNF174,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:1901699	0.849	0.233	11	164	cellular response to nitrogen compound	BP	1	SREBF1,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,PDXP,EZR,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0010821	0.849	0.316	3	49	regulation of mitochondrion	BP	1	PPARGC1A,MARCH5,BNIP3	up_ACOR_VSMC
GO:0018394	0.849	0.316	3	55	peptidyl-lysine acetylation	BP	1	IWS1,GATA3,ESCO1	up_VCAV_EC
GO:0030522	0.849	0.353	2	67	intracellular receptor signaling pathway	BP	1	KANK2,PARK7	down_VCAV_EC

GO:0071887	0.849	0.357	2	34	leukocyte apoptotic process	BP	1	BMP4,CD274	up_ACOR_VSMC
GO:0009100	0.849	0.351	2	139	glycoprotein metabolic process	BP	1	XYLT1,CSGALNACT2	up_AFEM_EC
GO:1903169	0.849	0.358	2	34	regulation of calcium ion transmembrane transport	BP	1	ABL1,CYBA	up_VSAP_EC
GO:0014812	0.849	0.449	1	21	muscle cell migration	BP	1	SIX4	down_ACOR_VSMC
GO:0043967	0.849	0.45	1	21	histone H4 acetylation	BP	1	DMAP1	down_ACOR_VSMC
GO:2000736	0.849	0.45	1	21	regulation of stem cell differentiation	BP	1	HSPA9	down_ACOR_VSMC
GO:0035305	0.849	0.444	1	37	negative regulation of dephosphorylation	BP	1	SPRED1	down_VCAV_EC
GO:0048024	0.849	0.447	1	30	regulation of mRNA splicing, via spliceosome	BP	1	REST	down_VSAP_EC
GO:0002063	0.849	0.452	1	18	chondrocyte development	BP	1	FGF18	up_ACOR_VSMC
GO:0002757	0.849	0.441	1	78	immune response-activating signal	BP	1	CYLD	up_AFEM_EC
GO:0061136	0.849	0.441	1	78	regulation of proteasomal protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:1903532	0.849	0.442	1	78	positive regulation of secretion by cell	BP	1	RAB7A	up_AFEM_EC
GO:0000271	0.849	0.45	1	22	polysaccharide biosynthetic process	BP	1	PDGFB	up_VCAV_EC
GO:0002637	0.849	0.451	1	20	regulation of immunoglobulin	BP	1	THOC1	up_VCAV_EC
GO:0043933	0.849	0.452	1	698	protein-containing complex subunit	BP	1	FBP1	up_VFEM_VSMC
GO:0042886	0.849	0.448	1	527	amide transport	BP	1	NR1H4	up_VPUL_EC
GO:0051173	0.849	0.458	1	874	positive regulation of nitrogen compound	BP	1	GATA5	up_VPUL_VSMC
GO:1905268	0.849	0.452	1	20	negative regulation of chromatin organization	BP	1	PHF1	up_VSAP_EC
GO:0009059	0.849295556	0.19809	36	1563	macromolecule biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,PKNOX2,GALNT5,PORCN,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,PIGS,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0055080	0.849781519	0.31061	3	176	cation homeostasis	BP	1	PTH1R,SLC9A9,TMTC2	up_ACOR_EC
GO:0051171	0.85	0.173	153	1697	regulation of nitrogen compound metabolic process	BP	1	ADRA1B,TLR1,SMAD6,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MEIS2,MBP,FBXL20,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ISG15,ZNF782,ZNF365,AR,ZNF484,SASH1,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,CDKN2B,CST3,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,NPNT,OS9,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,SH3RF1,PRKCE,CCNT1,FRS2,RNF19A,CCPG1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,MXI1,CHD7,JUP,TLE4,SPINK2,ZNF432,CCL5,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,OXR1,RNF141,AKTIP,DUSP26,CBX7,NOD2,LRRC4,ARID5B,FAM107A,ZNF629,PRKAG3,ZFP3,DDIT4,ENSCAFG00000018360,DISC1,SH3RF3,DCUN1D4,KLF11,HERPUD1,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,WDR48,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,Z	up_ACOR_VSMC
GO:0008152	0.85	0.22	27	3714	metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,HOXA3,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,ABHD5,FAM135A,RRP15,KLHL28,PUM3,TMEM68,EIF5,CCAR1,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC

GO:0045935	0.85	0.21	20	491	positive regulation of nucleobase-containing compound metabolic process	BP	1	DCN,LUM,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TMEM161A,TEAD1,GLI3,PARK7,ZFP36L1,MYDGF,MAVS,MAPRE3,SHC1,GREM1,THRB,ZBTB16	down_VCAV_EC
GO:0044248	0.85	0.225	13	691	cellular catabolic process	BP	1	LEP,CTSS,TENT5C,CLEC16A,CYLD,MOXD1,RAB7A,AXIN2,ACACB,CTIF,FAP,SAMD4B,RNF181	up_AFEM_EC
GO:0009987	0.85	0.319	9	5086	cellular process	BP	1	HOXA3,TBX5,GATA5,TMEM176A,TMEM176B,IL22RA1,PHEX,HOXB5,SLIT2	up_VPUL_VSMC
GO:0014706	0.85	0.246	8	112	striated muscle tissue development	BP	1	CDON,DLL1,SAV1,GTF3C5,SHOX2,FLOT1,NPRL3,CITED2	up_VSAP_EC
GO:0072006	0.85	0.291	4	59	nephron development	BP	1	BMP4,CLSTN1,NPNT,NID1	up_ACOR_VSMC
GO:0031123	0.85	0.315	3	48	RNA 3'-end processing	BP	1	EXOSC7,ZFP36L1,CDK9	up_VSAP_EC
GO:0006612	0.85	0.356	2	35	protein targeting to membrane	BP	1	TCAF1,INPP5K	up_ACOR_VSMC
GO:0022406	0.85	0.355	2	35	membrane docking	BP	1	STX11,BVES	up_ACOR_VSMC
GO:0006091	0.85	0.349	2	139	generation of precursor metabolites and energy	BP	1	LEP,PPARGC1A	up_AFEM_EC
GO:0009056	0.85	0.358	2	755	catabolic process	BP	1	TRIM9,CYP26B1	up_VFEM_EC
GO:0071674	0.85	0.448	1	23	mononuclear cell migration	BP	1	HMGB1	down_ACOR_VSMC
GO:0002065	0.85	0.442	1	37	columnar/cuboidal epithelial cell	BP	1	CDH2	down_VCAV_EC
GO:0060759	0.85	0.442	1	37	regulation of response to cytokine stimulus	BP	1	MAVS	down_VCAV_EC
GO:0006984	0.85	0.449	1	19	ER-nucleus signaling pathway	BP	1	WFS1	up_ACOR_VSMC
GO:0048194	0.85	0.451	1	18	Golgi vesicle budding	BP	1	SEC24B	up_ACOR_VSMC
GO:0006469	0.85	0.44	1	78	negative regulation of protein kinase activity	BP	1	LRRC15	up_AFEM_EC
GO:1905515	0.85	0.448	1	22	non-motile cilium assembly	BP	1	EXOC5	up_VCAV_EC
GO:0006270	0.85	0.449	1	19	DNA replication initiation	BP	1	CIZ1	up_VSAP_EC
GO:0072210	0.85	0.449	1	19	metanephric nephron development	BP	1	OSR1	up_VSAP_EC
GO:0006366	0.851	0.188	49	583	transcription by RNA polymerase II	BP	1	FZD1,THRB,HOXA7,HOXA9,CDON,INSIG2,ZNF367,PPARGC1B,ZHX3,HOXD3,ABL1,PEX2,HDAC7,DLL1,OSR1,KLF15,ANXA4,RARG,CBX7,STAT6,F2RL1,RBL2,GLIS2,ICE1,PIK3R1,BATF2,MYC,SSBP2,ZEB1,SHOX2,IKZF2,TFE3,LRP4,TRERF1,NPAS2,CDK9,KDM2B,RAF1,NFIB,ABHD14B,ZNF205,NCOA2,SMARCA2,ACVRL1,PPP3CB,NCK1,MAVS,HMOX1,CITED2	up_VSAP_EC
GO:0040011	0.851	0.193	37	505	locomotion	BP	1	FSCN1,HMGB1,ANLN,FMNL3,RACGAP1,NEDD4,SDC1,FBXO5,B3GNT2,CAV1,MMP14,GREM1,TRIM35,HOXA7,B4GALT1,PRCP,PPARD,RAP2C,RAC1,EMP2,NUP188,HMGB2,SMC3,CORO1A,SGPL1,PHACTR4,ASPM,ENSCAFG00000010224,ITGA2,ARHGEF2,TWIST2,NUS1,AMOTL1,SIX4,DEPDC1B,TTLL1,PIK3CD	down_ACOR_VSMC
GO:0000122	0.851	0.214	17	218	negative regulation of transcription by RNA polymerase II	BP	1	THRB,HOXA7,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,SHOX2,IKZF2,KDM2B,NFIB,ZNF205,NCOA2,NCK1	up_VSAP_EC
GO:0030595	0.851	0.313	3	57	leukocyte chemotaxis	BP	1	HMGB1,RAC1,CORO1A	down_ACOR_VSMC
GO:0012501	0.851	0.312	3	561	programmed cell death	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0035966	0.851	0.313	3	47	response to topologically incorrect protein	BP	1	PIK3R1,CREBRF,NCK1	up_VSAP_EC
GO:1902117	0.851	0.355	2	32	positive regulation of organelle assembly	BP	1	EDN1,ASAP1	up_ACOR_VSMC
GO:0042176	0.851	0.347	2	140	regulation of protein catabolic process	BP	1	CLEC16A,RAB7A	up_AFEM_EC
GO:0008630	0.851	0.353	2	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	USP28,SKIL	up_VCAV_EC
GO:0006396	0.851	0.442	1	368	RNA processing	BP	1	WDR12	down_ACOR_EC
GO:0030239	0.851	0.447	1	21	myofibril assembly	BP	1	SIX4	down_ACOR_VSMC
GO:0043500	0.851	0.447	1	21	muscle adaptation	BP	1	EZH2	down_ACOR_VSMC

GO:0016571	0.851	0.44	1	39	histone methylation	BP	1	PRMT6	down_VCAV_EC
GO:0048585	0.851	0.443	1	475	negative regulation of response to stimulus	BP	1	NR1H4	up_APUL_EC
GO:0019083	0.851	0.448	1	19	viral transcription	BP	1	MON1B	up_VSAP_EC
GO:0030166	0.851	0.448	1	19	proteoglycan biosynthetic process	BP	1	CHST7	up_VSAP_EC
GO:1903078	0.851	0.448	1	19	positive regulation of protein localization to	BP	1	STX4	up_VSAP_EC
GO:0018130	0.852	0.181	69	1261	heterocycle biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,PGK1,TPI1,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,NMNAT2,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A,CMPK1	down_VSAP_EC
GO:0043632	0.852	0.211	18	262	modification-dependent macromolecule catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C	down_ACOR_VSMC
GO:0048589	0.852	0.237	9	188	developmental growth	BP	1	CELF1,PTPN11,IFRD1,TMED2,ZPR1,CTNNB1,WWC3,SIX4,NRP1	down_VSAP_EC
GO:0009123	0.852	0.251	7	104	nucleoside monophosphate	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7	up_ACOR_VSMC
GO:0006936	0.852	0.272	5	74	muscle contraction	BP	1	TPCN2,KCNE3,CHRM1,TBXA2R,SULF2	up_VSAP_EC
GO:0043270	0.852	0.31	3	56	positive regulation of ion transport	BP	1	PRELID1,CAV1,GSTO1	down_ACOR_VSMC
GO:0050769	0.852	0.308	3	95	positive regulation of neurogenesis	BP	1	TRPV2,NUMBL,GLI3	down_VCAV_EC
GO:0006839	0.852	0.309	3	86	mitochondrial transport	BP	1	SLC25A16,BNIP3,SH3GLB1	down_VSAP_EC
GO:0031497	0.852	0.311	3	49	chromatin assembly	BP	1	ATRX,TSPYL5,SHPRH	up_ACOR_VSMC
GO:0140053	0.852	0.312	3	47	mitochondrial gene expression	BP	1	PPARGC1B,RPUSD4,LARS2	up_VSAP_EC
GO:0046425	0.852	0.351	2	39	regulation of JAK-STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0072329	0.852	0.352	2	34	monocarboxylic acid catabolic process	BP	1	LEP,ACAD11	up_ACOR_VSMC
GO:0090101	0.852	0.352	2	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SMAD6,TBX20	up_ACOR_VSMC
GO:0090101	0.852	0.352	2	34	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FZD1,ABL1	up_VSAP_EC
GO:0016574	0.852	0.445	1	21	histone ubiquitination	BP	1	UHRF1	down_ACOR_VSMC
GO:0006813	0.852	0.439	1	37	potassium ion transport	BP	1	PRNP	down_VCAV_EC
GO:0002181	0.852	0.439	1	35	cytoplasmic translation	BP	1	AARS	down_VSAP_EC
GO:0015718	0.852	0.441	1	30	monocarboxylic acid transport	BP	1	APOE	down_VSAP_EC
GO:0051973	0.852	0.446	1	19	positive regulation of telomerase activity	BP	1	HMBOX1	up_ACOR_VSMC
GO:0033554	0.852	0.448	1	708	cellular response to stress	BP	1	ANKRD6	up_VPOR_VSMC
GO:0010628	0.852	0.443	1	527	positive regulation of gene expression	BP	1	ARHGEF2	up_VPUL_EC
GO:0045184	0.852	0.443	1	532	establishment of protein localization	BP	1	NR1H4	up_VPUL_EC
GO:0031644	0.852	0.445	1	19	regulation of neurological system process	BP	1	WASF3	up_VSAP_EC
GO:0070534	0.852	0.445	1	19	protein K63-linked ubiquitination	BP	1	SASH1	up_VSAP_EC

GO:0044271	0.853	0.181	68	1501	cellular nitrogen compound biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,ADCY6,LARP6,KANK2,COA1,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,VDR,PRMT6,UROS,ENTPD3,ATP5MC1,CXXC5,EIF3K,TEAD1,ADK,MRPL37,CC2D1A,GLI3,PARK7,RPL27A,EEF2,ZFP36L1,MYDGF,RPL27,AMPD2,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,ENSCAFG00000015122,PYM1,CRCP,GREM1,FOXO3,THRB,ZBTB16,EIF4EBP1,RGMA,ACAT1	down_VCAV_EC
GO:0042886	0.853	0.191	37	527	amide transport	BP	1	HCLS1,GBP5,TMEM173,IWS1,FERMT1,CHD7,TLR4,GATA3,EDN1,RAB11A,RAB27A,EXOC6,PPP3CA,ARG2,HHEX,SCAMP1,ABCA1,SNX2,THOC1,AKAP12,APOD,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,MCU,HIF1A,IPO11,LMTK2,RABGAP1,USP6NL	up_VCAV_EC
GO:0051338	0.853	0.203	23	288	regulation of transferase activity	BP	1	MAP3K14,ARHGEF5,CEP85,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,CAMKK2,AMBRA1,RBL2,DDR2,TRAF7,PIK3R1,PIK3IP1,RTN4RL1,SASH1,FBXO7,ZER1,MAP2K2,TGFBR2,LATS2	up_VSAP_EC
GO:0018209	0.853	0.242	8	125	peptidyl-serine modification	BP	1	SLC29A1,CAV1,CDK1,AURKB,CDK2,CLSPN,TTK,MAST2	down_ACOR_VSMC
GO:0007517	0.853	0.258	6	100	muscle organ development	BP	1	FLNB,CAV1,GREM1,GLI1,MSC,SIX4	down_ACOR_VSMC
GO:0071214	0.853	0.306	3	93	cellular response to abiotic stimulus	BP	1	AKT2,TMEM161A,ZFP36L1	down_VCAV_EC
GO:0104004	0.853	0.306	3	93	cellular response to environmental stimulus	BP	1	AKT2,TMEM161A,ZFP36L1	down_VCAV_EC
GO:0071417	0.853	0.344	2	142	cellular response to organonitrogen	BP	1	CAMK2A,KANK1	up_AFEM_EC
GO:0006810	0.853	0.359	2	1244	transport	BP	1	NETO1,SLC16A12	up_VFEM_VSMC
GO:0032835	0.853	0.443	1	21	glomerulus development	BP	1	IQGAP1	down_ACOR_VSMC
GO:0046128	0.853	0.441	1	23	purine ribonucleoside metabolic process	BP	1	RAN	down_ACOR_VSMC
GO:2001238	0.853	0.442	1	23	positive regulation of extrinsic apoptotic	BP	1	CAV1	down_ACOR_VSMC
GO:0019935	0.853	0.437	1	38	cyclic-nucleotide-mediated signaling	BP	1	ADCY6	down_VCAV_EC
GO:0008277	0.853	0.438	1	31	regulation of G protein-coupled receptor signaling	BP	1	RGS2	down_VSAP_EC
GO:0043628	0.853	0.443	1	19	ncRNA 3'-end processing	BP	1	EXOSC7	up_VSAP_EC
GO:0042100	0.853	0.444	1	19	B cell proliferation	BP	1	ABL1	up_VSAP_EC
GO:0055017	0.853	0.445	1	19	cardiac muscle tissue growth	BP	1	SAV1	up_VSAP_EC
GO:1902893	0.853	0.444	1	19	regulation of pri-miRNA transcription by RNA polymerase II	BP	1	NFIB	up_VSAP_EC
GO:0006913	0.853838012	0.34309	2	124	nucleocytoplasmic transport	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0051169	0.853838012	0.34309	2	124	nuclear transport	BP	1	MAVS,PRKCD	up_ACOR_EC
GO:0002573	0.853955177	0.43235	1	71	myeloid leukocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0007051	0.853984517	0.43235	1	70	spindle organization	BP	1	CHMP4B	up_ACOR_EC
GO:1901701	0.854	0.206	19	271	cellular response to oxygen-containing compound	BP	1	SREBF1,IRAK1,MTDH,BIRC5,INSIG1,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,PDXP,CACTIN,HMGB2,ENSCAFG00000005299,EZR,SIGMAR1,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0070647	0.854	0.214	15	311	protein modification by small protein conjugation or removal	BP	1	PRICKLE1,HSPA5,SOCS5,WSB1,TRIB3,USP12,NXN,UCHL5,SPOPL,USP48,UBA5,BACH1,CUL2,SH3RF3,USP14	down_VSAP_EC
GO:2000147	0.854	0.227	11	169	positive regulation of cell motility	BP	1	HMGB1,FBXO5,CAV1,MMP14,RAC1,CORO1A,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0051247	0.854	0.235	9	502	positive regulation of protein metabolic process	BP	1	LEP,PRR16,F3,GREM1,DCUN1D3,RAB7A,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0002237	0.854	0.268	5	85	response to molecule of bacterial origin	BP	1	IRAK1,MTDH,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0045931	0.854	0.308	3	49	positive regulation of mitotic cell cycle	BP	1	CDC7,APP,EDN1	up_ACOR_VSMC

GO:1903707	0.854	0.308	3	48	negative regulation of hemopoiesis	BP	1	TMEM176B,TMEM176A,BMP4	up_ACOR_VSMC
GO:0008016	0.854	0.308	3	48	regulation of heart contraction	BP	1	THRB,IRX5,KCNE3	up_VSAP_EC
GO:0009791	0.854	0.347	2	38	post-embryonic development	BP	1	SGPL1,HMGN1	down_ACOR_VSMC
GO:0051896	0.854	0.347	2	39	regulation of protein kinase B signaling	BP	1	SLC29A1,MTDH	down_ACOR_VSMC
GO:0030073	0.854	0.347	2	42	insulin secretion	BP	1	MCU,HIF1A	up_VCAV_EC
GO:0097479	0.854	0.348	2	41	synaptic vesicle localization	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0071482	0.854	0.348	2	34	cellular response to light stimulus	BP	1	DDB2,PIK3R1	up_VSAP_EC
GO:1903578	0.854	0.44	1	22	regulation of ATP metabolic process	BP	1	CDK1	down_ACOR_VSMC
GO:0051246	0.854	0.446	1	832	regulation of protein metabolic process	BP	1	IVNS1ABP	down_AFEM_EC
GO:0048565	0.854	0.435	1	38	digestive tract development	BP	1	GLI3	down_VCAV_EC
GO:0010923	0.854	0.436	1	30	negative regulation of phosphatase activity	BP	1	ARFGEF3	down_VSAP_EC
GO:1903076	0.854	0.435	1	32	regulation of protein localization to plasma	BP	1	KIF5B	down_VSAP_EC
GO:0034330	0.854	0.432	1	80	cell junction organization	BP	1	GREM1	up_AFEM_EC
GO:0061035	0.854	0.438	1	24	regulation of cartilage development	BP	1	BMP2	up_VCAV_EC
GO:0010243	0.854	0.433	1	238	response to organonitrogen	BP	1	ARHGEF2	up_VPOR_EC
GO:0033619	0.854	0.443	1	19	membrane protein proteolysis	BP	1	TIMP2	up_VSAP_EC
GO:0030258	0.854451074	0.4314	1	71	lipid modification	BP	1	ENSCAFG00000004331	up_ACOR_EC
GO:0051783	0.854570148	0.43112	1	72	regulation of nuclear division	BP	1	CHMP4B	up_ACOR_EC
GO:0045935	0.855	0.186	42	491	positive regulation of nucleobase-containing compound metabolic process	BP	1	SMAD6,LBH,GATA5,GATA4,CDC7,PCGF5,MLLT3,BMP4,FGFR2,TP53BP1,ATRX,MED14,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,AR,LMO4,PLAC8B,F2RL1,EGLN1,CRLF3,NPNT,SMARCD3,CCNT1,CCPG1,PARP9,CHD6,APP,PSEN1,TGFBR1,CHD7,EDN1,NOD2,RPRD1B,INPP5K,ZKSCAN1,PARK7,TEAD1,HMBOX1,SSBP2	up_ACOR_VSMC
GO:0010558	0.855	0.191	32	392	negative regulation of macromolecule biosynthetic process	BP	1	FZD1,THRB,HOXA7,WNT11,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,ZFP36L1,SHOX2,H2AFJ,IKZF2,PASK,ANKHD1,LIMD1,PRMT2,KDM2B,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1	up_VSAP_EC
GO:0006897	0.855	0.228	10	158	endocytosis	BP	1	HMGB1,NEDD4,ARFGAP1,CAV1,GREM1,TFRC,HIST1H1A,EZR,CORO1A,JMJD6	down_ACOR_VSMC
GO:0018209	0.855	0.234	9	125	peptidyl-serine modification	BP	1	CAMKK2,TNKS1BP1,MORC3,RAF1,NCK1,ULK1,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0050804	0.855	0.255	6	87	modulation of chemical synaptic transmission	BP	1	FAM107A,ABL1,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0099177	0.855	0.255	6	87	regulation of trans-synaptic signaling	BP	1	FAM107A,ABL1,KCNB1,STX4,KCNC4,FLOT1	up_VSAP_EC
GO:0070507	0.855	0.268	5	73	regulation of microtubule cytoskeleton organization	BP	1	FGF13,MID1,PRKAA2,TUBB4A,FAM107A	up_ACOR_VSMC
GO:0043436	0.855	0.264	5	303	oxoacid metabolic process	BP	1	LEP,XYLT1,GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0043903	0.855	0.284	4	61	regulation of symbiosis, encompassing mutualism through parasitism	BP	1	F2RL1,MYD88,PC,MAVS	up_VSAP_EC
GO:0051716	0.855	0.328	3	2001	cellular response to stimulus	BP	1	GPSM2,IVNS1ABP,GABPA	down_AFEM_EC
GO:0051179	0.855	0.321	3	1747	localization	BP	1	NETO1,SLC16A12,EMX2	up_VFEM_VSMC
GO:0050866	0.855	0.307	3	48	negative regulation of cell activation	BP	1	CD274,TBC1D10C,FBXO7	up_VSAP_EC
GO:0034614	0.855	0.346	2	39	cellular response to reactive oxygen species	BP	1	EZH2,SIGMAR1	down_ACOR_VSMC
GO:0050890	0.855	0.342	2	67	cognition	BP	1	PRNP,BRSK1	down_VCAV_EC
GO:0034728	0.855	0.343	2	56	nucleosome organization	BP	1	SMARCA4,BRD2	down_VSAP_EC
GO:0030641	0.855	0.348	2	34	regulation of cellular pH	BP	1	SLC26A7,DMXL1	up_ACOR_VSMC

GO:1990138	0.855	0.346	2	35	neuron projection extension	BP	1	IFRD1,RAB11A	up_VCAV_EC
GO:0042752	0.855	0.348	2	34	regulation of circadian rhythm	BP	1	CHRM1,NR2F6	up_VSAP_EC
GO:0031325	0.855	0.445	1	914	positive regulation of cellular metabolic process	BP	1	CITED2	down_VPOR_EC
GO:0008333	0.855	0.44	1	19	endosome to lysosome transport	BP	1	AKTIP	up_ACOR_VSMC
GO:0009056	0.855	0.441	1	755	catabolic process	BP	1	LNPEP	up_AORT_EC
GO:0099175	0.855	0.44	1	21	regulation of postsynapse organization	BP	1	RELN	up_VCAV_EC
GO:0043412	0.855	0.453	1	1225	macromolecule modification	BP	1	LIMK1	up_VCAV_VSMC
GO:0032456	0.855	0.44	1	19	endocytic recycling	BP	1	RAB11B	up_VSAP_EC
GO:0009892	0.856	0.176	72	835	negative regulation of metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,INSIG2,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,SLIT2,CST3,ZHX3,ABL1,PEX2,HDAC7,OSR1,TENT5C,KLF15,RARG,CBX7,STAT6,RECK,PLPP3,ENSCAFG00000000071,EXOSC7,PYM1,F2RL1,RBL2,GLIS2,ZFP36L1,GAS1,MYC,PIK3IP1,SHOX2,TMEM225B,H2AFJ,ZC3H10,RTN4RL1,HOXC10,POLDIP2,IKZF2,PASK,ANKHD1,AZIN2,PHF1,SMG9,FBXO7,LIMD1,PC,CDK9,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ACVRL1,UBQLN2,HTRA2,TNRC6C,NCK1,HMOX1,BAG4,DDIT4,LATS2	up_VSAP_EC
GO:0043161	0.856	0.223	11	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	UBE2S,PSMD7,SLC29A1,SMARCC1,PLK3,UBE2J2,UBE2K,RAD23A,CDC20,PSMC1,UBE2C	down_ACOR_VSMC
GO:0009611	0.856	0.233	9	122	response to wounding	BP	1	LGR6,DCBLD2,LNPK,GJA1,F2RL1,ENPP4,PRKCE,NMNAT1,RREB1	up_ACOR_VSMC
GO:0006807	0.856	0.258	9	3221	nitrogen compound metabolic process	BP	1	NR1H4,STK32B,ENSCAFG00000028814,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0051962	0.856	0.246	7	112	positive regulation of nervous system	BP	1	SRRT,BEND6,CDC20,ASPM,ARHGEF2,GLI1,TPBG	down_ACOR_VSMC
GO:0034641	0.856	0.328	3	2171	cellular nitrogen compound metabolic	BP	1	HDAC7,CITED2,TBX15	down_VPOR_EC
GO:0031326	0.856	0.313	3	1176	regulation of cellular biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0046677	0.856	0.343	2	54	response to antibiotic	BP	1	CRYAB,KPNA4	down_VSAP_EC
GO:0044070	0.856	0.436	1	22	regulation of anion transport	BP	1	PRELID1	down_ACOR_VSMC
GO:1990266	0.856	0.435	1	24	neutrophil migration	BP	1	RAC1	down_ACOR_VSMC
GO:0071901	0.856	0.431	1	37	negative regulation of protein serine/threonine	BP	1	SPRED1	down_VCAV_EC
GO:2000278	0.856	0.43	1	37	regulation of DNA biosynthetic process	BP	1	GREM1	down_VCAV_EC
GO:0046632	0.856	0.433	1	29	alpha-beta T cell differentiation	BP	1	SOCS5	down_VSAP_EC
GO:0072210	0.856	0.438	1	19	metanephric nephron development	BP	1	BMP4	up_ACOR_VSMC
GO:0002764	0.856	0.428	1	80	immune response-regulating signaling	BP	1	CYLD	up_AFEM_EC
GO:0007260	0.856	0.437	1	19	tyrosine phosphorylation of STAT protein	BP	1	IL6R	up_VSAP_EC

GO:0051171	0.857	0.166	152	1697	regulation of nitrogen compound metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,TBC1D10C,CEP85,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,CBX7,STAT6,RECK,GATAD1,PLPP3,ENSCAFG00000000071,CAMKK2,TNKS1BP1,PYM1,F2RL1,RBL2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,CLYBL,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,ANKHD1,AZIN2,TRERF1,PHF1,E2F4,NPAS2,FBXO7,LIMD1,RNF166,RPUSD4,CDK9,PRMT2,KDM2B,FBLN1,OSBPL7,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,PQBP1,TIMP2,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,UBQLN2,ZNF517,HTRA2,ASS1,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,ZER1,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,KEAP1,DDIT4,ZNF772,SOAT1,LATS2	up_VSAP_EC
GO:0044267	0.857	0.166	140	1583	cellular protein metabolic process	BP	1	FGF13,ADRA1B,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MBP,ZRANB1,RECK,LIPT2,B3GALNT2,SKP2,PRKAA2,BMP4,B3GNT7,FGFR2,CCDC126,ABCA1,EIF4A2,ATRX,TARSL2,TLR3,SH3RF2,LATS2,PIGN,PDE5A,PIGS,ISG15,ZNRF3,SASH1,CTSS,PTPN3,FGF18,NDRG2,TMX3,CDKN2B,USP53,GRK7,CST3,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,ERO1B,DAPK1,CTSB,RBM4B,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,NRP1,UBR1,PTPN22,ULK2,DMPK,NPNT,OS9,STT3B,SMPD1,FUT11,UBE2H,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,FRS2,RNF19A,LYPLAL1,DAG1,FUT8,POMK,PARP9,APP,PSEN1,SYNJ2BP,SHPRH,PIK3C3,LAMP2,SPINK2,CCL5,DDR2,CLN8,PERP,PSKH1,DUSP22,SIAH1,EDN1,OXR1,RNF141,PHF20,AKTIP,CTSF,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PCYOX1,PRKAG3,DISC1,SH3RF3,EOGT,DCUN1D4,RNF181,USP20,HERPUD1,RPRD1B,MAP3K7,INPP5K,FAF2,CNOT4,KLHDC8B,WFS1,UBA52,KLHL36,WDR48,CTIF,DZIP3,ENSCAFG00000029553,PARK7,NGRN,ZDHHC21,LMF1,CRKL,CDKL2	up_ACOR_VSMC
GO:0009890	0.857	0.187	35	420	negative regulation of biosynthetic process	BP	1	LEP,NACC2,ITM2C,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,AR,ZNF174,ANKRD1,DAPK1,ENSCAFG00000006238,CLSTN1,ORMDL3,TBX20,DKKL1,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,DDIT4,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,PARK7,HMBOX1,RREB1	up_ACOR_VSMC
GO:0043436	0.857	0.196	24	303	oxoacid metabolic process	BP	1	LEP,ENOSF1,PRDX4,ENSCAFG00000002977,TARSL2,PPARGC1A,NIT2,ACAD11,ERO1B,EGLN1,CYP2J2,P4HA1,PRKCE,SARDH,SGSM2,EDN1,ALDOC,HPGD,PCYOX1,DDIT4,AZIN2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0034097	0.857	0.208	16	238	response to cytokine	BP	1	FLNB,IRAK1,SLC29A1,SLC25A5,B3GNT2,CAV1,ADIPOR2,CDK4,TFRC,NCL,CACTIN,CDC42EP4,CORO1A,CTH,ARHGEF2,MSC	down_ACOR_VSMC
GO:0043161	0.857	0.215	13	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	FOXRED2,ABTB1,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,RNF166,RNF216,UBQLN2,CDC26,KEAP1	up_VSAP_EC
GO:0006839	0.857	0.279	4	86	mitochondrial transport	BP	1	SH3GLB1,SLC25A25,PMAIP1,MCU	up_VCAV_EC
GO:0007596	0.857	0.304	3	47	blood coagulation	BP	1	LNPK,F2RL1,ENPP4	up_ACOR_VSMC
GO:0002062	0.857	0.303	3	48	chondrocyte differentiation	BP	1	BMP4,LNPK,FGF18	up_ACOR_VSMC
GO:0002793	0.857	0.341	2	54	positive regulation of peptide secretion	BP	1	NR1H4,HIF1A	down_VSAP_EC
GO:0050714	0.857	0.341	2	54	positive regulation of protein secretion	BP	1	NR1H4,HIF1A	down_VSAP_EC

GO:0062014	0.857	0.344	2	35	negative regulation of small molecule metabolic	BP	1	DKKL1,DDIT4	up_ACOR_VSMC
GO:0007269	0.857	0.344	2	34	neurotransmitter secretion	BP	1	STX4,KCNC4	up_VSAP_EC
GO:0018022	0.857	0.344	2	36	peptidyl-lysine methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:0050851	0.857	0.344	2	34	antigen receptor-mediated signaling	BP	1	ABL1,RBCK1	up_VSAP_EC
GO:0099643	0.857	0.344	2	34	signal release from synapse	BP	1	STX4,KCNC4	up_VSAP_EC
GO:0000271	0.857	0.433	1	22	polysaccharide biosynthetic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:0043618	0.857	0.434	1	22	regulation of transcription from RNA polymerase II promoter in response to	BP	1	NEDD4	down_ACOR_VSMC
GO:0043631	0.857	0.436	1	21	RNA polyadenylation	BP	1	WDR33	down_ACOR_VSMC
GO:0010604	0.857	0.443	1	919	positive regulation of macromolecule metabolic	BP	1	CITED2	down_VPOR_EC
GO:0019083	0.857	0.436	1	19	viral transcription	BP	1	INPP5K	up_ACOR_VSMC
GO:0043331	0.857	0.435	1	20	response to dsRNA	BP	1	TLR3	up_ACOR_VSMC
GO:0008088	0.857	0.435	1	21	axo-dendritic transport	BP	1	HIF1A	up_VCAV_EC
GO:0048640	0.857	0.436	1	21	negative regulation of developmental growth	BP	1	IFRD1	up_VCAV_EC
GO:0034654	0.857	0.451	1	1236	nucleobase-containing compound biosynthetic	BP	1	GATA5	up_VCAV_VSMC
GO:0061383	0.857	0.435	1	20	trabecula morphogenesis	BP	1	PPARGC1B	up_VSAP_EC
GO:0031346	0.857709702	0.42498	1	73	positive regulation of cell projection organization	BP	1	NRP1	up_ACOR_EC
GO:0009888	0.858	0.182	40	545	tissue development	BP	1	FLNB,HOXA3,CTDNEP1,FBXO5,NAB2,HNRNPH3,CAV1,CDK1,TIMELESS,NF2,MMP14,EZH2,GREM1,CDK4,PCNA,HOXA7,ARG2,HOXB7,DHCR24,POC1A,E2F8,B4GALT1,PPARD,RAP2C,PLK4,IQGAP1,HOXB5,EZR,TOX,HOXC4,NOLC1,PHACTR4,SLC20A1,ITGA2,SERPINH1,GLI1,MSC,SIX4,AMER1,ANXA7	down_ACOR_VSMC
GO:0044257	0.858	0.197	22	327	cellular protein catabolic process	BP	1	TNFAIP3,CTSC,WWP1,USP33,PSME4,PELI1,CASP8,ENC1,USP28,PMAIP1,RIPK1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0006875	0.858	0.235	8	129	cellular metal ion homeostasis	BP	1	HMGB1,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:1903362	0.858	0.243	7	100	regulation of cellular protein catabolic process	BP	1	SH3RF2,OS9,RNF19A,PSEN1,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0051603	0.858	0.26	5	305	proteolysis involved in cellular protein catabolic	BP	1	CTSS,CLEC16A,CYLD,FAP,RNF181	up_AFEM_EC
GO:0001837	0.858	0.302	3	48	epithelial to mesenchymal transition	BP	1	BMP4,DAG1,TGFBR1	up_ACOR_VSMC
GO:0043433	0.858	0.301	3	49	negative regulation of DNA-binding transcription factor activity	BP	1	EGLN1,CLSTN1,WFS1	up_ACOR_VSMC
GO:0007034	0.858	0.3	3	55	vacuolar transport	BP	1	HOOK3,GCC2,VPS54	up_VCAV_EC
GO:0032006	0.858	0.301	3	52	regulation of TOR signaling	BP	1	RELN,PREX2,HIF1A	up_VCAV_EC
GO:0007034	0.858	0.338	2	55	vacuolar transport	BP	1	HOOK3,TRAK1	down_VSAP_EC
GO:0018394	0.858	0.338	2	55	peptidyl-lysine acetylation	BP	1	IWS1,MORF4L2	down_VSAP_EC
GO:0033036	0.858	0.345	2	852	macromolecule localization	BP	1	NR1H4,NPNT	up_APUL_EC
GO:0009855	0.858	0.34	2	42	determination of bilateral symmetry	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0002706	0.858	0.341	2	35	regulation of lymphocyte mediated immunity	BP	1	STAT6,PPP3CB	up_VSAP_EC
GO:0010257	0.858	0.431	1	25	NADH dehydrogenase complex assembly	BP	1	FOXRED1	down_ACOR_VSMC
GO:0032642	0.858	0.433	1	22	regulation of chemokine production	BP	1	ARG2	down_ACOR_VSMC
GO:0032981	0.858	0.431	1	25	mitochondrial respiratory chain complex I assembly	BP	1	FOXRED1	down_ACOR_VSMC
GO:0033077	0.858	0.432	1	22	T cell differentiation in thymus	BP	1	JMJD6	down_ACOR_VSMC
GO:1905515	0.858	0.433	1	22	non-motile cilium assembly	BP	1	POC1A	down_ACOR_VSMC

GO:0010906	0.858	0.427	1	38	regulation of glucose metabolic process	BP	1	AKT2	down_VCAV_EC
GO:0043524	0.858	0.426	1	39	negative regulation of neuron apoptotic process	BP	1	PARK7	down_VCAV_EC
GO:0048813	0.858	0.427	1	39	dendrite morphogenesis	BP	1	TLX2	down_VCAV_EC
GO:0044774	0.858	0.43	1	30	mitotic DNA integrity checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0002204	0.858	0.436	1	18	somatic recombination of immunoglobulin genes involved in immune	BP	1	TP53BP1	up_ACOR_VSMC
GO:0002208	0.858	0.436	1	18	somatic diversification of immunoglobulins involved in immune response	BP	1	TP53BP1	up_ACOR_VSMC
GO:0045190	0.858	0.436	1	18	isotype switching	BP	1	TP53BP1	up_ACOR_VSMC
GO:0032886	0.858	0.424	1	81	regulation of microtubule-based process	BP	1	CYLD	up_AFEM_EC
GO:0006508	0.858	0.43	1	483	proteolysis	BP	1	PCSK1N	up_APUL_EC
GO:0031324	0.858	0.435	1	735	negative regulation of cellular metabolic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:0002709	0.858	0.434	1	19	regulation of T cell mediated immunity	BP	1	PPP3CB	up_VSAP_EC
GO:0045935	0.858922038	0.22316	10	491	positive regulation of nucleobase-containing compound metabolic	BP	1	GATA4,PKIB,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2,PRKCD	up_ACOR_EC
GO:0033036	0.859	0.171	74	852	macromolecule localization	BP	1	EXPH5,SH3TC2,FGF13,TLR1,ACTN2,LEP,MID1,HTR2B,TCAF1,USP6NL,MBP,NACC2,PRKAA2,FERMT1,BMP4,LCAT,EVI5L,TM7SF3,ABCA1,SCARB2,ATRX,SEC24B,LATS2,GLRB,CD274,AR,STX11,ANKRD1,F2RL1,MARCH5,APOL6,CDKN1A,ABCA4,NRP1,PTPN22,NPNT,OS9,SCP2,OSBPL1A,PRKCE,AGRN,SCG5,DAG1,PARP9,PSEN1,SGSM2,SYNJ2BP,PIK3C3,LAMP2,JUP,CCL5,RAB11B,NOD2,LRRC4,LMTK2,DISC1,AP2B1,PLIN2,SCAMP5,SAR1B,HERPUD1,CFI,SUN1,VPS26A,INPP5K,FAF2,RAB5C,PFKL,RPAIN,WASL,SH3BP4,PARK7,LMF1,PTPN14	up_ACOR_VSMC
GO:0044237	0.859	0.209	25	3491	cellular metabolic process	BP	1	BARX1,OSTC,CXHXorf57,OGA,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ASPN,ACVR2A,FBP1,MTDH,RSL24D1,RPL10L,ABHD5,FAM135A,RRP15,KLHL28,PUM3,EIF5,CCAR1,USP33,ENSCAFG00000032731,GNPNAT1,RNF6	up_VPOR_EC
GO:0006887	0.859	0.241	7	99	exocytosis	BP	1	F2RL1,RAB11B,SCFD2,STX4,VPS11,PPP3CB,RAB11FIP2	up_VSAP_EC
GO:0006399	0.859	0.25	6	87	tRNA metabolic process	BP	1	WARS2,EXOSC7,FARS2,RPUSD4,QARS,LARS2	up_VSAP_EC
GO:0006082	0.859	0.259	5	305	organic acid metabolic process	BP	1	LEP,XYLT1,GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0040029	0.859	0.298	3	74	regulation of gene expression, epigenetic	BP	1	MORF4L2,CTNNB1,CDYL	down_VSAP_EC
GO:0090305	0.859	0.3	3	49	nucleic acid phosphodiester bond	BP	1	EXOSC7,DFFB,RCL1	up_VSAP_EC
GO:0010634	0.859	0.336	2	68	positive regulation of epithelial cell migration	BP	1	GLIPR2,SASH1	down_VCAV_EC
GO:0044272	0.859	0.34	2	35	sulfur compound biosynthetic process	BP	1	MAT2B,ELOVL7	up_ACOR_VSMC
GO:0006733	0.859	0.338	2	45	oxidoreduction coenzyme metabolic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0032543	0.859	0.34	2	34	mitochondrial translation	BP	1	RPUSD4,LARS2	up_VSAP_EC
GO:0032204	0.859	0.34	2	35	regulation of telomere maintenance	BP	1	MYC,FBXO4	up_VSAP_EC
GO:0008217	0.859	0.426	1	38	regulation of blood pressure	BP	1	RNPEP	down_VCAV_EC
GO:0042147	0.859	0.426	1	38	retrograde transport, endosome to Golgi	BP	1	RAB7B	down_VCAV_EC
GO:0051668	0.859	0.425	1	39	localization within membrane	BP	1	CDH2	down_VCAV_EC
GO:0007031	0.859	0.432	1	20	peroxisome organization	BP	1	SCP2	up_ACOR_VSMC
GO:0070265	0.859	0.432	1	19	necrotic cell death	BP	1	TLR3	up_ACOR_VSMC
GO:0007018	0.859	0.422	1	82	microtubule-based movement	BP	1	KIF1A	up_AFEM_EC
GO:0045088	0.859	0.422	1	81	regulation of innate immune response	BP	1	LEP	up_AFEM_EC

GO:0010824	0.859	0.43	1	23	regulation of centrosome duplication	BP	1	PLK2	up_VCAV_EC
GO:0000165	0.859	0.423	1	236	MAPK cascade	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0016445	0.859	0.432	1	20	somatic diversification of immunoglobulins	BP	1	STAT6	up_VSAP_EC
GO:0016447	0.859	0.432	1	20	somatic recombination of immunoglobulin gene	BP	1	STAT6	up_VSAP_EC
GO:1903901	0.859	0.433	1	19	negative regulation of viral life cycle	BP	1	MAVS	up_VSAP_EC
GO:0045637	0.859001025	0.42246	1	73	regulation of myeloid cell differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0043085	0.859108768	0.24768	6	323	positive regulation of catalytic activity	BP	1	CDH3,PKIB,FZD5,DYNC1I1,PAK3,PRKCD	up_ACOR_EC
GO:0080090	0.86	0.162	156	1734	regulation of primary metabolic process	BP	1	ADRA1B,TLR1,SMAD6,LEP,PLCL1,LBH,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,MEIS2,MBP,FBXL20,RECK,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,SH3RF2,PPARGC1A,LATS2,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ISG15,ZNF782,ZNF365,AR,ZNF484,SASH1,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,CDKN2B,CST3,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NRP1,PTPN22,NPNT,OS9,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,SH3RF1,CCDC3,PRKCE,CCNT1,DKKL1,FRS2,RNF19A,CCPG1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,SYNJ2BP,MXI1,CHD7,JUP,TLE4,SPINK2,ZNF432,CCL5,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,OXR1,RNF141,AKTIP,DUSP26,CBX7,NOD2,LRRC4,ARID5B,FAM107A,ZNF629,PRKAG3,ZFP3,DDIT4,ENSCAFG00000018360,DISC1,SH3RF3,DCUN1D4,KLF11,HERPUD1,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,WDR48,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,T	up_ACOR_VSMC
GO:0070647	0.86	0.191	25	311	protein modification by small protein conjugation or removal	BP	1	FAM107A,ABL1,KLHL36,DTX2,DDB2,CISH,KLHL24,KLHDC8B,TRAF7,RBCK1,KBTBD12,RNF24,SASH1,FBXO4,RMND5A,FBXW5,FBXO7,ASB8,RNF166,CDK9,KDM2B,RNF216,CDC26,ZER1,KEAP1	up_VSAP_EC
GO:0060429	0.86	0.192	24	341	epithelium development	BP	1	FLNB,HNRNPH3,CAV1,CDK1,TIMELESS,NF2,MMP14,EZH2,GREM1,PCNA,HOXA7,ARG2,HOXB7,E2F8,B4GALT1,RAP2C,PLK4,IQGAP1,HOXB5,EZR,PHACTR4,GLI1,SIX4,ANXA7	down_ACOR_VSMC
GO:0006469	0.86	0.274	4	78	negative regulation of protein kinase activity	BP	1	TNFAIP3,HHEX,PREX2,SH3BP5	up_VCAV_EC
GO:0044782	0.86	0.295	3	96	cilium organization	BP	1	TTC8,IFT57,EVI5L	down_VCAV_EC
GO:0048232	0.86	0.295	3	95	male gamete generation	BP	1	ADAMTS2,MEA1,ZBTB16	down_VCAV_EC
GO:0009451	0.86	0.335	2	59	RNA modification	BP	1	AARS,MRPL1	down_VSAP_EC
GO:0033674	0.86	0.332	2	144	positive regulation of kinase activity	BP	1	LEP,ADAM17	up_AFEM_EC
GO:0008104	0.86	0.339	2	763	protein localization	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0035914	0.86	0.428	1	22	skeletal muscle cell differentiation	BP	1	SIX4	down_ACOR_VSMC
GO:0033036	0.86	0.434	1	852	macromolecule localization	BP	1	GPSM2	down_AFEM_EC
GO:0009062	0.86	0.425	1	31	fatty acid catabolic process	BP	1	SESN2	down_VSAP_EC
GO:0032008	0.86	0.43	1	19	positive regulation of TOR signaling	BP	1	LEP	up_ACOR_VSMC
GO:0032526	0.86	0.43	1	19	response to retinoic acid	BP	1	ABCA1	up_ACOR_VSMC
GO:0046426	0.86	0.43	1	20	negative regulation of JAK-STAT cascade	BP	1	LRRC4	up_ACOR_VSMC
GO:1904893	0.86	0.43	1	20	negative regulation of STAT cascade	BP	1	LRRC4	up_ACOR_VSMC
GO:0070192	0.86	0.429	1	20	chromosome organization involved in meiotic cell	BP	1	ATRX	up_VCAV_EC
GO:0008652	0.86	0.427	1	24	cellular amino acid biosynthetic process	BP	1	BCAT1	up_VCAV_EC

GO:1901607	0.86	0.427	1	24	alpha-amino acid biosynthetic process	BP	1	BCAT1	up_VCAV_EC
GO:0006810	0.86	0.445	1	1244	transport	BP	1	CA2	up_VCAV_VSMC
GO:1901565	0.86	0.424	1	442	organonitrogen compound catabolic	BP	1	TRIM9	up_VFEM_EC
GO:0010605	0.86	0.431	1	745	negative regulation of macromolecule metabolic	BP	1	SHOX2	up_VFEM_VSMC
GO:0065009	0.86	0.431	1	735	regulation of molecular function	BP	1	NETO1	up_VFEM_VSMC
GO:1901615	0.860575171	0.3314	2	128	organic hydroxy compound metabolic	BP	1	CDH3,NR1H4	up_ACOR_EC
GO:0098771	0.860722171	0.29307	3	180	inorganic ion homeostasis	BP	1	PTH1R,SLC9A9,TMTC2	up_ACOR_EC
GO:0048534	0.861	0.199	18	262	hematopoietic or lymphoid organ development	BP	1	HMGB1,ANLN,HOXA3,HSPA9,PRELID1,PRMT1,MMP14,HMGB3,HOXA7,PDCD2,HOXB7,TFRC,HMGB2,TOX,SGPL1,HOXA9,JMJD6,SIX4	down_ACOR_VSMC
GO:0022613	0.861	0.225	9	208	ribonucleoprotein complex biogenesis	BP	1	CELF1,MRPL1,PRPF3,DDX39B,CNOT7,PDCD11,STRAP,EIF2S1,RSL24D1	down_VSAP_EC
GO:0031401	0.861	0.246	6	358	positive regulation of protein modification	BP	1	LEP,GREM1,DCUN1D3,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:2001242	0.861	0.273	4	62	regulation of intrinsic apoptotic signaling	BP	1	ACKR3,PLEKHF1,PTPMT1,NCK1	up_VSAP_EC
GO:0007519	0.861	0.297	3	49	skeletal muscle tissue development	BP	1	CITED2,ANKRD1,BVES	up_ACOR_VSMC
GO:0090305	0.861	0.296	3	49	nucleic acid phosphodiester bond	BP	1	PNRC1,DCP1B,FAN1	up_ACOR_VSMC
GO:0017144	0.861	0.293	3	199	drug metabolic process	BP	1	ATP6V1B2,MOXD1,PPARGC1A	up_AFEM_EC
GO:0044085	0.861	0.303	3	1076	cellular component biogenesis	BP	1	TRIM9,SIX1,CDC42EP5	up_VFEM_EC
GO:0001666	0.861	0.333	2	67	response to hypoxia	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0036293	0.861	0.333	2	67	response to decreased oxygen levels	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0000956	0.861	0.333	2	55	nuclear-transcribed mRNA catabolic process	BP	1	SMG7,CNOT7	down_VSAP_EC
GO:0007626	0.861	0.334	2	53	locomotory behavior	BP	1	UBA6,APOE	down_VSAP_EC
GO:0007015	0.861	0.331	2	144	actin filament organization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0043410	0.861	0.331	2	144	positive regulation of MAPK cascade	BP	1	LEP,CCL5	up_AFEM_EC
GO:0033627	0.861	0.426	1	22	cell adhesion mediated by integrin	BP	1	ITGA2	down_ACOR_VSMC
GO:0030433	0.861	0.422	1	38	ubiquitin-dependent ERAD pathway	BP	1	SEC61B	down_VCAV_EC
GO:0048489	0.861	0.422	1	38	synaptic vesicle transport	BP	1	TMEM230	down_VCAV_EC
GO:0097480	0.861	0.422	1	38	establishment of synaptic vesicle localization	BP	1	TMEM230	down_VCAV_EC
GO:0019751	0.861	0.423	1	33	polyol metabolic process	BP	1	TPI1	down_VSAP_EC
GO:1901654	0.861	0.424	1	31	response to ketone	BP	1	MSN	down_VSAP_EC
GO:0010332	0.861	0.427	1	20	response to gamma radiation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0035987	0.861	0.43	1	17	endodermal cell differentiation	BP	1	LAMA3	up_ACOR_VSMC
GO:0033157	0.861	0.418	1	82	regulation of intracellular protein transport	BP	1	LEP	up_AFEM_EC
GO:0051188	0.861	0.419	1	81	cofactor biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0051702	0.861	0.426	1	24	interaction with symbiont	BP	1	SMARCA4	up_VCAV_EC
GO:0060393	0.861	0.429	1	19	regulation of pathway-restricted SMAD protein	BP	1	ACVRL1	up_VSAP_EC
GO:0034622	0.861265843	0.22978	8	421	cellular protein-containing complex assembly	BP	1	TMOD1,CALY,SOX9,SMAD6,PAK3,VPS16,PRKCD,TUBB4A	up_ACOR_EC

GO:0018130	0.862	0.164	111	1261	heterocycle biosynthetic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,ENSCAFG00000013986,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,PDK2,ICE1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,FBXO4,ENSCAFG00000016140,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,MOCOS,PCBD1,LIMD1,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,PNPO,DCAKD,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:0032268	0.862	0.172	58	778	regulation of cellular protein metabolic process	BP	1	HMGB1,SREBF1,IRAK1,ILF3,USP4,EIF4A3,HMGCR,HNRNPD,UBE2S,U2AF2,SLC29A1,PPP1R15B,PRELID1,BIRC5,CAV1,RAD51,FANCI,TRUB2,NF2,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,SMARCC1,PLK3,DHX33,CKS2,PDCD2,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,RAP2C,YWHAB,CYCS,NCL,RAC1,NUP62,EMP2,CACTIN,ENSCAFG00000005299,EZR,CLSPN,RBM14,RAD23A,NOLC1,CDC20,PUM3,AIFM1,ARHGEF2,TADA2A,TINF2,CCNB3,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0042886	0.862	0.177	44	527	amide transport	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,TBC1D10C,TBC1D2B,CDH1,ABL1,PEX2,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,PASK,NUP98,HPS4,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,STX4,VPS11,PPP3CB,PEX6,MAVS,BAG4,NCOA4,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0051253	0.862	0.185	29	359	negative regulation of RNA metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,TENT5C,RARG,CBX7,STAT6,GLIS2,SHOX2,H2AFJ,ZC3H10,IKZF2,LIMD1,CDK9,PRMT2,KDM2B,NFIB,ZNF205,NCOA2,QARS,SMARCA2,NCK1	up_VSAP_EC
GO:0006886	0.862	0.191	23	332	intracellular protein transport	BP	1	SREBF1,DDX39A,NEDD4,TIMM44,POLA2,HSPA9,RAN,HM13,INSIG1,PLK3,ENSCAFG00000011598,PREB,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,DDX39B,SNX15,PMPCA	down_ACOR_VSMC
GO:0061024	0.862	0.207	14	215	membrane organization	BP	1	STXBP6,SLC25A5,CTDNEP1,PRELID1,INSIG1,CAV1,AURKB,CHCHD3,DHCR24,PREB,EMP2,SAMM50,REEP4,CORO1A	down_ACOR_VSMC
GO:0030001	0.862	0.215	11	172	metal ion transport	BP	1	NEDD4,HOXA3,CAV1,SLC30A1,NKAIN1,TFRC,GSTO1,CDK2,NIPA2,CORO1A,REM1	down_ACOR_VSMC
GO:0048193	0.862	0.236	7	116	Golgi vesicle transport	BP	1	ACSL3,STXBP6,ZW10,INSIG1,PREB,ARCN1,TRAPPC6A	down_ACOR_VSMC
GO:1903362	0.862	0.245	6	100	regulation of cellular protein catabolic process	BP	1	SLC29A1,SMARCC1,PLK3,EZR,RAD23A,AMER1	down_ACOR_VSMC
GO:0055074	0.862	0.292	3	95	calcium ion homeostasis	BP	1	PRNP,THY1,CYBA	down_VCAV_EC
GO:0009889	0.862	0.303	3	1190	regulation of biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0006888	0.862	0.295	3	49	ER to Golgi vesicle-mediated transport	BP	1	LMF1,GAS1,ERGIC1	up_VSAP_EC
GO:1904892	0.862	0.334	2	40	regulation of STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0061025	0.862	0.33	2	69	membrane fusion	BP	1	AKT2,EVI5L	down_VCAV_EC
GO:0008654	0.862	0.331	2	58	phospholipid biosynthetic process	BP	1	NR1H4,SH3GLB1	down_VSAP_EC
GO:0009411	0.862	0.331	2	56	response to UV	BP	1	EIF2S1,CDKN1A	down_VSAP_EC
GO:0031347	0.862	0.328	2	144	regulation of defense response	BP	1	LEP,NAPEPLD	up_AFEM_EC
GO:0044772	0.862	0.329	2	144	mitotic cell cycle phase transition	BP	1	CAMK2A,DCUN1D3	up_AFEM_EC
GO:0006996	0.862	0.345	2	1301	organelle organization	BP	1	EYA1,ATP8B4	up_VFEM_VSMC
GO:1904375	0.862	0.336	2	35	regulation of protein localization to cell	BP	1	PIK3R1,STX4	up_VSAP_EC

GO:0007601	0.862	0.424	1	22	visual perception	BP	1	NOB1	down_ACOR_VSMC
GO:0050953	0.862	0.424	1	22	sensory perception of light stimulus	BP	1	NOB1	down_ACOR_VSMC
GO:1903510	0.862	0.425	1	22	mucopolysaccharide metabolic process	BP	1	XYLT1	down_ACOR_VSMC
GO:0042100	0.862	0.427	1	19	B cell proliferation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0051495	0.862	0.416	1	82	positive regulation of cytoskeleton organization	BP	1	CDC42EP5	up_AFEM_EC
GO:0019438	0.862	0.44	1	1258	aromatic compound biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0031325	0.862	0.432	1	914	positive regulation of cellular metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0048010	0.862	0.426	1	20	vascular endothelial growth factor receptor	BP	1	EPN2	up_VSAP_EC
GO:0016485	0.862026504	0.4165	1	73	protein processing	BP	1	PCSK1N	up_ACOR_EC
GO:0048511	0.862465168	0.41568	1	72	rhythmic process	BP	1	PTGDS	up_ACOR_EC
GO:0050896	0.863	0.157	212	2346	response to stimulus	BP	1	GPR1,FZD1,EMX2,NAPEPLD,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ACKR2,INSIG2,ENPP2,PTGFR,SLC8B1,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,LIMS2,FOXRED2,ARHGEF6,ACACB,IL6R,SLIT2,CRADD,LRRC28,HOXD3,CDH1,SLC6A4,FGF7,ABL1,GOT1,HDAC7,KLKB1,EMP2,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,CTSS,DTX2,PDGFD,TRAFD1,SAV1,RHPN1,TNFSF13,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,SEMA5A,CDC42EP2,HSD3B7,RARG,CCBE1,MGST1,STAT5A,STAT6,RECK,CISH,KLHL24,PLPP3,SLC25A12,CAMKK2,TNKS1BP1,RASD2,AMBRA1,F2RL1,RAB11B,NFE2L2,GLIS2,LPL,PDK2,MFN2,ZFP36L1,PDE6D,TRAF7,MT2A,FXN,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,BATF2,PLA2G6,NEIL2,MYC,PIK3IP1,ZEB1,DLC1,CTNS,SCARA5,TBXA2R,SULF2,SHOX2,ABAT,SLC12A6,HIC1,FGD4,RTN4RL1,SASH1,FBXO4,CREBRF,MYD88,NDUFS2,ATRIP,GABBR2,TFE3,LRP4,DPYSL2,GDPD5,PTPMT1,S100A4,TSPAN5,STK16,ACKR4,CASTOR1,HPS4,NCEH1,PHF1,WIPF1,CFD,NPAS2,FBXO7,ASB8,TMEM17,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CDK9,CD	up_VSAP_EC
GO:2000112	0.863	0.17	61	1119	regulation of cellular macromolecule biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,AARS,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:2000112	0.863	0.174	49	1119	regulation of cellular macromolecule biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,AKT2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,EIF3K,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0030162	0.863	0.203	15	202	regulation of proteolysis	BP	1	MBP,RECK,SH3RF2,PTPN3,CST3,DAPK1,OS9,SH3RF1,RNF19A,PSEN1,SPINK2,PERP,DISC1,HERPUD1,PARK7	up_ACOR_VSMC
GO:0019693	0.863	0.218	10	172	ribose phosphate metabolic process	BP	1	NPR1,PANK3,PIPOX,ADSS,GUCY1A1,ELOVL7,ENSCAFG00000024323,SLC25A25,GUCY1B1,HIF1A	up_VCAV_EC
GO:0071704	0.863	0.248	10	3535	organic substance metabolic process	BP	1	HOXA3,NR1H4,STK32B,ENSCAFG00000028814,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:1902115	0.863	0.255	5	77	regulation of organelle assembly	BP	1	ARHGEF5,FUZ,PIP4K2B,UBQLN2,NPRL3	up_VSAP_EC
GO:0031497	0.863	0.294	3	49	chromatin assembly	BP	1	NAA60,GATAD1,CENPP	up_VSAP_EC

GO:0032436	0.863	0.331	2	40	positive regulation of proteasomal ubiquitin-dependent protein	BP	1	PLK3,RAD23A	down_ACOR_VSMC
GO:1904375	0.863	0.334	2	35	regulation of protein localization to cell	BP	1	AR,DAG1	up_ACOR_VSMC
GO:0072657	0.863	0.328	2	144	protein localization to membrane	BP	1	LRRC15,REEP2	up_AFEM_EC
GO:0000045	0.863	0.331	2	46	autophagosome assembly	BP	1	RALB,SH3GLB1	up_VCAV_EC
GO:0006996	0.863	0.344	2	1301	organelle organization	BP	1	NKX2-5,CYP26B1	up_VPOR_VSMC
GO:0002244	0.863	0.334	2	35	hematopoietic progenitor cell differentiation	BP	1	EEF2,CITED2	up_VSAP_EC
GO:0032677	0.863	0.423	1	22	regulation of interleukin-8 production	BP	1	CACTIN	down_ACOR_VSMC
GO:0043624	0.863	0.416	1	39	cellular protein complex disassembly	BP	1	PLEKHH2	down_VCAV_EC
GO:0030279	0.863	0.424	1	19	negative regulation of ossification	BP	1	SMAD6	up_ACOR_VSMC
GO:0072659	0.863	0.415	1	82	protein localization to plasma membrane	BP	1	LRRC15	up_AFEM_EC
GO:0051128	0.863	0.425	1	790	regulation of cellular component organization	BP	1	TAOK1	up_AORT_EC
GO:0018130	0.863	0.439	1	1261	heterocycle biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0009056	0.863	0.427	1	755	catabolic process	BP	1	CYP26B1	up_VPOR_VSMC
GO:1905332	0.863	0.423	1	20	positive regulation of morphogenesis of an	BP	1	ABL1	up_VSAP_EC
GO:0033044	0.863661401	0.32603	2	127	regulation of chromosome organization	BP	1	PKIB,PYGO2	up_ACOR_EC
GO:0006082	0.864	0.187	24	305	organic acid metabolic process	BP	1	LEP,ENOSF1,PRDX4,ENSCAFG00000002977,TARSL2,PPARGC1A,NIT2,ACAD11,ERO1B,EGLN1,CYP2J2,P4HA1,PRKCE,SARDH,SGSM2,EDN1,ALDOC,HPGD,PCYOX1,DDIT4,AZIN2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0009894	0.864	0.194	19	277	regulation of catabolic process	BP	1	HMGB1,SREBF1,HNRNPD,NEDD4,PSMD3,SLC29A1,MTDH,THRAP3,ABHD5,CDK4,SMARCC1,PLK3,RNF152,FASTKD3,DTL,EZR,RAD23A,AIFM1,AMER1	down_ACOR_VSMC
GO:0019439	0.864	0.213	11	150	aromatic compound catabolic process	BP	1	PNRC1,PDE5A,MAOA,ENPP4,DCP1B,MOXD1,ALDOC,ENTPD3,DDIT4,CNOT4,CTIF	up_ACOR_VSMC
GO:0045862	0.864	0.227	8	112	positive regulation of proteolysis	BP	1	CRADD,MAP3K5,CCBE1,MYC,RNF166,OSBPL7,UBQLN2,HTRA2	up_VSAP_EC
GO:0043524	0.864	0.331	2	39	negative regulation of neuron apoptotic process	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0006633	0.864	0.415	1	38	fatty acid biosynthetic process	BP	1	THNSL2	down_VCAV_EC
GO:1902749	0.864	0.415	1	39	regulation of cell cycle G2/M phase transition	BP	1	BRSK1	down_VCAV_EC
GO:1903828	0.864	0.416	1	38	negative regulation of cellular protein	BP	1	PARK7	down_VCAV_EC
GO:0120162	0.864	0.418	1	31	positive regulation of cold-induced thermogenesis	BP	1	KDM3A	down_VSAP_EC
GO:2001021	0.864	0.418	1	30	negative regulation of response to DNA damage	BP	1	DDX39B	down_VSAP_EC
GO:0032268	0.864	0.425	1	778	regulation of cellular protein metabolic process	BP	1	TAOK1	up_AORT_EC
GO:0010604	0.864	0.429	1	919	positive regulation of macromolecule metabolic	BP	1	GATA5	up_VPUL_VSMC
GO:0006378	0.864	0.422	1	20	mRNA polyadenylation	BP	1	CDK9	up_VSAP_EC
GO:0048747	0.864	0.422	1	20	muscle fiber development	BP	1	SHOX2	up_VSAP_EC
GO:0021795	0.864	0.422	1	20	cerebral cortex cell migration	BP	1	SLIT2	up_VSAP_EC
GO:0030162	0.865	0.205	13	202	regulation of proteolysis	BP	1	HMGB1,SLC29A1,PRELID1,BIRC5,SMARCC1,PLK3,PDCD2,DHCR24,CYCS,ENSCAFG00000005299,RAD23A,AIFM1,DELE1	down_ACOR_VSMC
GO:0007049	0.865	0.215	10	560	cell cycle	BP	1	LEP,GAS1,OVOL1,CAMK2A,CYLD,MYBL1,DCUN1D3,AXIN2,FAP,ANXA11	up_AFEM_EC
GO:0060249	0.865	0.226	8	110	anatomical structure homeostasis	BP	1	ATRX,ZNF365,STN1,LAMP2,CLN8,NOD2,GAA,HMBOX1	up_ACOR_VSMC
GO:0010605	0.865	0.268	4	745	negative regulation of macromolecule metabolic	BP	1	CXHXorf57,ENSCAFG00000002015,ASPN,MTDH	up_VPOR_EC
GO:0010948	0.865	0.288	3	96	negative regulation of cell cycle process	BP	1	KANK2,ZFP36L1,BRSK1	down_VCAV_EC
GO:0044283	0.865	0.286	3	201	small molecule biosynthetic process	BP	1	LEP,MOXD1,ACACB	up_AFEM_EC

GO:0042180	0.865	0.29	3	61	cellular ketone metabolic process	BP	1	BMP2,PROX1,PTGS2	up_VCAV_EC
GO:0048583	0.865	0.296	3	1095	regulation of response to stimulus	BP	1	EYA1,TIAM1,CYP26B1	up_VFEM_EC
GO:0017015	0.865	0.328	2	40	regulation of transforming growth factor beta receptor signaling	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:1903844	0.865	0.328	2	40	regulation of cellular response to transforming growth factor beta	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:2000058	0.865	0.326	2	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	PARK7,CLEC16A	down_VCAV_EC
GO:0060021	0.865	0.33	2	34	roof of mouth development	BP	1	CHD7,ARID5B	up_ACOR_VSMC
GO:0055065	0.865	0.324	2	145	metal ion homeostasis	BP	1	CNNM4,DMPK	up_AFEM_EC
GO:0006879	0.865	0.417	1	23	cellular iron ion homeostasis	BP	1	TFRC	down_ACOR_VSMC
GO:0051851	0.865	0.418	1	23	modification by host of symbiont morphology or	BP	1	SMC3	down_ACOR_VSMC
GO:0008593	0.865	0.415	1	33	regulation of Notch signaling pathway	BP	1	HIF1AN	down_VSAP_EC
GO:0006270	0.865	0.42	1	19	DNA replication initiation	BP	1	CDC7	up_ACOR_VSMC
GO:0048814	0.865	0.421	1	19	regulation of dendrite morphogenesis	BP	1	SIPA1L1	up_ACOR_VSMC
GO:0051452	0.865	0.419	1	20	intracellular pH reduction	BP	1	DMXL1	up_ACOR_VSMC
GO:0006900	0.865	0.419	1	21	vesicle budding from membrane	BP	1	ATP8A1	up_VCAV_EC
GO:0030097	0.865	0.411	1	244	hemopoiesis	BP	1	ACVR2A	up_VPOR_EC
GO:0043549	0.865	0.411	1	244	regulation of kinase activity	BP	1	ASPN	up_VPOR_EC
GO:0010605	0.865	0.423	1	745	negative regulation of macromolecule metabolic	BP	1	NKX2-5	up_VPOR_VSMC
GO:0018958	0.865	0.419	1	20	phenol-containing compound metabolic	BP	1	SULT1A1	up_VSAP_EC
GO:0070482	0.865894544	0.40869	1	75	response to oxygen levels	BP	1	AQP1	up_ACOR_EC
GO:0051345	0.866	0.21	11	151	positive regulation of hydrolase activity	BP	1	ARHGEF5,PPARGC1B,TBC1D10C,CRADD,TBC1D2B,MAP3K5,F2RL1,LMF1,TIAM1,MYC,HTRA2	up_VSAP_EC
GO:0009987	0.866	0.357	5	5086	cellular process	BP	1	HOXC10,HOXA9,WNT7A,ARG2,ESR1	up_AORT_VSMC
GO:0050803	0.866	0.288	3	55	regulation of synapse structure or activity	BP	1	CDC20,SIX4,TPBG	down_ACOR_VSMC
GO:0050807	0.866	0.288	3	55	regulation of synapse organization	BP	1	CDC20,SIX4,TPBG	down_ACOR_VSMC
GO:0007599	0.866	0.288	3	48	hemostasis	BP	1	LNPK,F2RL1,ENPP4	up_ACOR_VSMC
GO:0072009	0.866	0.29	3	48	nephron epithelium development	BP	1	BMP4,CLSTN1,NPNT	up_ACOR_VSMC
GO:0032869	0.866	0.288	3	57	cellular response to insulin stimulus	BP	1	PPARG,BAIAP2L1,NCK1	up_VCAV_EC
GO:0051648	0.866	0.324	2	69	vesicle localization	BP	1	TMEM230,CDH2	down_VCAV_EC
GO:0009799	0.866	0.326	2	43	specification of symmetry	BP	1	MEF2C,HIF1A	up_VCAV_EC
GO:0044265	0.866	0.324	2	423	cellular macromolecule catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0042770	0.866	0.328	2	35	signal transduction in response to DNA damage	BP	1	CRADD,ABL1	up_VSAP_EC
GO:0060976	0.866	0.416	1	22	coronary vasculature development	BP	1	ADAMTS6	down_ACOR_VSMC
GO:1903557	0.866	0.415	1	22	positive regulation of tumor necrosis factor superfamily cytokine	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0032760	0.866	0.415	1	22	positive regulation of tumor necrosis factor	BP	1	ARHGEF2	down_ACOR_VSMC
GO:0009966	0.866	0.422	1	868	regulation of signal transduction	BP	1	IVNS1ABP	down_AFEM_EC
GO:0006885	0.866	0.41	1	39	regulation of pH	BP	1	ATP6V0C	down_VCAV_EC
GO:2001056	0.866	0.411	1	38	positive regulation of cysteine-type	BP	1	IFT57	down_VCAV_EC
GO:0110020	0.866	0.412	1	31	regulation of actomyosin structure organization	BP	1	NRP1	down_VSAP_EC

GO:0016043	0.866	0.454	1	1973	cellular component organization	BP	1	TGFBI	down_VSAP_VSMC
GO:0051972	0.866	0.417	1	20	regulation of telomerase activity	BP	1	HMBOX1	up_ACOR_VSMC
GO:0000209	0.866	0.408	1	83	protein polyubiquitination	BP	1	RNF181	up_AFEM_EC
GO:0006996	0.866	0.433	1	1301	organelle organization	BP	1	EYA1	up_AFEM_VSMC
GO:0010629	0.866	0.414	1	502	negative regulation of gene expression	BP	1	NR1H4	up_APUL_EC
GO:0016192	0.866	0.413	1	452	vesicle-mediated transport	BP	1	TRIM9	up_VFEM_EC
GO:0007613	0.866	0.419	1	20	memory	BP	1	CTNS	up_VSAP_EC
GO:0031529	0.866	0.418	1	20	ruffle organization	BP	1	BAG4	up_VSAP_EC
GO:0000070	0.86672279	0.40702	1	75	mitotic sister chromatid segregation	BP	1	CHMP4B	up_ACOR_EC
GO:0032879	0.867	0.166	57	767	regulation of localization	BP	1	ACSL3,HMGB1,SREBF1,STXBP6,RACGAP1,SREBF2,NEDD4,SLC29A1,HOXA3,SLC25A5,SDC1,ARFGAP1,FBXO5,RAN,CFAP298,PRELID1,BIRC5,INSIG1,CAV1,CDK1,NF2,MMP14,ABHD5,STMN1,SLC30A1,GREM1,CLIC1,PLK3,HOXA7,ARG2,NKAIN1,B4GALT1,PRCP,PREB,NDC80,RAP2C,ARHGDIA,HIST1H1A,RAC1,NUP62,EMP2,RSL1D1,GSTO1,DMAP1,ENSCAFG00000005299,EZR,RBM14,CORO1A,ENSCAFG00000010224,REM1,ARHGEF2,TWIST2,NUS1,CCT4,AMOTL1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0050789	0.867	0.199	23	3295	regulation of biological process	BP	1	C3AR1,BARX1,CXHXorf57,HOOK3,HOXA3,ARHGEF2,TCEA1,ENSCAFG00000002015,SEMA3A,ASPN,ACVR2A,FBP1,MTDH,GCC2,ABHD5,TWF1,PDE1C,PUM3,EIF5,CCAR1,STK17B,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0045934	0.867	0.195	16	407	negative regulation of nucleobase-containing compound metabolic	BP	1	NAB2,KANK2,NR3C1,HR,CLSTN1,PRMT6,CXXC5,CC2D1A,GLI3,LOXL3,TSC22D3,GLIS2,SHC1,FBH1,GREM1,THRB	down_VCAV_EC
GO:1905114	0.867	0.213	10	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	RELN,MEF2C,FERMT1,RAPGEF1,GATA3,PPP3CA,BMP2,HHEX,MCC,SMARCA4	up_VCAV_EC
GO:0050708	0.867	0.238	6	101	regulation of protein secretion	BP	1	HMGB1,SREBF1,BIRC5,ARG2,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0010506	0.867	0.249	5	86	regulation of autophagy	BP	1	HMGB1,SREBF1,MTDH,PLK3,RNF152	down_ACOR_VSMC
GO:0031396	0.867	0.249	5	90	regulation of protein ubiquitination	BP	1	TNFAIP3,PELI1,BCL10,UBE2D1,IVNS1ABP	up_VCAV_EC
GO:0007219	0.867	0.322	2	59	Notch signaling pathway	BP	1	NR1H4,HIF1AN	down_VSAP_EC
GO:0034641	0.867	0.355	2	2171	cellular nitrogen compound metabolic	BP	1	GATA5,ENSCAFG00000028814	up_VCAV_VSMC
GO:0051234	0.867	0.336	2	1283	establishment of localization	BP	1	NETO1,SLC16A12	up_VFEM_VSMC
GO:0060419	0.867	0.414	1	22	heart growth	BP	1	GLI1	down_ACOR_VSMC
GO:0048525	0.867	0.412	1	25	negative regulation of viral process	BP	1	PROX1	up_VCAV_EC
GO:0060425	0.867	0.412	1	25	lung morphogenesis	BP	1	HHEX	up_VCAV_EC
GO:0008104	0.867	0.419	1	763	protein localization	BP	1	LHFPL4	up_VPOR_VSMC
GO:0006284	0.867	0.416	1	20	base-excision repair	BP	1	NEIL2	up_VSAP_EC
GO:2000756	0.867	0.415	1	20	regulation of peptidyl-lysine acetylation	BP	1	KLF15	up_VSAP_EC
GO:0021766	0.867	0.415	1	20	hippocampus development	BP	1	EMX2	up_VSAP_EC
GO:0055086	0.867895822	0.25971	4	237	nucleobase-containing small molecule metabolic	BP	1	NMNAT2,GUCY1B1,AK7,ALDOC	up_ACOR_EC
GO:0044087	0.868	0.179	27	339	regulation of cellular component biogenesis	BP	1	FZD1,WNT11,FAM107A,ARHGEF5,AMIGO1,LRRN3,SLIT2,ABL1,CDC42EP5,FUZ,CDC42EP2,ENSCAFG00000000071,F2RL1,ICE1,PIK3R1,LCAT,PIP4K2B,RAF1,VPS11,ACVRL1,UBQLN2,FLOT1,NCK1,ULK1,NPRL3,BAG4,JCHAIN	up_VSAP_EC
GO:0006796	0.868	0.192	18	938	phosphate-containing compound metabolic process	BP	1	LEP,GPAM,MYO1D,ATP6V1B2,HCK,GREM1,CAMK2A,CYLD,LRRC15,AXIN2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,DMPK,ADAM17,AGPAT2	up_AFEM_EC

GO:0003008	0.868	0.2	13	336	system process	BP	1	KIRREL1,NDN,PRNP,LUM,ADCY6,CLSTN1,PEX5,RNPEP,ENSCAFG00000017708,IRX5,RDH10,THRB,BRSK1	down_VCAV_EC
GO:0055065	0.868	0.215	9	145	metal ion homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0007249	0.868	0.262	4	71	I-kappaB kinase/NF-kappaB signaling	BP	1	IRAK1,MTDH,NUP62,CTH	down_ACOR_VSMC
GO:0031346	0.868	0.261	4	73	positive regulation of cell projection organization	BP	1	FSCN1,ANLN,RAC1,CDC42EP4	down_ACOR_VSMC
GO:0071496	0.868	0.282	3	97	cellular response to external stimulus	BP	1	KANK2,GABARAP,CLEC16A	down_VCAV_EC
GO:1902532	0.868	0.281	3	204	negative regulation of intracellular signal	BP	1	CYLD,LRRC15,KANK1	up_AFEM_EC
GO:0007165	0.868	0.339	2	1496	signal transduction	BP	1	GPSM2,IVNS1ABP	down_AFEM_EC
GO:0000723	0.868	0.322	2	54	telomere maintenance	BP	1	SMG7,CTNNB1	down_VSAP_EC
GO:0007098	0.868	0.32	2	56	centrosome cycle	BP	1	PPP1R12A,CTNNB1	down_VSAP_EC
GO:0032200	0.868	0.322	2	54	telomere organization	BP	1	SMG7,CTNNB1	down_VSAP_EC
GO:0070374	0.868	0.321	2	57	positive regulation of ERK1 and ERK2 cascade	BP	1	PTPN11,NRP1	down_VSAP_EC
GO:0016125	0.868	0.323	2	41	sterol metabolic process	BP	1	ABCA1,LBR	up_VCAV_EC
GO:0002429	0.868	0.324	2	35	immune response-activating cell surface receptor signaling	BP	1	ABL1,RBCK1	up_VSAP_EC
GO:0006661	0.868	0.412	1	23	phosphatidylinositol biosynthetic process	BP	1	VAC14	down_ACOR_VSMC
GO:0045921	0.868	0.412	1	24	positive regulation of exocytosis	BP	1	SDC1	down_ACOR_VSMC
GO:0098781	0.868	0.413	1	22	ncRNA transcription	BP	1	NCL	down_ACOR_VSMC
GO:0051896	0.868	0.408	1	39	regulation of protein kinase B signaling	BP	1	MYDGF	down_VCAV_EC
GO:0046620	0.868	0.41	1	30	regulation of organ growth	BP	1	WWC3	down_VSAP_EC
GO:0032210	0.868	0.414	1	20	regulation of telomere maintenance via	BP	1	HMBOX1	up_ACOR_VSMC
GO:0051897	0.868	0.414	1	20	positive regulation of protein kinase B signaling	BP	1	LEP	up_ACOR_VSMC
GO:1904356	0.868	0.414	1	20	regulation of telomere maintenance via telomere lengthening	BP	1	HMBOX1	up_ACOR_VSMC
GO:0030850	0.868	0.414	1	20	prostate gland development	BP	1	RARG	up_VSAP_EC
GO:0061614	0.868	0.414	1	20	pri-miRNA transcription by RNA polymerase II	BP	1	NFIB	up_VSAP_EC
GO:0070228	0.868	0.413	1	20	regulation of lymphocyte apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0051716	0.869	0.151	179	2001	cellular response to stimulus	BP	1	GPR1,FZD1,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,INSIG2,PTGFR,SLC8B1,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,LIMS2,FOXRED2,ARHGEF6,IL6R,SLIT2,CRADD,LRRC28,HOXD3,CDH1,SLC6A4,FGF7,ABL1,GOT1,HDAC7,EMP2,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,DTX2,PDGFD,SAV1,RHPN1,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,HSD3B7,RARG,CCBE1,MGST1,STAT5A,STAT6,RECK,CISH,KLHL24,PLPP3,CAMKK2,TNKS1BP1,RASD2,AMBRA1,F2RL1,RAB11B,NFE2L2,GLIS2,PDK2,MFN2,ZFP36L1,TRAF7,MT2A,FXN,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,NEIL2,MYC,PIK3IP1,ZEB1,DLC1,SCARA5,TBXA2R,SULF2,SHOX2,SLC12A6,HIC1,FGD4,RTN4RL1,SASH1,FBXO4,CREBRF,MYD88,ATRIP,GABBR2,LRP4,GDPD5,PTPMT1,S100A4,TSPAN5,STK16,CASTOR1,NCEH1,PHF1,NPAS2,FBXO7,ASB8,TMEM17,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CDK9,CD83,PRMT2,FBLN1,AP5Z1,OSBPL7,ZFP36L2,HPGD,IGFBP6,YPEL3,RAF1,MAPKBP1,ZNF580,PPP2R5B,CYBA,ZNF205,NCOA2,STX4,ZBTB4,ZFAND5,PSD4,PQBP1,QARS,ARHGAP12,A	up_VSAP_EC

GO:0033036	0.869	0.16	73	852	macromolecule localization	BP	1	PEX7,WNT11,HNF4A,CD274,ARHGEF5,AXIN2,C5AR2,LIPC,SLC8B1,PLEKHF1,TBC1D10C,ACACB,TBC1D2B,CDH1,FGF7,ABL1,PEX2,EMP2,IL17RC,SCAMP4,ANXA4,RILPL2,ABCB11,VPS36,APOL5,TOM1,F2RL1,LMF1,RAB11B,GLIS2,MORC3,MFN2,ICE1,ZFP36L1,PIK3R1,CRACR2B,SLC27A6,CIZ1,FBXO4,LRP4,NUP98,TSPAN5,HPS4,FRMD6,ABCA9,STEAP3,FBXO7,KCNB1,LCAT,LONP2,SNUPN,OSBPL7,SCAMP2,RAF1,PNP,MAPKBP1,TAF8,STX4,VPS11,FLOT1,PPP3CB,PEX6,STK11IP,MAVS,ULK1,TGFBR2,BAG4,NCOA4,NAGPA,KEAP1,RAB11FIP2,SOAT1,LATS2	up_VSAP_EC
GO:0009893	0.869	0.169	43	995	positive regulation of metabolic process	BP	1	NOTCH2,PDGFRB,LRP1,DCN,PRNP,LUM,GLIPR2,LARP6,BMPR1A,NABP2,LMO4,TRPV2,CLIP3,ENSCAFG00000014978,SSBP2,AKT2,TFE3,CSPG4,TMEM161A,TEAD1,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,ARL2BP,IFT57,MAVS,CDH2,GSDME,MAPRE3,DDR2,SHC1,PYM1,FBH1,GREM1,SOAT1,THRB,PACSIN3,ZBTB16	down_VCAV_EC
GO:0045944	0.869	0.186	20	287	positive regulation of transcription by RNA polymerase II	BP	1	HMGB1,SREBF1,PPRC1,ATAD2,SREBF2,INSIG1,THRAP3,GREM1,SMARCC1,BRCA1,E2F8,NCL,HMGB2,RBM14,PSMC1,ARHGEF2,SUPT16H,HOXA9,GLI1,ENSCAFG00000017103	down_ACOR_VSMC
GO:0070647	0.869	0.244	5	311	protein modification by small protein conjugation	BP	1	USP54,KLHDC8B,CYLD,DCUN1D3,RNF181	up_AFEM_EC
GO:0031669	0.869	0.26	4	72	cellular response to nutrient levels	BP	1	ATF3,RALB,MTOR,PMAIP1	up_VCAV_EC
GO:0009987	0.869	0.418	3	5086	cellular process	BP	1	HOXA3,TBX5,HOXB5	up_APUL_VSMC
GO:0051128	0.869	0.323	2	790	regulation of cellular component organization	BP	1	CAV1,SHOX2	up_VSAP_VSMC
GO:0006259	0.869	0.407	1	354	DNA metabolic process	BP	1	ACVRL1	down_ACOR_EC
GO:0009206	0.869	0.405	1	39	purine ribonucleoside triphosphate biosynthetic	BP	1	ATP5MC1	down_VCAV_EC
GO:0050921	0.869	0.405	1	39	positive regulation of chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:0055123	0.869	0.405	1	40	digestive system development	BP	1	GLI3	down_VCAV_EC
GO:0006672	0.869	0.406	1	33	ceramide metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0019395	0.869	0.406	1	33	fatty acid oxidation	BP	1	SESN2	down_VSAP_EC
GO:1902806	0.869	0.407	1	33	regulation of cell cycle G1/S phase transition	BP	1	CDKN1A	down_VSAP_EC
GO:0046324	0.869	0.412	1	20	regulation of glucose import	BP	1	LEP	up_ACOR_VSMC
GO:0006816	0.869	0.403	1	84	calcium ion transport	BP	1	CAMK2A	up_AFEM_EC
GO:0031334	0.869	0.402	1	84	positive regulation of protein complex assembly	BP	1	CDC42EP5	up_AFEM_EC
GO:0019882	0.869	0.409	1	25	antigen processing and presentation	BP	1	RAB27A	up_VCAV_EC
GO:0051234	0.869	0.426	1	1283	establishment of localization	BP	1	CA2	up_VCAV_VSMC
GO:0042325	0.869	0.406	1	463	regulation of phosphorylation	BP	1	MAP2K6	up_VFEM_EC
GO:0007049	0.869	0.409	1	560	cell cycle	BP	1	ARHGEF2	up_VPUL_EC
GO:0006796	0.869	0.418	1	938	phosphate-containing compound metabolic	BP	1	SLIT2	up_VPUL_VSMC
GO:0042035	0.869	0.412	1	20	regulation of cytokine biosynthetic process	BP	1	MYD88	up_VSAP_EC
GO:0090559	0.869	0.412	1	20	regulation of membrane permeability	BP	1	ZNF205	up_VSAP_EC
GO:0007586	0.869	0.412	1	20	digestion	BP	1	CHRM1	up_VSAP_EC
GO:0022600	0.869	0.412	1	20	digestive system process	BP	1	CHRM1	up_VSAP_EC
GO:0043065	0.869272241	0.279	3	188	positive regulation of apoptotic process	BP	1	IFIT2,CLU,PRKCD	up_ACOR_EC

GO:0010468	0.87	0.154	113	1270	regulation of gene expression	BP	1	SMAD6,PLCG2,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,PRKAA2,MLLT3,FERMT1,BMP4,PNRC1,ZNF331,FGFR2,TP53BP1,EIF4A2,GJA1,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,PTPN22,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,MARF1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,STC2,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,CRKL	up_ACOR_VSMC
GO:1901360	0.87	0.206	13	2016	organic cyclic compound metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,AK5,ENSCAFG00000002015,ACVR2A,FBP1,MTDH,RRP15,CCAR1,GNPNAT1,RNF6	up_VPOR_EC
GO:0001838	0.87	0.281	3	56	embryonic epithelial tube formation	BP	1	GREM1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0001505	0.87	0.317	2	69	regulation of neurotransmitter levels	BP	1	MAOA,PARK7	down_VCAV_EC
GO:0034249	0.87	0.32	2	41	negative regulation of cellular amide metabolic	BP	1	ENC1,CNOT7	up_VCAV_EC
GO:0032268	0.87	0.323	2	778	regulation of cellular protein metabolic process	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0032602	0.87	0.408	1	23	chemokine production	BP	1	ARG2	down_ACOR_VSMC
GO:0007269	0.87	0.405	1	34	neurotransmitter secretion	BP	1	GSK3B	down_VSAP_EC
GO:0033047	0.87	0.404	1	33	regulation of mitotic sister chromatid segregation	BP	1	NAA10	down_VSAP_EC
GO:0099643	0.87	0.405	1	34	signal release from synapse	BP	1	GSK3B	down_VSAP_EC
GO:0048747	0.87	0.409	1	20	muscle fiber development	BP	1	BMP4	up_ACOR_VSMC
GO:0033673	0.87	0.399	1	84	negative regulation of kinase activity	BP	1	LRRC15	up_AFEM_EC
GO:0051047	0.87	0.4	1	84	positive regulation of secretion	BP	1	RAB7A	up_AFEM_EC
GO:0044267	0.87	0.433	1	1583	cellular protein metabolic process	BP	1	WNT7A	up_AORT_VSMC
GO:0009056	0.87	0.411	1	755	catabolic process	BP	1	FBP1	up_VFEM_VSMC
GO:0032879	0.87	0.411	1	767	regulation of localization	BP	1	NETO1	up_VFEM_VSMC
GO:0006893	0.87	0.41	1	20	Golgi to plasma membrane transport	BP	1	CCDC93	up_VSAP_EC
GO:0032210	0.87	0.409	1	20	regulation of telomere maintenance via	BP	1	FBXO4	up_VSAP_EC
GO:1904356	0.87	0.409	1	20	regulation of telomere maintenance via telomere lengthening	BP	1	FBXO4	up_VSAP_EC
GO:1901565	0.871	0.173	30	442	organonitrogen compound catabolic process	BP	1	PLK2,CDA,TNFAIP3,CTSC,TIPARP,WWP1,LYVE1,USP33,PIPOX,PSME4,PELI1,ODC1,CASP8,ENC1,USP28,PMAIP1,RIPK1,USP13,USP38,USP37,BLVRA,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMB9,PSMD12,TET2,ITCH	up_VCAV_EC
GO:0045597	0.871	0.188	17	253	positive regulation of cell differentiation	BP	1	HMGB1,SLC29A1,SRRT,FBXO5,PRMT1,NF2,MMP14,EZH2,GREM1,RAC1,HMGB2,TOX,RBM14,BEND6,ASPM,CTH,ARHGEF2	down_ACOR_VSMC
GO:0016070	0.871	0.217	9	1479	RNA metabolic process	BP	1	BARX1,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,RRP15,CCAR1,RNF6	up_VPOR_EC
GO:0050794	0.871	0.274	5	3075	regulation of cellular process	BP	1	GPSM2,IVNS1ABP,SRSF6,GABPA,FSCN1	down_AFEM_EC
GO:0006282	0.871	0.281	3	48	regulation of DNA repair	BP	1	TP53BP1,ZNF365,PARP9	up_ACOR_VSMC
GO:1901215	0.871	0.279	3	57	negative regulation of neuron death	BP	1	CD34,MEF2C,HIF1A	up_VCAV_EC
GO:0043491	0.871	0.28	3	50	protein kinase B signaling	BP	1	HPSE,ZFP36L1,BAG4	up_VSAP_EC
GO:0071219	0.871	0.28	3	50	cellular response to molecule of bacterial	BP	1	ABL1,SASH1,MYD88	up_VSAP_EC

GO:0045580	0.871	0.318	2	35	regulation of T cell differentiation	BP	1	CD83,BMP4	up_ACOR_VSMC
GO:0045995	0.871	0.318	2	40	regulation of embryonic development	BP	1	AMOT,GATA3	up_VCAV_EC
GO:0099173	0.871	0.318	2	40	postsynapse organization	BP	1	EPHB1,RELN	up_VCAV_EC
GO:1905037	0.871	0.316	2	47	autophagosome organization	BP	1	RALB,SH3GLB1	up_VCAV_EC
GO:0048701	0.871	0.406	1	25	embryonic cranial skeleton morphogenesis	BP	1	MEF2C	up_VCAV_EC
GO:0006996	0.871	0.422	1	1301	organelle organization	BP	1	LIMK1	up_VCAV_VSMC
GO:1901362	0.871	0.423	1	1293	organic cyclic compound biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0032387	0.871	0.407	1	20	negative regulation of intracellular transport	BP	1	BAG4	up_VSAP_EC
GO:1903573	0.871	0.407	1	20	negative regulation of response to endoplasmic	BP	1	NCK1	up_VSAP_EC
GO:0050794	0.872	0.146	281	3075	regulation of cellular process	BP	1	GPR1,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,NAPEPLD,TWIST2,HOXA9,ADGRD1,SEZ6L,CDON,NECAB3,WNT11,HNF4A,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,SLC8B1,RADIL,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,TBC1D10C,MAB21L1,CEP85,LIMS2,ARHGEF6,ACACB,TPCN2,EEF2K,DDHD1,IL6R,IRX5,SLIT2,CST3,CRADD,CRIP2,LRRC28,ZHX3,TBC1D2B,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,GOT1,BTG1,HDAC7,EMP2,KCNE3,CHRM1,DLL1,EPN2,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,DTX2,TENT5C,FUZ,ADAMTSL4,PDGFD,SAV1,RHPN1,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ANKRD54,CDC42EP2,ZNF688,ZBTB16,TOX,CNPPD1,RARG,CCBE1,PTGES2,CBX7,STAT5A,STAT6,RECK,GATAD1,CISH,KLHL24,PLPP3,ENSCAFG00000000071,CAMKK2,TNKS1BP1,RASD2,PYM1,AMBRA1,F2RL1,RBL2,LMF1,RAB11B,GLIS2,MORC3,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,RGL1,PIK3R1,RBCK1,FAM53B,TIAM1,GAS1,BATF2,MYC,PIK3IP1,PTGES,SSBP2,IRX3,ZEB1,DLC1,FBXW4,DLD,TBXA2R,SULF2,SHOX2,TMEM225B,H2AFJ,ZC3H10,TLE2,CIZ1,HIC1,FGD4,YBX3,CFAP69,EEF2,RTN4RL1,SASH1,CD	up_VSAP_EC
GO:0050877	0.872	0.199	12	164	nervous system process	BP	1	THRB,FAM107A,WASF3,CBR3,ABL1,CHRM1,PDE6D,FXN,CTNS,HOXC10,DOP1B,NR2F6	up_VSAP_EC
GO:0051259	0.872	0.206	10	140	protein complex oligomerization	BP	1	ACTN2,NACC2,PCBD1,TP53BP1,TRPS1,LRRC8C,EVL,KCNC4,SBF2,PFKL	up_ACOR_VSMC
GO:0031400	0.872	0.274	3	205	negative regulation of protein modification	BP	1	GREM1,CYLD,LRRC15	up_AFEM_EC
GO:0043170	0.872	0.318	3	2980	macromolecule metabolic process	BP	1	LIMK1,GATA5,C6	up_VCAV_VSMC
GO:0033135	0.872	0.315	2	40	regulation of peptidyl-serine phosphorylation	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:0002064	0.872	0.312	2	71	epithelial cell development	BP	1	B4GALT1,ADAMTSL4	down_VCAV_EC
GO:0006333	0.872	0.313	2	59	chromatin assembly or disassembly	BP	1	SMARCA4,BRD2	down_VSAP_EC
GO:0035265	0.872	0.314	2	54	organ growth	BP	1	PTPN11,WWC3	down_VSAP_EC
GO:0035966	0.872	0.315	2	47	response to topologically incorrect protein	BP	1	ATF3,NCK1	up_VCAV_EC
GO:0055067	0.872	0.315	2	42	monovalent inorganic cation homeostasis	BP	1	EDNRB,EDN1	up_VCAV_EC
GO:0007006	0.872	0.317	2	35	mitochondrial membrane organization	BP	1	MFN2,ZNF205	up_VSAP_EC
GO:0002381	0.872	0.406	1	19	immunoglobulin production involved in immunoglobulin	BP	1	TP53BP1	up_ACOR_VSMC
GO:0021695	0.872	0.405	1	20	cerebellar cortex development	BP	1	ZNF365	up_ACOR_VSMC
GO:0033692	0.872	0.406	1	20	cellular polysaccharide biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:2000756	0.872	0.406	1	20	regulation of peptidyl-lysine acetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0002697	0.872	0.396	1	85	regulation of immune effector process	BP	1	LEP	up_AFEM_EC
GO:0015031	0.872	0.402	1	510	protein transport	BP	1	NR1H4	up_APUL_EC

GO:0009063	0.872	0.404	1	25	cellular amino acid catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0043631	0.872	0.404	1	21	RNA polyadenylation	BP	1	TENT2	up_VCAV_EC
GO:0023014	0.872	0.396	1	248	signal transduction by protein phosphorylation	BP	1	ENSCAFG00000032731	up_VPOR_EC
GO:0032268	0.872	0.408	1	778	regulation of cellular protein metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0007405	0.872	0.405	1	21	neuroblast proliferation	BP	1	DAGLB	up_VSAP_EC
GO:0010332	0.872	0.406	1	20	response to gamma radiation	BP	1	MYC	up_VSAP_EC
GO:0045005	0.872	0.405	1	21	DNA-dependent DNA replication maintenance	BP	1	CDK9	up_VSAP_EC
GO:0010629	0.872204801	0.20501	10	502	negative regulation of gene expression	BP	1	NR1H4,TRPS1,SOX9,DUSP26,ZMYND8,PIAS1,FOXC2,CLSTN1,SFMBT2,RIOX2	up_ACOR_EC
GO:0009101	0.873	0.215	8	113	glycoprotein biosynthetic process	BP	1	NECAB3,GALNT15,LMF1,FKRP,GALNT11,CHST7,B3GALT4,SOAT1	up_VSAP_EC
GO:0001932	0.873	0.22	7	416	regulation of protein phosphorylation	BP	1	LEP,GREM1,CYLD,LRRC15,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0072522	0.873	0.229	6	91	purine-containing compound biosynthetic	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,ELOVL7	up_ACOR_VSMC
GO:0044248	0.873	0.316	2	691	cellular catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0009108	0.873	0.31	2	68	coenzyme biosynthetic process	BP	1	ACSS2,ACAT1	down_VCAV_EC
GO:2001056	0.873	0.315	2	38	positive regulation of cysteine-type	BP	1	DAPK1,PERP	up_ACOR_VSMC
GO:0097305	0.873	0.398	1	31	response to alcohol	BP	1	CTNNB1	down_VSAP_EC
GO:0070372	0.873	0.395	1	85	regulation of ERK1 and ERK2 cascade	BP	1	CCL5	up_AFEM_EC
GO:0046426	0.873	0.403	1	20	negative regulation of JAK-STAT cascade	BP	1	RTN4RL1	up_VSAP_EC
GO:1904893	0.873	0.403	1	20	negative regulation of STAT cascade	BP	1	RTN4RL1	up_VSAP_EC
GO:0016192	0.873	0.398	1	452	vesicle-mediated transport	BP	1	CAV1	up_VSAP_VSMC
GO:0034645	0.873076287	0.16989	35	1546	cellular macromolecule biosynthetic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,PKNOX2,GALNT5,PORCN,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,B3GNT7,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,PIGS,LRP4,CLSTN1,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0044092	0.874	0.182	18	270	negative regulation of molecular function	BP	1	IRAK1,HMGCR,NEDD4,BIRC5,CAV1,NF2,AURKB,CDKN2C,EZH2,STMN1,NEK2,DHCR24,NUP62,CACTIN,GSTO1,ENSCAFG00000005299,REM1,KNL1	down_ACOR_VSMC
GO:0055080	0.874	0.193	13	176	cation homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,PDK2,FXN,SLC25A28,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:0030163	0.874	0.227	6	365	protein catabolic process	BP	1	CTSS,CLEC16A,CYLD,RAB7A,FAP,RNF181	up_AFEM_EC
GO:0051321	0.874	0.254	4	61	meiotic cell cycle	BP	1	ATRX,MARF1,DMC1,SUN1	up_ACOR_VSMC
GO:0090304	0.874	0.265	4	1694	nucleic acid metabolic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0034612	0.874	0.254	4	63	response to tumor necrosis factor	BP	1	F2RL1,ZFP36L1,ZFP36L2,BAG4	up_VSAP_EC
GO:0030177	0.874	0.275	3	51	positive regulation of Wnt signaling pathway	BP	1	ABL1,FAM53B,SULF2	up_VSAP_EC
GO:0044242	0.874	0.309	2	57	cellular lipid catabolic process	BP	1	SESN2,ABHD5	down_VSAP_EC
GO:0009142	0.874	0.311	2	46	nucleoside triphosphate biosynthetic process	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0021510	0.874	0.399	1	23	spinal cord development	BP	1	HOXC10	down_ACOR_VSMC
GO:0042278	0.874	0.398	1	25	purine nucleoside metabolic process	BP	1	RAN	down_ACOR_VSMC
GO:1903034	0.874	0.394	1	40	regulation of response to wounding	BP	1	RGMA	down_VCAV_EC
GO:0071248	0.874	0.396	1	35	cellular response to metal ion	BP	1	BNIP3	down_VSAP_EC
GO:0016239	0.874	0.401	1	20	positive regulation of macroautophagy	BP	1	BNIP3	up_ACOR_VSMC
GO:0051056	0.874	0.392	1	87	regulation of small GTPase mediated signal	BP	1	KANK1	up_AFEM_EC
GO:0014812	0.874	0.401	1	21	muscle cell migration	BP	1	SLIT2	up_VSAP_EC

GO:0042325	0.874	0.396	1	463	regulation of phosphorylation	BP	1	CAV1	up_VSAP_VSMC
GO:0043068	0.874133991	0.2709	3	190	positive regulation of programmed cell death	BP	1	IFIT2,CLU,PRKCD	up_ACOR_EC
GO:0045893	0.874632256	0.21096	8	413	positive regulation of transcription, DNA-	BP	1	GATA4,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:1901362	0.875	0.154	70	1293	organic cyclic compound biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,PGK1,TPI1,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,NMNAT2,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,APOE,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A,CMPK1	down_VSAP_EC
GO:0010557	0.875	0.172	25	492	positive regulation of macromolecule biosynthetic process	BP	1	ARHGEF2,VEGFA,ILK,PPP1R12A,SMARCA4,SESN2,TGFBR1,HIF1A,ZPR1,YES1,PEG3,DDX39B,CNOT7,MAGED1,CTNNB1,KLF5,DDIT3,ATF3,GTF2H1,ARMCX3,INHBA,NR4A1,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0050801	0.875	0.187	15	200	ion homeostasis	BP	1	HNF4A,C5AR2,SLC8B1,ABL1,GOT1,F2RL1,PDK2,FXN,SLC25A28,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:0001933	0.875	0.206	9	146	negative regulation of protein phosphorylation	BP	1	HMGCR,PPP1R15B,CAV1,NF2,CDKN2C,GREM1,NUP62,CACTIN,EZR	down_ACOR_VSMC
GO:0003012	0.875	0.226	6	90	muscle system process	BP	1	TPCN2,KCNE3,CHRM1,KLF15,TBXA2R,SULF2	up_VSAP_EC
GO:0021700	0.875	0.252	4	65	developmental maturation	BP	1	SEZ6L,IRX5,RECK,NTN4	up_VSAP_EC
GO:0009156	0.875	0.274	3	50	ribonucleoside monophosphate	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0048593	0.875	0.31	2	41	camera-type eye morphogenesis	BP	1	PHACTR4,HMGN1	down_ACOR_VSMC
GO:0051607	0.875	0.308	2	58	defense response to virus	BP	1	CNOT7,BNIP3	down_VSAP_EC
GO:0032204	0.875	0.312	2	35	regulation of telomere maintenance	BP	1	ATRX,HMBOX1	up_ACOR_VSMC
GO:0022029	0.875	0.397	1	23	telencephalon cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0022607	0.875	0.405	1	969	cellular component assembly	BP	1	HDAC7	down_VPOR_EC
GO:0032231	0.875	0.395	1	32	regulation of actin filament bundle assembly	BP	1	NRP1	down_VSAP_EC
GO:0061013	0.875	0.395	1	32	regulation of mRNA catabolic process	BP	1	CNOT7	down_VSAP_EC
GO:0035924	0.875	0.398	1	21	cellular response to vascular endothelial growth factor stimulus	BP	1	NRP1	up_ACOR_VSMC
GO:0001508	0.875	0.396	1	25	action potential	BP	1	KCNJ2	up_VCAV_EC
GO:0070887	0.875	0.401	1	775	cellular response to chemical stimulus	BP	1	FBP1	up_VFEM_VSMC
GO:1902017	0.875	0.399	1	21	regulation of cilium assembly	BP	1	FUZ	up_VSAP_EC
GO:0099175	0.875	0.399	1	21	regulation of postsynapse organization	BP	1	LRP4	up_VSAP_EC
GO:0097190	0.876	0.188	14	217	apoptotic signaling pathway	BP	1	SLC25A5,PRELID1,CAV1,CASP2,NOC2L,PPARD,HMGB2,SGPL1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1	down_ACOR_VSMC
GO:0014070	0.876	0.197	11	172	response to organic cyclic compound	BP	1	TFPI,NEDD4,INSIG1,CAV1,RAD51,THRAP3,EZH2,CDK4,PDXP,HMGB2,EZR	down_ACOR_VSMC
GO:1990778	0.876	0.224	6	91	protein localization to cell periphery	BP	1	FGF13,ACTN2,AR,DAG1,JUP,INPP5K	up_ACOR_VSMC
GO:2001233	0.876	0.233	5	149	regulation of apoptotic signaling pathway	BP	1	SLC35F6,TMEM161A,PARK7,GSDME,FBH1	down_VCAV_EC
GO:0035264	0.876	0.271	3	56	multicellular organism growth	BP	1	CDK4,EZR,SGPL1	down_ACOR_VSMC
GO:0051495	0.876	0.27	3	82	positive regulation of cytoskeleton organization	BP	1	WDR1,ACTR3,NRP1	down_VSAP_EC
GO:0044249	0.876	0.289	3	1851	cellular biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0003018	0.876	0.308	2	42	vascular process in circulatory system	BP	1	CAV1,TRPV4	down_ACOR_VSMC
GO:0036294	0.876	0.31	2	37	cellular response to decreased oxygen levels	BP	1	BNIP3,PRKCE	up_ACOR_VSMC

GO:0071456	0.876	0.31	2	37	cellular response to hypoxia	BP	1	BNIP3,PRKCE	up_ACOR_VSMC
GO:0002687	0.876	0.309	2	36	positive regulation of leukocyte migration	BP	1	F2RL1,ZNF580	up_VSAP_EC
GO:0001578	0.876	0.396	1	23	microtubule bundle formation	BP	1	TTLL1	down_ACOR_VSMC
GO:0032411	0.876	0.396	1	24	positive regulation of transporter activity	BP	1	GSTO1	down_ACOR_VSMC
GO:0043966	0.876	0.394	1	25	histone H3 acetylation	BP	1	GATA3	up_VCAV_EC
GO:0060341	0.876	0.388	1	255	regulation of cellular localization	BP	1	GCC2	up_VPOR_EC
GO:0008150	0.877	0.167	129	5646	biological_process	BP	1	TBX15,HOXA9,CMKLR1,MT2A,TRAPPC3L,IRX3,IRX5,HOXC10,HOXA10,LEP,KCNC4,LBH,PRR16,USP54,CDH18,CRY2,ENSCAFG00000009113,VPS26C,RAB20,XYLT1,GAS1,F5,ANGPT4,HOXA7,COL8A2,CD40,DLL1,CRYAB,CPNE7,KCND1,CTSS,F3,VXN,PLXNA4,BPI,GPAM,FIBIN,MLLT11,NEFH,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,SLC17A5,TWIST2,MAB21L1,THRB,LGI4,MYO1D,MFAP4,ATP6V1B2,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,KLHDC8B,HTR1D,NFE2L1,OVOL1,FAM53B,TPST2,AVPR1A,TENT5C,CAMK2A,GREM2,HOXA6,CLEC16A,CYLD,DNAL1,RASGEF1B,POSTN,SDR42E1,FXYD1,CHCHD10,LRRC15,FAM13A,ICAM5,LUZP1,MYBL1,RECK,NR3C1,PTHLH,TBXA2R,EVI2B,KIF1A,MOXD1,DCUN1D3,CNNM4,TFPI2,UNC45B,REEP2,EAF1,BVES,LGR6,ACKR4,RAB7A,PTPRB,AXIN2,YEATS2,ATP6V0B,ALDH3B1,ACACB,NAPEPLD,PPARGC1A,SPATA6,NIPAL1,CSGALNACT2,SLC46A2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SLC43A1,SAMD4B,CLIC4,LRRN2,AGPAT2,HSPB2,GCNT4,FOSL2,KANK1,TNC,KXD1,RNF181,ANXA11,SOD1	up_AFEM_EC
GO:0009889	0.877	0.156	52	1190	regulation of biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,AKT2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,EIF3K,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,CYBA,MAVS,LOXL3,ORMDL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0015031	0.877	0.163	35	510	protein transport	BP	1	HCLS1,GBP5,TMEM173,IWS1,FERMT1,TLR4,GATA3,RAB11A,RAB27A,EXOC6,PPP3CA,ARG2,HHEX,SCAMP1,ABCA1,SNX2,THOC1,AKAP12,APOD,CD200,CTDSPL2,PAN3,GCC2,STX11,SMG7,HMGB1,TBC1D1,NOS2,NUP133,MCU,HIF1A,IPO11,LMTK2,RABGAP1,USP6NL	up_VCAV_EC
GO:0006807	0.877	0.222	10	3221	nitrogen compound metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,HOXA1,ENSCAFG00000028814	up_APUL_EC
GO:0009165	0.877	0.215	7	104	nucleotide biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0051345	0.877	0.231	5	151	positive regulation of hydrolase activity	BP	1	PDGFRB,SNX18,AKT2,IFT57,EVI5L	down_VCAV_EC
GO:0035303	0.877	0.248	4	65	regulation of dephosphorylation	BP	1	PPARGC1B,SH2D4A,TMEM225B,BAG4	up_VSAP_EC
GO:0006950	0.877	0.275	3	1102	response to stress	BP	1	TLR2,CAV1,F5	up_VSAP_VSMC
GO:1903305	0.877	0.308	2	36	regulation of regulated secretory pathway	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0061035	0.877	0.393	1	24	regulation of cartilage development	BP	1	GREM1	down_ACOR_VSMC
GO:0090263	0.877	0.391	1	33	positive regulation of canonical Wnt signaling	BP	1	ILK	down_VSAP_EC
GO:0038034	0.877	0.395	1	21	signal transduction in absence of ligand	BP	1	UNC5B	up_ACOR_VSMC
GO:0097192	0.877	0.395	1	21	extrinsic apoptotic signaling pathway in	BP	1	UNC5B	up_ACOR_VSMC
GO:0000819	0.877	0.386	1	87	sister chromatid segregation	BP	1	AXIN2	up_AFEM_EC
GO:0015833	0.877	0.391	1	521	peptide transport	BP	1	NR1H4	up_APUL_EC
GO:0009057	0.877	0.392	1	473	macromolecule catabolic process	BP	1	TRIM9	up_VFEM_EC

GO:0071705	0.877	0.392	1	582	nitrogen compound transport	BP	1	NR1H4	up_VPUL_EC
GO:0043631	0.877	0.394	1	21	RNA polyadenylation	BP	1	CDK9	up_VSAP_EC
GO:1902680	0.877770046	0.20647	8	415	positive regulation of RNA biosynthetic process	BP	1	GATA4,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:1903508	0.877770046	0.20647	8	415	positive regulation of nucleic acid-templated	BP	1	GATA4,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:0010959	0.877782518	0.38406	1	79	regulation of metal ion transport	BP	1	ACTN2	up_ACOR_EC
GO:0019438	0.878	0.152	68	1258	aromatic compound biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,PGK1,TPI1,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A,CMPK1	down_VSAP_EC
GO:0070201	0.878	0.19	12	187	regulation of establishment of protein localization	BP	1	ACSL3,HMGB1,SREBF1,RAN,BIRC5,INSIG1,PLK3,ARG2,DMAP1,ENSCAFG00000005299,EZR,CCT4	down_ACOR_VSMC
GO:0009100	0.878	0.197	10	139	glycoprotein metabolic process	BP	1	NECAB3,GALNT15,HPSE,LMF1,FKRP,SULF2,GALNT11,CHST7,B3GALT4,SOAT1	up_VSAP_EC
GO:0060271	0.878	0.221	6	89	cilium assembly	BP	1	EVI5L,IFT43,ASAP1,DISC1,ATXN10,ENSCAFG00000013536	up_ACOR_VSMC
GO:0007178	0.878	0.221	6	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	FERMT1,SMAD1,BMP2,CTDSPL2,SKIL,ZEB1	up_VCAV_EC
GO:0031396	0.878	0.222	6	90	regulation of protein ubiquitination	BP	1	FAM107A,ABL1,SASH1,FBXO4,CDK9,ZER1	up_VSAP_EC
GO:0006790	0.878	0.231	5	99	sulfur compound metabolic process	BP	1	PIPOX,ACPP,CHST7,CHST1,ELOVL7	up_VCAV_EC
GO:0032496	0.878	0.232	5	77	response to lipopolysaccharide	BP	1	PTGFR,ABL1,TBXA2R,SASH1,MYD88	up_VSAP_EC
GO:0060538	0.878	0.269	3	51	skeletal muscle organ development	BP	1	CITED2,ANKRD1,BVES	up_ACOR_VSMC
GO:0002440	0.878	0.269	3	51	production of molecular mediator of immune	BP	1	STAT6,F2RL1,STX4	up_VSAP_EC
GO:0034404	0.878	0.268	3	50	nucleobase-containing small molecule	BP	1	GALK1,ENTPD3,DDIT4	up_VSAP_EC
GO:0051702	0.878	0.391	1	24	interaction with symbiont	BP	1	SMC3	down_ACOR_VSMC
GO:0000018	0.878	0.387	1	31	regulation of DNA recombination	BP	1	TFRC	down_VSAP_EC
GO:0007040	0.878	0.388	1	33	lysosome organization	BP	1	HOOK3	down_VSAP_EC
GO:0080171	0.878	0.388	1	33	lytic vacuole organization	BP	1	HOOK3	down_VSAP_EC
GO:0045851	0.878	0.393	1	21	pH reduction	BP	1	DMXL1	up_ACOR_VSMC
GO:0006839	0.878	0.383	1	86	mitochondrial transport	BP	1	CAMK2A	up_AFEM_EC
GO:0060395	0.878	0.389	1	27	SMAD protein signal transduction	BP	1	BMP2	up_VCAV_EC
GO:0060976	0.878	0.392	1	22	coronary vasculature development	BP	1	APLNR	up_VCAV_EC
GO:1903047	0.878	0.385	1	257	mitotic cell cycle process	BP	1	MZT1	up_VPOR_EC
GO:0022607	0.878	0.4	1	969	cellular component assembly	BP	1	SLIT2	up_VPUL_VSMC
GO:0065004	0.878703447	0.38204	1	81	protein-DNA complex assembly	BP	1	SOX9	up_ACOR_EC
GO:0008219	0.879	0.157	44	611	cell death	BP	1	HMGB1,RNPS1,MNDA,SLC29A1,MTDH,SLC25A5,PRELID1,BIRC5,CAV1,CDK1,CASP2,FAM129B,NF2,AURKB,GREM1,MAP3K20,TRIM35,PLK3,BID,ARG2,PDCD2,RNF152,DHCR24,NOC2L,EIF5A,B4GALT1,PPARD,CYCS,NUP62,EMP2,RSL1D1,HMGB2,ENSCAFG00000005299,CORO1A,SGPL1,SIGMAR1,MELK,TXNDC12,CTH,AIFM1,ARHGEF2,DELE1,SIX4,PIK3CD	down_ACOR_VSMC
GO:0022402	0.879	0.172	20	407	cell cycle process	BP	1	MYH9,PLK3,MZT1,PPP1R12A,TUBB,NAA10,ZPR1,EIF4EBP1,CTNNB1,KPNB1,ANLN,SND1,DDIT3,PDS5B,BACH1,HTT,RBBP8,CALM1,INHBA,CDKN1A	down_VSAP_EC

GO:0006793	0.879	0.178	18	948	phosphorus metabolic process	BP	1	LEP,GPAM,MYO1D,ATP6V1B2,HCK,GREM1,CAMK2A,CYLD,LRRC15,AXIN2,ACACB,NAPEPLD,PPARGC1A,CCL5,CDC42EP5,DMPK,ADAM17,AGPAT2	up_AFEM_EC
GO:0010604	0.879	0.233	5	919	positive regulation of macromolecule metabolic	BP	1	ARHGEF2,ENSCAFG00000002015,ACVR2A,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0032872	0.879	0.265	3	77	regulation of stress-activated MAPK cascade	BP	1	TNIK,SH3RF3,MID1	down_VSAP_EC
GO:0009855	0.879	0.303	2	42	determination of bilateral symmetry	BP	1	GREM1,RTTN	down_ACOR_VSMC
GO:1903311	0.879	0.301	2	72	regulation of mRNA metabolic process	BP	1	SAMD4B,ZFP36L1	down_VCAV_EC
GO:0035601	0.879	0.304	2	36	protein deacylation	BP	1	PRKAA2,LYPLAL1	up_ACOR_VSMC
GO:0098732	0.879	0.304	2	36	macromolecule deacylation	BP	1	PRKAA2,LYPLAL1	up_ACOR_VSMC
GO:0033043	0.879	0.3	2	446	regulation of organelle organization	BP	1	ARHGEF2,TWF1	up_VPOR_EC
GO:0042307	0.879	0.39	1	23	positive regulation of protein import into	BP	1	DMAP1	down_ACOR_VSMC
GO:0030856	0.879	0.384	1	41	regulation of epithelial cell differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0071346	0.879	0.385	1	41	cellular response to interferon-gamma	BP	1	RAB7B	down_VCAV_EC
GO:0030534	0.879	0.386	1	33	adult behavior	BP	1	HOMER1	down_VSAP_EC
GO:1905269	0.879	0.385	1	32	positive regulation of chromatin organization	BP	1	CTNNB1	down_VSAP_EC
GO:0071840	0.879	0.427	1	2059	cellular component organization or biogenesis	BP	1	TGFBI	down_VSAP_VSMC
GO:0002637	0.879	0.391	1	20	regulation of immunoglobulin	BP	1	TP53BP1	up_ACOR_VSMC
GO:0090183	0.879	0.391	1	21	regulation of kidney development	BP	1	BMP4	up_ACOR_VSMC
GO:0031647	0.879	0.381	1	87	regulation of protein stability	BP	1	CRYAB	up_AFEM_EC
GO:0035637	0.879	0.39	1	21	multicellular organismal signaling	BP	1	KCNE3	up_VSAP_EC
GO:0043500	0.879	0.39	1	21	muscle adaptation	BP	1	KLF15	up_VSAP_EC
GO:0098781	0.879	0.389	1	22	ncRNA transcription	BP	1	ICE1	up_VSAP_EC
GO:1904377	0.879	0.391	1	21	positive regulation of protein localization to cell	BP	1	STX4	up_VSAP_EC
GO:0050865	0.879364983	0.29772	2	135	regulation of cell activation	BP	1	NOD2,PRKCD	up_ACOR_EC
GO:1902115	0.879645855	0.38022	1	77	regulation of organelle assembly	BP	1	CHMP4B	up_ACOR_EC
GO:0048523	0.88	0.142	123	1399	negative regulation of cellular process	BP	1	FZD1,THRB,HOXA7,TWIST2,HOXA9,WNT11,HNF4A,FAM107A,CD274,ACKR3,AXIN2,C5AR2,INSIG2,PTGFR,SLC8B1,PPARGC1B,SH2D4A,TBC1D10C,CEP85,LIMS2,ACACB,SLIT2,CST3,CRADD,ZHX3,CDH1,ABL1,PEX2,BTG1,HDAC7,KCNE3,DLL1,EPN2,SESN1,OSR1,TENT5C,FUZ,SAV1,KLF15,ANXA4,ZBTB16,RARG,CBX7,STAT6,RECK,PLPP3,ENSCAFG00000000071,AMBRA1,F2RL1,GLIS2,MORC3,MFN2,ZFP36L1,PIK3R1,RBCK1,GAS1,MYC,PIK3IP1,PTGES,IRX3,ZEB1,TBXA2R,SULF2,SHOX2,TMEM225B,H2AFJ,ZC3H10,HIC1,RTN4RL1,FBXO4,CREBRF,POLDIP2,IKZF2,ATRIP,LRP4,PASK,ANKHD1,GDPD5,ZADH2,CASTOR1,PHF1,NPAS2,FBXO7,KCNB1,WISP2,LIMD1,NLRX1,ENSCAFG00000011993,TKFC,CDK9,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,HPGD,RAF1,MAPKBP1,NFIB,CYBA,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ARHGAP12,ACVRL1,TPRA1,UBQLN2,ARHGAP10,HTRA2,ASS1,TNRC6C,NCK1,ULK1,HMOX1,NPRL3,CITED2,BAG4,LBH,DPT,DDIT4,LATS2	up_VSAP_EC
GO:0051248	0.88	0.166	25	316	negative regulation of protein metabolic process	BP	1	TBC1D10C,CEP85,SLIT2,CST3,ABL1,KLF15,RECK,PLPP3,F2RL1,ZFP36L1,GAS1,MYC,RTN4RL1,ANKHD1,AZIN2,PHF1,FBXO7,FBLN1,SAMD4B,ZFP36L2,TIMP2,QARS,TNRC6C,NCK1,LATS2	up_VSAP_EC
GO:0033365	0.88	0.175	18	276	protein localization to organelle	BP	1	HCLS1,GBP5,TNFAIP3,TMEM173,FERMT1,RAB11A,PPP3CA,HOOK3,HHEX,CEP68,SH3GLB1,APOD,GCC2,NUP133,RAD21,ZW10,IPO11,ATRX	up_VCAV_EC

GO:0044237	0.88	0.216	11	3491	cellular metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,LZTS1,ZDHHC16,NPNT,NTRK2,HOXA1,ENSCAFG00000028814	up_APUL_EC
GO:2001233	0.88	0.198	9	149	regulation of apoptotic signaling pathway	BP	1	SLC25A5,PRELID1,CAV1,CASP2,NOC2L,HMGB2,TXNDC12,CTH,ARHGEF2	down_ACOR_VSMC
GO:0006732	0.88	0.21	7	107	coenzyme metabolic process	BP	1	MAT2B,PCBD1,ALDOC,DDIT4,PTS,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0006486	0.88	0.228	5	91	protein glycosylation	BP	1	MPDU1,SLC35C2,B3GNT2,B4GALT1,NUS1	down_ACOR_VSMC
GO:0043413	0.88	0.228	5	91	macromolecule glycosylation	BP	1	MPDU1,SLC35C2,B3GNT2,B4GALT1,NUS1	down_ACOR_VSMC
GO:0044282	0.88	0.229	5	89	small molecule catabolic process	BP	1	PPARD,PDXP,GALE,ACADL,NUDT3	down_ACOR_VSMC
GO:0034654	0.88	0.272	3	1236	nucleobase-containing compound biosynthetic	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0046890	0.88	0.265	3	51	regulation of lipid biosynthetic process	BP	1	INSIG2,ENSCAFG00000000071,IDH1	up_VSAP_EC
GO:0048518	0.88	0.318	2	1676	positive regulation of biological process	BP	1	HDAC7,CITED2	down_VPOR_EC
GO:0002761	0.88	0.303	2	36	regulation of myeloid leukocyte differentiation	BP	1	RASSF2,CLSTN1	up_ACOR_VSMC
GO:0030330	0.88	0.386	1	25	DNA damage response, signal transduction by p53 class mediator	BP	1	CASP2	down_ACOR_VSMC
GO:0034754	0.88	0.386	1	24	cellular hormone metabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0033108	0.88	0.383	1	39	mitochondrial respiratory chain complex assembly	BP	1	COA1	down_VCAV_EC
GO:0009893	0.88	0.395	1	995	positive regulation of metabolic process	BP	1	CITED2	down_VPOR_EC
GO:2001020	0.88	0.379	1	88	regulation of response to DNA damage stimulus	BP	1	AXIN2	up_AFEM_EC
GO:0042886	0.88	0.384	1	527	amide transport	BP	1	NR1H4	up_APUL_EC
GO:0006355	0.88	0.394	1	974	regulation of transcription, DNA-	BP	1	GATA5	up_VPUL_VSMC
GO:1901976	0.88	0.389	1	21	regulation of cell cycle checkpoint	BP	1	FBXO4	up_VSAP_EC
GO:0090183	0.88	0.388	1	21	regulation of kidney development	BP	1	OSR1	up_VSAP_EC
GO:0048585	0.88	0.384	1	475	negative regulation of response to stimulus	BP	1	CAV1	up_VSAP_VSMC
GO:0051641	0.881	0.178	16	858	cellular localization	BP	1	LEP,KCNC4,CRY2,VPS26C,GAS1,CRYAB,CHRM2,MYO1D,CAMK2A,CYLD,LRRC15,REEP2,BVES,RAB7A,AXIN2,KXD1	up_AFEM_EC
GO:1990778	0.881	0.227	5	91	protein localization to cell periphery	BP	1	ACSL3,CAV1,MMP14,EMP2,EZR	down_ACOR_VSMC
GO:0044249	0.881	0.239	5	1851	cellular biosynthetic process	BP	1	NR1H4,GALNT17,ZDHHC16,NPNT,HOXA1	up_APUL_EC
GO:0048511	0.881	0.297	2	72	rhythmic process	BP	1	NAGLU,FOXO3	down_VCAV_EC
GO:1902905	0.881	0.295	2	72	positive regulation of supramolecular fiber	BP	1	KIRREL1,ACTR3B	down_VCAV_EC
GO:0034250	0.881	0.299	2	45	positive regulation of cellular amide metabolic	BP	1	MTOR,NCK1	up_VCAV_EC
GO:0043507	0.881	0.386	1	23	positive regulation of JUN kinase activity	BP	1	MAP3K20	down_ACOR_VSMC
GO:0043620	0.881	0.384	1	24	regulation of DNA-templated transcription in	BP	1	NEDD4	down_ACOR_VSMC
GO:0060411	0.881	0.381	1	33	cardiac septum morphogenesis	BP	1	NRP1	down_VSAP_EC
GO:0032270	0.881	0.382	1	479	positive regulation of cellular protein metabolic	BP	1	MAP2K6	up_VFEM_EC
GO:0051049	0.881	0.382	1	479	regulation of transport	BP	1	TRIM9	up_VFEM_EC
GO:1903506	0.881	0.393	1	977	regulation of nucleic acid-templated transcription	BP	1	GATA5	up_VPUL_VSMC
GO:0042089	0.881	0.386	1	21	cytokine biosynthetic process	BP	1	MYD88	up_VSAP_EC
GO:0031503	0.881862104	0.37541	1	79	protein-containing complex localization	BP	1	CALY	up_ACOR_EC

GO:0065009	0.882	0.147	62	735	regulation of molecular function	BP	1	FZD1,CDON,MAP3K14,ARHGEF5,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,CST3,CRADD,TBC1D2B,ABL1,EBF2,EMP2,KCNE3,OSR1,MAP3K5,PDGFD,SAV1,C1QTNF2,ANXA4,CNPPD1,RECK,KLHL24,PLPP3,CAMKK2,AMBRA1,F2RL1,RBL2,LMF1,GLIS2,DDR2,TRAF7,PIK3R1,RBCK1,TIAM1,MYC,PIK3IP1,TMEM225B,RTN4RL1,SASH1,SBF2,LARP6,MYD88,PRKAB1,FBXO7,CDK9,PRMT2,RAF1,FXYD1,TIMP2,EIF3D,HTRA2,FLOT1,MAVS,ZER1,MAP2K2,TGFBR2,BAG4,KEAP1,LATS2	up_VSAP_EC
GO:0051270	0.882	0.169	20	296	regulation of cellular component movement	BP	1	HMGB1,RACGAP1,FBXO5,CFAP298,CAV1,MMP14,STMN1,HOXA7,B4GALT1,PRCP,RAP2C,RAC1,EMP2,CORO1A,ENSCAFG00000010224,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0007010	0.882	0.173	17	441	cytoskeleton organization	BP	1	KIRREL1,TLN2,CLIP3,RHOD,ENSCAFG00000014978,GABARAP,SYDE1,WIPF1,THY1,ARHGAP10,MYO1B,MAST2,ACTR3B,SHC1,PLEKHH2,RAC2,BRSK1	down_VCAV_EC
GO:0043086	0.882	0.192	10	170	negative regulation of catalytic activity	BP	1	PPP2R5A,TNFAIP3,AMOT,HHEX,PREX2,SH3BP5,PAK2,PTGS2,KDM5A,FKBP15	up_VCAV_EC
GO:0070482	0.882	0.24	4	75	response to oxygen levels	BP	1	CAV1,PLK3,PPARD,SUV39H1	down_ACOR_VSMC
GO:1903708	0.882	0.241	4	65	positive regulation of hemopoiesis	BP	1	CD83,ISG15,FAM210B,CLSTN1	up_ACOR_VSMC
GO:2001236	0.882	0.26	3	59	regulation of extrinsic apoptotic signaling	BP	1	CAV1,HMGB2,ARHGEF2	down_ACOR_VSMC
GO:1901576	0.882	0.278	3	1877	organic substance biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0007259	0.882	0.297	2	42	JAK-STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0031346	0.882	0.293	2	73	positive regulation of cell projection organization	BP	1	TRPV2,RAC2	down_VCAV_EC
GO:0031023	0.882	0.295	2	58	microtubule organizing center organization	BP	1	PPP1R12A,CTNNB1	down_VSAP_EC
GO:0008286	0.882	0.299	2	36	insulin receptor signaling pathway	BP	1	SESN3,INPP5K	up_ACOR_VSMC
GO:0099504	0.882	0.298	2	42	synaptic vesicle cycle	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0045669	0.882	0.381	1	24	positive regulation of osteoblast differentiation	BP	1	FBXO5	down_ACOR_VSMC
GO:0009201	0.882	0.378	1	41	ribonucleoside triphosphate biosynthetic	BP	1	ATP5MC1	down_VCAV_EC
GO:0002822	0.882	0.378	1	42	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BP	1	LOXL3	down_VCAV_EC
GO:0030879	0.882	0.378	1	34	mammary gland development	BP	1	HIF1A	down_VSAP_EC
GO:1903050	0.882	0.375	1	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0030512	0.882	0.382	1	24	negative regulation of transforming growth factor beta receptor	BP	1	SKIL	up_VCAV_EC
GO:0034637	0.882	0.381	1	25	cellular carbohydrate biosynthetic process	BP	1	IMPA1	up_VCAV_EC
GO:1903845	0.882	0.382	1	24	negative regulation of cellular response to transforming growth	BP	1	SKIL	up_VCAV_EC
GO:2001141	0.882	0.391	1	979	regulation of RNA biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0051145	0.882	0.383	1	21	smooth muscle cell differentiation	BP	1	ZEB1	up_VSAP_EC
GO:0008306	0.882	0.383	1	21	associative learning	BP	1	CTNS	up_VSAP_EC
GO:0060348	0.882476317	0.37414	1	78	bone development	BP	1	SOX9	up_ACOR_EC
GO:0051348	0.883	0.224	5	90	negative regulation of transferase activity	BP	1	HMGCR,CAV1,NF2,CDKN2C,NUP62	down_ACOR_VSMC
GO:0071383	0.883	0.26	3	58	cellular response to steroid hormone stimulus	BP	1	TFPI,NEDD4,THRAP3	down_ACOR_VSMC
GO:0043408	0.883	0.256	3	211	regulation of MAPK cascade	BP	1	LEP,CYLD,CCL5	up_AFEM_EC
GO:0030512	0.883	0.38	1	24	negative regulation of transforming growth factor beta receptor	BP	1	CAV1	down_ACOR_VSMC

GO:0061053	0.883	0.381	1	24	somite development	BP	1	SIX4	down_ACOR_VSMC
GO:1903845	0.883	0.38	1	24	negative regulation of cellular response to transforming growth	BP	1	CAV1	down_ACOR_VSMC
GO:0034440	0.883	0.377	1	35	lipid oxidation	BP	1	SESN2	down_VSAP_EC
GO:1904375	0.883	0.377	1	35	regulation of protein localization to cell	BP	1	KIF5B	down_VSAP_EC
GO:0016445	0.883	0.382	1	20	somatic diversification of immunoglobulins	BP	1	TP53BP1	up_ACOR_VSMC
GO:0016447	0.883	0.382	1	20	somatic recombination of immunoglobulin gene	BP	1	TP53BP1	up_ACOR_VSMC
GO:0051246	0.883	0.386	1	832	regulation of protein metabolic process	BP	1	TAOK1	up_AORT_EC
GO:0002718	0.883	0.381	1	21	regulation of cytokine production involved in	BP	1	F2RL1	up_VSAP_EC
GO:0071103	0.883066481	0.37279	1	80	DNA conformation change	BP	1	SOX9	up_ACOR_EC
GO:0071902	0.883894667	0.37105	1	79	positive regulation of protein serine/threonine	BP	1	FZD5	up_ACOR_EC
GO:0061061	0.884	0.18	13	179	muscle structure development	BP	1	FZD1,CDON,BTG1,DLL1,MAP3K5,SAV1,GTF3C5,ZFP36L1,ZEB1,SHOX2,CDK9,FLOT1,CITED2	up_VSAP_EC
GO:0060627	0.884	0.183	12	165	regulation of vesicle-mediated transport	BP	1	TBC1D10C,TBC1D2B,DLL1,F2RL1,RAB11B,GAS1,CYBA,STX4,VPS11,UBQLN2,FLOT1,PPP3CB	up_VSAP_EC
GO:0032787	0.884	0.198	8	144	monocarboxylic acid metabolic process	BP	1	EDN1,PTGS1,PROX1,ELOVL7,ENSCAFG00000024323,PTGS2,HIF1A,ALDH1A3	up_VCAV_EC
GO:0022618	0.884	0.212	6	111	ribonucleoprotein complex assembly	BP	1	SCAF11,CNOT6,PAN3,PRPF39,CNOT7,LSM14A	up_VCAV_EC
GO:0051348	0.884	0.213	6	90	negative regulation of transferase activity	BP	1	CEP85,ABL1,PIK3IP1,RTN4RL1,FBXO7,LATS2	up_VSAP_EC
GO:0098813	0.884	0.234	4	102	nuclear chromosome segregation	BP	1	NAA10,CTNNB1,KPNB1,PDS5B	down_VSAP_EC
GO:0048523	0.884	0.244	4	1399	negative regulation of cellular process	BP	1	HOXA9,PITX1,CAV1,SHOX2	up_VSAP_VSMC
GO:0009124	0.884	0.259	3	51	nucleoside monophosphate	BP	1	GALK1,ENSCAFG00000013366,DDIT4	up_VSAP_EC
GO:0031398	0.884	0.258	3	51	positive regulation of protein ubiquitination	BP	1	FAM107A,FBXO4,CDK9	up_VSAP_EC
GO:0006633	0.884	0.294	2	38	fatty acid biosynthetic process	BP	1	EDN1,ELOVL7	up_ACOR_VSMC
GO:0009791	0.884	0.294	2	38	post-embryonic development	BP	1	ABL1,MORC3	up_VSAP_EC
GO:0007584	0.884	0.377	1	24	response to nutrient	BP	1	PDXP	down_ACOR_VSMC
GO:0021885	0.884	0.377	1	24	forebrain cell migration	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0038202	0.884	0.378	1	24	TORC1 signaling	BP	1	RNF152	down_ACOR_VSMC
GO:0072384	0.884	0.378	1	24	organelle transport along microtubule	BP	1	TRAK1	down_ACOR_VSMC
GO:0097237	0.884	0.374	1	42	cellular response to toxic substance	BP	1	PARK7	down_VCAV_EC
GO:0030490	0.884	0.375	1	35	maturation of SSU-rRNA	BP	1	PDCD11	down_VSAP_EC
GO:0072329	0.884	0.376	1	34	monocarboxylic acid catabolic process	BP	1	SESN2	down_VSAP_EC
GO:0033046	0.884	0.38	1	21	negative regulation of sister chromatid	BP	1	ATRX	up_ACOR_VSMC
GO:0033048	0.884	0.38	1	21	negative regulation of mitotic sister chromatid	BP	1	ATRX	up_ACOR_VSMC
GO:0043967	0.884	0.38	1	21	histone H4 acetylation	BP	1	PHF20	up_ACOR_VSMC
GO:0051985	0.884	0.38	1	21	negative regulation of chromosome segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0045132	0.884	0.379	1	23	meiotic chromosome segregation	BP	1	CENPC	up_VCAV_EC
GO:0042632	0.884	0.377	1	27	cholesterol homeostasis	BP	1	ABCA1	up_VCAV_EC
GO:0000959	0.884	0.38	1	21	mitochondrial RNA metabolic process	BP	1	PPARGC1B	up_VSAP_EC
GO:0007189	0.884	0.38	1	22	adenylate cyclase-activating G protein-coupled receptor signaling	BP	1	ADGRD1	up_VSAP_EC

GO:0050896	0.885	0.134	185	2346	response to stimulus	BP	1	ELK3,HMGB1,SREBF1,FLNB,USP1,IRAK1,MCM7,RPA1,DDX39A,CBX5,RACGAP1,HMGA1,HMGCR,HNRNPUL1,TFPI,SREBF2,SMC1A,TFPI2,HINFP,NEDD4,WDR76,INTS7,MNDA,POLA1,SLC29A1,MTDH,HEY1,RRBP1,TRIP13,SLC25A5,PPP1R15B,PARPBP,GINS4,SDC1,CTDNEP1,RAD54L,RANGAP1,POLE,SLC35C2,TENT4A,B3GNT2,PRELID1,HM13,UBE2T,RFC2,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CDK1,RFC5,RFC3,RAD51,CASP2,FANCI,FANCD2,TIMELESS,THRAP3,ENSCAFG00000008236,NF2,AURKB,PSD4,MMP14,TOPBP1,EZH2,STMN1,DEPDC1,SLC30A1,PPP2R5D,GREM1,MAP3K20,RFC4,ADIPOR2,FEN1,CDK4,TRIM35,SMARCC1,MND1,RNASEH2B,PLK3,PCNA,DHX33,TONSL,ARG2,ANXA5,MCM10,RNF152,DHCR24,BRCA1,NOC2L,B4GALT1,PRCP,TFRC,NRAS,PPARD,POLH,ITGB3,NEIL3,RAP2C,UBE2J2,ARHGDIA,YWHAB,FAM49B,AHSA1,NCL,RAC1,NUP62,EMP2,DTL,GNB2,PDXP,FOSL1,IQGAP1,SUV39H1,HASPIN,RSL1D1,IQGAP2,CACTIN,HMGB2,GSTO1,DMAP1,CDC42EP4,CDK2,FGF5,SMARCB1,DDX39B,ENSCAFG00000030087,CCNA2,SNX15,ENSCAFG00000005299,RBBP8,EZR,CLSPN,SMC6,RBM14,MIOS,RBM17,RAD23A,CORO1A,SGPL1,BEND6,POLR3F,PHACTR4,SIGMAR1,B	down_ACOR_VSMC
GO:0032269	0.885	0.16	24	306	negative regulation of cellular protein metabolic process	BP	1	TBC1D10C,CEP85,SLIT2,CST3,ABL1,KLF15,RECK,PLPP3,F2RL1,ZFP36L1,GAS1,MYC,RTN4RL1,ANKHD1,PHF1,FBXO7,FBLN1,SAMD4B,ZFP36L2,TIMP2,QARS,TNRC6C,NCK1,LATS2	up_VSAP_EC
GO:1901361	0.885	0.184	11	154	organic cyclic compound catabolic process	BP	1	PNRC1,PDE5A,MAOA,ENPP4,DCP1B,MOXD1,ALDOC,ENTPD3,DDIT4,CNOT4,CTIF	up_ACOR_VSMC
GO:0008150	0.885	0.278	10	5646	biological_process	BP	1	CST3,HDAC7,CITED2,GSTP1,RAB11B,ERGIC1,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0051301	0.885	0.197	8	117	cell division	BP	1	FGF7,DLL1,ZNF449,ZBTB16,MYC,ZFP36L2,TPRA1,LBH	up_VSAP_EC
GO:0002791	0.885	0.21	6	104	regulation of peptide secretion	BP	1	HMGB1,SREBF1,BIRC5,ARG2,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0051222	0.885	0.21	6	103	positive regulation of protein transport	BP	1	ACSL3,HMGB1,RAN,PLK3,DMAP1,EZR	down_ACOR_VSMC
GO:0062012	0.885	0.253	3	100	regulation of small molecule metabolic	BP	1	AKT2,PARK7,LONP2	down_VCAV_EC
GO:0009615	0.885	0.253	3	83	response to virus	BP	1	ACTA2,CNOT7,BNIP3	down_VSAP_EC
GO:0006810	0.885	0.263	3	1244	transport	BP	1	NR1H4,HOXA3,NTRK2	up_APUL_EC
GO:0042157	0.885	0.256	3	51	lipoprotein metabolic process	BP	1	APOL5,ZDHHC8,LCAT	up_VSAP_EC
GO:0007041	0.885	0.292	2	41	lysosomal transport	BP	1	NEDD4,TRAK1	down_ACOR_VSMC
GO:0045926	0.885	0.289	2	72	negative regulation of growth	BP	1	NOTCH2,MT2A	down_VCAV_EC
GO:0046578	0.885	0.288	2	77	regulation of Ras protein signal transduction	BP	1	NOTCH2,ARHGEF25	down_VCAV_EC
GO:1901565	0.885	0.289	2	442	organonitrogen compound catabolic	BP	1	USP33,RNF6	up_VPOR_EC
GO:0036294	0.885	0.292	2	37	cellular response to decreased oxygen levels	BP	1	ZFP36L1,HMOX1	up_VSAP_EC
GO:0071456	0.885	0.292	2	37	cellular response to hypoxia	BP	1	ZFP36L1,HMOX1	up_VSAP_EC
GO:0019882	0.885	0.376	1	25	antigen processing and presentation	BP	1	RAB35	down_ACOR_VSMC
GO:0055067	0.885	0.371	1	42	monovalent inorganic cation homeostasis	BP	1	ATP6V0C	down_VCAV_EC
GO:0060021	0.885	0.372	1	34	roof of mouth development	BP	1	INHBA	down_VSAP_EC
GO:0010718	0.885	0.378	1	21	positive regulation of epithelial to mesenchymal	BP	1	BMP4	up_ACOR_VSMC
GO:0038202	0.885	0.375	1	24	TORC1 signaling	BP	1	MTOR	up_VCAV_EC
GO:1901698	0.885	0.37	1	266	response to nitrogen compound	BP	1	ARHGEF2	up_VPOR_EC
GO:0055117	0.885	0.378	1	21	regulation of cardiac muscle contraction	BP	1	KCNE3	up_VSAP_EC
GO:0038034	0.885	0.378	1	21	signal transduction in absence of ligand	BP	1	HTRA2	up_VSAP_EC
GO:0097192	0.885	0.378	1	21	extrinsic apoptotic signaling pathway in	BP	1	HTRA2	up_VSAP_EC
GO:0002696	0.885603562	0.36731	1	80	positive regulation of leukocyte activation	BP	1	NOD2	up_ACOR_EC

GO:0008202	0.885886662	0.36669	1	80	steroid metabolic process	BP	1	NR1H4	up_ACOR_EC
GO:0031326	0.886	0.146	51	1176	regulation of cellular biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,AKT2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,EIF3K,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,MAVS,LOXL3,ORMDL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,FOXO3,SOAT1,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:1901566	0.886	0.147	48	598	organonitrogen compound biosynthetic process	BP	1	TLR1,GALNT3,GALNT10,ST3GAL5,B3GALNT2,ITM2C,LCAT,B3GNT7,PCBD1,CCDC126,ABCA1,EIF4A2,TARSL2,TLR3,PPARGC1A,PIGN,PIGS,UGCG,ADCY6,PIGG,FAM129A,DAPK1,RBM4B,MAGT1,STT3B,ORMDL3,SMPD1,FUT11,MOXD1,FUT8,ENSCAFG00000018611,POMK,APP,PSEN1,PIK3C3,ALDOC,DDIT4,EOGT,AZIN2,PTS,UBA52,CTIF,NMNAT1,PARK7,ELOVL7,NGRN,ZDHHC21,LMF1	up_ACOR_VSMC
GO:0070647	0.886	0.163	21	311	protein modification by small protein conjugation or removal	BP	1	USP1,USP4,UBE2S,U2AF2,SLC29A1,UBE2T,CAV1,FANCI,UHRF1,RNF152,BRCA1,UBE2J2,DTL,UBE2K,CDC20,BAP1,UBE2C,UBA2,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0019725	0.886	0.17	16	245	cellular homeostasis	BP	1	HMGB1,UBE2S,QSOX2,BIRC5,CAV1,SLC30A1,TFRC,GSTO1,ENSCAFG00000005299,CORO1A,PRDX1,ENSCAFG00000006478,TXNDC12,UBE2C,THADA,ANXA7	down_ACOR_VSMC
GO:0071840	0.886	0.185	13	2059	cellular component organization or biogenesis	BP	1	MZT1,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,FBP1,RSL24D1,GCC2,RPL10L,TWF1,RRP15,SRP54,RNF6	up_VPOR_EC
GO:0019220	0.886	0.19	9	525	regulation of phosphate metabolic process	BP	1	LEP,MYO1D,GREM1,CYLD,LRRC15,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0051174	0.886	0.19	9	525	regulation of phosphorus metabolic process	BP	1	LEP,MYO1D,GREM1,CYLD,LRRC15,AXIN2,PPARGC1A,CCL5,ADAM17	up_AFEM_EC
GO:0009141	0.886	0.202	7	110	nucleoside triphosphate metabolic process	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,ENTPD3,DDIT4,NMNAT1,PARK7	up_ACOR_VSMC
GO:0034976	0.886	0.209	6	112	response to endoplasmic reticulum stress	BP	1	CXCL8,ATF3,NCK1,PDIA5,USP13,ATP2A1	up_VCAV_EC
GO:0060271	0.886	0.22	5	89	cilium assembly	BP	1	CFAP298,POC1A,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0006887	0.886	0.252	3	99	exocytosis	BP	1	SDC4,RAB31,RAC2	down_VCAV_EC
GO:0007517	0.886	0.252	3	100	muscle organ development	BP	1	BMPR1A,TSC22D3,GREM1	down_VCAV_EC
GO:0140013	0.886	0.255	3	50	meiotic nuclear division	BP	1	MARF1,DMC1,SUN1	up_ACOR_VSMC
GO:1903052	0.886	0.254	3	51	positive regulation of proteolysis involved in cellular protein catabolic	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:0098656	0.886	0.289	2	42	anion transmembrane transport	BP	1	SLC35C2,SLC25A19	down_ACOR_VSMC
GO:0016571	0.886	0.29	2	39	histone methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:0008585	0.886	0.373	1	24	female gonad development	BP	1	SGPL1	down_ACOR_VSMC
GO:0002286	0.886	0.374	1	24	T cell activation involved in immune response	BP	1	HMGB1	down_ACOR_VSMC
GO:0002532	0.886	0.373	1	25	production of molecular mediator involved in inflammatory response	BP	1	BAP1	down_ACOR_VSMC
GO:0048278	0.886	0.372	1	25	vesicle docking	BP	1	CEP83	down_ACOR_VSMC
GO:0061515	0.886	0.373	1	24	myeloid cell development	BP	1	JMJD6	down_ACOR_VSMC
GO:0046545	0.886	0.373	1	24	development of primary female sexual	BP	1	SGPL1	down_ACOR_VSMC
GO:0030073	0.886	0.369	1	42	insulin secretion	BP	1	PARK7	down_VCAV_EC
GO:0033866	0.886	0.375	1	22	nucleoside bisphosphate biosynthetic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034030	0.886	0.375	1	22	ribonucleoside bisphosphate biosynthetic	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034033	0.886	0.375	1	22	purine nucleoside bisphosphate biosynthetic	BP	1	ELOVL7	up_ACOR_VSMC
GO:1902017	0.886	0.375	1	21	regulation of cilium assembly	BP	1	EVI5L	up_ACOR_VSMC
GO:0009893	0.886	0.383	1	995	positive regulation of metabolic process	BP	1	GATA5	up_VPUL_VSMC

GO:0000462	0.886	0.375	1	22	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S	BP	1	RCL1	up_VSAP_EC
GO:0042981	0.886	0.371	1	471	regulation of apoptotic process	BP	1	CAV1	up_VSAP_VSMC
GO:0048285	0.887	0.199	7	166	organelle fission	BP	1	MZT1,ENSCAFG00000007260,NAA10,KPNB1,BNIP3,PDS5B,SLC25A46	down_VSAP_EC
GO:0043603	0.887	0.206	6	372	cellular amide metabolic process	BP	1	PRR16,GPAM,ACACB,NAPEPLD,CTIF,SAMD4B	up_AFEM_EC
GO:0120031	0.887	0.215	5	154	plasma membrane bounded cell projection	BP	1	RHOD,TTC8,IFT57,EVI5L,RAC2	down_VCAV_EC
GO:0021537	0.887	0.232	4	73	telencephalon development	BP	1	NF2,WDR62,ASPM,ENSCAFG00000010224	down_ACOR_VSMC
GO:0009205	0.887	0.25	3	98	purine ribonucleoside triphosphate metabolic	BP	1	ATP5MC1,UQCR10,PARK7	down_VCAV_EC
GO:0009799	0.887	0.287	2	43	specification of symmetry	BP	1	GREM1,RTTN	down_ACOR_VSMC
GO:0030518	0.887	0.288	2	42	intracellular steroid hormone receptor	BP	1	NEDD4,THRAP3	down_ACOR_VSMC
GO:0042147	0.887	0.288	2	38	retrograde transport, endosome to Golgi	BP	1	SGSM2,VPS26A	up_ACOR_VSMC
GO:0043902	0.887	0.287	2	45	positive regulation of multi-organism process	BP	1	SMARCA4,CNOT7	up_VCAV_EC
GO:0002768	0.887	0.288	2	37	immune response-regulating cell surface receptor signaling	BP	1	ABL1,RBCK1	up_VSAP_EC
GO:0001508	0.887	0.372	1	25	action potential	BP	1	CAV1	down_ACOR_VSMC
GO:0015698	0.887	0.371	1	24	inorganic anion transport	BP	1	SLC20A1	down_ACOR_VSMC
GO:0030500	0.887	0.371	1	25	regulation of bone mineralization	BP	1	GREM1	down_ACOR_VSMC
GO:0060324	0.887	0.371	1	24	face development	BP	1	SGPL1	down_ACOR_VSMC
GO:0042471	0.887	0.368	1	34	ear morphogenesis	BP	1	SIX4	down_VSAP_EC
GO:0042136	0.887	0.374	1	21	neurotransmitter biosynthetic process	BP	1	MOXD1	up_ACOR_VSMC
GO:0071674	0.887	0.371	1	23	mononuclear cell migration	BP	1	CCL5	up_ACOR_VSMC
GO:0031349	0.887	0.364	1	90	positive regulation of defense response	BP	1	NAPEPLD	up_AFEM_EC
GO:0031396	0.887	0.364	1	90	regulation of protein ubiquitination	BP	1	DCUN1D3	up_AFEM_EC
GO:0009408	0.887	0.37	1	27	response to heat	BP	1	CD34	up_VCAV_EC
GO:0043271	0.887	0.37	1	28	negative regulation of ion transport	BP	1	STC1	up_VCAV_EC
GO:0006368	0.887	0.371	1	22	transcription elongation from RNA polymerase II	BP	1	CDK9	up_VSAP_EC
GO:1902105	0.887989252	0.3621	1	80	regulation of leukocyte differentiation	BP	1	CLSTN1	up_ACOR_EC
GO:0045892	0.888	0.155	26	328	negative regulation of transcription, DNA-templated	BP	1	LEP,NACC2,BMP4,FGFR2,ATRX,TRPS1,ZNF174,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0051726	0.888	0.163	19	393	regulation of cell cycle	BP	1	ASNS,PLK3,PTPN11,TNIK,NAA10,DDX39B,EIF4EBP1,CTNNB1,SND1,CDK8,DDIT3,CCNYL1,CALM1,RAD23A,PAK2,INHBA,NR4A1,CDKN1A,MADD	down_VSAP_EC
GO:0043436	0.888	0.163	19	303	oxoacid metabolic process	BP	1	PDGFB,ST6GAL1,EDN1,PIPOX,PTGS1,ODC1,ARG2,TARSL2,CHST7,AADAT,PROX1,CHST1,ELOVL7,ENSCAFG00000024323,PTGS2,GCH1,HIF1A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0006469	0.888	0.216	5	78	negative regulation of protein kinase activity	BP	1	CEP85,ABL1,RTN4RL1,FBXO7,LATS2	up_VSAP_EC
GO:0019438	0.888	0.258	3	1258	aromatic compound biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0090257	0.888	0.251	3	52	regulation of muscle system process	BP	1	KCNE3,CHRM1,TBXA2R	up_VSAP_EC
GO:0043966	0.888	0.368	1	25	histone H3 acetylation	BP	1	POLE3	down_ACOR_VSMC
GO:0071621	0.888	0.369	1	27	granulocyte chemotaxis	BP	1	RAC1	down_ACOR_VSMC
GO:0009116	0.888	0.366	1	39	nucleoside metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:0043487	0.888	0.367	1	33	regulation of RNA stability	BP	1	SMG7	down_VSAP_EC

GO:0099175	0.888	0.371	1	21	regulation of postsynapse organization	BP	1	EGLN1	up_ACOR_VSMC
GO:0051348	0.888	0.362	1	90	negative regulation of transferase activity	BP	1	LRRC15	up_AFEM_EC
GO:0051641	0.888	0.373	1	858	cellular localization	BP	1	ENSCAFG00000005494	up_AORT_EC
GO:0001578	0.888	0.37	1	23	microtubule bundle formation	BP	1	FES	up_VCAV_EC
GO:0001736	0.888	0.369	1	23	establishment of planar polarity	BP	1	EXOC5	up_VCAV_EC
GO:0007164	0.888	0.369	1	23	establishment of tissue polarity	BP	1	EXOC5	up_VCAV_EC
GO:0032880	0.888	0.363	1	266	regulation of protein localization	BP	1	GCC2	up_VPOR_EC
GO:0051341	0.888	0.371	1	22	regulation of oxidoreductase activity	BP	1	ABL1	up_VSAP_EC
GO:0050789	0.889	0.134	154	3295	regulation of biological process	BP	1	CST3,GPAM,NOTCH2,HSPB6,PDGFRB,SLC35F6,KIRREL1,FBLN2,SMAD9,ITGB5,LRP1,DCN,CFD,NAB2,NDN,ANGPT1,PRNP,LUM,MT2A,SDC4,VASN,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,SH3BP1,BMPR1A,NABP2,LMO4,EVC,RECK,FXYD1,IGFBP6,TRPV2,CLIP3,NUMBL,CHID1,ARHGEF25,RHOD,OSMR,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,DOCK10,PSMF1,LCAT,SAMD4B,EEF2K,TFE3,NR3C1,SYDE1,HR,SCP2,PDIA4,LAMA3,CLSTN1,PLCL1,CACNB3,CSPG4,TRIM8,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,CXXC5,SEMA3C,ASPN,POLDIP2,LRPAP1,GNAZ,EIF3K,THY1,NECAB3,RNF216,TEAD1,PEX5,ARHGAP10,TLX2,CC2D1A,ATP6V0C,B4GALT1,GLI3,PARK7,ZMAT3,ADAMTSL4,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,BPI,CYBA,ENSCAFG00000018194,RBM38,ARL2BP,IFT57,MAVS,CDH2,EDIL3,LOXL3,ORMDL3,GSDME,LSM10,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,MGARP,ACTR3B,RAB7B,A2M,SPNS1,IRX5,TSC22D3,UST,MAPRE3,GLIS2,TWIST2,ARHGAP1,PRKCSH,DDR2,SHC1,PYM1,CRCP,FBH1,OMD,GREM1,PLEKHH2,NPHP4,EVI5L,LONP2,RAC2,NAPEPLD,CLIC4,GLS2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,ANK	down_VCAV_EC
GO:1901293	0.889	0.198	7	106	nucleoside phosphate biosynthetic process	BP	1	PPARGC1A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,ELOVL7	up_ACOR_VSMC
GO:0061061	0.889	0.204	6	179	muscle structure development	BP	1	BMPR1A,ZFP36L1,RBM38,CDH2,TSC22D3,GREM1	down_VCAV_EC
GO:0045732	0.889	0.215	5	78	positive regulation of protein catabolic process	BP	1	SH3RF2,RNF19A,PSEN1,DISC1,HERPUD1	up_ACOR_VSMC
GO:0043588	0.889	0.228	4	74	skin development	BP	1	FLNB,STMN1,HOXA7,DHCR24	down_ACOR_VSMC
GO:0006473	0.889	0.229	4	66	protein acetylation	BP	1	NAA60,KLF15,EHHADH,DR1	up_VSAP_EC
GO:0031667	0.889	0.246	3	102	response to nutrient levels	BP	1	KANK2,GABARAP,CLEC16A	down_VCAV_EC
GO:0018130	0.889	0.256	3	1261	heterocycle biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0043588	0.889	0.281	2	74	skin development	BP	1	ADAMTS2,ZFP36L1	down_VCAV_EC
GO:0050770	0.889	0.285	2	39	regulation of axonogenesis	BP	1	IFRD1,RAB11A	up_VCAV_EC
GO:0006664	0.889	0.285	2	37	glycolipid metabolic process	BP	1	KDELC2,B3GALT4	up_VSAP_EC
GO:0016525	0.889	0.285	2	38	negative regulation of angiogenesis	BP	1	EPN2,TBXA2R	up_VSAP_EC
GO:1903509	0.889	0.285	2	37	liposaccharide metabolic process	BP	1	KDELC2,B3GALT4	up_VSAP_EC
GO:2000181	0.889	0.285	2	38	negative regulation of blood vessel	BP	1	EPN2,TBXA2R	up_VSAP_EC
GO:0006942	0.889	0.367	1	26	regulation of striated muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0010646	0.889	0.374	1	945	regulation of cell communication	BP	1	IVNS1ABP	down_AFEM_EC
GO:0006874	0.889	0.359	1	91	cellular calcium ion homeostasis	BP	1	DMPK	up_AFEM_EC
GO:0043648	0.889	0.366	1	26	dicarboxylic acid metabolic process	BP	1	AADAT	up_VCAV_EC
GO:0051310	0.889	0.368	1	22	metaphase plate congression	BP	1	TTL	up_VSAP_EC
GO:0006839	0.889944361	0.35756	1	86	mitochondrial transport	BP	1	SLC25A42	up_ACOR_EC

GO:0051130	0.89	0.151	27	342	positive regulation of cellular component organization	BP	1	SYNPO2L,ACTN2,PLCG2,LNPK,SYNPO2,ATRX,PPARGC1A,F2RL1,MARCH5,BNIP3,JMY,NRP1,EVL,SLITRK5,PRKCE,DAG1,APP,PSEN1,DDR2,EDN1,ASAP1,B2M,WASL,DOCK5,HMBOX1,RREB1,CRKL	up_ACOR_VSMC
GO:0003006	0.89	0.171	13	180	developmental process involved in reproduction	BP	1	HOXA11,HOXA9,HNF4A,GJB5,IRX5,SLIT2,OSR1,ZBTB16,RARG,PATZ1,DLX3,ZFP36L1,CITED2	up_VSAP_EC
GO:0009314	0.89	0.18	10	143	response to radiation	BP	1	MFAP4,HRH1,LRRN4,TP53INP1,RBM4B,CDKN1A,APP,XRRA1,DMC1,GNAQ	up_ACOR_VSMC
GO:0048568	0.89	0.201	6	148	embryonic organ development	BP	1	TMED2,HOXB7,HIF1A,CTNNB1,SH2B3,SIX4	down_VSAP_EC
GO:0030031	0.89	0.211	5	155	cell projection assembly	BP	1	RHOD,TTC8,IFT57,EVI5L,RAC2	down_VCAV_EC
GO:1901576	0.89	0.225	5	1877	organic substance biosynthetic process	BP	1	NR1H4,GALNT17,ZDHHC16,NPNT,HOXA1	up_APUL_EC
GO:0010256	0.89	0.224	4	129	endomembrane system organization	BP	1	ATP8B2,AKT2,PEX5,PACSIN3	down_VCAV_EC
GO:0006473	0.89	0.227	4	66	protein acetylation	BP	1	PRKAA2,PHF20,MAP3K7,PARK7	up_ACOR_VSMC
GO:0060560	0.89	0.247	3	58	developmental growth involved in	BP	1	SLC29A1,IQGAP1,SIX4	down_ACOR_VSMC
GO:0051260	0.89	0.245	3	100	protein homooligomerization	BP	1	PRNP,B4GALT1,SCARA5	down_VCAV_EC
GO:0008219	0.89	0.247	3	611	cell death	BP	1	ARHGEF2,MTDH,STK17B	up_VPOR_EC
GO:0009058	0.89	0.264	3	1910	biosynthetic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0046822	0.89	0.248	3	53	regulation of nucleocytoplasmic	BP	1	CDH1,PIK3R1,MAVS	up_VSAP_EC
GO:0055076	0.89	0.283	2	44	transition metal ion homeostasis	BP	1	SLC30A1,TFRC	down_ACOR_VSMC
GO:0097696	0.89	0.282	2	43	STAT cascade	BP	1	CAV1,NF2	down_ACOR_VSMC
GO:0033045	0.89	0.283	2	38	regulation of sister chromatid segregation	BP	1	AXIN2,CDC26	up_VSAP_EC
GO:0000288	0.89	0.365	1	25	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	BP	1	EXOSC5	down_ACOR_VSMC
GO:2001244	0.89	0.363	1	27	positive regulation of intrinsic apoptotic	BP	1	CAV1	down_ACOR_VSMC
GO:0070371	0.89	0.357	1	91	ERK1 and ERK2 cascade	BP	1	CCL5	up_AFEM_EC
GO:1990778	0.89	0.358	1	91	protein localization to cell periphery	BP	1	LRRC15	up_AFEM_EC
GO:0051246	0.89	0.37	1	832	regulation of protein metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0007601	0.89	0.365	1	22	visual perception	BP	1	PDE6D	up_VSAP_EC
GO:0050953	0.89	0.365	1	22	sensory perception of light stimulus	BP	1	PDE6D	up_VSAP_EC
GO:0008037	0.89	0.365	1	22	cell recognition	BP	1	AMIGO1	up_VSAP_EC
GO:0043067	0.89	0.363	1	479	regulation of programmed cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0001819	0.891	0.194	7	120	positive regulation of cytokine production	BP	1	HMGB1,IRAK1,DHX33,FAM49B,HMGB2,POLR3F,ARHGEF2	down_ACOR_VSMC
GO:0043393	0.891	0.224	4	77	regulation of protein binding	BP	1	HOXA3,CAV1,AURKB,STMN1	down_ACOR_VSMC
GO:0042113	0.891	0.226	4	64	B cell activation	BP	1	PLCG2,TP53BP1,CDKN1A,NOD2	up_ACOR_VSMC
GO:0010212	0.891	0.279	2	60	response to ionizing radiation	BP	1	CRYAB,CDKN1A	down_VSAP_EC
GO:0007498	0.891	0.281	2	38	mesoderm development	BP	1	BMP4,CITED2	up_ACOR_VSMC
GO:0010906	0.891	0.281	2	38	regulation of glucose metabolic process	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:0051171	0.891	0.298	2	1697	regulation of nitrogen compound metabolic	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0002312	0.891	0.363	1	24	B cell activation involved in immune response	BP	1	TFRC	down_ACOR_VSMC
GO:0072665	0.891	0.363	1	25	protein localization to vacuole	BP	1	NEDD4	down_ACOR_VSMC
GO:0034341	0.891	0.357	1	43	response to interferon-gamma	BP	1	RAB7B	down_VCAV_EC
GO:0006900	0.891	0.364	1	21	vesicle budding from membrane	BP	1	SEC24B	up_ACOR_VSMC
GO:0043618	0.891	0.364	1	22	regulation of transcription from RNA polymerase II promoter in response to	BP	1	CHD6	up_ACOR_VSMC

GO:0070972	0.891	0.363	1	23	protein localization to endoplasmic reticulum	BP	1	OS9	up_ACOR_VSMC
GO:0009060	0.891	0.359	1	31	aerobic respiration	BP	1	HIF1A	up_VCAV_EC
GO:0050806	0.891	0.362	1	25	positive regulation of synaptic transmission	BP	1	RELN	up_VCAV_EC
GO:0014855	0.891	0.363	1	22	striated muscle cell proliferation	BP	1	SAV1	up_VSAP_EC
GO:0060255	0.892	0.127	158	1782	regulation of macromolecule metabolic process	BP	1	HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,HNF4A,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PTGFR,ZNF367,PPARGC1B,TBC1D10C,CEP85,ACACB,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,HDAC7,EMP2,DLL1,OSR1,MAP3K5,TENT5C,PDGFD,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,CBX7,STAT6,RECK,GATAD1,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,TNKS1BP1,PYM1,F2RL1,RBL2,GLIS2,DDR2,ICE1,ZFP36L1,TRAF7,PIK3R1,RBCK1,GAS1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,PASK,NUP98,ANKHD1,AZIN2,TRERF1,PHF1,E2F4,NPAS2,PRKAB1,SMG9,FBXO7,LIMD1,RNF166,RPUSD4,PC,CDK9,PRMT2,KDM2B,FBLN1,OSBPL7,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ZNF580,ABHD14B,ZNF205,NCOA2,EIF3K,PQBP1,TIMP2,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,UBQLN2,ZNF517,HTRA2,FLOT1,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,ZER1,MAP2K2,TGFBR2,CITED2,BAG4,CXXC1,LBH,KEAP1,ZNF772,SOAT1,LATS2	up_VSAP_EC
GO:0010467	0.892	0.131	97	1787	gene expression	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,SERPINH1,CARS,MYH9,NR1H4,PLK3,SERPINE1,ETV6,MEIS2,ERO1A,PRKACB,ENSCAFG00000005575,CBX5,SARS,PGK1,AARS,TMED2,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,MSN,HIF1A,FOXP4,MRPL1,IWS1,ACTG2,NAA10,ZPR1,PTPN2,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,CRYAB,SND1,ENSCAFG00000002015,APOE,WWC3,PDCD11,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,CDC37,GTF2H1,ARMCX3,REST,ZMYND8,MAPK10,EIF2S1,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,CDYL,A2M,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,RTCB,SNRPA1,KDM3A	down_VSAP_EC
GO:0010556	0.892	0.137	61	1137	regulation of macromolecule biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,AARS,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0044255	0.892	0.167	13	293	cellular lipid metabolic process	BP	1	NR1H4,PTPN11,TRIB3,UGCG,SESN2,PTGS2,SEL1L,SLC45A3,APOE,LYN,SH3GLB1,ABHD5,RDH11	down_VSAP_EC
GO:0098771	0.892	0.168	13	180	inorganic ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,PDK2,FXN,SLC25A28,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:0032270	0.892	0.186	8	479	positive regulation of cellular protein metabolic	BP	1	LEP,PRR16,F3,GREM1,DCUN1D3,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:1901615	0.892	0.208	5	128	organic hydroxy compound metabolic	BP	1	NR1H4,TPI1,HIF1A,APOE,REST	down_VSAP_EC
GO:0007268	0.892	0.221	4	130	chemical synaptic transmission	BP	1	PLCL1,CACNB3,PARK7,BRSK1	down_VCAV_EC
GO:0098916	0.892	0.221	4	130	anterograde trans-synaptic signaling	BP	1	PLCL1,CACNB3,PARK7,BRSK1	down_VCAV_EC

GO:0046467	0.892	0.277	2	45	membrane lipid biosynthetic process	BP	1	ELOVL1,ELOVL6	down_ACOR_VSMC
GO:0008544	0.892	0.275	2	75	epidermis development	BP	1	NAB2,ZFP36L1	down_VCAV_EC
GO:0006635	0.892	0.36	1	25	fatty acid beta-oxidation	BP	1	PPARD	down_ACOR_VSMC
GO:0023051	0.892	0.368	1	954	regulation of signaling	BP	1	IVNS1ABP	down_AFEM_EC
GO:0051053	0.892	0.355	1	45	negative regulation of DNA metabolic process	BP	1	FBH1	down_VCAV_EC
GO:0030838	0.892	0.356	1	37	positive regulation of actin filament	BP	1	ACTR3	down_VSAP_EC
GO:2001238	0.892	0.36	1	23	positive regulation of extrinsic apoptotic	BP	1	ITM2C	up_ACOR_VSMC
GO:0002253	0.892	0.352	1	92	activation of immune response	BP	1	CYLD	up_AFEM_EC
GO:0044786	0.892	0.36	1	23	cell cycle DNA replication	BP	1	ATRX	up_VCAV_EC
GO:0035556	0.892	0.363	1	845	intracellular signal transduction	BP	1	FBP1	up_VFEM_VSMC
GO:0018023	0.892	0.362	1	23	peptidyl-lysine trimethylation	BP	1	WDR82	up_VSAP_EC
GO:0031060	0.892	0.361	1	23	regulation of histone methylation	BP	1	PHF1	up_VSAP_EC
GO:0045944	0.892020921	0.20797	5	287	positive regulation of transcription by RNA polymerase II	BP	1	SOX9,FZD5,NOD2,SMAD6,MAVS	up_ACOR_EC
GO:0051234	0.893	0.128	112	1283	establishment of localization	BP	1	SLC43A1,PEX7,HNF4A,DNM1,CD274,ACKR3,ARHGEF5,C5AR2,LIPC,AMIGO1,CALHM2,SLC8B1,TBC1D10C,SLC43A3,GABRE,MFSD3,TPCN2,NIPAL3,TBC1D2B,CDH1,SLC6A4,FGF7,ABL1,PEX2,SLC16A12,EMP2,KCNE3,CHRM1,DLL1,EPN2,OSR1,IL17RC,SCAMP4,CLIC5,KLF15,C1QTNF2,ANXA4,RILPL2,ANKRD54,ABCB11,CCS,VPS36,AP5B1,KLHL24,SLC25A12,APOL5,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,ZFP36L1,PIK3R1,SLC25A28,CRACR2B,GAS1,SLC27A6,CTNS,SCARA5,SLC10A6,NIPAL1,ERGIC1,PASK,MON1B,NUP98,SCFD2,AZIN2,HPS4,CCDC93,ABCA9,CLCN2,STEAP3,FBXO7,KCNB1,LCAT,LONP2,SNUPN,DOP1B,DENND5A,AP5Z1,OSBPL7,FTL,MYO1B,SCAMP2,ENSCAFG00000013366,RAF1,PNP,MAPKBP1,ZFYVE21,CYBA,ZNF205,XKR8,FXYD1,STX4,TTL,VPS11,KCNC4,ARHGAP12,UBQLN2,FLOT1,PPP3CB,PEX6,SLC25A40,MAVS,CEP19,TGFBR2,BAG4,NCOA4,NAGPA,RAB11FIP2,SOAT1	up_VSAP_EC
GO:0006082	0.893	0.156	19	305	organic acid metabolic process	BP	1	PDGFB,ST6GAL1,EDN1,PIPOX,PTGS1,ODC1,ARG2,TARSL2,CHST7,AADAT,PROX1,CHST1,ELOVL7,ENSCAFG00000024323,PTGS2,GCH1,HIF1A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0071704	0.893	0.197	11	3535	organic substance metabolic process	BP	1	NR1H4,MAPK10,HOXA3,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,HOXA1,ENSCAFG00000028814	up_APUL_EC
GO:0009205	0.893	0.198	6	98	purine ribonucleoside triphosphate metabolic	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,PARK7	up_ACOR_VSMC
GO:0007276	0.893	0.219	4	130	gamete generation	BP	1	ADAMTS2,MEA1,FOXO3,ZBTB16	down_VCAV_EC
GO:0090150	0.893	0.241	3	64	establishment of protein localization to membrane	BP	1	ACSL3,TRAM1,SAMM50	down_ACOR_VSMC
GO:0042060	0.893	0.24	3	103	wound healing	BP	1	SDC4,VKORC1,B4GALT1	down_VCAV_EC
GO:0050878	0.893	0.273	2	75	regulation of body fluid levels	BP	1	VKORC1,CYBA	down_VCAV_EC
GO:0035107	0.893	0.274	2	60	appendage morphogenesis	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0035108	0.893	0.274	2	60	limb morphogenesis	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0050896	0.893	0.305	2	2346	response to stimulus	BP	1	TLR2,EYA1	up_AFEM_VSMC
GO:0042127	0.893	0.274	2	452	regulation of cell proliferation	BP	1	HOXA3,CCAR1	up_VPOR_EC
GO:0051668	0.893	0.277	2	39	localization within membrane	BP	1	RILPL2,LRP4	up_VSAP_EC
GO:0035556	0.893	0.279	2	845	intracellular signal transduction	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0006479	0.893	0.354	1	45	protein methylation	BP	1	PRMT6	down_VCAV_EC

GO:0008213	0.893	0.354	1	45	protein alkylation	BP	1	PRMT6	down_VCAV_EC
GO:0035023	0.893	0.353	1	46	regulation of Rho protein signal transduction	BP	1	ARHGEF25	down_VCAV_EC
GO:0002819	0.893	0.352	1	44	regulation of adaptive immune response	BP	1	LOXL3	down_VCAV_EC
GO:0000271	0.893	0.359	1	22	polysaccharide biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0016574	0.893	0.36	1	21	histone ubiquitination	BP	1	PCGF5	up_ACOR_VSMC
GO:1905515	0.893	0.359	1	22	non-motile cilium assembly	BP	1	DISC1	up_ACOR_VSMC
GO:0019538	0.893	0.383	1	1713	protein metabolic process	BP	1	WNT7A	up_AORT_VSMC
GO:0007049	0.893	0.356	1	560	cell cycle	BP	1	LZTS1	up_APUL_EC
GO:0019080	0.893	0.357	1	26	viral gene expression	BP	1	SMARCA4	up_VCAV_EC
GO:0051247	0.893	0.355	1	502	positive regulation of protein metabolic process	BP	1	MAP2K6	up_VFEM_EC
GO:0044281	0.893	0.359	1	622	small molecule metabolic process	BP	1	NR1H4	up_VPUL_EC
GO:0000380	0.893	0.359	1	22	alternative mRNA splicing, via spliceosome	BP	1	PQBP1	up_VSAP_EC
GO:0042107	0.893	0.36	1	22	cytokine metabolic process	BP	1	MYD88	up_VSAP_EC
GO:0032612	0.893	0.358	1	22	interleukin-1 production	BP	1	F2RL1	up_VSAP_EC
GO:0043618	0.893	0.359	1	22	regulation of transcription from RNA polymerase II promoter in response to	BP	1	NCK1	up_VSAP_EC
GO:0050867	0.893878046	0.3489	1	83	positive regulation of cell activation	BP	1	NOD2	up_ACOR_EC
GO:0090304	0.894	0.126	130	1694	nucleic acid metabolic process	BP	1	EDNRB,HCLS1,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,TARSL2,MTOR,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,TLR3,NCK1,ESCO1,TRMT9B,TIMELESS,OTUD4,LDB2,CD200,JAG1,NSD1,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,ENSCAFG00000002897,ASF1A,HMGB1,AHR,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC
GO:0051649	0.894	0.137	45	630	establishment of localization in cell	BP	1	SREBF1,DDX39A,NEDD4,ZW10,CENPA,TIMM44,POLA2,HSPA9,RAN,HM13,BIRC5,INSIG1,CAV1,RANBP1,AAAS,PLK3,KIF22,CDCA8,ENSCAFG00000011598,PREB,TRAM1,NDC80,IPO4,YWHAB,NUP62,EMP2,NUP188,TOMM34,SAMM50,GSTO1,TRAK1,DMAP1,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,RBM14,CORO1A,CYC1,TRAPPC6A,PMPCA,NUS1,CEP83,ZWINT	down_ACOR_VSMC
GO:0001501	0.894	0.165	13	178	skeletal system development	BP	1	RASSF2,BMP4,LNPK,FGFR2,CITED2,FGF18,BBX,PSEN1,CHD7,EDN1,ARID5B,WDR48,ACP2	up_ACOR_VSMC
GO:0044772	0.894	0.175	10	144	mitotic cell cycle phase transition	BP	1	CDC7,SKP2,NACC2,LATS2,CDKN2B,CDKN1A,CRLF3,APP,FAM107A,KLF11	up_ACOR_VSMC
GO:0016055	0.894	0.183	8	134	Wnt signaling pathway	BP	1	SDC1,CTDNEP1,CAV1,GREM1,ASPM,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0198738	0.894	0.183	8	134	cell-cell signaling by wnt	BP	1	SDC1,CTDNEP1,CAV1,GREM1,ASPM,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0007610	0.894	0.196	6	146	behavior	BP	1	HIF1A,UBA6,APOE,HTT,ARF4,HOMER1	down_VSAP_EC
GO:0048608	0.894	0.218	4	129	reproductive structure development	BP	1	ZFP36L1,IRX5,RDH10,FOXO3	down_VCAV_EC

GO:0010038	0.894	0.24	3	62	response to metal ion	BP	1	CAV1,SLC30A1,IQGAP1	down_ACOR_VSMC
GO:0030705	0.894	0.241	3	56	cytoskeleton-dependent intracellular transport	BP	1	KIF3C,HOOK3,HIF1A	up_VCAV_EC
GO:0023052	0.894	0.289	2	1602	signaling	BP	1	GPSM2,IVNS1ABP	down_AFEM_EC
GO:0019827	0.894	0.272	2	59	stem cell population maintenance	BP	1	HOOK3,KDM3A	down_VSAP_EC
GO:0050821	0.894	0.273	2	48	protein stabilization	BP	1	CREB1,USP13	up_VCAV_EC
GO:0048639	0.894	0.274	2	39	positive regulation of developmental growth	BP	1	ACACB,DLL1	up_VSAP_EC
GO:0051246	0.894	0.276	2	832	regulation of protein metabolic process	BP	1	PRR16,CAV1	up_VSAP_VSMC
GO:0016233	0.894	0.358	1	22	telomere capping	BP	1	STN1	up_ACOR_VSMC
GO:0019915	0.894	0.357	1	22	lipid storage	BP	1	PLIN2	up_ACOR_VSMC
GO:0061640	0.894	0.355	1	23	cytoskeleton-dependent cytokinesis	BP	1	MITD1	up_ACOR_VSMC
GO:1904019	0.894	0.358	1	22	epithelial cell apoptotic process	BP	1	WFS1	up_ACOR_VSMC
GO:1990542	0.894	0.354	1	32	mitochondrial transmembrane transport	BP	1	MCU	up_VCAV_EC
GO:0009892	0.894	0.361	1	835	negative regulation of metabolic process	BP	1	NKX2-5	up_VPOR_VSMC
GO:1903510	0.894	0.357	1	22	mucopolysaccharide metabolic process	BP	1	CHST7	up_VSAP_EC
GO:0010498	0.895	0.167	12	194	proteasomal protein catabolic process	BP	1	UBE2S,PSMD7,SLC29A1,HM13,SMARCC1,PLK3,UBE2J2,UBE2K,RAD23A,CDC20,PSMC1,UBE2C	down_ACOR_VSMC
GO:0034762	0.895	0.188	7	122	regulation of transmembrane transport	BP	1	NEDD4,CAV1,SLC30A1,CLIC1,GSTO1,CORO1A,REM1	down_ACOR_VSMC
GO:0006302	0.895	0.195	6	97	double-strand break repair	BP	1	FIGNL1,TIMELESS,BLM,SMC5,RAD21,GINS4	up_VCAV_EC
GO:0051235	0.895	0.204	5	90	maintenance of location	BP	1	PDE4D,CHD7,APLNR,PLCG2,ATP2A1	up_VCAV_EC
GO:0099537	0.895	0.216	4	131	trans-synaptic signaling	BP	1	PLCL1,CACNB3,PARK7,BRSK1	down_VCAV_EC
GO:0009199	0.895	0.236	3	100	ribonucleoside triphosphate metabolic	BP	1	ATP5MC1,UQCR10,PARK7	down_VCAV_EC
GO:0006464	0.895	0.243	3	1162	cellular protein modification process	BP	1	EYA1,MAP2K6,CDC42EP5	up_VFEM_EC
GO:0036211	0.895	0.243	3	1162	protein modification process	BP	1	EYA1,MAP2K6,CDC42EP5	up_VFEM_EC
GO:0046474	0.895	0.272	2	44	glycerophospholipid biosynthetic process	BP	1	ACSL3,VAC14	down_ACOR_VSMC
GO:0050731	0.895	0.272	2	44	positive regulation of peptidyl-tyrosine	BP	1	GREM1,ARHGEF2	down_ACOR_VSMC
GO:0034404	0.895	0.271	2	50	nucleobase-containing small molecule	BP	1	ENSCAFG00000024323,HIF1A	up_VCAV_EC
GO:0030433	0.895	0.273	2	38	ubiquitin-dependent ERAD pathway	BP	1	FOXRED2,UBQLN2	up_VSAP_EC
GO:1903828	0.895	0.273	2	38	negative regulation of cellular protein	BP	1	FBXO4,BAG4	up_VSAP_EC
GO:0006664	0.895	0.35	1	37	glycolipid metabolic process	BP	1	UGCG	down_VSAP_EC
GO:1903509	0.895	0.35	1	37	liposaccharide metabolic process	BP	1	UGCG	down_VSAP_EC
GO:1903828	0.895	0.35	1	38	negative regulation of cellular protein	BP	1	TAX1BP3	down_VSAP_EC
GO:0055092	0.895	0.352	1	28	sterol homeostasis	BP	1	ABCA1	up_VCAV_EC
GO:1903578	0.895	0.354	1	22	regulation of ATP metabolic process	BP	1	DDIT4	up_VSAP_EC
GO:0045069	0.895	0.354	1	22	regulation of viral genome replication	BP	1	MAVS	up_VSAP_EC
GO:0030097	0.896	0.157	16	244	hemopoiesis	BP	1	HMGB1,ANLN,HSPA9,PRELID1,PRMT1,MMP14,HMGB3,HOXA7,PDCD2,HOXB7,TFRC,HMGB2,TOX,SGPL1,HOXA9,JMJD6	down_ACOR_VSMC
GO:0061024	0.896	0.176	9	215	membrane organization	BP	1	MYH9,SEC24D,SEC23A,USO1,APOE,BNIP3,SH3GLB1,SLC25A46,SEC13	down_VSAP_EC
GO:0060348	0.896	0.203	5	78	bone development	BP	1	BMP4,FGFR2,CITED2,FGF18,BBX	up_ACOR_VSMC
GO:0008344	0.896	0.35	1	25	adult locomotory behavior	BP	1	ARCN1	down_ACOR_VSMC
GO:1904591	0.896	0.351	1	25	positive regulation of protein import	BP	1	DMAP1	down_ACOR_VSMC
GO:0006813	0.896	0.347	1	37	potassium ion transport	BP	1	KIF5B	down_VSAP_EC

GO:0001706	0.896	0.355	1	20	endoderm formation	BP	1	LAMA3	up_ACOR_VSMC
GO:0045582	0.896	0.352	1	22	positive regulation of T cell differentiation	BP	1	CD83	up_ACOR_VSMC
GO:0090501	0.896	0.349	1	29	RNA phosphodiester bond hydrolysis	BP	1	MOV10	up_VCAV_EC
GO:0044092	0.896	0.345	1	270	negative regulation of molecular function	BP	1	ASPN	up_VPOR_EC
GO:0009247	0.896	0.352	1	22	glycolipid biosynthetic process	BP	1	B3GALT4	up_VSAP_EC
GO:0031330	0.896157975	0.34368	1	85	negative regulation of cellular catabolic process	BP	1	CHMP4B	up_ACOR_EC
GO:0010942	0.896292182	0.23274	3	200	positive regulation of cell death	BP	1	IFIT2,CLU,PRKCD	up_ACOR_EC
GO:0044772	0.896886393	0.26457	2	144	mitotic cell cycle phase transition	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0009653	0.897	0.13	57	773	anatomical structure morphogenesis	BP	1	ELK3,FSCN1,FLNB,FMNL3,EIF4A3,SLC29A1,MTDH,HOXA3,NAB2,B3GNT2,CFAP298,INSIG1,CAV1,TIMELESS,NF2,ANPEP,MMP14,STMN1,GREM1,MAP3K20,ADIPOR2,SMARCC1,HOXA7,HOXC10,HOXB7,GMNN,POC1A,E2F8,B4GALT1,PRCP,NCL,RAC1,UGDH,EMP2,IQGAP1,CDC42EP4,HOXB5,EZR,HOXC4,CORO1A,SGPL1,NOLC1,PHACTR4,TBX15,ENSCAFG00000010224,RADIL,ITGA2,ARHGEF2,HOXA9,SERPINH1,GLI1,JMJD6,NUS1,HMGN1,TBCC,SIX4,ANXA7	down_ACOR_VSMC
GO:0030003	0.897	0.168	11	157	cellular cation homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,FXN,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:0007005	0.897	0.171	10	175	mitochondrion organization	BP	1	SREBF1,SLC25A5,TIMM44,PRELID1,CHCHD3,FASTKD3,TOMM34,SAMM50,FOXRED1,PMPCA	down_ACOR_VSMC
GO:0032870	0.897	0.171	10	162	cellular response to hormone stimulus	BP	1	SREBF1,TFPI,NEDD4,CAV1,THRAP3,ADIPOR2,CDK4,SMARCC1,PRCP,NCOA5	down_ACOR_VSMC
GO:0044772	0.897	0.171	10	144	mitotic cell cycle phase transition	BP	1	FAM107A,CRADD,ZFP36L1,E2F4,FBXO7,ZFP36L2,TPRA1,CDC26,LSM10,LATS2	up_VSAP_EC
GO:0007186	0.897	0.185	7	124	G protein-coupled receptor signaling	BP	1	CAV1,STMN1,YWHAB,IQGAP2,EZR,PRMT5,RGS9	down_ACOR_VSMC
GO:0060562	0.897	0.185	7	120	epithelial tube morphogenesis	BP	1	TIMELESS,MMP14,GREM1,HOXB7,B4GALT1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0006139	0.897	0.252	3	1909	nucleobase-containing compound metabolic	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0022412	0.897	0.266	2	76	cellular process involved in reproduction in multicellular organism	BP	1	FOXO3,ZBTB16	down_VCAV_EC
GO:0034620	0.897	0.268	2	38	cellular response to unfolded protein	BP	1	PIK3R1,NCK1	up_VSAP_EC
GO:0070373	0.897	0.347	1	26	negative regulation of ERK1 and ERK2 cascade	BP	1	EZR	down_ACOR_VSMC
GO:0043484	0.897	0.344	1	43	regulation of RNA splicing	BP	1	RBM38	down_VCAV_EC
GO:0030282	0.897	0.346	1	37	bone mineralization	BP	1	HIF1A	down_VSAP_EC
GO:0006879	0.897	0.351	1	23	cellular iron ion homeostasis	BP	1	EGLN1	up_ACOR_VSMC
GO:0007032	0.897	0.35	1	22	endosome organization	BP	1	AKTIP	up_ACOR_VSMC
GO:1901990	0.897	0.341	1	94	regulation of mitotic cell cycle phase transition	BP	1	DCUN1D3	up_AFEM_EC
GO:0033036	0.897	0.354	1	852	macromolecule localization	BP	1	LHFPL4	up_VPOR_VSMC
GO:0002200	0.897	0.35	1	23	somatic diversification of immune receptors	BP	1	STAT6	up_VSAP_EC
GO:0002562	0.897	0.35	1	23	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	STAT6	up_VSAP_EC
GO:0016444	0.897	0.35	1	23	somatic cell DNA recombination	BP	1	STAT6	up_VSAP_EC
GO:0051899	0.897	0.35	1	22	membrane depolarization	BP	1	TPCN2	up_VSAP_EC
GO:0046034	0.897108091	0.34141	1	88	ATP metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0007018	0.897471093	0.3408	1	82	microtubule-based movement	BP	1	DYNC1I1	up_ACOR_EC

GO:0019438	0.898	0.122	109	1258	aromatic compound biosynthetic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,ENSCAFG00000013986,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,PDK2,ICE1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,FBXO4,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,PCBD1,LIMD1,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,PNPO,DCAKD,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:0019222	0.898	0.126	87	1934	regulation of metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,NDN,PRNP,LUM,FBN1,GLIPR2,BGN,LARP6,KANK2,BMPR1A,NABP2,LMO4,RECK,TRPV2,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,PSMF1,SAMD4B,EEF2K,TFE3,NR3C1,HR,CLSTN1,PLCL1,CSPG4,PRMT6,TMEM161A,CXXC5,ASPN,POLDIP2,LRPAP1,EIF3K,THY1,NECAB3,TEAD1,CC2D1A,GLI3,PARK7,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,CYBA,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,FUT8,SPRED1,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,FBH1,GREM1,LONP2,RAC2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0044248	0.898	0.132	50	691	cellular catabolic process	BP	1	HMGB1,RNPS1,SREBF1,USP1,USP4,EIF4A3,EDC3,HNRNPD,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,MTDH,HM13,PSMD13,THRAP3,EDC4,ABHD5,FEN1,SMARCC1,RNASEH2B,PLK3,SMG9,RNF152,DIS3,FASTKD3,PPARD,UBE2J2,DTL,PDXP,GSTO1,EZR,UBE2K,RAD23A,SGPL1,CDC20,BAP1,PSMC1,AIFM1,ENSCAFG00000015189,LIPC,RNASEH2C,NUDT1,EXOSC5,UBE2C,ACADL,AMER1,NUDT3,ANXA7	down_ACOR_VSMC
GO:0043009	0.898	0.153	17	227	chordate embryonic development	BP	1	SHROOM3,BMP4,FGFR2,GJA1,SEC24B,LATS2,CITED2,SPINT1,LMO4,EGLN1,ENSCAFG00000006238,SPINT2,FZD3,PSEN1,CHD7,EDN1,INPP5K	up_ACOR_VSMC
GO:0098657	0.898	0.166	11	181	import into cell	BP	1	HMGB1,NEDD4,ARFGAP1,CAV1,SLC30A1,GREM1,TFRC,HIST1H1A,EZR,CORO1A,JMJD6	down_ACOR_VSMC
GO:0016567	0.898	0.168	10	232	protein ubiquitination	BP	1	PRICKLE1,HSPA5,SOCS5,WSB1,TRIB3,NXN,SPOPL,BACH1,CUL2,SH3RF3	down_VSAP_EC
GO:0016050	0.898	0.178	8	119	vesicle organization	BP	1	USP6NL,SYT16,EVI5L,ABCA1,SEC24B,STX11,SGSM2,AKTIP	up_ACOR_VSMC
GO:0006950	0.898	0.194	6	1102	response to stress	BP	1	C3AR1,CXHXorf57,ARHGEF2,OAS3,SLC7A11,ENSCAFG00000032731	up_VPOR_EC
GO:0010256	0.898	0.2	5	129	endomembrane system organization	BP	1	PLK3,HOOK3,LMAN1,HTT,BLZF1	down_VSAP_EC
GO:1903829	0.898	0.2	5	91	positive regulation of cellular protein	BP	1	HCLS1,TMEM173,EPB41,SH3GLB1,CTDSPL2	up_VCAV_EC
GO:0051054	0.898	0.2	5	81	positive regulation of DNA metabolic process	BP	1	STAT6,MYC,CIZ1,FBXO4,NPAS2	up_VSAP_EC
GO:0072175	0.898	0.232	3	60	epithelial tube formation	BP	1	GREM1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0045859	0.898	0.23	3	219	regulation of protein kinase activity	BP	1	LEP,LRRC15,ADAM17	up_AFEM_EC
GO:0090288	0.898	0.267	2	44	negative regulation of cellular response to growth factor stimulus	BP	1	CAV1,GREM1	down_ACOR_VSMC
GO:0007154	0.898	0.281	2	1622	cell communication	BP	1	GPSM2,IVNS1ABP	down_AFEM_EC
GO:1902115	0.898	0.263	2	77	regulation of organelle assembly	BP	1	SDC4,EVI5L	down_VCAV_EC
GO:1990823	0.898	0.267	2	39	response to leukemia inhibitory factor	BP	1	EIF4A2,ARID5B	up_ACOR_VSMC
GO:1990830	0.898	0.267	2	39	cellular response to leukemia inhibitory factor	BP	1	EIF4A2,ARID5B	up_ACOR_VSMC
GO:0043524	0.898	0.267	2	39	negative regulation of neuron apoptotic process	BP	1	AMBRA1,KDM2B	up_VSAP_EC

GO:0050680	0.898	0.341	1	44	negative regulation of epithelial cell proliferation	BP	1	IFT57	down_VCAV_EC
GO:0032204	0.898	0.342	1	35	regulation of telomere maintenance	BP	1	CTNNB1	down_VSAP_EC
GO:0019217	0.898	0.346	1	27	regulation of fatty acid metabolic process	BP	1	PTGS2	up_VCAV_EC
GO:0035556	0.898	0.351	1	845	intracellular signal transduction	BP	1	ANKRD6	up_VPOR_VSMC
GO:0051641	0.898	0.351	1	858	cellular localization	BP	1	LHFPL4	up_VPOR_VSMC
GO:0051649	0.898	0.346	1	630	establishment of localization in cell	BP	1	NR1H4	up_VPUL_EC
GO:0019438	0.899	0.121	110	1258	aromatic compound biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,MOXD1,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,PTS,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0019219	0.899	0.122	99	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,TENT5C,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT6,GATAD1,PLPP3,F2RL1,RBL2,GLIS2,DDR2,PDK2,ICE1,ZFP36L1,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,MYD88,IKZF2,TFE3,LRP4,NUP98,TRERF1,E2F4,NPAS2,LIMD1,CDK9,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:0051172	0.899	0.129	55	663	negative regulation of nitrogen compound metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,PPARGC1B,TBC1D10C,CEP85,SLIT2,CST3,ZHX3,ABL1,PEX2,HDAC7,OSR1,TENT5C,KLF15,RARG,CBX7,STAT6,RECK,PLPP3,ENSCAFG00000000071,F2RL1,GLIS2,ZFP36L1,GAS1,MYC,SHOX2,H2AFJ,ZC3H10,RTN4RL1,IKZF2,ANKHD1,AZIN2,PHF1,FBXO7,LIMD1,CDK9,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ACVRL1,TNRC6C,NCK1,DDIT4,LATS2	up_VSAP_EC
GO:0045859	0.899	0.156	14	219	regulation of protein kinase activity	BP	1	IRAK1,HMGCR,SLC29A1,CAV1,NF2,CDKN2C,EZH2,MAP3K20,CKS2,RAP2C,NUP62,EMP2,CLSPN,CCNB3	down_ACOR_VSMC
GO:0010638	0.899	0.181	7	207	positive regulation of organelle organization	BP	1	KIRREL1,DCN,SDC4,NABP2,AKT2,CLEC16A,ACTR3B	down_VCAV_EC
GO:0051179	0.899	0.209	5	1747	localization	BP	1	TRIM9,HOXA7,SIX1,TIAM1,CA9	up_VFEM_EC
GO:0001666	0.899	0.212	4	67	response to hypoxia	BP	1	ZFP36L1,LIMD1,HMOX1,DDIT4	up_VSAP_EC
GO:0036293	0.899	0.212	4	67	response to decreased oxygen levels	BP	1	ZFP36L1,LIMD1,HMOX1,DDIT4	up_VSAP_EC
GO:0042692	0.899	0.228	3	105	muscle cell differentiation	BP	1	RBM38,CDH2,GREM1	down_VCAV_EC
GO:0006996	0.899	0.238	3	1301	organelle organization	BP	1	NR1H4,TUBB4A,PDLIM3	up_APUL_EC
GO:0046677	0.899	0.231	3	54	response to antibiotic	BP	1	ABL1,MAP3K5,ZNF580	up_VSAP_EC
GO:0051186	0.899	0.261	2	159	cofactor metabolic process	BP	1	GPAM,ACACB	up_AFEM_EC

GO:0080090	0.899	0.282	2	1734	regulation of primary metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0051896	0.899	0.265	2	39	regulation of protein kinase B signaling	BP	1	HPSE,BAG4	up_VSAP_EC
GO:0035904	0.899	0.345	1	25	aorta development	BP	1	ADAMTS6	down_ACOR_VSMC
GO:0043506	0.899	0.344	1	25	regulation of JUN kinase activity	BP	1	MAP3K20	down_ACOR_VSMC
GO:0050852	0.899	0.343	1	26	T cell receptor signaling pathway	BP	1	EZR	down_ACOR_VSMC
GO:1900542	0.899	0.344	1	26	regulation of purine nucleotide metabolic	BP	1	CDK1	down_ACOR_VSMC
GO:0046631	0.899	0.34	1	35	alpha-beta T cell activation	BP	1	SOCS5	down_VSAP_EC
GO:0050769	0.899	0.338	1	95	positive regulation of neurogenesis	BP	1	IRX3	up_AFEM_EC
GO:0006446	0.899	0.343	1	27	regulation of translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0051641	0.899	0.348	1	858	cellular localization	BP	1	NETO1	up_VFEM_VSMC
GO:0046785	0.899	0.345	1	23	microtubule polymerization	BP	1	ABL1	up_VSAP_EC
GO:0048872	0.899824516	0.33529	1	85	homeostasis of number of cells	BP	1	SOX9	up_ACOR_EC
GO:0016070	0.9	0.139	29	1479	RNA metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0098657	0.9	0.157	13	181	import into cell	BP	1	DNM1,ACKR3,SLC6A4,ABL1,DLL1,EPN2,F2RL1,CYBA,XKR8,ARHGAP12,UBQLN2,FLOT1,PPP3CB	up_VSAP_EC
GO:0048589	0.9	0.161	12	188	developmental growth	BP	1	SLC29A1,GINS4,EZH2,CDK4,POC1A,PPARD,IQGAP1,EZR,SGPL1,ASPM,GLI1,SIX4	down_ACOR_VSMC
GO:0097193	0.9	0.187	6	109	intrinsic apoptotic signaling pathway	BP	1	CAV1,NOC2L,MELK,TXNDC12,AIFM1,ARHGEF2	down_ACOR_VSMC
GO:0051056	0.9	0.188	6	87	regulation of small GTPase mediated signal	BP	1	ABCA1,ARHGEF26,CHN2,F2RL1,NRP1,SIPA1L1	up_ACOR_VSMC
GO:0009058	0.9	0.209	5	1910	biosynthetic process	BP	1	NR1H4,GALNT17,ZDHHC16,NPNT,HOXA1	up_APUL_EC
GO:0061458	0.9	0.208	4	131	reproductive system development	BP	1	ZFP36L1,IRX5,RDH10,FOXO3	down_VCAV_EC
GO:1901362	0.9	0.237	3	1293	organic cyclic compound biosynthetic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0070588	0.9	0.23	3	54	calcium ion transmembrane transport	BP	1	SLC8B1,ABL1,CYBA	up_VSAP_EC
GO:0071897	0.9	0.229	3	54	DNA biosynthetic process	BP	1	MYC,FBXO4,ACVRL1	up_VSAP_EC
GO:0070482	0.9	0.26	2	75	response to oxygen levels	BP	1	VASN,ZFP36L1	down_VCAV_EC
GO:0098727	0.9	0.26	2	60	maintenance of cell number	BP	1	HOOK3,KDM3A	down_VSAP_EC
GO:0006892	0.9	0.263	2	39	post-Golgi vesicle-mediated transport	BP	1	KLHL20,MYO1B	up_ACOR_VSMC
GO:0033036	0.9	0.266	2	852	macromolecule localization	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0002088	0.9	0.342	1	26	lens development in camera-type eye	BP	1	NF2	down_ACOR_VSMC
GO:0043648	0.9	0.342	1	26	dicarboxylic acid metabolic process	BP	1	AADAT	down_ACOR_VSMC
GO:0006355	0.9	0.35	1	974	regulation of transcription, DNA-	BP	1	GABPA	down_AFEM_EC
GO:0043535	0.9	0.338	1	45	regulation of blood vessel endothelial cell migration	BP	1	SPRED1	down_VCAV_EC
GO:0046661	0.9	0.337	1	45	male sex differentiation	BP	1	BMPR1A	down_VCAV_EC
GO:0055074	0.9	0.335	1	95	calcium ion homeostasis	BP	1	DMPK	up_AFEM_EC
GO:0051252	0.9	0.35	1	1051	regulation of RNA metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0022029	0.9	0.342	1	23	telencephalon cell migration	BP	1	SLIT2	up_VSAP_EC
GO:0046849	0.9	0.342	1	23	bone remodeling	BP	1	PPARGC1B	up_VSAP_EC
GO:0055065	0.900010843	0.25848	2	145	metal ion homeostasis	BP	1	PTH1R,TMTC2	up_ACOR_EC
GO:0051254	0.900999414	0.17251	8	431	positive regulation of RNA metabolic process	BP	1	GATA4,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:0007169	0.901	0.161	11	178	transmembrane receptor protein tyrosine kinase	BP	1	SREBF1,STMN1,CDK4,SMARCC1,RAC1,NUP62,IQGAP1,FGF5,SGPL1,NCOA5,NUS1	down_ACOR_VSMC

GO:0051716	0.901	0.197	6	2001	cellular response to stimulus	BP	1	NETO1,SALL1,TLR2,CAV1,SHOX2,FGF5	up_VSAP_VSMC
GO:0044281	0.901	0.227	3	622	small molecule metabolic process	BP	1	AK5,FBP1,GNPNAT1	up_VPOR_EC
GO:0009056	0.901	0.262	2	755	catabolic process	BP	1	USP28,NEDD4	down_ACOR_EC
GO:0006090	0.901	0.339	1	26	pyruvate metabolic process	BP	1	PDHA1	down_ACOR_VSMC
GO:0060996	0.901	0.34	1	26	dendritic spine development	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:1904064	0.901	0.339	1	27	positive regulation of cation transmembrane	BP	1	GSTO1	down_ACOR_VSMC
GO:0050905	0.901	0.34	1	26	neuromuscular process	BP	1	HOXC10	down_ACOR_VSMC
GO:1903506	0.901	0.348	1	977	regulation of nucleic acid-templated transcription	BP	1	GABPA	down_AFEM_EC
GO:2001141	0.901	0.347	1	979	regulation of RNA biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0006368	0.901	0.342	1	22	transcription elongation from RNA polymerase II	BP	1	ELL2	up_ACOR_VSMC
GO:0010507	0.901	0.338	1	26	negative regulation of autophagy	BP	1	MTOR	up_VCAV_EC
GO:0031647	0.901524394	0.33128	1	87	regulation of protein stability	BP	1	CLU	up_ACOR_EC
GO:0007610	0.902	0.164	10	146	behavior	BP	1	THRB,SEZ6L,SLC6A4,FXN,CTNS,ABAT,CREBRF,NCOA2,HTRA2,PPP3CB	up_VSAP_EC
GO:0072659	0.902	0.193	5	82	protein localization to plasma membrane	BP	1	FGF13,ACTN2,AR,JUP,INPP5K	up_ACOR_VSMC
GO:0006886	0.902	0.191	5	332	intracellular protein transport	BP	1	LEP,CRY2,VPS26C,REEP2,RAB7A	up_AFEM_EC
GO:0099536	0.902	0.204	4	133	synaptic signaling	BP	1	PLCL1,CACNB3,PARK7,BRSK1	down_VCAV_EC
GO:0048284	0.902	0.256	2	66	organelle fusion	BP	1	USO1,BNIP3	down_VSAP_EC
GO:0051641	0.902	0.261	2	858	cellular localization	BP	1	NETO1,CAV1	up_VSAP_VSMC
GO:0008203	0.902	0.333	1	37	cholesterol metabolic process	BP	1	APOE	down_VSAP_EC
GO:0001776	0.902	0.338	1	23	leukocyte homeostasis	BP	1	JAM3	up_ACOR_VSMC
GO:0019220	0.902	0.336	1	525	regulation of phosphate metabolic process	BP	1	MAP2K6	up_VFEM_EC
GO:0051174	0.902	0.336	1	525	regulation of phosphorus metabolic process	BP	1	MAP2K6	up_VFEM_EC
GO:0010824	0.902	0.339	1	23	regulation of centrosome duplication	BP	1	FBXW5	up_VSAP_EC
GO:0031400	0.903	0.15	15	205	negative regulation of protein modification process	BP	1	TBC1D10C,CEP85,SLIT2,ABL1,KLF15,PLPP3,F2RL1,MYC,RTN4RL1,PHF1,FBXO7,FBLN1,QARS,NCK1,LATS2	up_VSAP_EC
GO:0007346	0.903	0.166	9	210	regulation of mitotic cell cycle	BP	1	ASNS,PTPN11,TNIK,NAA10,EIF4EBP1,CTNNB1,CDK8,PAK2,CDKN1A	down_VSAP_EC
GO:0030855	0.903	0.182	6	183	epithelial cell differentiation	BP	1	B4GALT1,ADAMTSL4,ZFP36L1,CDH2,GREM1,THRB	down_VCAV_EC
GO:0016032	0.903	0.183	6	94	viral process	BP	1	MON1B,PC,EIF3G,EIF3L,EIF3D,MAVS	up_VSAP_EC
GO:0070085	0.903	0.192	5	95	glycosylation	BP	1	MPDU1,SLC35C2,B3GNT2,B4GALT1,NUS1	down_ACOR_VSMC
GO:0051346	0.903	0.205	4	78	negative regulation of hydrolase activity	BP	1	BIRC5,DHCR24,ENSCAFG00000005299,KNL1	down_ACOR_VSMC
GO:0044057	0.903	0.204	4	110	regulation of system process	BP	1	PTPN11,CALM1,RAB11FIP1,INHBA	down_VSAP_EC
GO:0042391	0.903	0.205	4	81	regulation of membrane potential	BP	1	RELN,MEF2C,PPP3CA,KCNJ2	up_VCAV_EC
GO:0043087	0.903	0.221	3	83	regulation of GTPase activity	BP	1	ENSCAFG00000002015,GSK3B,TAX1BP3	down_VSAP_EC
GO:0050792	0.903	0.224	3	55	regulation of viral process	BP	1	MX1,ISG15,INPP5K	up_ACOR_VSMC
GO:0010950	0.903	0.331	1	44	positive regulation of endopeptidase activity	BP	1	IFT57	down_VCAV_EC
GO:0050684	0.903	0.331	1	46	regulation of mRNA processing	BP	1	ZFP36L1	down_VCAV_EC
GO:0051701	0.903	0.33	1	45	interaction with host	BP	1	TRIM8	down_VCAV_EC
GO:0044085	0.903	0.343	1	1076	cellular component biogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0072527	0.903	0.336	1	23	pyrimidine-containing compound metabolic	BP	1	ALDH6A1	up_VSAP_EC
GO:0015908	0.903	0.336	1	23	fatty acid transport	BP	1	SLC27A6	up_VSAP_EC

GO:0000280	0.903511736	0.25159	2	145	nuclear division	BP	1	FIGNL1,CHMP4B	up_ACOR_EC
GO:0043412	0.904	0.124	53	1225	macromolecule modification	BP	1	NOTCH2,PDGFRB,KIRREL1,SMAD9,DCN,PRNP,GLIPR2,BGN,BMPR1A,KRTCAP2,VKORC1,CLIP3,AKT1S1,AKT2,EEF2K,HR,PLCL1,DDOST,CSPG4,PRMT6,GFPT2,ASPN,PIGS,HS3ST3B1,THY1,RNF216,WDR45,B4GALT1,PARK7,MAST2,ZFP36L1,MYDGF,SASH1,COPS7A,ARL2BP,MAVS,CDH2,LOXL3,GSDME,CAMK2D,FUT8,SPRED1,MAPRE3,CDKL2,DDR2,SHC1,CRTAP,FBH1,GREM1,RPN2,KLHL29,BRSK1,CDK14	down_VCAV_EC
GO:0031327	0.904	0.131	33	412	negative regulation of cellular biosynthetic process	BP	1	LEP,NACC2,ITM2C,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,ZNF174,ANKRD1,DAPK1,ENSCAFG00000006238,CLSTN1,ORMDL3,TBX20,DKKL1,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,DDIT4,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0009057	0.904	0.131	32	473	macromolecule catabolic process	BP	1	PLK2,TNFAIP3,CTSC,TIPARP,WWP1,LYVE1,USP33,PSME4,PELI1,ODC1,CASP8,TENT2,CNOT6,ENC1,PAN3,USP28,CNOT7,SMG7,PMAIP1,RIPK1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,DCP2,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0031329	0.904	0.143	18	241	regulation of cellular catabolic process	BP	1	LEP,HTR2B,FEZ1,PRKAA2,SH3RF2,TP53INP1,PTPN3,DAPK1,BNIP3,OS9,RNF19A,PSEN1,DDIT4,DISC1,HERPUD1,FEZ2,SH3BP4,PARK7	up_ACOR_VSMC
GO:0030155	0.904	0.158	11	180	regulation of cell adhesion	BP	1	HMGB1,CAV1,NF2,GREM1,HOXA7,ARG2,TFRC,FAM49B,RAC1,EMP2,CORO1A	down_ACOR_VSMC
GO:0032446	0.904	0.157	11	255	protein modification by small protein conjugation	BP	1	PRICKLE1,HSPA5,SOCS5,WSB1,TRIB3,NXN,SPOPL,UBA5,BACH1,CUL2,SH3RF3	down_VSAP_EC
GO:0055114	0.904	0.163	9	157	oxidation-reduction process	BP	1	NNT,PRELID1,CDK1,FASTKD3,SUCLG1,PPARD,CYCS,CYC1,PDHA1	down_ACOR_VSMC
GO:0007346	0.904	0.172	7	210	regulation of mitotic cell cycle	BP	1	KANK2,NABP2,POLDIP2,ZFP36L1,LSM10,EIF4EBP1,BRSK1	down_VCAV_EC
GO:0007033	0.904	0.202	4	82	vacuole organization	BP	1	RALB,HOOK3,ABCA1,SH3GLB1	up_VCAV_EC
GO:0048592	0.904	0.222	3	53	eye morphogenesis	BP	1	BMP4,CITED2,FRS2	up_ACOR_VSMC
GO:0051402	0.904	0.222	3	64	neuron apoptotic process	BP	1	MEF2C,GATA3,HIF1A	up_VCAV_EC
GO:0006464	0.904	0.228	3	1162	cellular protein modification process	BP	1	GALNT17,TLR2,CAV1	up_VSAP_VSMC
GO:0036211	0.904	0.228	3	1162	protein modification process	BP	1	GALNT17,TLR2,CAV1	up_VSAP_VSMC
GO:0055002	0.904	0.254	2	45	striated muscle cell development	BP	1	SDC1,SIX4	down_ACOR_VSMC
GO:0045727	0.904	0.254	2	40	positive regulation of translation	BP	1	FAM129A,NGRN	up_ACOR_VSMC
GO:0002699	0.904	0.329	1	46	positive regulation of immune effector process	BP	1	RAC2	down_VCAV_EC
GO:0006334	0.904	0.327	1	45	nucleosome assembly	BP	1	CABIN1	down_VCAV_EC
GO:0046330	0.904	0.326	1	47	positive regulation of JNK cascade	BP	1	SASH1	down_VCAV_EC
GO:0035305	0.904	0.329	1	37	negative regulation of dephosphorylation	BP	1	ARFGEF3	down_VSAP_EC
GO:0072503	0.904	0.324	1	97	cellular divalent inorganic cation homeostasis	BP	1	DMPK	up_AFEM_EC
GO:0072655	0.904	0.33	1	33	establishment of protein localization to	BP	1	SH3GLB1	up_VCAV_EC
GO:1902531	0.904	0.331	1	536	regulation of intracellular signal transduction	BP	1	TIAM1	up_VFEM_EC
GO:0006351	0.904	0.34	1	1069	transcription, DNA-templated	BP	1	GATA5	up_VPUL_VSMC
GO:0046928	0.904	0.333	1	23	regulation of neurotransmitter	BP	1	KCNC4	up_VSAP_EC
GO:1901992	0.904	0.332	1	23	positive regulation of mitotic cell cycle phase	BP	1	LSM10	up_VSAP_EC
GO:0032206	0.904	0.333	1	23	positive regulation of telomere maintenance	BP	1	FBXO4	up_VSAP_EC
GO:0015031	0.904	0.331	1	510	protein transport	BP	1	TLR2	up_VSAP_VSMC

GO:0008150	0.905	0.114	527	5646	biological_process	BP	1	SYNPO2L,EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,RHOT1,FMOD,EPB41L4A,ADRA1B,VEGFD,SEMA5A,TMEM176B,TLR1,TMEM176A,DNAJC6,SMAD6,GALNT3,PIP5K1B,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,DNAH7,CASP10,IFNGR1,LEP,PLCL1,GALNT10,LBH,DCBLD2,ST3GAL5,AFF3,MAP3K8,SNAP91,MID1,SLC26A7,KCNE3,GATA5,BCL2,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,PCGF5,ENSCAFG00000016285,EPYC,HTR2B,RASSF2,TPST2,ENOSF1,TCAF1,MEIS2,USP6NL,INTS9,FNDC5,MBP,TMEM255A,ZRANB1,FBXL20,C28H10orf71,PRDX4,RECK,SHROOM3,LIPT2,B3GALNT2,FEZ1,ENSCAFG00000002977,SKP2,MAT2B,NACC2,COCH,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,SYT16,PNRC1,CPXM1,LCAT,ZNF331,TPC3,EVI5L,AHCYL1,CRIM1,LNPK,SYNPO2,TBX18,TUBB4A,TM7SF3,B3GNT7,NPPB,CHPT1,CNNM2,FGFR2,PCBD1,TP53BP1,MX1,FAXDC2,CCDC126,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,SCARB2,ATRX,MED14,HRH1,CASTOR1,TARSL2,TRPS1,TLR3,LRRN4,SH3RF2,SEC24B,XIRP1,ELL2,WASF3,PPARGC1A,LATS2,LPL,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,RERG,SPINT1,GLRB,PKP4,ARHGAP29,CCNG2,MAOA,PIGS,ZBTB40,ISG15,UGCG,ACSL6,ZNRF3,ZNF782,	up_ACOR_VSMC
GO:0030154	0.905	0.118	78	1040	cell differentiation	BP	1	ELK3,HMGB1,SREBF1,FLNB,ANLN,ACSL4,HINFP,NEDD4,SLC29A1,TRIP13,SF1,SRRT,SDC1,FBXO5,HSPA9,NAB2,HNRNPH3,B3GNT2,PRELID1,INSIG1,PRMT1,CAV1,CDK1,CASP2,NF2,ANPEP,MMP14,EZH2,STMN1,GREM1,HMGB3,PCNA,HOXA7,PDCD2,HOXC10,HOXB7,POC1A,WDR62,E2F8,B4GALT1,NAV2,TFRC,PPARD,RAP2C,RAC1,EMP2,PLK4,IQGAP1,HMGB2,SMARCB1,RAB35,HOXB5,EZR,TOX,RBM14,SGPL1,NOLC1,BEND6,PHACTR4,ERF,ASPM,ENSCAFG00000010224,ELF4,TXNDC12,RADIL,ITGA2,CTH,ARHGEF2,TWIST2,HOXA9,SERPINH1,GLI1,JMJD6,CDC5L,SIX4,TTLL1,AMER1,ANXA7	down_ACOR_VSMC
GO:1901135	0.905	0.13	31	390	carbohydrate derivative metabolic process	BP	1	NECAB3,ACSM3,ACACB,GALNT15,KDELC2,HPSE,COQ9,NDUFS1,ENSCAFG00000004260,LMF1,PDK2,FXN,GALK1,FKRP,CTNS,SULF2,NDUFS2,NT5C2,GALNT11,ACSS2,RENBP,MVK,DCAKD,ENSCAFG00000013366,PNP,NDUFV1,CHST7,B3GALT4,GNPDA1,DDIT4,SOAT1	up_VSAP_EC
GO:0044283	0.905	0.148	14	201	small molecule biosynthetic process	BP	1	PLCG2,LEP,PCBD1,PDE5A,PPIP5K1,MOXD1,DKKL1,EDN1,ALDOC,ENTPD3,DDIT4,PTS,PARK7,ELOVL7	up_ACOR_VSMC
GO:0016043	0.905	0.159	12	1973	cellular component organization	BP	1	MZT1,HOOK3,ARHGEF2,ENSCAFG00000002015,SEMA3A,FBP1,RSL24D1,GCC2,RPL10L,TWF1,SRP54,RNF6	up_VPOR_EC
GO:0090304	0.905	0.165	10	1694	nucleic acid metabolic process	BP	1	BARX1,CXHXorf57,ARHGEF2,TCEA1,ENSCAFG00000002015,ACVR2A,MTDH,RRP15,CCAR1,RNF6	up_VPOR_EC
GO:0016570	0.905	0.163	9	143	histone modification	BP	1	IWS1,GATA3,ARID4B,PRKD2,NSD1,KDM5A,KDM3A,ATRX,TET2	up_VCAV_EC
GO:0009199	0.905	0.18	6	100	ribonucleoside triphosphate metabolic	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,PARK7	up_ACOR_VSMC
GO:0032147	0.905	0.201	4	77	activation of protein kinase activity	BP	1	IRAK1,MAP3K20,EMP2,CLSPN	down_ACOR_VSMC
GO:0061136	0.905	0.201	4	78	regulation of proteasomal protein catabolic process	BP	1	SLC29A1,SMARCC1,PLK3,RAD23A	down_ACOR_VSMC
GO:0016482	0.905	0.219	3	63	cytosolic transport	BP	1	EMP2,EZR,CORO1A	down_ACOR_VSMC
GO:0006066	0.905	0.218	3	89	alcohol metabolic process	BP	1	TPI1,APOE,REST	down_VSAP_EC
GO:0046483	0.905	0.237	3	1948	heterocycle metabolic process	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:2000060	0.905	0.251	2	45	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	PLK3,RAD23A	down_ACOR_VSMC
GO:0009057	0.905	0.252	2	473	macromolecule catabolic process	BP	1	USP33,RNF6	up_VPOR_EC
GO:0046425	0.905	0.252	2	39	regulation of JAK-STAT cascade	BP	1	IL6R,RTN4RL1	up_VSAP_EC
GO:0016064	0.905	0.329	1	26	immunoglobulin mediated immune	BP	1	TFRC	down_ACOR_VSMC

GO:0019724	0.905	0.329	1	26	B cell mediated immunity	BP	1	TFRC	down_ACOR_VSMC
GO:0021954	0.905	0.33	1	26	central nervous system neuron development	BP	1	SLC29A1	down_ACOR_VSMC
GO:0002377	0.905	0.33	1	26	immunoglobulin production	BP	1	TFRC	down_ACOR_VSMC
GO:0046364	0.905	0.329	1	27	monosaccharide biosynthetic process	BP	1	PGD	down_ACOR_VSMC
GO:0019722	0.905	0.324	1	45	calcium-mediated signaling	BP	1	PRNP	down_VCAV_EC
GO:0032774	0.905	0.338	1	1073	RNA biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0044085	0.905	0.34	1	1076	cellular component biogenesis	BP	1	SLIT2	up_VPUL_VSMC
GO:0097659	0.905	0.339	1	1072	nucleic acid-templated transcription	BP	1	GATA5	up_VPUL_VSMC
GO:0071674	0.905	0.331	1	23	mononuclear cell migration	BP	1	SLIT2	up_VSAP_EC
GO:0000819	0.905476752	0.32201	1	87	sister chromatid segregation	BP	1	CHMP4B	up_ACOR_EC
GO:0044270	0.905889011	0.24684	2	147	cellular nitrogen compound catabolic	BP	1	ALDOC,PM20D1	up_ACOR_EC
GO:0016310	0.906	0.155	11	641	phosphorylation	BP	1	LEP,HCK,GREM1,CAMK2A,CYLD,LRRC15,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17	up_AFEM_EC
GO:0006725	0.906	0.234	3	1956	cellular aromatic compound metabolic	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0032637	0.906	0.326	1	26	interleukin-8 production	BP	1	CACTIN	down_ACOR_VSMC
GO:0042475	0.906	0.328	1	26	odontogenesis of dentin-containing tooth	BP	1	NF2	down_ACOR_VSMC
GO:0010675	0.906	0.322	1	46	regulation of cellular carbohydrate metabolic	BP	1	AKT2	down_VCAV_EC
GO:0071222	0.906	0.322	1	46	cellular response to lipopolysaccharide	BP	1	SASH1	down_VCAV_EC
GO:0006720	0.906	0.328	1	25	isoprenoid metabolic process	BP	1	GGPS1	up_ACOR_VSMC
GO:0016053	0.906	0.321	1	97	organic acid biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0046394	0.906	0.321	1	97	carboxylic acid biosynthetic process	BP	1	ACACB	up_AFEM_EC
GO:0061515	0.906	0.328	1	24	myeloid cell development	BP	1	CITED2	up_VSAP_EC
GO:0019220	0.906	0.325	1	525	regulation of phosphate metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0051174	0.906	0.325	1	525	regulation of phosphorus metabolic process	BP	1	CAV1	up_VSAP_VSMC
GO:0010628	0.90671947	0.15615	10	527	positive regulation of gene expression	BP	1	CDH3,GATA4,SOX9,ENSCAFG00000004331,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:1901575	0.907	0.122	46	643	organic substance catabolic process	BP	1	RNPS1,USP1,USP4,EIF4A3,EDC3,HNRNPD,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,THRAP3,EDC4,ABHD5,FEN1,CDK4,SMARCC1,RNASEH2B,PLK3,SMG9,DIS3,FASTKD3,PPARD,UBE2J2,DTL,PDXP,EZR,UBE2K,RAD23A,SGPL1,CDC20,BAP1,PSMC1,GALE,AIFM1,ENSCAFG00000015189,LIPC,RNASEH2C,NUDT1,EXOSC5,UBE2C,ACADL,AMER1,NUDT3	down_ACOR_VSMC
GO:0045786	0.907	0.146	14	195	negative regulation of cell cycle	BP	1	NACC2,BMP4,TP53BP1,ATRX,LATS2,TP53INP1,PTPN3,CDKN2B,CDKN1A,JMY,CRLF3,FZD3,HPGD,FAM107A	up_ACOR_VSMC
GO:0010498	0.907	0.145	14	194	proteasomal protein catabolic process	BP	1	FOXRED2,ABTB1,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,RNF166,RNF216,OSBPL7,UBQLN2,CDC26,KEAP1	up_VSAP_EC
GO:0007264	0.907	0.151	12	164	small GTPase mediated signal transduction	BP	1	ABCA1,DOCK3,ARHGEF26,CHN2,F2RL1,CDKN1A,NRP1,RND1,SYNJ2BP,SIPA1L1,RASGRP2,DOCK5	up_ACOR_VSMC
GO:1903827	0.907	0.156	10	164	regulation of cellular protein localization	BP	1	HCLS1,PPP2R5A,TMEM173,IWS1,FERMT1,EPB41,SH3GLB1,APOD,CTDSPL2,GCC2	up_VCAV_EC
GO:0016311	0.907	0.214	3	106	dephosphorylation	BP	1	PDGFRB,THNSL2,SPRED1	down_VCAV_EC
GO:0043281	0.907	0.216	3	57	regulation of cysteine-type endopeptidase activity involved in	BP	1	DAPK1,SH3RF1,PARK7	up_ACOR_VSMC
GO:0140053	0.907	0.249	2	47	mitochondrial gene expression	BP	1	TRUB2,FASTKD3	down_ACOR_VSMC
GO:0048588	0.907	0.249	2	44	developmental cell growth	BP	1	SLC29A1,IQGAP1	down_ACOR_VSMC
GO:0045732	0.907	0.246	2	78	positive regulation of protein catabolic process	BP	1	LRP1,PACSIN3	down_VCAV_EC

GO:1902749	0.907	0.249	2	39	regulation of cell cycle G2/M phase transition	BP	1	CDC7,APP	up_ACOR_VSMC
GO:0009116	0.907	0.249	2	39	nucleoside metabolic process	BP	1	NT5C2,PNP	up_VSAP_EC
GO:0048675	0.907	0.325	1	26	axon extension	BP	1	SLC29A1	down_ACOR_VSMC
GO:0060395	0.907	0.324	1	27	SMAD protein signal transduction	BP	1	RBM14	down_ACOR_VSMC
GO:0042221	0.907	0.332	1	1012	response to chemical	BP	1	GABPA	down_AFEM_EC
GO:0002703	0.907	0.32	1	47	regulation of leukocyte mediated immunity	BP	1	RAC2	down_VCAV_EC
GO:0007596	0.907	0.32	1	47	blood coagulation	BP	1	VKORC1	down_VCAV_EC
GO:0022900	0.907	0.321	1	46	electron transport chain	BP	1	NDUFA4L2	down_VSAP_EC
GO:0009064	0.907	0.327	1	23	glutamine family amino acid metabolic process	BP	1	NIT2	up_ACOR_VSMC
GO:0097194	0.907	0.327	1	23	execution phase of apoptosis	BP	1	FZD3	up_ACOR_VSMC
GO:0006814	0.907	0.324	1	28	sodium ion transport	BP	1	SPTBN4	up_VCAV_EC
GO:0016070	0.907	0.343	1	1479	RNA metabolic process	BP	1	GATA5	up_VCAV_VSMC
GO:0003208	0.907	0.326	1	24	cardiac ventricle morphogenesis	BP	1	TGFBR2	up_VSAP_EC
GO:0044089	0.908	0.149	12	170	positive regulation of cellular component	BP	1	SYNPO2L,SYNPO2,F2RL1,JMY,NRP1,EVL,SLITRK5,PRKCE,DAG1,EDN1,ASAP1,WASL	up_ACOR_VSMC
GO:0032886	0.908	0.184	5	81	regulation of microtubule-based process	BP	1	FGF13,MID1,PRKAA2,TUBB4A,FAM107A	up_ACOR_VSMC
GO:0034728	0.908	0.215	3	56	nucleosome organization	BP	1	NAA60,SMARCD2,CENPP	up_VSAP_EC
GO:0042177	0.908	0.246	2	47	negative regulation of protein catabolic process	BP	1	SLC29A1,SMARCC1	down_ACOR_VSMC
GO:0032496	0.908	0.243	2	77	response to lipopolysaccharide	BP	1	ENSCAFG00000013404,SASH1	down_VCAV_EC
GO:1903532	0.908	0.244	2	78	positive regulation of secretion by cell	BP	1	SDC4,MAVS	down_VCAV_EC
GO:0060255	0.908	0.262	2	1782	regulation of macromolecule metabolic	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0017015	0.908	0.248	2	40	regulation of transforming growth factor beta receptor signaling	BP	1	ZEB1,CITED2	up_VSAP_EC
GO:1903844	0.908	0.248	2	40	regulation of cellular response to transforming growth factor beta	BP	1	ZEB1,CITED2	up_VSAP_EC
GO:0003014	0.908	0.323	1	27	renal system process	BP	1	EMP2	down_ACOR_VSMC
GO:0030510	0.908	0.323	1	27	regulation of BMP signaling pathway	BP	1	GREM1	down_ACOR_VSMC
GO:0009913	0.908	0.319	1	47	epidermal cell differentiation	BP	1	ZFP36L1	down_VCAV_EC
GO:0010976	0.908	0.319	1	47	positive regulation of neuron projection	BP	1	TRPV2	down_VCAV_EC
GO:0006094	0.908	0.324	1	24	gluconeogenesis	BP	1	LEP	up_ACOR_VSMC
GO:0051338	0.908	0.316	1	288	regulation of transferase activity	BP	1	ASPN	up_VPOR_EC
GO:0006342	0.908	0.324	1	24	chromatin silencing	BP	1	H2AFJ	up_VSAP_EC
GO:0050871	0.908	0.324	1	24	positive regulation of B cell activation	BP	1	STAT6	up_VSAP_EC
GO:0015833	0.908	0.321	1	521	peptide transport	BP	1	TLR2	up_VSAP_VSMC

GO:1901564	0.909	0.107	180	2053	organonitrogen compound metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,LEP,PLCL1,GALNT10,ST3GAL5,MAP3K8,MID1,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,ENSCAFG00000002977,SKP2,PRKAA2,ITM2C,BMP4,CPXM1,LCAT,B3GNT7,FGFR2,PCBD1,CCDC126,ABCA1,EIF4A2,ATRX,TARSL2,TLR3,SH3RF2,PPARGC1A,LATS2,PIGN,PDE5A,MAOA,PIGS,ISG15,UGCG,ZNRF3,SASH1,CTSS,PTPN3,FGF18,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,USP53,GRK7,CST3,PIGG,KLHL20,F2RL1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,ERO1B,DAPK1,APOL6,CTSB,RBM4B,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,C1S,NRP1,UBR1,PTPN22,ULK2,DMPK,NPNT,OS9,ENSCAFG00000028814,STT3B,ORMDL3,SMPD1,PTGDR,FUT11,C7,UBE2H,MOXD1,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,SARDH,FRS2,RNF19A,LYPLAL1,SCG5,DAG1,FUT8,ENSCAFG00000018611,POMK,PARP9,APP,PSEN1,PCSK6,SGSM2,SYNJ2BP,SHPRH,PIK3C3,LAMP2,SPINK2,CCL5,DDR2,CLN8,PERP,PSKH1,DUSP22,SIAH1,EDN1,OXR1,RNF141,PHF20,ALDOC,AKTIP,CTSF,DUSP26,NOD2,LRRC4,LMTK2,FAM107A,PCYOX1,PRKAG3,DDIT4,DISC1,SH3RF3,SERINC3,EOGT,DCUN1D4,RNF181,NEU3,USP20,HERPUD1,S	up_ACOR_VSMC
GO:0045184	0.909	0.121	43	532	establishment of protein localization	BP	1	PEX7,HNF4A,CD274,ARHGEF5,C5AR2,SLC8B1,TBC1D10C,TBC1D2B,CDH1,ABL1,PEX2,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,TOM1,F2RL1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,NUP98,HPS4,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,STX4,VPS11,PPP3CB,PEX6,MAVS,BAG4,NCOA4,NAGPA,RAB11FIP2	up_VSAP_EC
GO:0006873	0.909	0.15	11	160	cellular ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,FXN,MYC,SCARA5,FTL,CYBA,HMOX1,NCOA4	up_VSAP_EC
GO:1901565	0.909	0.165	7	442	organonitrogen compound catabolic	BP	1	CTSS,CLEC16A,CYLD,MOXD1,RAB7A,FAP,RNF181	up_AFEM_EC
GO:0061025	0.909	0.195	4	69	membrane fusion	BP	1	TBC1D10C,TBC1D2B,STX4,VPS11	up_VSAP_EC
GO:0051049	0.909	0.242	2	479	regulation of transport	BP	1	HOXA3,GCC2	up_VPOR_EC
GO:0010467	0.909	0.261	2	1787	gene expression	BP	1	HOXA3,GATA5	up_VPUL_VSMC
GO:0031323	0.909	0.26	2	1788	regulation of cellular metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:2000241	0.909	0.245	2	40	regulation of reproductive process	BP	1	CFAP69,CITED2	up_VSAP_EC
GO:0007009	0.909	0.318	1	27	plasma membrane organization	BP	1	CAV1	down_ACOR_VSMC
GO:0016579	0.909	0.315	1	49	protein deubiquitination	BP	1	PARK7	down_VCAV_EC
GO:1901657	0.909	0.317	1	43	glycosyl compound metabolic process	BP	1	ENTPD4	down_VSAP_EC
GO:1902652	0.909	0.316	1	38	secondary alcohol metabolic process	BP	1	APOE	down_VSAP_EC
GO:0008652	0.909	0.322	1	24	cellular amino acid biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1901607	0.909	0.322	1	24	alpha-amino acid biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:0007173	0.909	0.319	1	27	epidermal growth factor receptor signaling	BP	1	FES	up_VCAV_EC
GO:0015918	0.909	0.319	1	27	sterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0030301	0.909	0.319	1	27	cholesterol transport	BP	1	ABCA1	up_VCAV_EC
GO:0019752	0.909	0.315	1	283	carboxylic acid metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0051345	0.909259176	0.24002	2	151	positive regulation of hydrolase activity	BP	1	DYNC1I1,PRKCD	up_ACOR_EC
GO:0046777	0.909358239	0.31278	1	86	protein autophosphorylation	BP	1	GRK7	up_ACOR_EC
GO:0051223	0.91	0.149	11	181	regulation of protein transport	BP	1	ACSL3,HMGB1,SREBF1,RAN,BIRC5,INSIG1,PLK3,ARG2,DMAP1,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0045333	0.91	0.192	4	74	cellular respiration	BP	1	PPARGC1A,BNIP3,SLC25A12,PARK7	up_ACOR_VSMC
GO:0031348	0.91	0.242	2	46	negative regulation of defense response	BP	1	ARG2,CACTIN	down_ACOR_VSMC

GO:0002699	0.91	0.242	2	46	positive regulation of immune effector process	BP	1	TFRC,FAM49B	down_ACOR_VSMC
GO:0046328	0.91	0.241	2	61	regulation of JNK cascade	BP	1	TNIK,SH3RF3	down_VSAP_EC
GO:0048738	0.91	0.241	2	64	cardiac muscle tissue development	BP	1	FHL2,NEXN	down_VSAP_EC
GO:0048167	0.91	0.317	1	28	regulation of synaptic plasticity	BP	1	CDC20	down_ACOR_VSMC
GO:0006605	0.91	0.311	1	99	protein targeting	BP	1	RAB7A	up_AFEM_EC
GO:0070585	0.91	0.316	1	34	protein localization to mitochondrion	BP	1	SH3GLB1	up_VCAV_EC
GO:0055085	0.91	0.313	1	284	transmembrane transport	BP	1	SRP54	up_VPOR_EC
GO:0031110	0.91	0.319	1	24	regulation of microtubule polymerization or depolymerization	BP	1	ABL1	up_VSAP_EC
GO:0009117	0.910690996	0.2067	3	208	nucleotide metabolic process	BP	1	NMNAT2,GUCY1B1,ALDOC	up_ACOR_EC
GO:0045892	0.911	0.127	25	328	negative regulation of transcription, DNA-templated	BP	1	FZD1,THRB,HOXA7,WNT11,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,SHOX2,H2AFJ,IKZF2,LIMD1,PRMT2,KDM2B,NFIB,ZNF205,NCOA2,QARS,SMARCA2,NCK1	up_VSAP_EC
GO:0022414	0.911	0.129	22	294	reproductive process	BP	1	HOXA11,THRB,HOXA9,HNF4A,GJB5,IRX5,SLIT2,EMP2,OSR1,ZNF449,HERPUD2,ZBTB16,RARG,RECK,PATZ1,DLX3,ZFP36L1,CFAP69,CREBRF,KDM2B,HPGD,CITED2	up_VSAP_EC
GO:0009792	0.911	0.135	17	231	embryo development ending in birth or egg hatching	BP	1	SHROOM3,BMP4,FGFR2,GJA1,SEC24B,LATS2,CITED2,SPINT1,LMO4,EGLN1,ENSCAFG00000006238,SPINT2,FZD3,PSEN1,CHD7,EDN1,INPP5K	up_ACOR_VSMC
GO:0019752	0.911	0.134	17	283	carboxylic acid metabolic process	BP	1	PDGFB,ST6GAL1,EDN1,PIPOX,PTGS1,ODC1,ARG2,TARSL2,AADAT,PROX1,ELOVL7,ENSCAFG00000024323,PTGS2,GCH1,HIF1A,BCAT1,ALDH1A3	up_VCAV_EC
GO:0008152	0.911	0.175	10	3714	metabolic process	BP	1	HOXA3,NR1H4,STK32B,ENSCAFG00000028814,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0006790	0.911	0.171	6	99	sulfur compound metabolic process	BP	1	TPST2,MAT2B,ENSCAFG00000028814,PCYOX1,PARK7,ELOVL7	up_ACOR_VSMC
GO:1901135	0.911	0.168	6	390	carbohydrate derivative metabolic process	BP	1	XYLT1,GPAM,ATP6V1B2,ACACB,PPARGC1A,CSGALNACT2	up_AFEM_EC
GO:0034641	0.911	0.192	5	2171	cellular nitrogen compound metabolic	BP	1	NR1H4,ENSCAFG00000028814,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0140014	0.911	0.189	4	110	mitotic nuclear division	BP	1	MZT1,NAA10,KPNB1,PDS5B	down_VSAP_EC
GO:0019752	0.911	0.189	4	283	carboxylic acid metabolic process	BP	1	LEP,GPAM,ACACB,PPARGC1A	up_AFEM_EC
GO:0071897	0.911	0.21	3	54	DNA biosynthetic process	BP	1	ANKRD1,CDKN1A,HMBOX1	up_ACOR_VSMC
GO:0045598	0.911	0.239	2	47	regulation of fat cell differentiation	BP	1	INSIG1,PPARD	down_ACOR_VSMC
GO:0007018	0.911	0.237	2	82	microtubule-based movement	BP	1	IFT57,MGARP	down_VCAV_EC
GO:1903008	0.911	0.24	2	47	organelle disassembly	BP	1	MRRF,HIF1A	up_VCAV_EC
GO:0007188	0.911	0.24	2	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	ADGRD1,CHRM1	up_VSAP_EC
GO:0035051	0.911	0.24	2	41	cardiocyte differentiation	BP	1	DLL1,CITED2	up_VSAP_EC
GO:0042158	0.911	0.242	2	40	lipoprotein biosynthetic process	BP	1	ZDHHC8,LCAT	up_VSAP_EC
GO:0007605	0.911	0.314	1	27	sensory perception of sound	BP	1	NAV2	down_ACOR_VSMC
GO:0021761	0.911	0.315	1	27	limbic system development	BP	1	NF2	down_ACOR_VSMC
GO:0042733	0.911	0.314	1	27	embryonic digit morphogenesis	BP	1	MAP3K20	down_ACOR_VSMC
GO:0006937	0.911	0.312	1	40	regulation of muscle contraction	BP	1	CALM1	down_VSAP_EC
GO:0042158	0.911	0.313	1	40	lipoprotein biosynthetic process	BP	1	APOE	down_VSAP_EC
GO:0044271	0.911	0.332	1	1501	cellular nitrogen compound biosynthetic	BP	1	GATA5	up_VCAV_VSMC
GO:0006950	0.911	0.323	1	1102	response to stress	BP	1	IL22RA1	up_VPUL_VSMC
GO:0001658	0.911	0.317	1	24	branching involved in ureteric bud	BP	1	HOXA11	up_VSAP_EC

GO:0010941	0.911	0.313	1	524	regulation of cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0042886	0.911	0.314	1	527	amide transport	BP	1	TLR2	up_VSAP_VSMC
GO:0071824	0.911763536	0.30675	1	92	protein-DNA complex subunit organization	BP	1	SOX9	up_ACOR_EC
GO:0051253	0.912	0.124	28	359	negative regulation of RNA metabolic process	BP	1	LEP,NACC2,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,ZNF174,ENSCAFG00000006238,CLSTN1,TBX20,CCNT1,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0044265	0.912	0.123	28	423	cellular macromolecule catabolic process	BP	1	TNFAIP3,CTSC,WWP1,USP33,PSME4,PELI1,CASP8,TENT2,CNOT6,ENC1,PAN3,USP28,CNOT7,SMG7,PMAIP1,RIPK1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,DCP2,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0055085	0.912	0.133	18	284	transmembrane transport	BP	1	NNT,NEDD4,TIMM44,SLC35C2,CAV1,SLC30A1,CLIC1,SLC17A9,TRAM1,GSTO1,CORO1A,CYC1,ATP5F1A,ENSCAFG00000013366,REM1,MRPL18,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0071345	0.912	0.137	15	210	cellular response to cytokine stimulus	BP	1	IFNGR1,LEP,EIF4A2,ANKRD1,F2RL1,DAPK1,CREBRF,NPNT,EVL,CCDC3,PARP9,CCL5,LRRC4,ARID5B,INPP5K	up_ACOR_VSMC
GO:0033043	0.912	0.161	7	446	regulation of organelle organization	BP	1	MLLT11,CLEC16A,CYLD,AXIN2,PPARGC1A,CDC42EP5,KANK1	up_AFEM_EC
GO:0006091	0.912	0.161	7	139	generation of precursor metabolites and energy	BP	1	PCDH12,ADGRF5,MTOR,ENSCAFG00000024323,SLC25A25,PPP1CB,HIF1A	up_VCAV_EC
GO:0006520	0.912	0.167	6	114	cellular amino acid metabolic process	BP	1	PIPOX,ODC1,ARG2,TARSL2,AADAT,BCAT1	up_VCAV_EC
GO:0010632	0.912	0.177	5	95	regulation of epithelial cell migration	BP	1	HMGB1,PRCP,EMP2,NUS1,AMOTL1	down_ACOR_VSMC
GO:0043406	0.912	0.208	3	62	positive regulation of MAP kinase activity	BP	1	IRAK1,EZH2,MAP3K20	down_ACOR_VSMC
GO:1901800	0.912	0.237	2	46	positive regulation of proteasomal protein catabolic process	BP	1	PLK3,RAD23A	down_ACOR_VSMC
GO:0045834	0.912	0.239	2	41	positive regulation of lipid metabolic process	BP	1	C1QTNF2,AMBRA1	up_VSAP_EC
GO:1903900	0.912	0.239	2	40	regulation of viral life cycle	BP	1	PC,MAVS	up_VSAP_EC
GO:0031124	0.912	0.311	1	27	mRNA 3'-end processing	BP	1	WDR33	down_ACOR_VSMC
GO:0007599	0.912	0.308	1	48	hemostasis	BP	1	VKORC1	down_VCAV_EC
GO:0031123	0.912	0.308	1	48	RNA 3'-end processing	BP	1	ZFP36L1	down_VCAV_EC
GO:2001251	0.912	0.309	1	49	negative regulation of chromosome organization	BP	1	PRMT6	down_VCAV_EC
GO:0043620	0.912	0.315	1	24	regulation of DNA-templated transcription in	BP	1	CHD6	up_ACOR_VSMC
GO:0030900	0.912	0.307	1	101	forebrain development	BP	1	PLXNA4	up_AFEM_EC
GO:1903362	0.912	0.307	1	100	regulation of cellular protein catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:1901983	0.912	0.314	1	24	regulation of protein acetylation	BP	1	KLF15	up_VSAP_EC
GO:0008585	0.912	0.312	1	24	female gonad development	BP	1	SLIT2	up_VSAP_EC
GO:0033209	0.912	0.313	1	24	tumor necrosis factor-mediated signaling	BP	1	F2RL1	up_VSAP_EC
GO:0046545	0.912	0.312	1	24	development of primary female sexual	BP	1	SLIT2	up_VSAP_EC
GO:0050790	0.912	0.312	1	532	regulation of catalytic activity	BP	1	CAV1	up_VSAP_VSMC
GO:0031396	0.912166438	0.30583	1	90	regulation of protein ubiquitination	BP	1	NOD2	up_ACOR_EC
GO:0010558	0.913	0.121	31	392	negative regulation of macromolecule biosynthetic process	BP	1	LEP,NACC2,ITM2C,BMP4,FGFR2,EIF4A2,ATRX,TRPS1,AR,ZNF174,ANKRD1,DAPK1,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0006954	0.913	0.147	10	147	inflammatory response	BP	1	NAPEPLD,C5AR2,ACKR2,IL17RC,TBXA2R,MYD88,NLRX1,CYBA,HMOX1,SAA1	up_VSAP_EC
GO:0034655	0.913	0.151	9	135	nucleobase-containing compound catabolic	BP	1	PNRC1,PDE5A,ENPP4,DCP1B,ALDOC,ENTPD3,DDIT4,CNOT4,CTIF	up_ACOR_VSMC
GO:0051186	0.913	0.155	8	159	cofactor metabolic process	BP	1	PANK3,PIPOX,AADAT,ELOVL7,ENSCAFG00000024323,GCH1,BLVRA,HIF1A	up_VCAV_EC

GO:0032984	0.913	0.188	4	70	protein-containing complex disassembly	BP	1	SMARCD2,PYM1,F2RL1,DDIT4	up_VSAP_EC
GO:0018394	0.913	0.206	3	55	peptidyl-lysine acetylation	BP	1	PRKAA2,PHF20,MAP3K7	up_ACOR_VSMC
GO:0007420	0.913	0.233	2	169	brain development	BP	1	DLL1,PLXNA4	up_AFEM_EC
GO:0071346	0.913	0.236	2	41	cellular response to interferon-gamma	BP	1	CDC42EP2,STX4	up_VSAP_EC
GO:1904892	0.913	0.237	2	40	regulation of STAT cascade	BP	1	IL6R,RTN4RL1	up_VSAP_EC
GO:0006140	0.913	0.31	1	28	regulation of nucleotide metabolic process	BP	1	CDK1	down_ACOR_VSMC
GO:0140056	0.913	0.309	1	28	organelle localization by membrane tethering	BP	1	CEP83	down_ACOR_VSMC
GO:0006836	0.913	0.306	1	47	neurotransmitter transport	BP	1	PARK7	down_VCAV_EC
GO:0010952	0.913	0.307	1	46	positive regulation of peptidase activity	BP	1	IFT57	down_VCAV_EC
GO:1905330	0.913	0.306	1	48	regulation of morphogenesis of an	BP	1	GREM1	down_VCAV_EC
GO:0016444	0.913	0.311	1	23	somatic cell DNA recombination	BP	1	TP53BP1	up_ACOR_VSMC
GO:0002200	0.913	0.311	1	23	somatic diversification of immune receptors	BP	1	TP53BP1	up_ACOR_VSMC
GO:0002562	0.913	0.311	1	23	somatic diversification of immune receptors via germline recombination within a single locus	BP	1	TP53BP1	up_ACOR_VSMC
GO:0035306	0.913	0.311	1	24	positive regulation of dephosphorylation	BP	1	PPARGC1B	up_VSAP_EC
GO:0043620	0.913	0.312	1	24	regulation of DNA-templated transcription in	BP	1	NCK1	up_VSAP_EC
GO:1901565	0.914	0.116	35	442	organonitrogen compound catabolic process	BP	1	ENPP2,RNPEP,FOXRED2,GDA,ABTB1,GOT1,CTSS,ADHFE1,HPSE,ALDH6A1,VPS36,RBCK1,RNF24,FBXW4,BCKDHB,FBXO4,RMND5A,AZIN2,FBXW5,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,ENSCAFG00000002977,PNP,TIMP2,UBQLN2,CTSF,CDC26,HTRA2,HMOX1,KEAP1,IDO2	up_VSAP_EC
GO:1902679	0.914	0.123	25	329	negative regulation of RNA biosynthetic process	BP	1	FZD1,THRB,HOXA7,WNT11,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,SHOX2,H2AFJ,IKZF2,LIMD1,PRMT2,KDM2B,NFIB,ZNF205,NCOA2,QARS,SMARCA2,NCK1	up_VSAP_EC
GO:1903507	0.914	0.123	25	329	negative regulation of nucleic acid-templated transcription	BP	1	FZD1,THRB,HOXA7,WNT11,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,RARG,CBX7,STAT6,GLIS2,SHOX2,H2AFJ,IKZF2,LIMD1,PRMT2,KDM2B,NFIB,ZNF205,NCOA2,QARS,SMARCA2,NCK1	up_VSAP_EC
GO:0000003	0.914	0.125	22	295	reproduction	BP	1	HOXA11,THRB,HOXA9,HNF4A,GJB5,IRX5,SLIT2,EMP2,OSR1,ZNF449,HERPUD2,ZBTB16,RARG,RECK,PATZ1,DLX3,ZFP36L1,CFAP69,CREBRF,KDM2B,HPGD,CITED2	up_VSAP_EC
GO:0045786	0.914	0.153	8	195	negative regulation of cell cycle	BP	1	PTPN11,NAA10,DDX39B,CTNNB1,DDIT3,INHBA,NR4A1,CDKN1A	down_VSAP_EC
GO:0031334	0.914	0.175	5	84	positive regulation of protein complex assembly	BP	1	JMY,EVL,PRKCE,ASAP1,WASL	up_ACOR_VSMC
GO:0043543	0.914	0.174	5	84	protein acylation	BP	1	PRKAA2,PHF20,MAP3K7,PARK7,ZDHHC21	up_ACOR_VSMC
GO:0000209	0.914	0.185	4	83	protein polyubiquitination	BP	1	TNFAIP3,PELI1,C7H18orf25,UBE2D1	up_VCAV_EC
GO:0048284	0.914	0.202	3	66	organelle fusion	BP	1	STXBP6,CHCHD3,CORO1A	down_ACOR_VSMC
GO:0009411	0.914	0.204	3	56	response to UV	BP	1	MFAP4,TP53INP1,CDKN1A	up_ACOR_VSMC
GO:1901991	0.914	0.203	3	56	negative regulation of mitotic cell cycle phase	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC
GO:0050684	0.914	0.233	2	46	regulation of mRNA processing	BP	1	IWS1,WTAP	up_VCAV_EC
GO:0006508	0.914	0.234	2	483	proteolysis	BP	1	USP33,RNF6	up_VPOR_EC
GO:0032436	0.914	0.235	2	40	positive regulation of proteasomal ubiquitin-dependent protein	BP	1	RNF166,UBQLN2	up_VSAP_EC
GO:0031056	0.914	0.302	1	50	regulation of histone modification	BP	1	PRMT6	down_VCAV_EC
GO:0098813	0.914	0.3	1	102	nuclear chromosome segregation	BP	1	AXIN2	up_AFEM_EC
GO:0090329	0.914	0.307	1	25	regulation of DNA-dependent DNA	BP	1	CIZ1	up_VSAP_EC

GO:0045184	0.914	0.306	1	532	establishment of protein localization	BP	1	TLR2	up_VSAP_VSMC
GO:0006874	0.914577901	0.29988	1	91	cellular calcium ion homeostasis	BP	1	PTH1R	up_ACOR_EC
GO:0006807	0.915	0.104	150	3221	nitrogen compound metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,MAOA,CFD,NAB2,NDN,PRNP,LUM,UBA52,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,NUMBL,CHID1,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,TFE3,NR3C1,H6PD,HR,RPL23,RPL13,CLSTN1,PCSK7,PLCL1,DDOST,CSPG4,VDR,PRMT6,UROS,NT5C2,ENTPD3,THNSL2,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,ASPN,PIGS,HS3ST3B1,EIF3K,THY1,NECAB3,RNF216,TEAD1,SUOX,ADK,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RNPEP,RPL27,COPS7A,RBM38,ARL2BP,AMPD2,IFT57,BTD,MAVS,MRPS11,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,CDKL2,HM13,PRKCSH,DDR2,SHC1,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,ATOX1,LONP2,NAPEPLD,GLS2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA,BCKDHB,ACAT1,BRSK1,CDK14	down_VCAV_EC
GO:0006351	0.915	0.11	56	1069	transcription, DNA-templated	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0006816	0.915	0.173	5	84	calcium ion transport	BP	1	SLC8B1,TPCN2,ABL1,CRACR2B,CYBA	up_VSAP_EC
GO:0071902	0.915	0.183	4	79	positive regulation of protein serine/threonine	BP	1	IRAK1,EZH2,MAP3K20,CKS2	down_ACOR_VSMC
GO:0044249	0.915	0.195	4	1851	cellular biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0010921	0.915	0.232	2	46	regulation of phosphatase activity	BP	1	SLC29A1,KNL1	down_ACOR_VSMC
GO:0043401	0.915	0.231	2	46	steroid hormone mediated signaling	BP	1	NEDD4,THRAP3	down_ACOR_VSMC
GO:1903008	0.915	0.231	2	47	organelle disassembly	BP	1	SREBF1,PLK3	down_ACOR_VSMC
GO:0007492	0.915	0.306	1	27	endoderm development	BP	1	MMP14	down_ACOR_VSMC
GO:0032007	0.915	0.305	1	27	negative regulation of TOR signaling	BP	1	RNF152	down_ACOR_VSMC
GO:0051224	0.915	0.302	1	47	negative regulation of protein transport	BP	1	PARK7	down_VCAV_EC
GO:1904950	0.915	0.302	1	47	negative regulation of establishment of protein localization	BP	1	PARK7	down_VCAV_EC
GO:0030512	0.915	0.306	1	24	negative regulation of transforming growth factor beta receptor	BP	1	SMAD6	up_ACOR_VSMC
GO:1903409	0.915	0.307	1	24	reactive oxygen species biosynthetic process	BP	1	PARK7	up_ACOR_VSMC
GO:1903845	0.915	0.306	1	24	negative regulation of cellular response to transforming growth	BP	1	SMAD6	up_ACOR_VSMC
GO:0021549	0.915	0.304	1	26	cerebellum development	BP	1	PROX1	up_VCAV_EC
GO:2000045	0.915	0.305	1	29	regulation of G1/S transition of mitotic cell	BP	1	CUL4A	up_VCAV_EC
GO:2000112	0.915	0.314	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0051493	0.916	0.135	13	188	regulation of cytoskeleton organization	BP	1	WNT11,FAM107A,ARHGEF5,CEP85,SLIT2,ABL1,CDC42EP5,CDC42EP2,F2RL1,PIK3R1,FBXW5,NCK1,BAG4	up_VSAP_EC

GO:0044770	0.916	0.14	11	161	cell cycle phase transition	BP	1	FAM107A,CRADD,ZFP36L1,CDC25B,E2F4,FBXO7,ZFP36L2,TPRA1,CDC26,LSM10,LATS2	up_VSAP_EC
GO:0050789	0.916	0.198	5	3295	regulation of biological process	BP	1	GPSM2,IVNS1ABP,SRSF6,GABPA,FSCN1	down_AFEM_EC
GO:0051216	0.916	0.182	4	70	cartilage development	BP	1	BMP4,LNPK,FGF18,EDN1	up_ACOR_VSMC
GO:0055001	0.916	0.229	2	47	muscle cell development	BP	1	SDC1,SIX4	down_ACOR_VSMC
GO:0044089	0.916	0.226	2	170	positive regulation of cellular component	BP	1	RAB7A,CDC42EP5	up_AFEM_EC
GO:0010633	0.916	0.302	1	28	negative regulation of epithelial cell migration	BP	1	HMGB1	down_ACOR_VSMC
GO:0030072	0.916	0.299	1	48	peptide hormone secretion	BP	1	PARK7	down_VCAV_EC
GO:0060968	0.916	0.305	1	23	regulation of gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:1903320	0.916	0.297	1	102	regulation of protein modification by small protein conjugation or	BP	1	DCUN1D3	up_AFEM_EC
GO:0006400	0.916	0.3	1	33	tRNA modification	BP	1	TRMT9B	up_VCAV_EC
GO:0048024	0.916	0.302	1	30	regulation of mRNA splicing, via spliceosome	BP	1	WTAP	up_VCAV_EC
GO:0031399	0.916	0.301	1	559	regulation of protein modification process	BP	1	MAP2K6	up_VFEM_EC
GO:0000075	0.916188855	0.29589	1	91	cell cycle checkpoint	BP	1	BRSK1	up_ACOR_EC
GO:0034645	0.917	0.117	30	1546	cellular macromolecule biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,XYLT1,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CSGALNACT2,CTIF,SAMD4B	up_AFEM_EC
GO:0002520	0.917	0.125	18	279	immune system development	BP	1	HMGB1,ANLN,HOXA3,HSPA9,PRELID1,PRMT1,MMP14,HMGB3,HOXA7,PDCD2,HOXB7,TFRC,HMGB2,TOX,SGPL1,HOXA9,JMJD6,SIX4	down_ACOR_VSMC
GO:0009144	0.917	0.16	6	103	purine nucleoside triphosphate metabolic	BP	1	PPARGC1A,ENSCAFG00000018611,ALDOC,DDIT4,NMNAT1,PARK7	up_ACOR_VSMC
GO:0072659	0.917	0.18	4	82	protein localization to plasma membrane	BP	1	ACSL3,MMP14,EMP2,EZR	down_ACOR_VSMC
GO:0031647	0.917	0.18	4	87	regulation of protein stability	BP	1	BMP2,CREB1,USP28,USP13	up_VCAV_EC
GO:0009991	0.917	0.196	3	110	response to extracellular stimulus	BP	1	KANK2,GABARAP,CLEC16A	down_VCAV_EC
GO:0043412	0.917	0.204	3	1225	macromolecule modification	BP	1	EYA1,MAP2K6,CDC42EP5	up_VFEM_EC
GO:0002011	0.917	0.299	1	28	morphogenesis of an epithelial sheet	BP	1	PHACTR4	down_ACOR_VSMC
GO:0065008	0.917	0.308	1	1056	regulation of biological quality	BP	1	GPSM2	down_AFEM_EC
GO:0001894	0.917	0.296	1	49	tissue homeostasis	BP	1	NCDN	down_VCAV_EC
GO:0007030	0.917	0.295	1	49	Golgi organization	BP	1	ATP8B2	down_VCAV_EC
GO:0002698	0.917	0.301	1	25	negative regulation of immune effector process	BP	1	DUSP22	up_ACOR_VSMC
GO:0061053	0.917	0.302	1	24	somite development	BP	1	PSEN1	up_ACOR_VSMC
GO:0090398	0.917	0.302	1	24	cellular senescence	BP	1	CDKN1A	up_ACOR_VSMC
GO:0051222	0.917	0.294	1	103	positive regulation of protein transport	BP	1	LEP	up_AFEM_EC
GO:0006355	0.917	0.306	1	974	regulation of transcription, DNA-	BP	1	HOXA9	up_AORT_EC
GO:0065003	0.917	0.299	1	616	protein-containing complex assembly	BP	1	TUBB4A	up_APUL_EC

GO:1901362	0.918	0.0996	112	1293	organic cyclic compound biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SCP2,SMARCD3,TBX20,MOXD1,CCNT1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,PTS,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0034654	0.918	0.0999	107	1236	nucleobase-containing compound biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0065008	0.918	0.102	78	1056	regulation of biological quality	BP	1	HMGB1,LSS,SREBF1,RPA1,USP4,FMNL3,TFPI,HNRNPD,SREBF2,TFPI2,RALY,UBE2S,NEDD4,QSOX2,CAPG,SLC29A1,HOXA3,SLC25A5,HSPA9,PRELID1,BIRC5,INSIG1,PRMT1,CAV1,RAD51,THRAP3,LIMA1,FAM129B,NF2,AURKB,ABHD5,EZH2,STMN1,SLC30A1,NEK2,ADIPOR2,HOXC10,TRPV4,FASTKD3,NAV2,PRCP,TFRC,ITGB3,YWHAB,RAC1,EMP2,PDXP,IQGAP2,HMGB2,GSTO1,CDC42EP4,ENSCAFG00000005299,EZR,SMC6,ELOVL6,RAD23A,CORO1A,SGPL1,CDC20,BAP1,PRDX1,ASPM,ARPC1B,ENSCAFG00000006478,TXNDC12,NCOA5,TADA2A,TINF2,JMJD6,LIPC,UBE2C,NUS1,CCT4,SIX4,THADA,TPBG,ANXA7,PIK3CD	down_ACOR_VSMC
GO:0097659	0.918	0.106	56	1072	nucleic acid-templated transcription	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0051252	0.918	0.107	55	1051	regulation of RNA metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC

GO:0044092	0.918	0.122	20	270	negative regulation of molecular function	BP	1	SH2D4A,CEP85,ACACB,CST3,ABL1,KCNE3,OSR1,ANXA4,RECK,GLIS2,RBCK1,PIK3IP1,TMEM225B,RTN4RL1,FBXO7,PRMT2,TIMP2,BAG4,KEAP1,LATS2	up_VSAP_EC
GO:0030334	0.918	0.125	17	267	regulation of cell migration	BP	1	HMGB1,RACGAP1,FBXO5,CAV1,MMP14,HOXA7,PRCP,RAP2C,RAC1,EMP2,CORO1A,ENSCAFG00000010224,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0061024	0.918	0.151	7	215	membrane organization	BP	1	SLC35F6,SNX18,AKT2,PEX5,CDH2,EVI5L,PACSIN3	down_VCAV_EC
GO:0034976	0.918	0.159	6	112	response to endoplasmic reticulum stress	BP	1	PPP1R15B,HM13,UBE2J2,TXNDC12,PSMC1,AIFM1	down_ACOR_VSMC
GO:0030111	0.918	0.158	6	108	regulation of Wnt signaling pathway	BP	1	FERMT1,RAPGEF1,BMP2,HHEX,MCC,SMARCA4	up_VCAV_EC
GO:0044282	0.918	0.178	4	89	small molecule catabolic process	BP	1	CDA,PIPOX,GALE,IMPA1	up_VCAV_EC
GO:0045165	0.918	0.225	2	65	cell fate commitment	BP	1	ARHGEF2,CTNNB1	down_VSAP_EC
GO:0034249	0.918	0.226	2	41	negative regulation of cellular amide metabolic	BP	1	DAPK1,ORMDL3	up_ACOR_VSMC
GO:0002062	0.918	0.226	2	48	chondrocyte differentiation	BP	1	MEF2C,BMP2	up_VCAV_EC
GO:0008589	0.918	0.296	1	28	regulation of smoothened signaling pathway	BP	1	GLI1	down_ACOR_VSMC
GO:0002285	0.918	0.293	1	50	lymphocyte activation involved in immune	BP	1	LOXL3	down_VCAV_EC
GO:0090305	0.918	0.294	1	49	nucleic acid phosphodiester bond	BP	1	FBH1	down_VCAV_EC
GO:0008630	0.918	0.294	1	39	intrinsic apoptotic signaling pathway in response to DNA damage	BP	1	CDKN1A	down_VSAP_EC
GO:0018023	0.918	0.298	1	23	peptidyl-lysine trimethylation	BP	1	ATRX	up_ACOR_VSMC
GO:0043966	0.918	0.299	1	25	histone H3 acetylation	BP	1	MAP3K7	up_ACOR_VSMC
GO:1903506	0.918	0.304	1	977	regulation of nucleic acid-templated transcription	BP	1	HOXA9	up_AORT_EC
GO:2001141	0.918	0.303	1	979	regulation of RNA biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0001738	0.918	0.296	1	27	morphogenesis of a polarized epithelium	BP	1	EXOC5	up_VCAV_EC
GO:0008589	0.918	0.298	1	28	regulation of smoothened signaling pathway	BP	1	CTNNA1	up_VCAV_EC
GO:0034645	0.918	0.315	1	1546	cellular macromolecule biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0071702	0.918	0.299	1	687	organic substance transport	BP	1	NR1H4	up_VPUL_EC
GO:0044238	0.919	0.0988	158	3383	primary metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,CFD,NAB2,NDN,PRNP,LUM,UBA52,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,NUMBL,CHID1,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,TFE3,ACAA1,NR3C1,H6PD,HSD3B7,HR,SCP2,RPL23,RPL13,GLB1L,CLSTN1,PCSK7,PLCL1,DDOST,CSPG4,CYB5R3,VDR,PRMT6,NT5C2,ENTPD3,THNSL2,PGLS,POFUT1,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,ASPN,PIGS,HS3ST3B1,EIF3K,THY1,NECAB3,RNF216,TEAD1,CYP1B1,ADK,WDR45,MRPL37,PEX5,CC2D1A,B4GALT1,RETSAT,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,ABHD15,CLEC16A,RNPEP,RPL27,COPS7A,RBM38,ARL2BP,AMPD2,IFT57,MAVS,MRPS11,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,ACSS2,TSC22D3,SLC3A2,MAPRE3,GLIS2,CDKL2,HM13,PRKCSH,DDR2,SHC1,RDH10,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,ATOX1,LONP2,NAPEPLD,GLS2,FOXO3,SOAT1,THRB	down_VCAV_EC
GO:0071345	0.919	0.126	15	210	cellular response to cytokine stimulus	BP	1	SLIT2,CDC42EP2,RARG,STAT6,F2RL1,ZFP36L1,RTN4RL1,CREBRF,CDK9,ZFP36L2,STX4,HTRA2,MAVS,BAG4,KEAP1	up_VSAP_EC
GO:0008150	0.919	0.198	12	5646	biological_process	BP	1	CHL1,FGF5,HOXA3,BARX1,COL4A5,NKX2-5,LHFPL4,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC

GO:0009306	0.919	0.151	7	127	protein secretion	BP	1	HMGB1,SREBF1,BIRC5,ARG2,PREB,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0006996	0.919	0.155	7	1301	organelle organization	BP	1	MZT1,HOOK3,ARHGEF2,RSL24D1,GCC2,RPL10L,TWF1	up_VPOR_EC
GO:0043604	0.919	0.175	4	288	amide biosynthetic process	BP	1	PRR16,ACACB,CTIF,SAMD4B	up_AFEM_EC
GO:0016567	0.919	0.191	3	232	protein ubiquitination	BP	1	KLHDC8B,DCUN1D3,RNF181	up_AFEM_EC
GO:1901564	0.919	0.209	3	2053	organonitrogen compound metabolic	BP	1	LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0008016	0.919	0.223	2	48	regulation of heart contraction	BP	1	SREBF1,CAV1	down_ACOR_VSMC
GO:0006413	0.919	0.224	2	42	translational initiation	BP	1	EIF4A2,CTIF	up_ACOR_VSMC
GO:0043161	0.919	0.22	2	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	CLEC16A,RNF181	up_AFEM_EC
GO:0010629	0.919	0.222	2	502	negative regulation of gene expression	BP	1	ENSCAFG00000002015,MTDH	up_VPOR_EC
GO:0001704	0.919	0.225	2	43	formation of primary germ layer	BP	1	HOXA11,WNT11	up_VSAP_EC
GO:0002702	0.919	0.294	1	28	positive regulation of production of molecular mediator of immune	BP	1	TFRC	down_ACOR_VSMC
GO:0046660	0.919	0.294	1	28	female sex differentiation	BP	1	SGPL1	down_ACOR_VSMC
GO:0002274	0.919	0.293	1	40	myeloid leukocyte activation	BP	1	LYN	down_VSAP_EC
GO:0009791	0.919	0.292	1	38	post-embryonic development	BP	1	MYO1E	down_VSAP_EC
GO:0051865	0.919	0.293	1	31	protein autoubiquitination	BP	1	UHRF2	up_VCAV_EC
GO:0006796	0.919	0.301	1	938	phosphate-containing compound metabolic	BP	1	ANKRD6	up_VPOR_VSMC
GO:0010556	0.919	0.305	1	1137	regulation of macromolecule	BP	1	GATA5	up_VPUL_VSMC
GO:0010557	0.919070216	0.14119	9	492	positive regulation of macromolecule biosynthetic process	BP	1	GATA4,PKIB,SOX9,FZD5,RASL11A,NOD2,SMAD6,MAVS,TP53INP2	up_ACOR_EC
GO:0018130	0.92	0.0969	109	1261	heterocycle biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,PTS,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0032774	0.92	0.104	56	1073	RNA biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0043933	0.92	0.114	28	698	protein-containing complex subunit organization	BP	1	ADAMTS2,KIRREL1,PRNP,LUM,COA1,LOX,LMO4,RPS10,COL6A1,CLIP3,ENSCAFG00000014978,LCAT,CLSTN1,CABIN1,EIF3K,B4GALT1,SCARA5,CLEC16A,CYBA,MRPS11,RPS27,NCLN,ACTR3B,DDR2,PYM1,GREM1,PLEKHH2,SOAT1	down_VCAV_EC
GO:0010243	0.92	0.123	17	238	response to organonitrogen compound	BP	1	FOXRED2,SLIT2,CDH1,GOT1,PDGFD,KLF15,STAT5A,PDK2,ZFP36L1,PIK3R1,ZEB1,ABAT,MYD88,CASTOR1,UBQLN2,NCK1,BGLAP	up_VSAP_EC

GO:0007186	0.92	0.145	8	124	G protein-coupled receptor signaling	BP	1	GPR1,ADGRD1,C5AR2,CHRM1,F2RL1,GABBR2,HPGD,UBQLN2	up_VSAP_EC
GO:0014706	0.92	0.156	6	112	striated muscle tissue development	BP	1	FLNB,CAV1,GREM1,GLI1,MSC,SIX4	down_ACOR_VSMC
GO:0070646	0.92	0.191	3	63	protein modification by small protein removal	BP	1	USP1,USP4,BAP1	down_ACOR_VSMC
GO:0051962	0.92	0.19	3	112	positive regulation of nervous system	BP	1	TRPV2,NUMBL,GLI3	down_VCAV_EC
GO:1901343	0.92	0.222	2	42	negative regulation of vasculature development	BP	1	EPN2,TBXA2R	up_VSAP_EC
GO:0006641	0.92	0.293	1	25	triglyceride metabolic process	BP	1	LMF1	up_ACOR_VSMC
GO:0031060	0.92	0.293	1	23	regulation of histone methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0043900	0.92	0.286	1	104	regulation of multi-organism process	BP	1	RAB7A	up_AFEM_EC
GO:0009628	0.92	0.288	1	302	response to abiotic stimulus	BP	1	ARHGEF2	up_VPOR_EC
GO:0070227	0.92	0.292	1	25	lymphocyte apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0031399	0.92	0.291	1	559	regulation of protein modification process	BP	1	CAV1	up_VSAP_VSMC
GO:1901990	0.920225215	0.28565	1	94	regulation of mitotic cell cycle phase transition	BP	1	BRSK1	up_ACOR_EC
GO:0006886	0.921	0.117	21	332	intracellular protein transport	BP	1	HCLS1,TMEM173,IWS1,FERMT1,RAB27A,PPP3CA,HHEX,SNX2,THOC1,AKAP12,APOD,CTDSPL2,PAN3,GCC2,STX11,SMG7,TBC1D1,NUP133,IPO11,RABGAP1,USP6NL	up_VCAV_EC
GO:0010628	0.921	0.117	20	527	positive regulation of gene expression	BP	1	DCN,LUM,LARP6,BMPR1A,LMO4,ENSCAFG00000014978,SSBP2,TFE3,TEAD1,GLI3,PARK7,EEF2,MYDGF,MAVS,MAPRE3,SHC1,PYM1,GREM1,THRB,ZBTB16	down_VCAV_EC
GO:0009056	0.921	0.128	13	755	catabolic process	BP	1	LEP,CTSS,TENT5C,CLEC16A,CYLD,MOXD1,RAB7A,AXIN2,ACACB,CTIF,FAP,SAMD4B,RNF181	up_AFEM_EC
GO:1903827	0.921	0.133	11	164	regulation of cellular protein localization	BP	1	CDH1,RAB11B,GLIS2,ICE1,PIK3R1,FBXO4,LRP4,KCNB1,STX4,MAVS,BAG4	up_VSAP_EC
GO:1901576	0.921	0.184	4	1877	organic substance biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0060047	0.921	0.189	3	57	heart contraction	BP	1	THRB,IRX5,KCNE3	up_VSAP_EC
GO:0019932	0.921	0.216	2	82	second-messenger-mediated signaling	BP	1	PRNP,ADCY6	down_VCAV_EC
GO:0051056	0.921	0.216	2	87	regulation of small GTPase mediated signal	BP	1	NOTCH2,ARHGEF25	down_VCAV_EC
GO:0006997	0.921	0.22	2	42	nucleus organization	BP	1	DMPK,SUN1	up_ACOR_VSMC
GO:0010770	0.921	0.288	1	29	positive regulation of cell morphogenesis involved in differentiation	BP	1	RAC1	down_ACOR_VSMC
GO:0006351	0.921	0.298	1	1069	transcription, DNA-templated	BP	1	GABPA	down_AFEM_EC
GO:0007519	0.921	0.286	1	49	skeletal muscle tissue development	BP	1	TSC22D3	down_VCAV_EC
GO:0050817	0.921	0.285	1	50	coagulation	BP	1	VKORC1	down_VCAV_EC
GO:0034637	0.921	0.29	1	25	cellular carbohydrate biosynthetic process	BP	1	INPP5K	up_ACOR_VSMC
GO:0042775	0.921	0.291	1	28	mitochondrial ATP synthesis coupled	BP	1	PARK7	up_ACOR_VSMC
GO:0046605	0.921	0.288	1	30	regulation of centrosome cycle	BP	1	PLK2	up_VCAV_EC
GO:0009059	0.921	0.308	1	1563	macromolecule biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0006793	0.921	0.295	1	948	phosphorus metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0043966	0.921	0.29	1	25	histone H3 acetylation	BP	1	DR1	up_VSAP_EC
GO:0098693	0.921	0.29	1	25	regulation of synaptic vesicle cycle	BP	1	PPP3CB	up_VSAP_EC
GO:0019882	0.921	0.291	1	25	antigen processing and presentation	BP	1	CTSS	up_VSAP_EC
GO:0009205	0.921385881	0.28258	1	98	purine ribonucleoside triphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0006310	0.921512628	0.2824	1	93	DNA recombination	BP	1	FIGNL1	up_ACOR_EC

GO:0009058	0.922	0.0959	102	1910	biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,SERPINH1,CARS,PLOD2,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,PUM3,UGCG,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,CHSY1,HIF1A,FOXP4,SLC45A3,MRPL1,IWS1,NMNAT2,GALNT1,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,APOE,WWC3,PPP1R3C,PLOD3,KLF5,STRAP,DDIT3,BACH1,STT3A,EIF5,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,SH3GLB1,REST,ZMYND8,EIF2S1,PRMT1,P3H4,NR4A2,EXT1,RAB11FIP1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,BCAT1,RPN1,KDM3A,CMPK1	down_VSAP_EC
GO:0031399	0.922	0.105	39	559	regulation of protein modification process	BP	1	HMGB1,SREBF1,IRAK1,USP4,HMGCR,UBE2S,U2AF2,SLC29A1,PPP1R15B,CAV1,RAD51,FANCI,NF2,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,BRCA1,NOC2L,RAP2C,YWHAB,RAC1,NUP62,EMP2,CACTIN,EZR,CLSPN,CDC20,PUM3,ARHGEF2,TADA2A,TINF2,CCNB3,MTBP,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0044093	0.922	0.108	34	437	positive regulation of molecular function	BP	1	FZD1,MAP3K14,ARHGEF5,PPARGC1B,TBC1D10C,CRADD,TBC1D2B,ABL1,EBF2,EMP2,MAP3K5,PDGFD,SAV1,C1QTNF2,PLPP3,CAMKK2,AMBRA1,F2RL1,LMF1,DDR2,TRAF7,RBCK1,TIAM1,MYC,SASH1,LARP6,MYD88,CDK9,EIF3D,HTRA2,FLOT1,MAVS,MAP2K2,TGFBR2	up_VSAP_EC
GO:0051260	0.922	0.152	6	100	protein homooligomerization	BP	1	ACTN2,NACC2,PCBD1,TP53BP1,EVL,KCNC4	up_ACOR_VSMC
GO:0031647	0.922	0.16	5	87	regulation of protein stability	BP	1	RASSF2,LAMP2,FAM107A,WFS1,PARK7	up_ACOR_VSMC
GO:0050794	0.922	0.197	4	3075	regulation of cellular process	BP	1	CST3,HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0045861	0.922	0.171	4	71	negative regulation of proteolysis	BP	1	CST3,RECK,GAS1,TIMP2	up_VSAP_EC
GO:0032388	0.922	0.188	3	62	positive regulation of intracellular transport	BP	1	HCLS1,TMEM173,CTDSPL2	up_VCAV_EC
GO:0006323	0.922	0.188	3	58	DNA packaging	BP	1	NAA60,GATAD1,CENPP	up_VSAP_EC
GO:0051495	0.922	0.215	2	82	positive regulation of cytoskeleton organization	BP	1	KIRREL1,ACTR3B	down_VCAV_EC
GO:0099504	0.922	0.218	2	42	synaptic vesicle cycle	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0010927	0.922	0.287	1	28	cellular component assembly involved in	BP	1	SIX4	down_ACOR_VSMC
GO:0032774	0.922	0.296	1	1073	RNA biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0097659	0.922	0.296	1	1072	nucleic acid-templated transcription	BP	1	GABPA	down_AFEM_EC
GO:0001936	0.922	0.284	1	49	regulation of endothelial cell proliferation	BP	1	MYDGF	down_VCAV_EC
GO:0031497	0.922	0.282	1	49	chromatin assembly	BP	1	CABIN1	down_VCAV_EC
GO:0099003	0.922	0.283	1	50	vesicle-mediated transport in synapse	BP	1	TMEM230	down_VCAV_EC
GO:0001707	0.922	0.288	1	25	mesoderm formation	BP	1	BMP4	up_ACOR_VSMC
GO:0044281	0.922	0.286	1	622	small molecule metabolic process	BP	1	NR1H4	up_APUL_EC
GO:0051649	0.922	0.287	1	630	establishment of localization in cell	BP	1	NR1H4	up_APUL_EC
GO:0032465	0.922	0.287	1	29	regulation of cytokinesis	BP	1	RAB11A	up_VCAV_EC
GO:0034613	0.922	0.286	1	576	cellular protein localization	BP	1	SIX1	up_VFEM_EC
GO:0019219	0.922	0.298	1	1151	regulation of nucleobase-containing compound metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0006915	0.922	0.287	1	550	apoptotic process	BP	1	CAV1	up_VSAP_VSMC

GO:0071704	0.923	0.0893	323	3535	organic substance metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,NAPEPLD,HOXA9,CDON,NECAB3,WNT11,HNF4A,ACSM3,DHDH,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,OSR2,INSIG2,ENPP2,PTGFR,ZNF367,PPARGC1B,RNPEP,TBC1D10C,PLBD1,ACAA1,MRPL37,CEP85,FOXRED2,ALDH3B1,ACACB,EEF2K,IL6R,IRX5,SLIT2,GDA,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,SLC6A4,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,HDAC7,KLKB1,EMP2,DLL1,DLST,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,GLUL,CTSS,GALNT15,DTX2,TENT5C,PGM2L1,ADHFE1,ENSCAFG00000013986,PDGFD,CERS4,HSD17B14,WARS2,VDR,DHRS4,NAA60,SAV1,KDELC2,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,PAFAH2,ABHD15,HSD3B7,ZNF688,ZBTB16,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,TRMT2A,VPS36,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,RECK,GATAD1,CISH,KLHL24,HSD17B8,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,FAAH,APOL5,TNKS1BP1,KLHDC8B,PYM1,AMBRA1,F2RL1,RBL2,LMF1,PHKA2,RAB11B,NFE2L2,GLIS2,LPL,DFFB,PPIP5K1,MORC3,DDR2,PDK2,ICE1,ZFP36L1,TRAF7,GALK2,HSF4,FXN,GALK1,RETSAT,PIK3R1,RBCK1,KBTBD12,ENTPD3,GAS1,BATF	up_VSAP_EC
GO:0006468	0.923	0.105	38	544	protein phosphorylation	BP	1	HMGB1,IRAK1,ILF3,HMGCR,SLC29A1,PPP1R15B,BIRC5,CAV1,CDK1,RAD51,NF2,AURKB,CDKN2C,EZH2,GREM1,MAP3K20,NEK2,CDK4,DHX33,CKS2,RAP2C,RAC1,NUP62,EMP2,HASPIN,CACTIN,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,TTK,MAST2,MELK,ARHGEF2,TADA2A,CCNB3,PIK3CD	down_ACOR_VSMC
GO:0044265	0.923	0.107	33	423	cellular macromolecule catabolic process	BP	1	ZRANB1,SKP2,PNRC1,SH3RF2,ISG15,ZNRF3,CTSS,KLHL20,CTSB,BNIP3,DCP1B,UBR1,OS9,STT3B,UBE2H,RNF24,RNF19A,PSEN1,LAMP2,CLN8,SIAH1,CTSF,PCYOX1,DISC1,RNF181,USP20,HERPUD1,FAF2,CNOT4,WFS1,CTIF,DZIP3,PARK7	up_ACOR_VSMC
GO:0031329	0.923	0.121	15	241	regulation of cellular catabolic process	BP	1	HMGB1,SREBF1,HNRNPD,SLC29A1,MTDH,THRAP3,ABHD5,SMARCC1,PLK3,RNF152,FASTKD3,EZR,RAD23A,AIFM1,AMER1	down_ACOR_VSMC
GO:0090087	0.923	0.129	11	185	regulation of peptide transport	BP	1	ACSL3,HMGB1,SREBF1,RAN,BIRC5,INSIG1,PLK3,ARG2,DMAP1,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0006325	0.923	0.132	10	234	chromatin organization	BP	1	NR1H4,SMARCA4,IWS1,MORF4L2,BRD2,CTNNB1,REST,ZMYND8,PRMT1,KDM3A	down_VSAP_EC
GO:0046330	0.923	0.214	2	47	positive regulation of JNK cascade	BP	1	HMGB1,MAP3K20	down_ACOR_VSMC
GO:0048736	0.923	0.214	2	66	appendage development	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0060173	0.923	0.214	2	66	limb development	BP	1	SULF1,CTNNB1	down_VSAP_EC
GO:0060048	0.923	0.283	1	30	cardiac muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0071219	0.923	0.281	1	50	cellular response to molecule of bacterial	BP	1	SASH1	down_VCAV_EC
GO:0070301	0.923	0.286	1	25	cellular response to hydrogen peroxide	BP	1	PARK7	up_ACOR_VSMC
GO:0016311	0.923	0.278	1	106	dephosphorylation	BP	1	MYO1D	up_AFEM_EC
GO:0043436	0.923	0.279	1	303	oxoacid metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0022607	0.923	0.289	1	969	cellular component assembly	BP	1	NKX2-5	up_VPOR_VSMC
GO:0070727	0.923	0.283	1	579	cellular macromolecule localization	BP	1	SIX1	up_VFEM_EC
GO:0006464	0.923	0.294	1	1162	cellular protein modification process	BP	1	SLIT2	up_VPUL_VSMC
GO:0036211	0.923	0.294	1	1162	protein modification process	BP	1	SLIT2	up_VPUL_VSMC
GO:0014074	0.923	0.284	1	26	response to purine-containing compound	BP	1	ZFP36L1	up_VSAP_EC
GO:0046683	0.923	0.284	1	26	response to organophosphorus	BP	1	ZFP36L1	up_VSAP_EC
GO:0007346	0.923195679	0.18319	3	210	regulation of mitotic cell cycle	BP	1	BRSK1,PAK3,CHMP4B	up_ACOR_EC
GO:0030003	0.923694247	0.21004	2	157	cellular cation homeostasis	BP	1	PTH1R,SLC9A9	up_ACOR_EC

GO:0009987	0.924	0.0896	471	5086	cellular process	BP	1	SYNPO2L,EXPH5,TNNT2,SH3TC2,PDLIM3,FGF13,RHOT1,FMOD,EPB41L4A,ADRA1B,VEGFD,TMEM176B,TLR1,TMEM176A,DNAJC6,SMAD6,GALNT3,PIP5K1B,ATRNL1,ARHGAP28,ACTN2,LGR6,PLCG2,DNAH7,CASP10,IFNGR1,LEP,PLCL1,GALNT10,LBH,DCBLD2,ST3GAL5,MAP3K8,SNAP91,MID1,SLC26A7,KCNE3,GATA5,BCL2,GATA4,ADGRD1,CD83,EFNB2,CDC7,ANGPT1,PCGF5,ENSCAFG00000016285,EPYC,HTR2B,RASSF2,TPST2,ENOSF1,TCAF1,MEIS2,USP6NL,INTS9,FNDC5,MBP,ZRANB1,FBXL20,C28H10orf71,PRDX4,RECK,SHROOM3,LIPT2,B3GALNT2,FEZ1,ENSCAFG00000002977,SKP2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,SYT16,PNRC1,LCAT,ZNF331,EVI5L,AHCYL1,CRIM1,LNPK,SYNPO2,TBX18,TUBB4A,TM7SF3,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,MX1,CCDC126,MFAP4,ABCA1,EIF4A2,GJA1,DOCK3,ELF1,ATRX,MED14,HRH1,CASTOR1,TARSL2,TRPS1,TLR3,SH3RF2,SEC24B,XIRP1,ELL2,WASF3,PPARGC1A,LATS2,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,RERG,SPINT1,GLRB,PKP4,ARHGAP29,CCNG2,MAOA,PIGS,ZBTB40,ISG15,UGCG,ACSL6,ZNRF3,ZNF782,CD274,ZNF365,PLPP2,MARCKSL1,AR,PTGIR,ZNF484,SASH1,CTSS,SLC2A5,STX11,GPR1	up_ACOR_VSMC
GO:0044238	0.924	0.0921	188	3383	primary metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,ENSCAFG00000009211,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,PUM3,UGCG,PM20D2,ILK,FHL2,BHLHE40,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CHSY1,MSN,SEL1L,HIF1A,FOXP4,SLC45A3,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,MOGS,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,AK5,GTF2H1,ARMCX3,CUL2,SH3GLB1,GALE,HTT,REST,ABHD5,RBBP8,ZMYND8,MAPK10,EIF2S1,PRMT1,RDH11,P3H4,NR4A2,EXT1,SPOP,CALM1,RAB	down_VSAP_EC
GO:0051336	0.924	0.116	18	251	regulation of hydrolase activity	BP	1	ARHGEF5,PPARGC1B,SH2D4A,TBC1D10C,CST3,CRADD,TBC1D2B,ABL1,MAP3K5,RECK,F2RL1,LMF1,TIAM1,MYC,TMEM225B,SBF2,HTRA2,BAG4	up_VSAP_EC
GO:0019953	0.924	0.131	10	152	sexual reproduction	BP	1	HOXA11,THRB,HOXA9,ZNF449,HERPUD2,ZBTB16,PATZ1,CFAP69,KDM2B,HPGD	up_VSAP_EC
GO:0002237	0.924	0.156	5	85	response to molecule of bacterial origin	BP	1	PTGFR,ABL1,TBXA2R,SASH1,MYD88	up_VSAP_EC
GO:0006261	0.924	0.169	4	68	DNA-dependent DNA replication	BP	1	CDC7,ATRX,ZNF365,RPAIN	up_ACOR_VSMC
GO:0043412	0.924	0.189	3	1225	macromolecule modification	BP	1	GALNT17,TLR2,CAV1	up_VSAP_VSMC
GO:2001022	0.924	0.213	2	42	positive regulation of response to DNA damage	BP	1	MYC,NPAS2	up_VSAP_EC
GO:0002042	0.924	0.282	1	29	cell migration involved in sprouting angiogenesis	BP	1	GREM1	down_ACOR_VSMC
GO:0006611	0.924	0.278	1	51	protein export from nucleus	BP	1	PARK7	down_VCAV_EC
GO:0002700	0.924	0.278	1	40	regulation of production of molecular mediator of immune response	BP	1	TFRC	down_VSAP_EC
GO:0016125	0.924	0.278	1	41	sterol metabolic process	BP	1	APOE	down_VSAP_EC
GO:0071241	0.924	0.278	1	42	cellular response to inorganic substance	BP	1	BNIP3	down_VSAP_EC
GO:0019319	0.924	0.282	1	26	hexose biosynthetic process	BP	1	LEP	up_ACOR_VSMC

GO:1903312	0.924	0.283	1	25	negative regulation of mRNA metabolic process	BP	1	CCNT1	up_ACOR_VSMC
GO:1904888	0.924	0.28	1	31	cranial skeletal system development	BP	1	MEF2C	up_VCAV_EC
GO:0032269	0.924	0.277	1	306	negative regulation of cellular protein metabolic	BP	1	ASPN	up_VPOR_EC
GO:0030330	0.924	0.283	1	25	DNA damage response, signal transduction by p53 class mediator	BP	1	CRADD	up_VSAP_EC
GO:0048525	0.924	0.283	1	25	negative regulation of viral process	BP	1	MAVS	up_VSAP_EC
GO:0009150	0.924776524	0.20769	2	161	purine ribonucleotide metabolic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0010605	0.925	0.0962	61	745	negative regulation of macromolecule metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,PPARGC1B,TBC1D10C,CEP85,ACACB,SLIT2,CST3,ZHX3,ABL1,PEX2,HDAC7,OSR1,TENT5C,KLF15,RARG,CBX7,STAT6,RECK,PLPP3,EXOSC7,PYM1,F2RL1,RBL2,GLIS2,ZFP36L1,GAS1,MYC,SHOX2,H2AFJ,ZC3H10,RTN4RL1,IKZF2,PASK,ANKHD1,AZIN2,PHF1,SMG9,FBXO7,LIMD1,PC,CDK9,PRMT2,KDM2B,FBLN1,SAMD4B,ZFP36L2,NFIB,ZNF205,NCOA2,TIMP2,QARS,SMARCA2,ACVRL1,UBQLN2,TNRC6C,NCK1,LATS2	up_VSAP_EC
GO:0000902	0.925	0.115	17	266	cell morphogenesis	BP	1	FLNB,FMNL3,SLC29A1,B3GNT2,CFAP298,STMN1,GREM1,RAC1,IQGAP1,CDC42EP4,EZR,CORO1A,ENSCAFG00000010224,RADIL,ARHGEF2,TBCC,ANXA7	down_ACOR_VSMC
GO:0010563	0.925	0.124	12	203	negative regulation of phosphorus metabolic process	BP	1	HMGCR,PPP1R15B,CAV1,NF2,CDKN2C,GREM1,YWHAB,NUP62,IQGAP1,CACTIN,EZR,KNL1	down_ACOR_VSMC
GO:0045936	0.925	0.124	12	203	negative regulation of phosphate metabolic process	BP	1	HMGCR,PPP1R15B,CAV1,NF2,CDKN2C,GREM1,YWHAB,NUP62,IQGAP1,CACTIN,EZR,KNL1	down_ACOR_VSMC
GO:0044237	0.925	0.152	9	3491	cellular metabolic process	BP	1	NR1H4,STK32B,ENSCAFG00000028814,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0062012	0.925	0.154	5	100	regulation of small molecule metabolic	BP	1	SREBF1,INSIG1,CAV1,CDK1,BRCA1	down_ACOR_VSMC
GO:0040029	0.925	0.165	4	74	regulation of gene expression, epigenetic	BP	1	H2AFJ,ZC3H10,LIMD1,TNRC6C	up_VSAP_EC
GO:0070507	0.925	0.165	4	73	regulation of microtubule cytoskeleton organization	BP	1	FAM107A,CEP85,ABL1,FBXW5	up_VSAP_EC
GO:0071478	0.925	0.183	3	58	cellular response to radiation	BP	1	MFAP4,TP53INP1,CDKN1A	up_ACOR_VSMC
GO:0000187	0.925	0.28	1	28	activation of MAPK activity	BP	1	MAP3K20	down_ACOR_VSMC
GO:0050848	0.925	0.28	1	30	regulation of calcium-mediated signaling	BP	1	GSTO1	down_ACOR_VSMC
GO:0030177	0.925	0.274	1	51	positive regulation of Wnt signaling pathway	BP	1	ATP6V0C	down_VCAV_EC
GO:0022037	0.925	0.278	1	27	metencephalon development	BP	1	PROX1	up_VCAV_EC
GO:0006082	0.925	0.275	1	305	organic acid metabolic process	BP	1	FBP1	up_VPOR_EC
GO:0007492	0.925	0.279	1	27	endoderm development	BP	1	ZFP36L1	up_VSAP_EC
GO:0012501	0.925	0.277	1	561	programmed cell death	BP	1	CAV1	up_VSAP_VSMC
GO:0009126	0.925517372	0.27186	1	100	purine nucleoside monophosphate metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0009167	0.925517372	0.27186	1	100	purine ribonucleoside monophosphate metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0009199	0.925707098	0.27137	1	100	ribonucleoside triphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0050769	0.925890354	0.27102	1	95	positive regulation of neurogenesis	BP	1	NRP1	up_ACOR_EC
GO:0006950	0.926	0.0993	46	1102	response to stress	BP	1	GPAM,LRP1,CFD,PRNP,SDC4,VASN,BMPR1A,VKORC1,NABP2,TRPV2,CHID1,ENSCAFG00000014978,GABARAP,PDIA4,CLSTN1,TRIM8,PRMT6,ENSCAFG00000013404,TMEM161A,THY1,RNF216,B4GALT1,PARK7,SCARA5,ZFP36L1,SASH1,CLEC16A,BPI,CYBA,MAVS,LOXL3,MPV17,FUT8,SPRED1,RAB7B,A2M,SEC61B,TSC22D3,HM13,SHC1,FBH1,ATOX1,NAPEPLD,FOXO3,RGMA,BRSK1	down_VCAV_EC
GO:0010243	0.926	0.117	15	238	response to organonitrogen compound	BP	1	SREBF1,SREBF2,HM13,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,UBE2J2,PDXP,EZR,PSMC1,NCOA5,ARHGEF2	down_ACOR_VSMC

GO:0070925	0.926	0.126	10	293	organelle assembly	BP	1	SDC4,RPS10,GABARAP,TTC8,WDR45,IFT57,MRPS11,EMC6,RPS27,EVI5L	down_VCAV_EC
GO:0002366	0.926	0.18	3	65	leukocyte activation involved in immune	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0000209	0.926	0.207	2	83	protein polyubiquitination	BP	1	RNF216,SASH1	down_VCAV_EC
GO:0044267	0.926	0.221	2	1583	cellular protein metabolic process	BP	1	ERC1,TAOK1	up_AORT_EC
GO:0099003	0.926	0.208	2	50	vesicle-mediated transport in synapse	BP	1	SNAP23,STX11	up_VCAV_EC
GO:0048771	0.926	0.208	2	43	tissue remodeling	BP	1	PPARGC1B,ACVRL1	up_VSAP_EC
GO:0001935	0.926	0.273	1	50	endothelial cell proliferation	BP	1	MYDGF	down_VCAV_EC
GO:0051303	0.926	0.276	1	26	establishment of chromosome localization	BP	1	SUN1	up_ACOR_VSMC
GO:1904951	0.926	0.269	1	108	positive regulation of establishment of protein localization	BP	1	LEP	up_AFEM_EC
GO:0031326	0.926	0.286	1	1176	regulation of cellular biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0002708	0.926	0.276	1	26	positive regulation of lymphocyte mediated	BP	1	STAT6	up_VSAP_EC
GO:0010469	0.926	0.276	1	26	regulation of signaling receptor activity	BP	1	KLHL24	up_VSAP_EC
GO:0034613	0.926	0.274	1	576	cellular protein localization	BP	1	CAV1	up_VSAP_VSMC
GO:0022407	0.926129638	0.27037	1	96	regulation of cell-cell adhesion	BP	1	PRKCD	up_ACOR_EC
GO:0010948	0.926708995	0.26885	1	96	negative regulation of cell cycle process	BP	1	BRSK1	up_ACOR_EC
GO:0045930	0.926995983	0.26807	1	97	negative regulation of mitotic cell cycle	BP	1	BRSK1	up_ACOR_EC
GO:0006725	0.927	0.0876	147	1956	cellular aromatic compound metabolic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,SNCAIP,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,TARSL2,MTOR,ACPP,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,ESCO1,TRMT9B,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,JAG1,NSD1,GUCY1B1,TOP1,ETAA1,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,GCH1,ENSCAFG00000002897,DCK,ASF1A,HMGB1,AHR,NOS2,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,BLVRA,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC
GO:0043412	0.927	0.0909	91	1225	macromolecule modification	BP	1	HMGB1,SREBF1,POLE3,USP1,IRAK1,ILF3,USP4,HMGCR,UBE2S,U2AF2,SLC29A1,METAP2,PPM1G,PPP1R15B,MPDU1,NOP56,SLC35C2,B3GNT2,UBE2T,BIRC5,PRMT1,CAV1,CDK1,RAD51,FANCI,TRUB2,NF2,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,DHX33,UHRF1,CKS2,RNF152,BRCA1,NOC2L,B4GALT1,RAP2C,UBE2J2,YWHAB,RAC1,NUP62,EMP2,DTL,HASPIN,THUMPD2,CACTIN,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,RBM14,OSGEP,CDC20,TTK,BAP1,ENSCAFG00000019620,PUM3,MAST2,METTL1,MELK,PRMT5,CTH,NOP58,ARHGEF2,TADA2A,WTAP,TINF2,JMJD6,EMG1,EXOSC5,CCNB3,UBE2C,NUS1,MIS18A,UBA2,MTBP,TTLL1,AMER1,DCUN1D5,PPIB,PIK3CD	down_ACOR_VSMC

GO:0010467	0.927	0.103	35	1787	gene expression	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,GAS1,HOXA7,DLL1,CRYAB,F3,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B,TNC	up_AFEM_EC
GO:0006955	0.927	0.109	21	327	immune response	BP	1	HMGB1,FLNB,IRAK1,MNDA,SLC29A1,CAV1,TRIM35,ARG2,TFRC,FAM49B,EMP2,CACTIN,HMGB2,CDC42EP4,EZR,RBM14,CORO1A,POLR3F,ELF4,ARHGEF2,PIK3CD	down_ACOR_VSMC
GO:0022402	0.927	0.143	6	407	cell cycle process	BP	1	OVOL1,CAMK2A,DCUN1D3,AXIN2,FAP,ANXA11	up_AFEM_EC
GO:0051052	0.927	0.16	4	145	regulation of DNA metabolic process	BP	1	NABP2,TMEM161A,FBH1,GREM1	down_VCAV_EC
GO:0007600	0.927	0.162	4	73	sensory perception	BP	1	THRB,PDE6D,FXN,NR2F6	up_VSAP_EC
GO:0000075	0.927	0.177	3	91	cell cycle checkpoint	BP	1	PTPN11,DDX39B,CDKN1A	down_VSAP_EC
GO:0003015	0.927	0.179	3	58	heart process	BP	1	THRB,IRX5,KCNE3	up_VSAP_EC
GO:1901343	0.927	0.206	2	42	negative regulation of vasculature development	BP	1	BMP4,SYNJ2BP	up_ACOR_VSMC
GO:0034341	0.927	0.207	2	43	response to interferon-gamma	BP	1	CDC42EP2,STX4	up_VSAP_EC
GO:0035967	0.927	0.208	2	42	cellular response to topologically incorrect	BP	1	PIK3R1,NCK1	up_VSAP_EC
GO:0050715	0.927	0.274	1	29	positive regulation of cytokine secretion	BP	1	HMGB1	down_ACOR_VSMC
GO:0055072	0.927	0.273	1	30	iron ion homeostasis	BP	1	TFRC	down_ACOR_VSMC
GO:0006950	0.927	0.283	1	1102	response to stress	BP	1	SRSF6	down_AFEM_EC
GO:0009987	0.927	0.468	1	5086	cellular process	BP	1	CST3	down_AORT_EC
GO:0046467	0.927	0.27	1	45	membrane lipid biosynthetic process	BP	1	UGCG	down_VSAP_EC
GO:0035850	0.927	0.274	1	25	epithelial cell differentiation involved in	BP	1	BMP4	up_ACOR_VSMC
GO:1903076	0.927	0.272	1	32	regulation of protein localization to plasma	BP	1	PPP2R5A	up_VCAV_EC
GO:0006278	0.927	0.274	1	26	RNA-dependent DNA biosynthetic process	BP	1	FBXO4	up_VSAP_EC
GO:0007004	0.927	0.274	1	26	telomere maintenance via telomerase	BP	1	FBXO4	up_VSAP_EC
GO:0051303	0.927	0.275	1	26	establishment of chromosome localization	BP	1	TTL	up_VSAP_EC
GO:1901879	0.927	0.274	1	26	regulation of protein depolymerization	BP	1	F2RL1	up_VSAP_EC
GO:0072503	0.927722046	0.26616	1	97	cellular divalent inorganic cation homeostasis	BP	1	PTH1R	up_ACOR_EC
GO:0050790	0.928	0.0968	42	532	regulation of catalytic activity	BP	1	MAP3K14,ARHGEF5,PPARGC1B,SH2D4A,TBC1D10C,CEP85,ACACB,CST3,CRADD,TBC1D2B,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CNPPD1,RECK,CAMKK2,AMBRA1,F2RL1,RBL2,LMF1,DDR2,TRAF7,PIK3R1,TIAM1,MYC,PIK3IP1,TMEM225B,RTN4RL1,SASH1,SBF2,PRKAB1,FBXO7,RAF1,TIMP2,HTRA2,ZER1,MAP2K2,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0009059	0.928	0.103	30	1563	macromolecule biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,XYLT1,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,YEATS2,PPARGC1A,CSGALNACT2,CTIF,SAMD4B	up_AFEM_EC
GO:0044257	0.928	0.107	21	327	cellular protein catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,EZR,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C,AMER1	down_ACOR_VSMC
GO:0051047	0.928	0.159	4	84	positive regulation of secretion	BP	1	ACSL3,HMGB1,SDC1,EZR	down_ACOR_VSMC
GO:0051259	0.928	0.159	4	140	protein complex oligomerization	BP	1	PRNP,COL6A1,B4GALT1,SCARA5	down_VCAV_EC
GO:0009058	0.928	0.171	4	1910	biosynthetic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0080135	0.928	0.173	3	240	regulation of cellular response to stress	BP	1	LEP,CYLD,AXIN2	up_AFEM_EC
GO:0006109	0.928	0.267	1	51	regulation of carbohydrate metabolic	BP	1	AKT2	down_VCAV_EC
GO:0006081	0.928	0.27	1	27	cellular aldehyde metabolic process	BP	1	PARK7	up_ACOR_VSMC

GO:0045739	0.928	0.27	1	26	positive regulation of DNA repair	BP	1	PARP9	up_ACOR_VSMC
GO:1901575	0.928	0.272	1	643	organic substance catabolic process	BP	1	PLCL1	up_APUL_EC
GO:0045454	0.928	0.268	1	35	cell redox homeostasis	BP	1	PDIA5	up_VCAV_EC
GO:0009889	0.928	0.279	1	1190	regulation of biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0007605	0.928	0.271	1	27	sensory perception of sound	BP	1	THRB	up_VSAP_EC
GO:0070727	0.928	0.271	1	579	cellular macromolecule localization	BP	1	CAV1	up_VSAP_VSMC
GO:0006873	0.928855241	0.19891	2	160	cellular ion homeostasis	BP	1	PTH1R,SLC9A9	up_ACOR_EC
GO:0019219	0.929	0.088	99	1151	regulation of nucleobase-containing compound metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TRPS1,TLR3,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0043069	0.929	0.109	19	262	negative regulation of programmed cell death	BP	1	WNT11,ACKR3,PTGFR,LIMS2,ABL1,DLL1,OSR1,RARG,AMBRA1,PIK3R1,RBCK1,MYC,ENSCAFG00000011993,KDM2B,RAF1,QARS,ARHGAP10,HMOX1,CITED2	up_VSAP_EC
GO:0009416	0.929	0.158	4	88	response to light stimulus	BP	1	MAPK13,ENSCAFG00000010596,USP28,HIF1A	up_VCAV_EC
GO:0006139	0.929	0.168	4	1909	nucleobase-containing compound metabolic	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0006643	0.929	0.174	3	68	membrane lipid metabolic process	BP	1	ELOVL1,ELOVL6,SGPL1	down_ACOR_VSMC
GO:0030217	0.929	0.175	3	65	T cell differentiation	BP	1	HMGB1,PRELID1,JMJD6	down_ACOR_VSMC
GO:0016331	0.929	0.174	3	66	morphogenesis of embryonic epithelium	BP	1	GREM1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0035148	0.929	0.174	3	66	tube formation	BP	1	GREM1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0006323	0.929	0.175	3	58	DNA packaging	BP	1	ATRX,TSPYL5,SHPRH	up_ACOR_VSMC
GO:0043543	0.929	0.199	2	84	protein acylation	BP	1	CLIP3,PARK7	down_VCAV_EC
GO:0030010	0.929	0.202	2	41	establishment of cell polarity	BP	1	FERMT1,JAM3	up_ACOR_VSMC
GO:0046890	0.929	0.264	1	51	regulation of lipid biosynthetic process	BP	1	ORMDL3	down_VCAV_EC
GO:0060538	0.929	0.264	1	51	skeletal muscle organ development	BP	1	TSC22D3	down_VCAV_EC
GO:0002831	0.929	0.265	1	42	regulation of response to biotic stimulus	BP	1	PVR	down_VSAP_EC
GO:0007188	0.929	0.265	1	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	GNAQ	down_VSAP_EC
GO:0032273	0.929	0.264	1	44	positive regulation of protein polymerization	BP	1	ACTR3	down_VSAP_EC
GO:0019080	0.929	0.269	1	26	viral gene expression	BP	1	INPP5K	up_ACOR_VSMC
GO:0048584	0.929	0.267	1	592	positive regulation of response to stimulus	BP	1	EYA1	up_VFEM_EC
GO:0030071	0.929	0.27	1	26	regulation of mitotic metaphase/anaphase	BP	1	CDC26	up_VSAP_EC
GO:0045739	0.929	0.269	1	26	positive regulation of DNA repair	BP	1	NPAS2	up_VSAP_EC
GO:1902099	0.929	0.27	1	26	regulation of metaphase/anaphase transition of cell cycle	BP	1	CDC26	up_VSAP_EC
GO:0015893	0.929	0.269	1	26	drug transport	BP	1	SLC6A4	up_VSAP_EC

GO:0044770	0.929139468	0.19828	2	161	cell cycle phase transition	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0062012	0.929697843	0.26083	1	100	regulation of small molecule metabolic	BP	1	NR1H4	up_ACOR_EC
GO:0006790	0.929823992	0.26052	1	99	sulfur compound metabolic process	BP	1	ENSCAFG00000028814	up_ACOR_EC
GO:0071704	0.93	0.0855	165	3535	organic substance metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,MAOA,CFD,NAB2,NDN,PRNP,LUM,UBA52,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,NUMBL,CHID1,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,TFE3,ACAA1,ME3,NR3C1,H6PD,HSD3B7,HR,SCP2,RPL23,RPL13,GLB1L,CLSTN1,PCSK7,PLCL1,DDOST,CSPG4,CYB5R3,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,THNSL2,PGLS,POFUT1,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,ASPN,PIGS,HS3ST3B1,LRPAP1,EIF3K,THY1,NECAB3,RNF216,TEAD1,SUOX,CYP1B1,ADK,WDR45,MRPL37,PEX5,CC2D1A,B4GALT1,RETSAT,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,ABHD15,CLEC16A,RNPEP,RPL27,COPS7A,RBM38,ARL2BP,AMPD2,IFT57,MAVS,MRPS11,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,ACSS2,TSC22D3,SLC3A2,MAPRE3,GLIS2,CDKL2,RAB31,HM13,PRKCSH,DDR2,SHC1,RDH10,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,A	down_VCAV_EC
GO:0042325	0.93	0.132	7	463	regulation of phosphorylation	BP	1	LEP,GREM1,CYLD,LRRC15,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0048736	0.93	0.172	3	66	appendage development	BP	1	CHD7,ITGA6,ATRX	up_VCAV_EC
GO:0060173	0.93	0.172	3	66	limb development	BP	1	CHD7,ITGA6,ATRX	up_VCAV_EC
GO:0032501	0.93	0.214	2	1782	multicellular organismal process	BP	1	SRSF6,GABPA	down_AFEM_EC
GO:0042133	0.93	0.264	1	30	neurotransmitter metabolic process	BP	1	CAV1	down_ACOR_VSMC
GO:0046632	0.93	0.264	1	29	alpha-beta T cell differentiation	BP	1	HMGB1	down_ACOR_VSMC
GO:0001890	0.93	0.261	1	51	placenta development	BP	1	ZFP36L1	down_VCAV_EC
GO:0010595	0.93	0.261	1	52	positive regulation of endothelial cell migration	BP	1	SASH1	down_VCAV_EC
GO:0006334	0.93	0.262	1	45	nucleosome assembly	BP	1	BRD2	down_VSAP_EC
GO:0010720	0.93	0.261	1	110	positive regulation of cell development	BP	1	IRX3	up_AFEM_EC
GO:0031331	0.93	0.259	1	110	positive regulation of cellular catabolic process	BP	1	CLEC16A	up_AFEM_EC
GO:0051248	0.93	0.26	1	316	negative regulation of protein metabolic process	BP	1	ASPN	up_VPOR_EC
GO:0022607	0.93	0.27	1	969	cellular component assembly	BP	1	FBP1	up_VFEM_VSMC
GO:0002367	0.93	0.267	1	26	cytokine production involved in immune	BP	1	F2RL1	up_VSAP_EC
GO:0009144	0.930798069	0.25782	1	103	purine nucleoside triphosphate metabolic	BP	1	ALDOC	up_ACOR_EC
GO:0034654	0.931	0.0845	105	1236	nucleobase-containing compound biosynthetic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,PDK2,ICE1,HSF4,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,TLE2,YBX3,FBXO4,MYD88,IKZF2,TFE3,LRP4,TRERF1,E2F4,NPAS2,LIMD1,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,DCAKD,ESRRA,ENSCAFG00000013366,YEATS2,RAF1,PNP,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,PPP3CB,NCK1,ZNF444,MAVS,HMOX1,ZNF662,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC

GO:0009968	0.931	0.0992	26	392	negative regulation of signal transduction	BP	1	HMGCR,SLC25A5,PRELID1,INSIG1,CAV1,NF2,MMP14,EZH2,STMN1,GREM1,RNF152,NOC2L,YWHAB,NUP62,CACTIN,HMGB2,GSTO1,EZR,BEND6,PHACTR4,TXNDC12,CTH,NCOA5,ARHGEF2,GLI1,AMER1	down_ACOR_VSMC
GO:0005996	0.931	0.154	4	85	monosaccharide metabolic process	BP	1	B4GALT1,GSTO1,GALE,PGD	down_ACOR_VSMC
GO:0031334	0.931	0.195	2	84	positive regulation of protein complex assembly	BP	1	KIRREL1,ACTR3B	down_VCAV_EC
GO:0030258	0.931	0.196	2	71	lipid modification	BP	1	SESN2,APOE	down_VSAP_EC
GO:0006479	0.931	0.198	2	45	protein methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:0008213	0.931	0.198	2	45	protein alkylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:0006796	0.931	0.201	2	938	phosphate-containing compound metabolic	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0006029	0.931	0.263	1	29	proteoglycan metabolic process	BP	1	XYLT1	down_ACOR_VSMC
GO:1903725	0.931	0.263	1	30	regulation of phospholipid metabolic process	BP	1	ACSL3	down_ACOR_VSMC
GO:2000112	0.931	0.271	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0000045	0.931	0.26	1	46	autophagosome assembly	BP	1	SH3GLB1	down_VSAP_EC
GO:0046364	0.931	0.262	1	27	monosaccharide biosynthetic process	BP	1	LEP	up_ACOR_VSMC
GO:0006942	0.931	0.265	1	26	regulation of striated muscle contraction	BP	1	KCNE3	up_VSAP_EC
GO:0050852	0.931	0.265	1	26	T cell receptor signaling pathway	BP	1	RBCK1	up_VSAP_EC
GO:0009161	0.93138845	0.25623	1	103	ribonucleoside monophosphate	BP	1	ALDOC	up_ACOR_EC
GO:0045934	0.932	0.0962	31	407	negative regulation of nucleobase-containing compound metabolic process	BP	1	FZD1,THRB,HOXA7,WNT11,AXIN2,PPARGC1B,ZHX3,PEX2,HDAC7,OSR1,TENT5C,RARG,CBX7,STAT6,GLIS2,SHOX2,H2AFJ,ZC3H10,IKZF2,LIMD1,CDK9,PRMT2,KDM2B,NFIB,ZNF205,NCOA2,QARS,SMARCA2,ACVRL1,NCK1,DDIT4	up_VSAP_EC
GO:1904018	0.932	0.168	3	69	positive regulation of vasculature development	BP	1	MTDH,GREM1,CTH	down_ACOR_VSMC
GO:0009267	0.932	0.169	3	60	cellular response to starvation	BP	1	SESN1,MAP3K5,NPRL3	up_VSAP_EC
GO:0001894	0.932	0.195	2	49	tissue homeostasis	BP	1	TFRC,CORO1A	down_ACOR_VSMC
GO:0043491	0.932	0.194	2	50	protein kinase B signaling	BP	1	SLC29A1,MTDH	down_ACOR_VSMC
GO:0016573	0.932	0.196	2	50	histone acetylation	BP	1	IWS1,GATA3	up_VCAV_EC
GO:0010923	0.932	0.26	1	30	negative regulation of phosphatase activity	BP	1	KNL1	down_ACOR_VSMC
GO:0034767	0.932	0.258	1	31	positive regulation of ion transmembrane transport	BP	1	GSTO1	down_ACOR_VSMC
GO:0042552	0.932	0.26	1	30	myelination	BP	1	NAB2	down_ACOR_VSMC
GO:0009408	0.932	0.262	1	27	response to heat	BP	1	TP53INP1	up_ACOR_VSMC
GO:0048332	0.932	0.261	1	26	mesoderm morphogenesis	BP	1	BMP4	up_ACOR_VSMC
GO:0007492	0.932	0.261	1	27	endoderm development	BP	1	HHEX	up_VCAV_EC
GO:0045814	0.932	0.262	1	27	negative regulation of gene expression,	BP	1	H2AFJ	up_VSAP_EC
GO:0071705	0.932	0.26	1	582	nitrogen compound transport	BP	1	TLR2	up_VSAP_VSMC
GO:0006302	0.932101584	0.25445	1	97	double-strand break repair	BP	1	FIGNL1	up_ACOR_EC
GO:0051604	0.932675723	0.25277	1	102	protein maturation	BP	1	PCSK1N	up_ACOR_EC
GO:0009259	0.932911016	0.18996	2	166	ribonucleotide metabolic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0033365	0.933	0.101	20	276	protein localization to organelle	BP	1	LEP,MID1,FERMT1,BMP4,SCARB2,ATRX,MARCH5,CDKN1A,NRP1,PTPN22,OS9,DAG1,PARP9,PSEN1,LAMP2,JUP,SUN1,RPAIN,SH3BP4,PARK7	up_ACOR_VSMC
GO:0072594	0.933	0.117	10	155	establishment of protein localization to organelle	BP	1	LEP,FERMT1,BMP4,SCARB2,CDKN1A,PTPN22,PSEN1,LAMP2,JUP,RPAIN	up_ACOR_VSMC

GO:0051186	0.933	0.117	10	159	cofactor metabolic process	BP	1	MAT2B,PCBD1,ENSCAFG00000028814,ALDOC,DDIT4,PTS,CAT,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0010498	0.933	0.133	6	194	proteasomal protein catabolic process	BP	1	PSMF1,RNF216,PARK7,CLEC16A,SEC61B,HM13	down_VCAV_EC
GO:0044260	0.933	0.169	4	2593	cellular macromolecule metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0032102	0.933	0.166	3	67	negative regulation of response to external	BP	1	TFPI,ARG2,CACTIN	down_ACOR_VSMC
GO:0010970	0.933	0.192	2	48	transport along microtubule	BP	1	KIF3C,HIF1A	up_VCAV_EC
GO:0099111	0.933	0.192	2	48	microtubule-based transport	BP	1	KIF3C,HIF1A	up_VCAV_EC
GO:0006793	0.933	0.195	2	948	phosphorus metabolic process	BP	1	TLR2,CAV1	up_VSAP_VSMC
GO:0050954	0.933	0.258	1	30	sensory perception of mechanical stimulus	BP	1	NAV2	down_ACOR_VSMC
GO:0043901	0.933	0.253	1	44	negative regulation of multi-organism process	BP	1	REST	down_VSAP_EC
GO:0006278	0.933	0.258	1	26	RNA-dependent DNA biosynthetic process	BP	1	HMBOX1	up_ACOR_VSMC
GO:0007004	0.933	0.258	1	26	telomere maintenance via telomerase	BP	1	HMBOX1	up_ACOR_VSMC
GO:0051962	0.933	0.252	1	112	positive regulation of nervous system	BP	1	IRX3	up_AFEM_EC
GO:0051252	0.933	0.263	1	1051	regulation of RNA metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0010923	0.933	0.258	1	30	negative regulation of phosphatase activity	BP	1	FKBP15	up_VCAV_EC
GO:1905897	0.933	0.255	1	34	regulation of response to endoplasmic reticulum	BP	1	NCK1	up_VCAV_EC
GO:0006974	0.933	0.254	1	333	cellular response to DNA damage stimulus	BP	1	CXHXorf57	up_VPOR_EC
GO:0006383	0.933	0.257	1	28	transcription by RNA polymerase III	BP	1	ICE1	up_VSAP_EC
GO:0009123	0.93327098	0.25111	1	104	nucleoside monophosphate	BP	1	ALDOC	up_ACOR_EC
GO:0010564	0.933708776	0.16263	3	217	regulation of cell cycle process	BP	1	BRSK1,SOX9,CHMP4B	up_ACOR_EC
GO:0006508	0.934	0.0926	31	483	proteolysis	BP	1	PRCP,TNFAIP3,TNIP1,CTSC,KLKB1,WWP1,USP33,PSME4,PELI1,ENSCAFG00000010893,CASP8,ENC1,PAK2,OTUD4,PTGS2,BCL10,SENP6,USP28,HMGB1,PMAIP1,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMB9,PSMD12,ITCH	up_VCAV_EC
GO:0006974	0.934	0.0978	22	333	cellular response to DNA damage stimulus	BP	1	PSME4,FIGNL1,MTOR,THOC1,TIMELESS,ETAA1,USP28,TAOK1,ENSCAFG00000002897,ASF1A,HMGB1,PMAIP1,BLM,SMC5,RAD21,RAD17,SKIL,CUL4A,ATRX,TOPBP1,RBBP6,GINS4	up_VCAV_EC
GO:0016071	0.934	0.106	15	248	mRNA metabolic process	BP	1	MOV10,IWS1,QKI,SOX18,TENT2,SCAF11,CNOT6,PAN3,PRPF39,CNOT7,SMG7,WTAP,RBBP6,ZC3H13,DCP2	up_VCAV_EC
GO:0072521	0.934	0.111	12	185	purine-containing compound metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENPP4,PTGDR,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0009725	0.934	0.113	11	188	response to hormone	BP	1	SREBF1,TFPI,NEDD4,CAV1,THRAP3,ADIPOR2,CDK4,SMARCC1,PRCP,HMGB2,NCOA5	down_ACOR_VSMC
GO:0044089	0.934	0.138	5	170	positive regulation of cellular component	BP	1	KIRREL1,SDC4,THY1,ACTR3B,RAC2	down_VCAV_EC
GO:0043087	0.934	0.148	4	83	regulation of GTPase activity	BP	1	EZH2,IQGAP1,IQGAP2,TRAPPC6A	down_ACOR_VSMC
GO:0009314	0.934	0.147	4	143	response to radiation	BP	1	NABP2,AKT2,TMEM161A,BRSK1	down_VCAV_EC
GO:0051173	0.934	0.151	4	874	positive regulation of nitrogen compound	BP	1	ARHGEF2,ACVR2A,ENSCAFG00000032731,RNF6	up_VPOR_EC
GO:0043549	0.934	0.163	3	244	regulation of kinase activity	BP	1	LEP,LRRC15,ADAM17	up_AFEM_EC
GO:0000077	0.934	0.164	3	60	DNA damage checkpoint	BP	1	CRADD,FBXO4,ATRIP	up_VSAP_EC
GO:0021953	0.934	0.191	2	49	central nervous system neuron differentiation	BP	1	SLC29A1,HOXC10	down_ACOR_VSMC
GO:0019222	0.934	0.207	2	1934	regulation of metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:1901657	0.934	0.191	2	43	glycosyl compound metabolic process	BP	1	NT5C2,PNP	up_VSAP_EC
GO:0051817	0.934	0.254	1	31	modification of morphology or physiology of other organism	BP	1	SMC3	down_ACOR_VSMC

GO:0090100	0.934	0.253	1	31	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SLC29A1	down_ACOR_VSMC
GO:0010556	0.934	0.262	1	1137	regulation of macromolecule	BP	1	GABPA	down_AFEM_EC
GO:0042274	0.934	0.251	1	47	ribosomal small subunit biogenesis	BP	1	PDCD11	down_VSAP_EC
GO:0019217	0.934	0.256	1	27	regulation of fatty acid metabolic process	BP	1	PPARGC1A	up_ACOR_VSMC
GO:0050000	0.934	0.255	1	27	chromosome localization	BP	1	SUN1	up_ACOR_VSMC
GO:0043412	0.934	0.265	1	1225	macromolecule modification	BP	1	SLIT2	up_VPUL_VSMC
GO:0007173	0.934	0.254	1	27	epidermal growth factor receptor signaling	BP	1	ABL1	up_VSAP_EC
GO:0044260	0.935	0.0761	231	2593	cellular macromolecule metabolic process	BP	1	FGF13,ADRA1B,SMAD6,GALNT3,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MEIS2,MBP,ZRANB1,RECK,LIPT2,B3GALNT2,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,PNRC1,LCAT,ZNF331,TBX18,B3GNT7,FGFR2,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,PIGS,ISG15,ZNRF3,ZNF782,ZNF365,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,TMX3,CDKN2B,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,STN1,FAM129A,CAMK2D,MARCH5,ERO1B,DAPK1,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,OS9,STT3B,PFDN5,SMARCD3,SMPD1,TBX20,FUT11,UBE2H,SH3RF1,PYGM,RNF24,P4HA1,PRKCE,CCNT1,MARF1,FRS2,RNF19A,CCPG1,LYPLAL1,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,FUT8,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,PCSK6,SYNJ2BP,MXI1,CHD7,SHPRH,PIK3C3,LAMP2,JUP,TLE4,SPINK2,ZNF432,CCL5,	up_ACOR_VSMC
GO:0006139	0.935	0.0788	143	1909	nucleobase-containing compound metabolic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,TARSL2,MTOR,ACPP,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,ESCO1,TRMT9B,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,JAG1,NSD1,GUCY1B1,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,ENSCAFG00000002897,DCK,ASF1A,HMGB1,AHR,NOS2,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC

GO:0044249	0.935	0.0818	98	1851	cellular biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,CARS,PLOD2,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,PUM3,UGCG,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,CHSY1,HIF1A,FOXP4,SLC45A3,MRPL1,IWS1,NMNAT2,GALNT1,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,APOE,WWC3,PPP1R3C,PLOD3,KLF5,STRAP,DDIT3,BACH1,STT3A,EIF5,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,SH3GLB1,REST,ZMYND8,EIF2S1,PRMT1,NR4A2,EXT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,BCAT1,RPN1,KDM3A,CMPK1	down_VSAP_EC
GO:0010648	0.935	0.0936	27	407	negative regulation of cell communication	BP	1	SREBF1,HMGCR,SLC25A5,PRELID1,INSIG1,CAV1,NF2,MMP14,EZH2,STMN1,GREM1,RNF152,NOC2L,YWHAB,NUP62,CACTIN,HMGB2,GSTO1,EZR,BEND6,PHACTR4,TXNDC12,CTH,NCOA5,ARHGEF2,GLI1,AMER1	down_ACOR_VSMC
GO:0060341	0.935	0.101	18	255	regulation of cellular localization	BP	1	CDH1,ABL1,RAB11B,GLIS2,ICE1,ZFP36L1,PIK3R1,GAS1,FBXO4,LRP4,KCNB1,CYBA,STX4,TTL,KCNC4,PPP3CB,MAVS,BAG4	up_VSAP_EC
GO:0009617	0.935	0.125	7	133	response to bacterium	BP	1	IRAK1,MTDH,CAV1,CDK4,ARG2,CACTIN,HMGB2	down_ACOR_VSMC
GO:0048193	0.935	0.124	7	116	Golgi vesicle transport	BP	1	LMF1,GAS1,ERGIC1,CCDC93,DOP1B,MYO1B,CEP19	up_VSAP_EC
GO:0040013	0.935	0.137	5	100	negative regulation of locomotion	BP	1	HMGB1,TRIM35,HOXA7,RAP2C,ENSCAFG00000010224	down_ACOR_VSMC
GO:0031346	0.935	0.147	4	73	positive regulation of cell projection organization	BP	1	F2RL1,NRP1,PSEN1,RREB1	up_ACOR_VSMC
GO:0044267	0.935	0.154	4	1583	cellular protein metabolic process	BP	1	EYA1,MAP2K6,TRIM9,CDC42EP5	up_VFEM_EC
GO:1903322	0.935	0.163	3	59	positive regulation of protein modification by small protein conjugation	BP	1	FAM107A,FBXO4,CDK9	up_VSAP_EC
GO:0002237	0.935	0.187	2	85	response to molecule of bacterial origin	BP	1	ENSCAFG00000013404,SASH1	down_VCAV_EC
GO:0050804	0.935	0.187	2	87	modulation of chemical synaptic transmission	BP	1	PLCL1,BRSK1	down_VCAV_EC
GO:0099177	0.935	0.187	2	87	regulation of trans-synaptic signaling	BP	1	PLCL1,BRSK1	down_VCAV_EC
GO:0000910	0.935	0.187	2	52	cytokinesis	BP	1	RAB11A,STMN1	up_VCAV_EC
GO:0018393	0.935	0.187	2	51	internal peptidyl-lysine acetylation	BP	1	IWS1,GATA3	up_VCAV_EC
GO:0030307	0.935	0.251	1	31	positive regulation of cell growth	BP	1	MMP14	down_ACOR_VSMC
GO:0097530	0.935	0.251	1	33	granulocyte migration	BP	1	RAC1	down_ACOR_VSMC
GO:0000723	0.935	0.247	1	54	telomere maintenance	BP	1	NABP2	down_VCAV_EC
GO:0032200	0.935	0.247	1	54	telomere organization	BP	1	NABP2	down_VCAV_EC
GO:0034250	0.935	0.249	1	45	positive regulation of cellular amide metabolic	BP	1	PLK3	down_VSAP_EC
GO:1905037	0.935	0.248	1	47	autophagosome organization	BP	1	SH3GLB1	down_VSAP_EC
GO:0006446	0.935	0.254	1	27	regulation of translational initiation	BP	1	CTIF	up_ACOR_VSMC
GO:0002377	0.935	0.252	1	26	immunoglobulin production	BP	1	TP53BP1	up_ACOR_VSMC
GO:0045862	0.935	0.247	1	112	positive regulation of proteolysis	BP	1	F3	up_AFEM_EC
GO:1905477	0.935	0.251	1	32	positive regulation of protein localization to	BP	1	SH3GLB1	up_VCAV_EC
GO:0000278	0.935	0.248	1	331	mitotic cell cycle	BP	1	MZT1	up_VPOR_EC
GO:0007091	0.935	0.251	1	27	metaphase/anaphase transition of mitotic cell	BP	1	CDC26	up_VSAP_EC
GO:0010965	0.935	0.251	1	27	regulation of mitotic sister chromatid separation	BP	1	CDC26	up_VSAP_EC
GO:0044784	0.935	0.251	1	27	metaphase/anaphase transition of cell cycle	BP	1	CDC26	up_VSAP_EC
GO:0021761	0.935	0.254	1	27	limbic system development	BP	1	EMX2	up_VSAP_EC

GO:0071704	0.936	0.0774	196	3535	organic substance metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,ENSCAFG00000009211,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,ENSCAFG00000028814,TRIB3,PGAM1,TMED2,PUM3,UGCG,PM20D2,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,HIF1A,FOXP4,SLC45A3,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,ACTG2,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,MOGS,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,AK5,GTF2H1,ARMCX3,CUL2,SH3GLB1,GALE,HTT,REST,ABHD5,RBBP8,ZMYN	down_VSAP_EC
GO:0008104	0.936	0.083	62	763	protein localization	BP	1	PEX7,WNT11,HNF4A,CD274,ARHGEF5,AXIN2,C5AR2,SLC8B1,PLEKHF1,TBC1D10C,TBC1D2B,CDH1,FGF7,ABL1,PEX2,EMP2,IL17RC,SCAMP4,ANXA4,RILPL2,VPS36,TOM1,F2RL1,LMF1,RAB11B,GLIS2,MORC3,MFN2,ICE1,PIK3R1,CRACR2B,CIZ1,FBXO4,LRP4,NUP98,TSPAN5,HPS4,FRMD6,STEAP3,FBXO7,KCNB1,LONP2,SNUPN,SCAMP2,RAF1,PNP,MAPKBP1,TAF8,STX4,VPS11,FLOT1,PPP3CB,PEX6,STK11IP,MAVS,ULK1,BAG4,NCOA4,NAGPA,KEAP1,RAB11FIP2,LATS2	up_VSAP_EC
GO:0002376	0.936	0.0865	43	622	immune system process	BP	1	HMGB1,FLNB,IRAK1,ANLN,MNDA,SLC29A1,HOXA3,HSPA9,PRELID1,PRMT1,CAV1,TXLNA,MMP14,TRIM35,HMGB3,HOXA7,ARG2,PDCD2,HOXB7,B4GALT1,TFRC,FAM49B,RAC1,EMP2,CACTIN,HMGB2,CDC42EP4,RAB35,EZR,TOX,RBM14,CORO1A,SGPL1,POLR3F,BAP1,ELF4,ARHGEF2,HOXA9,JMJD6,EXOSC5,SIX4,CTPS1,PIK3CD	down_ACOR_VSMC
GO:0042326	0.936	0.115	9	163	negative regulation of phosphorylation	BP	1	HMGCR,PPP1R15B,CAV1,NF2,CDKN2C,GREM1,NUP62,CACTIN,EZR	down_ACOR_VSMC
GO:0010817	0.936	0.136	5	102	regulation of hormone levels	BP	1	SREBF1,BIRC5,FAM129B,ENSCAFG00000005299,SGPL1	down_ACOR_VSMC
GO:0090596	0.936	0.145	4	84	sensory organ morphogenesis	BP	1	INSIG1,PHACTR4,HMGN1,SIX4	down_ACOR_VSMC
GO:0010634	0.936	0.161	3	68	positive regulation of epithelial cell migration	BP	1	HMGB1,NUS1,AMOTL1	down_ACOR_VSMC
GO:0010212	0.936	0.16	3	60	response to ionizing radiation	BP	1	TNKS1BP1,MYC,FBXO4	up_VSAP_EC
GO:0048839	0.936	0.185	2	50	inner ear development	BP	1	INSIG1,SIX4	down_ACOR_VSMC
GO:0005975	0.936	0.182	2	183	carbohydrate metabolic process	BP	1	LEP,ACACB	up_AFEM_EC
GO:0046474	0.936	0.186	2	44	glycerophospholipid biosynthetic process	BP	1	PLA2G6,LCAT	up_VSAP_EC
GO:0002793	0.936	0.246	1	54	positive regulation of peptide secretion	BP	1	MAVS	down_VCAV_EC
GO:0050714	0.936	0.246	1	54	positive regulation of protein secretion	BP	1	MAVS	down_VCAV_EC
GO:0097529	0.936	0.246	1	52	myeloid leukocyte migration	BP	1	RAC2	down_VCAV_EC
GO:0034654	0.936	0.259	1	1236	nucleobase-containing compound biosynthetic	BP	1	GATA5	up_VPUL_VSMC
GO:0031667	0.936609719	0.24198	1	102	response to nutrient levels	BP	1	PCSK1N	up_ACOR_EC
GO:0033043	0.937	0.0883	35	446	regulation of organelle organization	BP	1	SYNPO2L,FGF13,ARHGAP28,ACTN2,MID1,USP6NL,FEZ1,PRKAA2,BMP4,EVI5L,LNPK,SYNPO2,TUBB4A,ATRX,SEC24B,PPARGC1A,ATXN2,F2RL1,MARCH5,BNIP3,JMY,NRP1,EVL,PRKCE,SGSM2,SSH3,EDN1,ASAP1,FAM107A,JAM3,KIF9,FEZ2,INPP5K,WASL,HMBOX1	up_ACOR_VSMC

GO:0035295	0.937	0.0938	23	356	tube development	BP	1	ELK3,MTDH,HOXA3,CAV1,TIMELESS,ANPEP,MMP14,GREM1,ADIPOR2,HOXA7,ARG2,HOXB7,E2F8,B4GALT1,PRCP,NCL,EMP2,SGPL1,PHACTR4,GLI1,JMJD6,NUS1,SIX4	down_ACOR_VSMC
GO:0006952	0.937	0.0957	20	319	defense response	BP	1	HMGB1,FLNB,IRAK1,SLC29A1,CAV1,TRIM35,ARG2,B4GALT1,PRCP,CACTIN,HMGB2,CDC42EP4,RBM14,CORO1A,POLR3F,BAP1,ELF4,ARHGEF2,EXOSC5,PIK3CD	down_ACOR_VSMC
GO:0006511	0.937	0.102	15	253	ubiquitin-dependent protein catabolic process	BP	1	TNFAIP3,WWP1,USP33,PELI1,USP28,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMD12,ITCH	up_VCAV_EC
GO:0005975	0.937	0.106	12	183	carbohydrate metabolic process	BP	1	LEP,ST3GAL5,ENOSF1,PPIP5K1,PYGM,GLB1L,PRKCE,ALDOC,DDIT4,NEU3,GAA,INPP5K	up_ACOR_VSMC
GO:0051656	0.937	0.118	8	129	establishment of organelle localization	BP	1	RHOT1,FBXL20,STX11,PSEN1,RAB11B,SUN1,PREPL,DYNC1I1	up_ACOR_VSMC
GO:0007276	0.937	0.118	8	130	gamete generation	BP	1	HOXA11,HOXA9,ZNF449,HERPUD2,ZBTB16,PATZ1,KDM2B,HPGD	up_VSAP_EC
GO:0051098	0.937	0.117	8	129	regulation of binding	BP	1	CDON,ABL1,EBF2,TIAM1,LARP6,CDK9,EIF3D,FLOT1	up_VSAP_EC
GO:0019221	0.937	0.133	5	102	cytokine-mediated signaling pathway	BP	1	IRAK1,SLC29A1,CAV1,ADIPOR2,CACTIN	down_ACOR_VSMC
GO:0009416	0.937	0.134	5	88	response to light stimulus	BP	1	CHRM1,DDB2,PIK3R1,CTNS,NR2F6	up_VSAP_EC
GO:0006631	0.937	0.142	4	93	fatty acid metabolic process	BP	1	EDN1,PTGS1,ELOVL7,PTGS2	up_VCAV_EC
GO:0046483	0.937	0.154	4	1948	heterocycle metabolic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0050727	0.937	0.143	4	74	regulation of inflammatory response	BP	1	NAPEPLD,IL17RC,MYD88,NLRX1	up_VSAP_EC
GO:2001234	0.937	0.144	4	75	negative regulation of apoptotic signaling	BP	1	ACKR3,RAF1,QARS,HMOX1	up_VSAP_EC
GO:0006412	0.937	0.156	3	245	translation	BP	1	PRR16,CTIF,SAMD4B	up_AFEM_EC
GO:0045927	0.937	0.159	3	61	positive regulation of growth	BP	1	ACACB,DLL1,KDM2B	up_VSAP_EC
GO:0050731	0.937	0.185	2	44	positive regulation of peptidyl-tyrosine	BP	1	NRP1,PARP9	up_ACOR_VSMC
GO:0042306	0.937	0.245	1	31	regulation of protein import into nucleus	BP	1	DMAP1	down_ACOR_VSMC
GO:0046620	0.937	0.246	1	30	regulation of organ growth	BP	1	GLI1	down_ACOR_VSMC
GO:0055007	0.937	0.244	1	31	cardiac muscle cell differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0071897	0.937	0.243	1	54	DNA biosynthetic process	BP	1	GREM1	down_VCAV_EC
GO:0007187	0.937	0.243	1	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	GNAQ	down_VSAP_EC
GO:0070936	0.937	0.246	1	28	protein K48-linked ubiquitination	BP	1	UBE2H	up_ACOR_VSMC
GO:0006351	0.937	0.254	1	1069	transcription, DNA-templated	BP	1	HOXA9	up_AORT_EC
GO:0032774	0.937	0.251	1	1073	RNA biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0097659	0.937	0.252	1	1072	nucleic acid-templated transcription	BP	1	HOXA9	up_AORT_EC
GO:0043170	0.937	0.296	1	2980	macromolecule metabolic process	BP	1	HOXA3	up_APUL_VSMC
GO:0051651	0.937	0.245	1	31	maintenance of location in cell	BP	1	ATP2A1	up_VCAV_EC
GO:0090304	0.937	0.264	1	1694	nucleic acid metabolic process	BP	1	GATA5	up_VCAV_VSMC
GO:0006810	0.937	0.257	1	1244	transport	BP	1	HOXA3	up_VPUL_VSMC
GO:0014031	0.937	0.247	1	27	mesenchymal cell development	BP	1	CITED2	up_VSAP_EC
GO:0014032	0.937	0.247	1	27	neural crest cell development	BP	1	CITED2	up_VSAP_EC
GO:0030203	0.937	0.248	1	27	glycosaminoglycan metabolic process	BP	1	CHST7	up_VSAP_EC
GO:0062013	0.937	0.247	1	27	positive regulation of small molecule metabolic	BP	1	C1QTNF2	up_VSAP_EC
GO:2000117	0.937	0.248	1	27	negative regulation of cysteine-type	BP	1	CST3	up_VSAP_EC
GO:0007005	0.937625735	0.17935	2	175	mitochondrion organization	BP	1	IFI6,ENSCAFG00000010493	up_ACOR_EC

GO:0044260	0.938	0.077	117	2593	cellular macromolecule metabolic process	BP	1	CST3,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,NAB2,PRNP,LUM,UBA52,FBN1,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,SAMD4B,EEF2K,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,PLCL1,DDOST,CSPG4,VDR,PRMT6,TMEM161A,CXXC5,GFPT2,ASPN,PIGS,HS3ST3B1,LRPAP1,EIF3K,THY1,NECAB3,RNF216,TEAD1,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RPL27,COPS7A,ARL2BP,IFT57,MAVS,MRPS11,CDH2,LOXL3,GSDME,CAMK2D,RPS27,FUT8,SPRED1,RAB7B,A2M,SEC61B,IRX5,TSC22D3,MAPRE3,GLIS2,CDKL2,RAB31,HM13,PRKCSH,DDR2,SHC1,CRTAP,PCSK6,ENSCAFG00000000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,LONP2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:0009628	0.938	0.0925	22	302	response to abiotic stimulus	BP	1	WNT11,MAP3K14,CRADD,CHRM1,OSR1,DDB2,TNKS1BP1,RAB11B,ZFP36L1,PIK3R1,MYC,CTNS,SCARA5,SLC12A6,FBXO4,LIMD1,NR2F6,DENND5A,RAF1,HTRA2,HMOX1,DDIT4	up_VSAP_EC
GO:0060537	0.938	0.125	6	117	muscle tissue development	BP	1	FLNB,CAV1,GREM1,GLI1,MSC,SIX4	down_ACOR_VSMC
GO:1903320	0.938	0.126	6	102	regulation of protein modification by small protein conjugation or	BP	1	FAM107A,ABL1,SASH1,FBXO4,CDK9,ZER1	up_VSAP_EC
GO:0006725	0.938	0.151	4	1956	cellular aromatic compound metabolic	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:0044403	0.938	0.155	3	116	symbiont process	BP	1	TRIM8,MAVS,NAPEPLD	down_VCAV_EC
GO:0045930	0.938	0.154	3	97	negative regulation of mitotic cell cycle	BP	1	NAA10,CTNNB1,CDKN1A	down_VSAP_EC
GO:1901564	0.938	0.17	3	2053	organonitrogen compound metabolic	BP	1	EYA1,GATM,FBP1	up_VFEM_VSMC
GO:0008361	0.938	0.182	2	50	regulation of cell size	BP	1	RAC1,ANXA7	down_ACOR_VSMC
GO:0051403	0.938	0.179	2	89	stress-activated MAPK cascade	BP	1	ZFP36L1,SASH1	down_VCAV_EC
GO:0045619	0.938	0.181	2	44	regulation of lymphocyte differentiation	BP	1	CD83,BMP4	up_ACOR_VSMC
GO:0071453	0.938	0.181	2	46	cellular response to oxygen levels	BP	1	BNIP3,PRKCE	up_ACOR_VSMC
GO:0048704	0.938	0.182	2	46	embryonic skeletal system morphogenesis	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:1905475	0.938	0.181	2	52	regulation of protein localization to membrane	BP	1	PPP2R5A,SH3GLB1	up_VCAV_EC
GO:0007050	0.938	0.239	1	53	cell cycle arrest	BP	1	NOTCH2	down_VCAV_EC
GO:0050920	0.938	0.24	1	53	regulation of chemotaxis	BP	1	RAC2	down_VCAV_EC
GO:2000573	0.938	0.243	1	28	positive regulation of DNA biosynthetic process	BP	1	HMBOX1	up_ACOR_VSMC
GO:0016079	0.938	0.245	1	27	synaptic vesicle exocytosis	BP	1	STX4	up_VSAP_EC
GO:0098813	0.938483624	0.23675	1	102	nuclear chromosome segregation	BP	1	CHMP4B	up_ACOR_EC
GO:0048285	0.938769501	0.17684	2	166	organelle fission	BP	1	FIGNL1,CHMP4B	up_ACOR_EC
GO:0023057	0.939	0.0886	27	409	negative regulation of signaling	BP	1	SREBF1,HMGCR,SLC25A5,PRELID1,INSIG1,CAV1,NF2,MMP14,EZH2,STMN1,GREM1,RNF152,NOC2L,YWHAB,NUP62,CACTIN,HMGB2,GSTO1,EZR,BEND6,PHACTR4,TXNDC12,CTH,NCOA5,ARHGEF2,GLI1,AMER1	down_ACOR_VSMC
GO:0031401	0.939	0.0902	23	358	positive regulation of protein modification process	BP	1	HMGB1,SREBF1,IRAK1,UBE2S,SLC29A1,CAV1,FANCI,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,BRCA1,RAP2C,RAC1,EMP2,CLSPN,CDC20,ARHGEF2,TADA2A,AMER1,DCUN1D5	down_ACOR_VSMC
GO:0040012	0.939	0.0937	19	303	regulation of locomotion	BP	1	HMGB1,RACGAP1,FBXO5,CAV1,MMP14,TRIM35,HOXA7,PRCP,RAP2C,RAC1,EMP2,SMC3,CORO1A,ENSCAFG00000010224,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0051603	0.939	0.094	19	305	proteolysis involved in cellular protein catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C	down_ACOR_VSMC

GO:0002790	0.939	0.117	7	133	peptide secretion	BP	1	HMGB1,SREBF1,BIRC5,ARG2,PREB,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0071704	0.939	0.146	6	3535	organic substance metabolic process	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0019221	0.939	0.123	6	102	cytokine-mediated signaling pathway	BP	1	SLIT2,STAT6,F2RL1,RTN4RL1,CREBRF,MAVS	up_VSAP_EC
GO:0031667	0.939	0.13	5	102	response to nutrient levels	BP	1	SREBF1,SREBF2,RNF152,PDXP,MIOS	down_ACOR_VSMC
GO:0060828	0.939	0.139	4	82	regulation of canonical Wnt signaling pathway	BP	1	FERMT1,RAPGEF1,BMP2,MCC	up_VCAV_EC
GO:0051146	0.939	0.14	4	76	striated muscle cell differentiation	BP	1	CDON,DLL1,SHOX2,FLOT1	up_VSAP_EC
GO:0016050	0.939	0.153	3	119	vesicle organization	BP	1	SDC4,AKT2,EVI5L	down_VCAV_EC
GO:0010212	0.939	0.154	3	60	response to ionizing radiation	BP	1	CDKN1A,XRRA1,DMC1	up_ACOR_VSMC
GO:0090150	0.939	0.154	3	64	establishment of protein localization to membrane	BP	1	TCAF1,RAB11B,INPP5K	up_ACOR_VSMC
GO:0043043	0.939	0.152	3	247	peptide biosynthetic process	BP	1	PRR16,CTIF,SAMD4B	up_AFEM_EC
GO:0031570	0.939	0.154	3	61	DNA integrity checkpoint	BP	1	CRADD,FBXO4,ATRIP	up_VSAP_EC
GO:0051701	0.939	0.18	2	45	interaction with host	BP	1	CTSB,DAG1	up_ACOR_VSMC
GO:0006334	0.939	0.18	2	45	nucleosome assembly	BP	1	NAA60,CENPP	up_VSAP_EC
GO:0031532	0.939	0.241	1	31	actin cytoskeleton reorganization	BP	1	EZR	down_ACOR_VSMC
GO:0035821	0.939	0.24	1	32	modification of morphology or physiology	BP	1	SMC3	down_ACOR_VSMC
GO:0008104	0.939	0.242	1	763	protein localization	BP	1	NR1H4	up_VPUL_EC
GO:0019438	0.939	0.249	1	1258	aromatic compound biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0009987	0.94	0.159	8	5086	cellular process	BP	1	CST3,HDAC7,CITED2,RAB11B,MGAT4B,HSD3B7,TBX15,GBGT1	down_VPOR_EC
GO:0070482	0.94	0.137	4	75	response to oxygen levels	BP	1	ZFP36L1,LIMD1,HMOX1,DDIT4	up_VSAP_EC
GO:0002263	0.94	0.152	3	68	cell activation involved in immune response	BP	1	HMGB1,TFRC,CORO1A	down_ACOR_VSMC
GO:0044419	0.94	0.15	3	117	interspecies interaction between organisms	BP	1	TRIM8,MAVS,NAPEPLD	down_VCAV_EC
GO:2001252	0.94	0.152	3	61	positive regulation of chromosome organization	BP	1	FBXO4,PHF1,CDK9	up_VSAP_EC
GO:1903052	0.94	0.177	2	51	positive regulation of proteolysis involved in cellular protein catabolic	BP	1	PLK3,RAD23A	down_ACOR_VSMC
GO:0006364	0.94	0.175	2	87	rRNA processing	BP	1	RPL27,MRPS11	down_VCAV_EC
GO:0051171	0.94	0.188	2	1697	regulation of nitrogen compound metabolic	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0006352	0.94	0.176	2	56	DNA-templated transcription, initiation	BP	1	IRF8,HMGB1	up_VCAV_EC
GO:0022607	0.94	0.179	2	969	cellular component assembly	BP	1	EMP1,CAV1	up_VSAP_VSMC
GO:0007623	0.94	0.234	1	55	circadian rhythm	BP	1	NAGLU	down_VCAV_EC
GO:0038127	0.94	0.236	1	32	ERBB signaling pathway	BP	1	FES	up_VCAV_EC
GO:0018130	0.94	0.248	1	1261	heterocycle biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0046660	0.94	0.237	1	28	female sex differentiation	BP	1	SLIT2	up_VSAP_EC
GO:0009056	0.941	0.0777	53	755	catabolic process	BP	1	HMGB1,RNPS1,SREBF1,USP1,USP4,EIF4A3,EDC3,HNRNPD,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,MTDH,HM13,PSMD13,THRAP3,EDC4,MMP14,ABHD5,FEN1,CDK4,SMARCC1,RNASEH2B,PLK3,SMG9,RNF152,DIS3,FASTKD3,PPARD,UBE2J2,DTL,PDXP,GSTO1,EZR,UBE2K,RAD23A,SGPL1,CDC20,BAP1,PSMC1,GALE,AIFM1,ENSCAFG00000015189,LIPC,RNASEH2C,NUDT1,EXOSC5,UBE2C,ACADL,AMER1,NUDT3,ANXA7	down_ACOR_VSMC
GO:0006508	0.941	0.0836	32	483	proteolysis	BP	1	HMGB1,USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,PRELID1,HM13,PSMD13,BIRC5,CASP2,MMP14,SMARCC1,PLK3,PDCD2,DHCR24,PRCP,UBE2J2,CYCS,DTL,ENSCAFG00000005299,UBE2K,RAD23A,CDC20,BAP1,PSMC1,AIFM1,PMPCA,DELE1,UBE2C	down_ACOR_VSMC

GO:0030336	0.941	0.135	4	86	negative regulation of cell migration	BP	1	HMGB1,HOXA7,RAP2C,ENSCAFG00000010224	down_ACOR_VSMC
GO:0034641	0.941	0.165	3	2171	cellular nitrogen compound metabolic	BP	1	BARX1,NKX2-5,BAMBI	up_VPOR_VSMC
GO:0071216	0.941	0.151	3	61	cellular response to biotic stimulus	BP	1	ABL1,SASH1,MYD88	up_VSAP_EC
GO:0030316	0.941	0.235	1	31	osteoclast differentiation	BP	1	TFRC	down_ACOR_VSMC
GO:0035296	0.941	0.233	1	32	regulation of tube diameter	BP	1	CAV1	down_ACOR_VSMC
GO:0097746	0.941	0.233	1	32	regulation of blood vessel diameter	BP	1	CAV1	down_ACOR_VSMC
GO:0031326	0.941	0.244	1	1176	regulation of cellular biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0006470	0.941	0.232	1	54	protein dephosphorylation	BP	1	PDGFRB	down_VCAV_EC
GO:0007098	0.941	0.231	1	56	centrosome cycle	BP	1	BRSK1	down_VCAV_EC
GO:0043409	0.941	0.232	1	54	negative regulation of MAPK cascade	BP	1	SPRED1	down_VCAV_EC
GO:0006836	0.941	0.23	1	47	neurotransmitter transport	BP	1	GSK3B	down_VSAP_EC
GO:0050777	0.941	0.235	1	28	negative regulation of immune response	BP	1	DUSP22	up_ACOR_VSMC
GO:0043933	0.941	0.235	1	698	protein-containing complex subunit	BP	1	TUBB4A	up_APUL_EC
GO:0044248	0.941	0.236	1	691	cellular catabolic process	BP	1	LZTS1	up_APUL_EC
GO:0034440	0.941	0.234	1	35	lipid oxidation	BP	1	APOD	up_VCAV_EC
GO:0061013	0.941	0.235	1	32	regulation of mRNA catabolic process	BP	1	CNOT7	up_VCAV_EC
GO:1902806	0.941	0.234	1	33	regulation of cell cycle G1/S phase transition	BP	1	CUL4A	up_VCAV_EC
GO:0010468	0.941	0.243	1	1270	regulation of gene expression	BP	1	GATA5	up_VPUL_VSMC
GO:0007062	0.941	0.235	1	29	sister chromatid cohesion	BP	1	AXIN2	up_VSAP_EC
GO:0050868	0.941	0.235	1	28	negative regulation of T cell activation	BP	1	CD274	up_VSAP_EC
GO:0051928	0.941	0.236	1	28	positive regulation of calcium ion transport	BP	1	ABL1	up_VSAP_EC
GO:0044773	0.941	0.236	1	28	mitotic DNA damage checkpoint	BP	1	CRADD	up_VSAP_EC
GO:0019693	0.941199148	0.17125	2	172	ribose phosphate metabolic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0045860	0.942	0.113	7	132	positive regulation of protein kinase activity	BP	1	IRAK1,SLC29A1,EZH2,MAP3K20,CKS2,EMP2,CLSPN	down_ACOR_VSMC
GO:0051046	0.942	0.123	5	174	regulation of secretion	BP	1	GPAM,SDC4,CYBA,MAVS,RAC2	down_VCAV_EC
GO:0009126	0.942	0.132	4	100	purine nucleoside monophosphate metabolic process	BP	1	ADSS,ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0009167	0.942	0.132	4	100	purine ribonucleoside monophosphate metabolic process	BP	1	ADSS,ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:1903364	0.942	0.148	3	61	positive regulation of cellular protein catabolic	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:0050920	0.942	0.172	2	53	regulation of chemotaxis	BP	1	HMGB1,RAC1	down_ACOR_VSMC
GO:0001704	0.942	0.173	2	43	formation of primary germ layer	BP	1	BMP4,LAMA3	up_ACOR_VSMC
GO:0051130	0.942	0.229	1	342	positive regulation of cellular component	BP	1	ENSCAFG00000002015	up_VPOR_EC
GO:0051234	0.942	0.24	1	1283	establishment of localization	BP	1	HOXA3	up_VPUL_VSMC
GO:1905818	0.942	0.233	1	28	regulation of chromosome separation	BP	1	CDC26	up_VSAP_EC
GO:0070936	0.942	0.233	1	28	protein K48-linked ubiquitination	BP	1	RNF216	up_VSAP_EC
GO:0044265	0.943	0.081	32	423	cellular macromolecule catabolic process	BP	1	AXIN2,FOXRED2,ABTB1,CTSS,TENT5C,HPSE,VPS36,EXOSC7,PYM1,DFFB,ZFP36L1,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,SMG9,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,SAMD4B,ZFP36L2,UBQLN2,CTSF,CDC26,HTRA2,TNRC6C,KEAP1	up_VSAP_EC
GO:0009150	0.943	0.102	10	161	purine ribonucleotide metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC

GO:0042692	0.943	0.116	6	105	muscle cell differentiation	BP	1	CDON,DLL1,ZEB1,SHOX2,CDK9,FLOT1	up_VSAP_EC
GO:0045862	0.943	0.123	5	112	positive regulation of proteolysis	BP	1	TNIP1,CASP8,BCL10,HMGB1,PMAIP1	up_VCAV_EC
GO:2000060	0.943	0.171	2	45	positive regulation of ubiquitin-dependent protein catabolic process	BP	1	RNF166,UBQLN2	up_VSAP_EC
GO:0009889	0.943	0.238	1	1190	regulation of biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0032874	0.943	0.226	1	57	positive regulation of stress-activated MAPK	BP	1	SASH1	down_VCAV_EC
GO:0034728	0.943	0.225	1	56	nucleosome organization	BP	1	CABIN1	down_VCAV_EC
GO:0051168	0.943	0.225	1	57	nuclear export	BP	1	PARK7	down_VCAV_EC
GO:0006259	0.943	0.226	1	354	DNA metabolic process	BP	1	CXHXorf57	up_VPOR_EC
GO:0044085	0.943	0.236	1	1076	cellular component biogenesis	BP	1	NKX2-5	up_VPOR_VSMC
GO:0006163	0.943244032	0.16652	2	174	purine nucleotide metabolic process	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0044281	0.943427458	0.09855	11	622	small molecule metabolic process	BP	1	NR1H4,THNSL2,NMNAT2,SARDH,NIT2,PTGDS,GUCY1B1,AK7,ALDOC,AZIN2,PM20D1	up_ACOR_EC
GO:0044089	0.94370553	0.16548	2	170	positive regulation of cellular component	BP	1	SYNPO2,NRP1	up_ACOR_EC
GO:0046483	0.944	0.068	145	1948	heterocycle metabolic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,TARSL2,MTOR,ACPP,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,ESCO1,TRMT9B,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,JAG1,NSD1,GUCY1B1,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,GCH1,ENSCAFG00000002897,DCK,ASF1A,HMGB1,AHR,NOS2,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,BLVRA,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,GINS4	up_VCAV_EC
GO:0007017	0.944	0.0864	20	273	microtubule-based process	BP	1	FGF13,RHOT1,DNAH7,MID1,PRKAA2,TUBB4A,ATRX,TMEM108,IFT43,KIF1A,DAG1,APP,DYNC1I2,FAM107A,DISC1,KIF9,TACC1,SUN1,DYNC1I1,ENSCAFG00000013536	up_ACOR_VSMC
GO:0045786	0.944	0.0948	13	195	negative regulation of cell cycle	BP	1	FAM107A,CRADD,ABL1,ZFP36L1,GAS1,FBXO4,ATRIP,FBXO7,CDK9,ZFP36L2,HPGD,TPRA1,LATS2	up_VSAP_EC
GO:0009987	0.944	0.139	10	5086	cellular process	BP	1	CHL1,FGF5,HOXA3,BARX1,NKX2-5,BAMBI,TRPC4,ANKRD6,CYP26B1,C3AR1	up_VPOR_VSMC
GO:0006091	0.944	0.11	7	139	generation of precursor metabolites and energy	BP	1	PRELID1,CDK1,FASTKD3,SUCLG1,CYCS,CYC1,PDHA1	down_ACOR_VSMC
GO:0008015	0.944	0.114	6	120	blood circulation	BP	1	SREBF1,CAV1,TRPV4,NAV2,PRCP,EMP2	down_ACOR_VSMC
GO:0030900	0.944	0.121	5	101	forebrain development	BP	1	NF2,WDR62,ASPM,ENSCAFG00000010224,GLI1	down_ACOR_VSMC
GO:0071824	0.944	0.121	5	92	protein-DNA complex subunit organization	BP	1	ATRX,TSPYL5,SMARCD3,SHPRH,DMC1	up_ACOR_VSMC
GO:2001020	0.944	0.122	5	88	regulation of response to DNA damage stimulus	BP	1	NACC2,TP53BP1,ZNF365,ANKRD1,PARP9	up_ACOR_VSMC
GO:0008152	0.944	0.147	5	3714	metabolic process	BP	1	HOXA3,GATA5,ARSI,PHEX,SLIT2	up_VPUL_VSMC
GO:0006874	0.944	0.122	5	91	cellular calcium ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:0044267	0.944	0.136	4	1583	cellular protein metabolic process	BP	1	GALNT17,PRR16,TLR2,CAV1	up_VSAP_VSMC
GO:0006511	0.944	0.142	3	253	ubiquitin-dependent protein catabolic process	BP	1	CLEC16A,CYLD,RNF181	up_AFEM_EC
GO:0000075	0.944	0.165	2	91	cell cycle checkpoint	BP	1	NABP2,BRSK1	down_VCAV_EC

GO:0031396	0.944	0.165	2	90	regulation of protein ubiquitination	BP	1	PARK7,SASH1	down_VCAV_EC
GO:0006939	0.944	0.224	1	32	smooth muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0006665	0.944	0.223	1	48	sphingolipid metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0008589	0.944	0.225	1	28	regulation of smoothened signaling pathway	BP	1	FGFR2	up_ACOR_VSMC
GO:0044773	0.944	0.226	1	28	mitotic DNA damage checkpoint	BP	1	CDKN1A	up_ACOR_VSMC
GO:0043467	0.944	0.224	1	35	regulation of generation of precursor metabolites	BP	1	HIF1A	up_VCAV_EC
GO:2001021	0.944	0.225	1	30	negative regulation of response to DNA damage	BP	1	THOC1	up_VCAV_EC
GO:0051179	0.944	0.245	1	1747	localization	BP	1	CA2	up_VCAV_VSMC
GO:1901362	0.944	0.235	1	1293	organic cyclic compound biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0050773	0.944	0.226	1	29	regulation of dendrite development	BP	1	PQBP1	up_VSAP_EC
GO:0051649	0.944	0.225	1	630	establishment of localization in cell	BP	1	CAV1	up_VSAP_VSMC
GO:1901987	0.944004757	0.2209	1	107	regulation of cell cycle phase transition	BP	1	BRSK1	up_ACOR_EC
GO:0007275	0.945	0.0687	102	1370	multicellular organism development	BP	1	ELK3,HMGB1,FLNB,USP1,ANLN,ACSL4,EIF4A3,HINFP,NEDD4,SLC29A1,MTDH,HEY1,HOXA3,SF1,SRRT,GINS4,RAD54L,FBXO5,HSPA9,NAB2,B3GNT2,PRELID1,INSIG1,PRMT1,CAV1,XYLT1,TIMELESS,NF2,ANPEP,MMP14,EZH2,STMN1,SLC30A1,GREM1,MAP3K20,NEK2,ADIPOR2,CDK4,SMARCC1,RNASEH2B,HMGB3,HOXA7,SMG9,ARG2,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,POC1A,BRCA1,WDR62,E2F8,B4GALT1,NAV2,PRCP,TFRC,ADAMTS6,PPARD,NCL,RAC1,UGDH,EMP2,FOSL1,PLK4,IQGAP1,HOXC6,HMGB2,ARCN1,CDK2,SMARCB1,RAB35,HOXB5,RBBP8,TOX,HOXC4,SGPL1,NOLC1,BEND6,PHACTR4,CDC20,SLC20A1,ASPM,PRPS1,TBX15,ENSCAFG00000010224,ITGA2,CTH,ARHGEF2,HOXA9,SERPINH1,GLI1,JMJD6,MSC,EMG1,RTTN,RTCB,NUS1,HMGN1,SIX4,TPBG,AMER1	down_ACOR_VSMC
GO:0044281	0.945	0.074	48	622	small molecule metabolic process	BP	1	PLCG2,LEP,ENOSF1,PRDX4,ENSCAFG00000002977,MAT2B,LCAT,AHCYL1,PCBD1,ABCA1,TARSL2,PPARGC1A,PDE5A,NIT2,ADCY6,PPIP5K1,ACAD11,ENPP4,ERO1B,EGLN1,LIPE,CYP2J2,PTGDR,MOXD1,P4HA1,PRKCE,SARDH,DKKL1,FUT8,ENSCAFG00000018611,APP,SGSM2,CLN8,EDN1,ALDOC,HPGD,ENTPD3,PCYOX1,DDIT4,EXTL2,INPP5K,AZIN2,PTS,NT5C2,NMNAT1,PARK7,ELOVL7,LMF1	up_ACOR_VSMC
GO:0045934	0.945	0.0786	31	407	negative regulation of nucleobase-containing compound metabolic process	BP	1	LEP,NACC2,BMP4,FGFR2,TP53BP1,EIF4A2,ATRX,TRPS1,ZNF174,ANKRD1,ENSCAFG00000006238,CLSTN1,TBX20,CCNT1,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,DDIT4,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0040008	0.945	0.0982	10	179	regulation of growth	BP	1	MMP14,CDKN2C,CDK4,TKT,PPARD,EZR,SGPL1,BAP1,GLI1,SIX4	down_ACOR_VSMC
GO:0018205	0.945	0.14	3	122	peptidyl-lysine modification	BP	1	PRMT6,PARK7,LOXL3	down_VCAV_EC
GO:0016072	0.945	0.14	3	102	rRNA metabolic process	BP	1	SMARCA4,MRPL1,PDCD11	down_VSAP_EC
GO:0016070	0.945	0.147	3	1479	RNA metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0006310	0.945	0.162	2	93	DNA recombination	BP	1	NABP2,FBH1	down_VCAV_EC
GO:0080090	0.945	0.175	2	1734	regulation of primary metabolic process	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0007049	0.945	0.164	2	560	cell cycle	BP	1	MZT1,ARHGEF2	up_VPOR_EC
GO:0006810	0.945	0.171	2	1244	transport	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:0044264	0.945	0.224	1	32	cellular polysaccharide metabolic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:1901215	0.945	0.22	1	57	negative regulation of neuron death	BP	1	PARK7	down_VCAV_EC
GO:0042773	0.945	0.222	1	32	ATP synthesis coupled electron transport	BP	1	PARK7	up_ACOR_VSMC

GO:0045621	0.945	0.223	1	28	positive regulation of lymphocyte	BP	1	CD83	up_ACOR_VSMC
GO:2000112	0.945	0.23	1	1119	regulation of cellular macromolecule biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0006996	0.945	0.231	1	1301	organelle organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0065003	0.945	0.222	1	616	protein-containing complex assembly	BP	1	CAV1	up_VSAP_VSMC
GO:2000145	0.946	0.0857	17	279	regulation of cell motility	BP	1	HMGB1,RACGAP1,FBXO5,CAV1,MMP14,HOXA7,PRCP,RAP2C,RAC1,EMP2,CORO1A,ENSCAFG00000010224,ARHGEF2,TWIST2,NUS1,AMOTL1,PIK3CD	down_ACOR_VSMC
GO:0019941	0.946	0.0883	15	258	modification-dependent protein catabolic process	BP	1	TNFAIP3,WWP1,USP33,PELI1,USP28,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMD12,ITCH	up_VCAV_EC
GO:0019637	0.946	0.0894	14	342	organophosphate metabolic process	BP	1	NR1H4,ENPP1,PGK1,TPI1,PGAM1,HIF1A,NMNAT2,ENTPD4,ALDOC,PAPSS1,LYN,AK5,SH3GLB1,CMPK1	down_VSAP_EC
GO:1903047	0.946	0.102	8	257	mitotic cell cycle process	BP	1	SNX18,KANK2,NABP2,ZFP36L1,LSM10,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0065007	0.946	0.141	5	3499	biological regulation	BP	1	GPSM2,IVNS1ABP,SRSF6,GABPA,FSCN1	down_AFEM_EC
GO:1903050	0.946	0.125	4	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	SLC29A1,SMARCC1,PLK3,RAD23A	down_ACOR_VSMC
GO:0043393	0.946	0.126	4	77	regulation of protein binding	BP	1	CDON,ABL1,TIAM1,FLOT1	up_VSAP_EC
GO:0032446	0.946	0.137	3	255	protein modification by small protein conjugation	BP	1	KLHDC8B,DCUN1D3,RNF181	up_AFEM_EC
GO:0060322	0.946	0.16	2	193	head development	BP	1	DLL1,PLXNA4	up_AFEM_EC
GO:0006475	0.946	0.163	2	54	internal protein amino acid acetylation	BP	1	IWS1,GATA3	up_VCAV_EC
GO:0071453	0.946	0.164	2	46	cellular response to oxygen levels	BP	1	ZFP36L1,HMOX1	up_VSAP_EC
GO:0006672	0.946	0.219	1	33	ceramide metabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0019395	0.946	0.22	1	33	fatty acid oxidation	BP	1	PPARD	down_ACOR_VSMC
GO:1904589	0.946	0.219	1	33	regulation of protein import	BP	1	DMAP1	down_ACOR_VSMC
GO:0016358	0.946	0.216	1	58	dendrite development	BP	1	TLX2	down_VCAV_EC
GO:0070304	0.946	0.217	1	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	SASH1	down_VCAV_EC
GO:0031497	0.946	0.217	1	49	chromatin assembly	BP	1	BRD2	down_VSAP_EC
GO:0006383	0.946	0.219	1	28	transcription by RNA polymerase III	BP	1	GTF3C1	up_ACOR_VSMC
GO:0009060	0.946	0.22	1	31	aerobic respiration	BP	1	BNIP3	up_ACOR_VSMC
GO:0071479	0.946	0.219	1	29	cellular response to ionizing radiation	BP	1	CDKN1A	up_ACOR_VSMC
GO:0000422	0.946	0.218	1	34	autophagy of mitochondrion	BP	1	HIF1A	up_VCAV_EC
GO:0007292	0.946	0.22	1	32	female gamete generation	BP	1	FBXO5	up_VCAV_EC
GO:0061726	0.946	0.218	1	34	mitochondrion disassembly	BP	1	HIF1A	up_VCAV_EC
GO:0051249	0.946024402	0.215	1	107	regulation of lymphocyte activation	BP	1	NOD2	up_ACOR_EC

GO:0044238	0.947	0.0624	306	3383	primary metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,NAPEPLD,HOXA9,CDON,NECAB3,WNT11,HNF4A,ACSM3,DHDH,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,RNPEP,TBC1D10C,PLBD1,ACAA1,MRPL37,CEP85,FOXRED2,ACACB,EEF2K,IL6R,IRX5,SLIT2,GDA,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,HDAC7,KLKB1,EMP2,DLL1,DLST,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,GLUL,CTSS,GALNT15,DTX2,TENT5C,PGM2L1,ADHFE1,PDGFD,CERS4,HSD17B14,WARS2,VDR,DHRS4,NAA60,SAV1,KDELC2,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,PAFAH2,ABHD15,HSD3B7,ZNF688,ZBTB16,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,TRMT2A,VPS36,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,RECK,GATAD1,CISH,KLHL24,HSD17B8,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,FAAH,APOL5,TNKS1BP1,KLHDC8B,PYM1,AMBRA1,F2RL1,RBL2,LMF1,PHKA2,NFE2L2,GLIS2,LPL,DFFB,PPIP5K1,MORC3,DDR2,PDK2,ICE1,ZFP36L1,TRAF7,GALK2,HSF4,FXN,GALK1,RETSAT,PIK3R1,RBCK1,KBTBD12,ENTPD3,GAS1,BATF2,PLA2G6,NEIL2,MYC,PIK3IP1,PTGES,SSBP2,IRX3,ZEB1,	up_VSAP_EC
GO:1901360	0.947	0.0641	150	2016	organic cyclic compound metabolic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,MOV10,IWS1,MEF2C,ATF3,CHD7,TIPARP,DLL4,WWP1,TLR4,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,SNCAIP,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,TARSL2,MTOR,ACPP,TENT2,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,CCAR1,ABCA1,RIOK3,PROX1,UHRF2,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,ESCO1,TRMT9B,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,JAG1,NSD1,GUCY1B1,TOP1,ETAA1,RAPGEF2,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,GCH1,ENSCAFG00000002897,DCK,ASF1A,HMGB1,AHR,NOS2,BDP1,LBR,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,BLVRA,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609,G	up_VCAV_EC
GO:0003013	0.947	0.109	6	121	circulatory system process	BP	1	SREBF1,CAV1,TRPV4,NAV2,PRCP,EMP2	down_ACOR_VSMC
GO:0032006	0.947	0.16	2	52	regulation of TOR signaling	BP	1	RNF152,MIOS	down_ACOR_VSMC
GO:0007040	0.947	0.216	1	33	lysosome organization	BP	1	CORO1A	down_ACOR_VSMC
GO:0080171	0.947	0.216	1	33	lytic vacuole organization	BP	1	CORO1A	down_ACOR_VSMC
GO:0048645	0.947	0.215	1	33	animal organ formation	BP	1	HOXA3	down_ACOR_VSMC
GO:0031023	0.947	0.215	1	58	microtubule organizing center organization	BP	1	BRSK1	down_VCAV_EC
GO:1902275	0.947	0.214	1	60	regulation of chromatin organization	BP	1	PRMT6	down_VCAV_EC
GO:0008016	0.947	0.213	1	48	regulation of heart contraction	BP	1	CALM1	down_VSAP_EC
GO:0051306	0.947	0.216	1	29	mitotic sister chromatid separation	BP	1	CDC26	up_VSAP_EC
GO:0048864	0.947	0.216	1	29	stem cell development	BP	1	CITED2	up_VSAP_EC
GO:0050954	0.947	0.216	1	30	sensory perception of mechanical stimulus	BP	1	THRB	up_VSAP_EC
GO:2000106	0.947	0.218	1	29	regulation of leukocyte apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0006417	0.947809228	0.20968	1	109	regulation of translation	BP	1	KLHL25	up_ACOR_EC

GO:0051179	0.948	0.0641	131	1747	localization	BP	1	ACSL3,FSCN1,HMGB1,SREBF1,RPA1,ANLN,DDX39A,STXBP6,USP4,FMNL3,RACGAP1,NNT,SREBF2,HINFP,NEDD4,ZW10,CENPA,SLC29A1,HOXA3,NDC1,RRBP1,SLC25A5,TIMM44,POLA2,SDC1,ARFGAP1,CTDNEP1,FBXO5,HSPA9,SLC35C2,SLC25A15,RAN,CFAP298,PRELID1,HM13,BIRC5,INSIG1,CAV1,CDK1,RANBP1,LIMA1,FAM129B,NF2,AURKB,AAAS,MMP14,ABHD5,EZH2,STMN1,SLC30A1,GREM1,FBL,CLIC1,PLK3,HOXA7,ARG2,KIF22,NKAIN1,CDCA8,SLC17A9,DHCR24,ENSCAFG00000011598,B4GALT1,PRCP,PREB,TFRC,PPARD,TRAM1,NDC80,IPO4,RAP2C,ARHGDIA,YWHAB,HIST1H1A,RAC1,NUP62,EMP2,NUP188,HASPIN,RSL1D1,TOMM34,SAMM50,HMGB2,GSTO1,TRAK1,DMAP1,ARCN1,CDK2,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,NIPA2,RBM14,MIOS,CORO1A,SGPL1,CYC1,PHACTR4,TTK,SLC20A1,ASPM,ATP5F1A,ENSCAFG00000013366,ENSCAFG00000010224,REM1,ITGA2,NOP58,SLC25A16,ARHGEF2,TRAPPC6A,KNL1,TWIST2,PMPCA,TINF2,JMJD6,MRPL18,LIPC,NUS1,CCT4,AMOTL1,SIX4,CEP83,MTBP,DEPDC1B,ZWINT,SLC25A19,TTLL1,ATP5F1D,PIK3CD	down_ACOR_VSMC
GO:0051726	0.948	0.075	29	393	regulation of cell cycle	BP	1	FAM107A,MAP3K14,AXIN2,CEP85,CRADD,SLC6A4,ABL1,CNPPD1,RBL2,ZFP36L1,GAS1,CDC25B,FBXO4,POLDIP2,ATRIP,GDPD5,FBXW5,FBXO7,CDK9,TTC28,ZFP36L2,HPGD,TTL,TPRA1,CDC26,LSM10,MAP2K2,CITED2,LATS2	up_VSAP_EC
GO:0002521	0.948	0.0997	8	149	leukocyte differentiation	BP	1	HMGB1,PRELID1,MMP14,HMGB3,HOXA7,TFRC,TOX,JMJD6	down_ACOR_VSMC
GO:0042493	0.948	0.113	5	178	response to drug	BP	1	PRNP,FOLR2,ADCY6,NR3C1,PARK7	down_VCAV_EC
GO:1901360	0.948	0.13	4	2016	organic cyclic compound metabolic process	BP	1	NR1H4,NR4A2,ARHGEF2,NEO1	up_VPUL_EC
GO:1901988	0.948	0.135	3	63	negative regulation of cell cycle phase transition	BP	1	NACC2,CDKN1A,FAM107A	up_ACOR_VSMC
GO:0006906	0.948	0.159	2	55	vesicle fusion	BP	1	STXBP6,CORO1A	down_ACOR_VSMC
GO:0048592	0.948	0.158	2	53	eye morphogenesis	BP	1	PHACTR4,HMGN1	down_ACOR_VSMC
GO:0051179	0.948	0.17	2	1747	localization	BP	1	ENSCAFG00000005494,GPR155	up_AORT_EC
GO:0009411	0.948	0.157	2	56	response to UV	BP	1	MAPK13,USP28	up_VCAV_EC
GO:0030534	0.948	0.213	1	33	adult behavior	BP	1	ARCN1	down_ACOR_VSMC
GO:0006810	0.948	0.223	1	1244	transport	BP	1	ANKRD50	down_AFEM_EC
GO:0061005	0.948	0.213	1	28	cell differentiation involved in kidney	BP	1	BMP4	up_ACOR_VSMC
GO:0010556	0.948	0.222	1	1137	regulation of macromolecule	BP	1	HOXA9	up_AORT_EC
GO:0009991	0.948744902	0.20687	1	110	response to extracellular stimulus	BP	1	PCSK1N	up_ACOR_EC

GO:0044237	0.949	0.0626	192	3491	cellular metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,ENSCAFG00000009211,MEIS2,SGK1,ERO1A,HSP90B1,ENPP1,ERRFI1,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,ENSCAFG00000028814,TRIB3,PGAM1,ENSCAFG00000007260,PUM3,UGCG,PM20D2,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,ENSCAFG00000008716,HIF1A,NDUFA4L2,DYNLL1,FOXP4,SLC45A3,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,AK5,GTF2H1,ARMCX3,CUL2,SH3GLB1,HTT,REST,ABHD5,RBBP8,ZMYND8,MAPK10,E	down_VSAP_EC
GO:0034645	0.949	0.0655	80	1546	cellular macromolecule biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,AARS,ENSCAFG00000032470,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,CHSY1,HIF1A,FOXP4,MRPL1,IWS1,GALNT1,ZPR1,PTPN2,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,PPP1R3C,PLOD3,KLF5,STRAP,DDIT3,BACH1,STT3A,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,NR4A2,EXT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,RPN1,KDM3A	down_VSAP_EC
GO:0046903	0.949	0.0975	8	255	secretion	BP	1	GPAM,SDC4,PARK7,CYBA,MAVS,RAB31,PCSK6,RAC2	down_VCAV_EC
GO:0065004	0.949	0.12	4	81	protein-DNA complex assembly	BP	1	ATRX,TSPYL5,SHPRH,DMC1	up_ACOR_VSMC
GO:0090092	0.949	0.132	3	72	regulation of transmembrane receptor protein serine/threonine	BP	1	SLC29A1,CAV1,GREM1	down_ACOR_VSMC
GO:0007163	0.949	0.134	3	60	establishment or maintenance of cell	BP	1	FERMT1,SPINT2,JAM3	up_ACOR_VSMC
GO:0019941	0.949	0.132	3	258	modification-dependent protein catabolic process	BP	1	CLEC16A,CYLD,RNF181	up_AFEM_EC
GO:0042594	0.949	0.133	3	64	response to starvation	BP	1	SESN1,MAP3K5,NPRL3	up_VSAP_EC
GO:1902107	0.949	0.155	2	47	positive regulation of leukocyte differentiation	BP	1	CD83,CLSTN1	up_ACOR_VSMC
GO:0010498	0.949	0.153	2	194	proteasomal protein catabolic process	BP	1	CLEC16A,RNF181	up_AFEM_EC
GO:0000422	0.949	0.211	1	34	autophagy of mitochondrion	BP	1	SREBF1	down_ACOR_VSMC
GO:0006612	0.949	0.211	1	35	protein targeting to membrane	BP	1	TRAM1	down_ACOR_VSMC
GO:0061726	0.949	0.211	1	34	mitochondrion disassembly	BP	1	SREBF1	down_ACOR_VSMC
GO:0034654	0.949	0.22	1	1236	nucleobase-containing compound biosynthetic	BP	1	GABPA	down_AFEM_EC
GO:0006323	0.949	0.209	1	58	DNA packaging	BP	1	CABIN1	down_VCAV_EC
GO:0019219	0.949	0.216	1	1151	regulation of nucleobase-containing compound metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0006022	0.949	0.212	1	29	aminoglycan metabolic process	BP	1	CHST7	up_VSAP_EC
GO:0019079	0.949	0.21	1	29	viral genome replication	BP	1	MAVS	up_VSAP_EC
GO:2001021	0.949	0.211	1	30	negative regulation of response to DNA damage	BP	1	ACKR3	up_VSAP_EC
GO:0140014	0.949360271	0.20503	1	110	mitotic nuclear division	BP	1	CHMP4B	up_ACOR_EC

GO:0032989	0.95	0.0791	18	292	cellular component morphogenesis	BP	1	FLNB,FMNL3,SLC29A1,B3GNT2,CFAP298,STMN1,GREM1,RAC1,IQGAP1,CDC42EP4,EZR,CORO1A,ENSCAFG00000010224,RADIL,ARHGEF2,TBCC,SIX4,ANXA7	down_ACOR_VSMC
GO:0044262	0.95	0.118	4	89	cellular carbohydrate metabolic process	BP	1	B3GNT2,B4GALT1,PGD,GK5	down_ACOR_VSMC
GO:0009161	0.95	0.117	4	103	ribonucleoside monophosphate	BP	1	ADSS,ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0044271	0.95	0.137	3	1501	cellular nitrogen compound biosynthetic	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0048738	0.95	0.132	3	64	cardiac muscle tissue development	BP	1	DLL1,SAV1,NPRL3	up_VSAP_EC
GO:1903008	0.95	0.154	2	47	organelle disassembly	BP	1	GABARAPL1,KIF9	up_ACOR_VSMC
GO:0000226	0.95	0.15	2	197	microtubule cytoskeleton organization	BP	1	CYLD,DNAL1	up_AFEM_EC
GO:0036503	0.95	0.153	2	47	ERAD pathway	BP	1	FOXRED2,UBQLN2	up_VSAP_EC
GO:0042177	0.95	0.153	2	47	negative regulation of protein catabolic process	BP	1	AZIN2,TIMP2	up_VSAP_EC
GO:0051092	0.95	0.153	2	47	positive regulation of NF-kappaB transcription	BP	1	RBCK1,MYD88	up_VSAP_EC
GO:0071248	0.95	0.206	1	35	cellular response to metal ion	BP	1	IQGAP1	down_ACOR_VSMC
GO:0090305	0.95	0.205	1	49	nucleic acid phosphodiester bond	BP	1	MRPL1	down_VSAP_EC
GO:0006950	0.95	0.212	1	1102	response to stress	BP	1	EYA1	up_VFEM_VSMC
GO:0044085	0.95	0.213	1	1076	cellular component biogenesis	BP	1	FBP1	up_VFEM_VSMC
GO:0000018	0.95	0.208	1	31	regulation of DNA recombination	BP	1	STAT6	up_VSAP_EC
GO:0006354	0.95	0.209	1	30	DNA-templated transcription, elongation	BP	1	CDK9	up_VSAP_EC
GO:0010720	0.950649939	0.20113	1	110	positive regulation of cell development	BP	1	NRP1	up_ACOR_EC
GO:0034645	0.951	0.0601	132	1546	cellular macromolecule biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,GALNT15,WARS2,VDR,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,DDR2,ICE1,ZFP36L1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,FKRP,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,TRERF1,GALNT11,E2F4,NPAS2,ZDHHC8,FARS2,LCAT,LIMD1,UBA52,RPUSD4,RPL15,CDK9,NR2F6,PRMT2,KDM2B,EIF3G,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,COA1,PPP3CB,NCK1,ZNF444,MRPL4,MAVS,CHST7,HMOX1,ZNF662,LARS2,CITED2,B3GALT4,CXXC1,LBH,KEAP1,ZNF772,SOAT1	up_VSAP_EC
GO:2000113	0.951	0.0711	29	387	negative regulation of cellular macromolecule biosynthetic process	BP	1	LEP,NACC2,ITM2C,BMP4,FGFR2,ATRX,TRPS1,ZNF174,ANKRD1,DAPK1,ENSCAFG00000006238,CLSTN1,TBX20,PARP9,PSEN1,MXI1,NR3C1,WWC2,DUSP22,EDN1,DUSP26,CBX7,KLF11,INPP5K,WFS1,ENSCAFG00000029553,ID3,HMBOX1,RREB1	up_ACOR_VSMC
GO:0010498	0.951	0.0894	10	194	proteasomal protein catabolic process	BP	1	WWP1,PSME4,PELI1,ENC1,PMAIP1,USP13,C7H18orf25,CUL4A,TNFAIP1,PSMD12	up_VCAV_EC
GO:1905114	0.951	0.0942	8	150	cell surface receptor signaling pathway involved in cell-cell	BP	1	SDC1,CTDNEP1,CAV1,GREM1,ASPM,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0032940	0.951	0.0971	7	231	secretion by cell	BP	1	GPAM,SDC4,PARK7,MAVS,RAB31,PCSK6,RAC2	down_VCAV_EC
GO:0006486	0.951	0.107	5	91	protein glycosylation	BP	1	GALNT15,LMF1,FKRP,GALNT11,B3GALT4	up_VSAP_EC
GO:0043413	0.951	0.107	5	91	macromolecule glycosylation	BP	1	GALNT15,LMF1,FKRP,GALNT11,B3GALT4	up_VSAP_EC
GO:0050789	0.951	0.137	4	3295	regulation of biological process	BP	1	CST3,HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0006402	0.951	0.116	4	77	mRNA catabolic process	BP	1	PNRC1,DCP1B,CNOT4,CTIF	up_ACOR_VSMC

GO:0016049	0.951	0.127	3	124	cell growth	BP	1	NDN,IGFBP6,TRPV2	down_VCAV_EC
GO:1903311	0.951	0.128	3	72	regulation of mRNA metabolic process	BP	1	IWS1,CNOT7,WTAP	up_VCAV_EC
GO:0007088	0.951	0.128	3	64	regulation of mitotic nuclear division	BP	1	CEP85,FBXW5,CDC26	up_VSAP_EC
GO:0007611	0.951	0.15	2	54	learning or memory	BP	1	HMGCR,AAAS	down_ACOR_VSMC
GO:0002793	0.951	0.149	2	54	positive regulation of peptide secretion	BP	1	HMGB1,EZR	down_ACOR_VSMC
GO:0050714	0.951	0.149	2	54	positive regulation of protein secretion	BP	1	HMGB1,EZR	down_ACOR_VSMC
GO:0090174	0.951	0.151	2	56	organelle membrane fusion	BP	1	STXBP6,CORO1A	down_ACOR_VSMC
GO:0051053	0.951	0.15	2	45	negative regulation of DNA metabolic process	BP	1	TP53BP1,ANKRD1	up_ACOR_VSMC
GO:0060255	0.951	0.161	2	1782	regulation of macromolecule metabolic	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0090150	0.951	0.149	2	64	establishment of protein localization to membrane	BP	1	RAB11A,SH3GLB1	up_VCAV_EC
GO:0000077	0.951	0.201	1	60	DNA damage checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:2001236	0.951	0.201	1	59	regulation of extrinsic apoptotic signaling	BP	1	PARK7	down_VCAV_EC
GO:0042157	0.951	0.202	1	51	lipoprotein metabolic process	BP	1	APOE	down_VSAP_EC
GO:0048524	0.951	0.204	1	30	positive regulation of viral process	BP	1	PC	up_VSAP_EC
GO:0050794	0.952	0.0605	139	3075	regulation of cellular process	BP	1	CST3,GPAM,NOTCH2,PDGFRB,SLC35F6,KIRREL1,SMAD9,ITGB5,LRP1,DCN,NAB2,NDN,ANGPT1,PRNP,LUM,SDC4,VASN,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,SH3BP1,BMPR1A,NABP2,LMO4,EVC,RECK,IGFBP6,TRPV2,CLIP3,NUMBL,ARHGEF25,RHOD,OSMR,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,AKT2,DOCK10,PSMF1,LCAT,SAMD4B,EEF2K,TFE3,NR3C1,SYDE1,HR,PDIA4,LAMA3,CLSTN1,PLCL1,CSPG4,PRMT6,ENSCAFG00000013404,TMEM161A,RASSF8,CXXC5,SEMA3C,ASPN,POLDIP2,LRPAP1,GNAZ,EIF3K,THY1,NECAB3,TEAD1,ARHGAP10,TLX2,CC2D1A,ATP6V0C,B4GALT1,GLI3,PARK7,ZMAT3,ADAMTSL4,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,CLEC16A,BPI,CYBA,ENSCAFG00000018194,RBM38,ARL2BP,IFT57,MAVS,CDH2,LOXL3,ORMDL3,GSDME,LSM10,CAMK2D,FUT8,NCLN,ENSCAFG00000017708,SPRED1,MGARP,ACTR3B,RAB7B,A2M,SPNS1,IRX5,TSC22D3,UST,MAPRE3,GLIS2,TWIST2,ARHGAP1,PRKCSH,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,PLEKHH2,NPHP4,EVI5L,LONP2,RAC2,NAPEPLD,GLS2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,ANKRD54,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:1901576	0.952	0.0605	98	1877	organic substance biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,ASNS,CARS,PLOD2,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,ENSCAFG00000032470,TRIB3,PGAM1,PUM3,UGCG,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,CHSY1,HIF1A,FOXP4,SLC45A3,MRPL1,IWS1,NMNAT2,GALNT1,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,ENSCAFG00000002015,APOE,WWC3,PPP1R3C,PLOD3,KLF5,STRAP,DDIT3,BACH1,STT3A,EIF5,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,SH3GLB1,REST,ZMYND8,EIF2S1,PRMT1,NR4A2,EXT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,BCAT1,RPN1,KDM3A,CMPK1	down_VSAP_EC

GO:0044260	0.952	0.067	52	2593	cellular macromolecule metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,MLLT11,LMCD1,THRB,HCK,TMEM100,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,RNF181	up_AFEM_EC
GO:0043632	0.952	0.0789	15	262	modification-dependent macromolecule catabolic process	BP	1	TNFAIP3,WWP1,USP33,PELI1,USP28,USP13,USP38,USP37,C7H18orf25,CUL4A,UBE2D1,RBBP6,TNFAIP1,PSMD12,ITCH	up_VCAV_EC
GO:0043933	0.952	0.0856	11	698	protein-containing complex subunit organization	BP	1	KCNC4,CRYAB,KCND1,PLAGL2,GREM1,CLEC16A,CYLD,DNAL1,ACACB,CDC42EP5,KANK1	up_AFEM_EC
GO:0044270	0.952	0.0904	9	147	cellular nitrogen compound catabolic	BP	1	PNRC1,PDE5A,ENPP4,DCP1B,ALDOC,ENTPD3,DDIT4,CNOT4,CTIF	up_ACOR_VSMC
GO:0046700	0.952	0.0897	9	147	heterocycle catabolic process	BP	1	PNRC1,PDE5A,ENPP4,DCP1B,ALDOC,ENTPD3,DDIT4,CNOT4,CTIF	up_ACOR_VSMC
GO:0007088	0.952	0.126	3	64	regulation of mitotic nuclear division	BP	1	BMP4,ATRX,EDN1	up_ACOR_VSMC
GO:0043632	0.952	0.124	3	262	modification-dependent macromolecule catabolic	BP	1	CLEC16A,CYLD,RNF181	up_AFEM_EC
GO:0007626	0.952	0.148	2	53	locomotory behavior	BP	1	NAV2,ARCN1	down_ACOR_VSMC
GO:0006302	0.952	0.146	2	97	double-strand break repair	BP	1	NABP2,FBH1	down_VCAV_EC
GO:0010976	0.952	0.148	2	47	positive regulation of neuron projection	BP	1	NRP1,PSEN1	up_ACOR_VSMC
GO:0031323	0.952	0.157	2	1788	regulation of cellular metabolic process	BP	1	HOXA9,TAOK1	up_AORT_EC
GO:0051234	0.952	0.154	2	1283	establishment of localization	BP	1	HOXA3,NR1H4	up_VPUL_EC
GO:0016052	0.952	0.201	1	34	carbohydrate catabolic process	BP	1	GALE	down_ACOR_VSMC
GO:0018130	0.952	0.21	1	1261	heterocycle biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0019438	0.952	0.211	1	1258	aromatic compound biosynthetic process	BP	1	GABPA	down_AFEM_EC
GO:0006333	0.952	0.197	1	59	chromatin assembly or disassembly	BP	1	CABIN1	down_VCAV_EC
GO:0046328	0.952	0.197	1	61	regulation of JNK cascade	BP	1	SASH1	down_VCAV_EC
GO:0006638	0.952	0.2	1	30	neutral lipid metabolic process	BP	1	LMF1	up_ACOR_VSMC
GO:0006639	0.952	0.2	1	30	acylglycerol metabolic process	BP	1	LMF1	up_ACOR_VSMC
GO:0006418	0.952	0.201	1	31	tRNA aminoacylation for protein translation	BP	1	TARSL2	up_VCAV_EC
GO:0030490	0.952	0.201	1	35	maturation of SSU-rRNA	BP	1	RIOK3	up_VCAV_EC
GO:0031397	0.952	0.201	1	30	negative regulation of protein ubiquitination	BP	1	ABL1	up_VSAP_EC
GO:0060048	0.952	0.2	1	30	cardiac muscle contraction	BP	1	KCNE3	up_VSAP_EC
GO:0010833	0.952	0.202	1	30	telomere maintenance via telomere lengthening	BP	1	FBXO4	up_VSAP_EC
GO:0014033	0.952	0.2	1	30	neural crest cell differentiation	BP	1	CITED2	up_VSAP_EC
GO:0044774	0.952	0.203	1	30	mitotic DNA integrity checkpoint	BP	1	CRADD	up_VSAP_EC
GO:1901566	0.952664049	0.086	10	598	organonitrogen compound biosynthetic	BP	1	NMNAT2,GALNT5,PORCN,B3GNT7,KLHL25,GUCY1B1,PIGS,ALDOC,AZIN2,PRKCD	up_ACOR_EC
GO:1901575	0.953	0.0651	42	643	organic substance catabolic process	BP	1	PLK2,CDA,TNFAIP3,CTSC,TIPARP,WWP1,LYVE1,USP33,PIPOX,PSME4,PELI1,ODC1,CASP8,TENT2,CNOT6,ENC1,GALE,ENSCAFG00000024323,PLCG2,PAN3,USP28,CNOT7,SMG7,LIPA,PMAIP1,RIPK1,USP13,USP38,IMPA1,USP37,BLVRA,C7H18orf25,CUL4A,UBE2D1,HIF1A,RBBP6,DCP2,TNFAIP1,PSMB9,PSMD12,TET2,ITCH	up_VCAV_EC
GO:0051049	0.953	0.0679	31	479	regulation of transport	BP	1	ACSL3,HMGB1,SREBF1,STXBP6,SREBF2,NEDD4,HOXA3,SLC25A5,SDC1,ARFGAP1,RAN,PRELID1,BIRC5,INSIG1,CAV1,SLC30A1,GREM1,CLIC1,PLK3,ARG2,NKAIN1,PREB,HIST1H1A,GSTO1,DMAP1,ENSCAFG00000005299,EZR,RBM14,CORO1A,REM1,NUS1	down_ACOR_VSMC

GO:0043085	0.953	0.0714	23	323	positive regulation of catalytic activity	BP	1	MAP3K14,ARHGEF5,PPARGC1B,TBC1D10C,CRADD,TBC1D2B,ABL1,EMP2,MAP3K5,PDGFD,C1QTNF2,CAMKK2,AMBRA1,F2RL1,LMF1,DDR2,TRAF7,TIAM1,MYC,SASH1,HTRA2,MAP2K2,TGFBR2	up_VSAP_EC
GO:0006629	0.953	0.0771	16	382	lipid metabolic process	BP	1	NR1H4,PTPN11,TRIB3,UGCG,SESN2,PTGS2,SEL1L,SLC45A3,PLCL1,APOE,LYN,SH3GLB1,REST,ABHD5,RDH11,YWHAH	down_VSAP_EC
GO:0060322	0.953	0.0834	11	193	head development	BP	1	NF2,PFAS,MMP14,EZH2,SMG9,WDR62,ARCN1,SGPL1,ASPM,ENSCAFG00000010224,GLI1	down_ACOR_VSMC
GO:0044770	0.953	0.0862	10	161	cell cycle phase transition	BP	1	CDC7,SKP2,NACC2,LATS2,CDKN2B,CDKN1A,CRLF3,APP,FAM107A,KLF11	up_ACOR_VSMC
GO:0043086	0.953	0.0871	9	170	negative regulation of catalytic activity	BP	1	HMGCR,BIRC5,CAV1,NF2,CDKN2C,DHCR24,NUP62,ENSCAFG00000005299,KNL1	down_ACOR_VSMC
GO:0016049	0.953	0.0979	6	124	cell growth	BP	1	IFRD1,CDA,EDN1,RAB11A,MTOR,SMARCA4	up_VCAV_EC
GO:0009123	0.953	0.112	4	104	nucleoside monophosphate	BP	1	ADSS,ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0007600	0.953	0.125	3	73	sensory perception	BP	1	B3GNT2,NAV2,NOB1	down_ACOR_VSMC
GO:0051650	0.953	0.124	3	65	establishment of vesicle localization	BP	1	RAB11B,STX4,CEP19	up_VSAP_EC
GO:0007034	0.953	0.145	2	55	vacuolar transport	BP	1	NEDD4,TRAK1	down_ACOR_VSMC
GO:0006888	0.953	0.147	2	49	ER to Golgi vesicle-mediated transport	BP	1	SEC24B,LMF1	up_ACOR_VSMC
GO:0005976	0.953	0.198	1	34	polysaccharide metabolic process	BP	1	B3GNT2	down_ACOR_VSMC
GO:0035195	0.953	0.199	1	28	gene silencing by miRNA	BP	1	BMP4	up_ACOR_VSMC
GO:0033044	0.953	0.193	1	127	regulation of chromosome organization	BP	1	AXIN2	up_AFEM_EC
GO:0031326	0.953	0.204	1	1176	regulation of cellular biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0018193	0.953	0.194	1	368	peptidyl-amino acid modification	BP	1	ARHGEF2	up_VPOR_EC
GO:0007166	0.953	0.199	1	686	cell surface receptor signaling pathway	BP	1	EYA1	up_VFEM_EC
GO:0051962	0.953981788	0.19088	1	112	positive regulation of nervous system	BP	1	NRP1	up_ACOR_EC
GO:0051128	0.954	0.061	63	790	regulation of cellular component organization	BP	1	FZD1,WNT11,HNF4A,FAM107A,ARHGEF5,AXIN2,WASF3,AMIGO1,ENPP2,LRRN3,TBC1D10C,CEP85,DDHD1,SLIT2,TBC1D2B,ABL1,DLL1,CDC42EP5,FUZ,PLXNA4,CDC42EP2,F2RL1,DDR2,MFN2,ICE1,PIK3R1,MYC,SHOX2,RTN4RL1,FBXO4,LRP4,DPYSL2,PHF1,FBXW5,FBXO7,WISP2,LCAT,LIMD1,CDK9,KDM2B,FBLN1,PIP4K2B,IGFBP6,RAF1,CYBA,ZNF205,PQBP1,TTL,VPS11,SMARCA2,ACVRL1,UBQLN2,CDC26,HTRA2,FLOT1,PPP3CB,NCK1,MAVS,ULK1,MAP2K2,NPRL3,BAG4,JCHAIN	up_VSAP_EC
GO:0051640	0.954	0.0822	11	174	organelle localization	BP	1	RHOT1,FBXL20,STX11,POLR2M,PSEN1,RAB11B,SUN1,PREPL,WASL,DYNC1I1,BVES	up_ACOR_VSMC
GO:0009100	0.954	0.092	7	139	glycoprotein metabolic process	BP	1	MPDU1,SLC35C2,B3GNT2,XYLT1,B4GALT1,NUS1,NECAB3	down_ACOR_VSMC
GO:0016055	0.954	0.0915	7	134	Wnt signaling pathway	BP	1	FERMT1,RAPGEF1,GATA3,BMP2,HHEX,MCC,SMARCA4	up_VCAV_EC
GO:0198738	0.954	0.0915	7	134	cell-cell signaling by wnt	BP	1	FERMT1,RAPGEF1,GATA3,BMP2,HHEX,MCC,SMARCA4	up_VCAV_EC
GO:0022604	0.954	0.0961	6	122	regulation of cell morphogenesis	BP	1	FMNL3,RAC1,CDC42EP4,EZR,CORO1A,ANXA7	down_ACOR_VSMC
GO:0034641	0.954	0.111	5	2171	cellular nitrogen compound metabolic	BP	1	NR1H4,PCSK1N,NPNT,HOXA1,ENSCAFG00000028814	up_APUL_EC
GO:0006605	0.954	0.11	4	99	protein targeting	BP	1	RAB27A,AKAP12,PAN3,GCC2	up_VCAV_EC
GO:0051402	0.954	0.123	3	64	neuron apoptotic process	BP	1	THRB,AMBRA1,KDM2B	up_VSAP_EC
GO:0033002	0.954	0.144	2	55	muscle cell proliferation	BP	1	PPARD,GLI1	down_ACOR_VSMC
GO:0031123	0.954	0.144	2	48	RNA 3'-end processing	BP	1	CCNT1,APP	up_ACOR_VSMC
GO:0007030	0.954	0.144	2	49	Golgi organization	BP	1	RAB30,ATP8B2	up_VSAP_EC
GO:0031056	0.954	0.144	2	50	regulation of histone modification	BP	1	PHF1,CDK9	up_VSAP_EC
GO:0034440	0.954	0.195	1	35	lipid oxidation	BP	1	PPARD	down_ACOR_VSMC
GO:0045778	0.954	0.194	1	35	positive regulation of ossification	BP	1	FBXO5	down_ACOR_VSMC

GO:0031570	0.954	0.193	1	61	DNA integrity checkpoint	BP	1	BRSK1	down_VCAV_EC
GO:0007059	0.954	0.192	1	127	chromosome segregation	BP	1	AXIN2	up_AFEM_EC
GO:0006396	0.954	0.192	1	368	RNA processing	BP	1	RRP15	up_VPOR_EC
GO:0048024	0.954	0.196	1	30	regulation of mRNA splicing, via spliceosome	BP	1	NUP98	up_VSAP_EC
GO:0055007	0.954	0.195	1	31	cardiac muscle cell differentiation	BP	1	DLL1	up_VSAP_EC
GO:0098657	0.954288	0.14017	2	181	import into cell	BP	1	CALY,SLC9A9	up_ACOR_EC
GO:0051240	0.955	0.0647	32	489	positive regulation of multicellular organismal process	BP	1	HMGB1,IRAK1,MTDH,SRRT,FBXO5,PRMT1,CAV1,MMP14,EZH2,GREM1,ADIPOR2,DHX33,PDCD2,HOXB7,B4GALT1,TFRC,FAM49B,HMGB2,EZR,TOX,ELOVL6,BEND6,POLR3F,CDC20,ASPM,CTH,ARHGEF2,GLI1,NUS1,AMOTL1,SIX4,TPBG	down_ACOR_VSMC
GO:0009259	0.955	0.0816	10	166	ribonucleotide metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:1901566	0.955	0.0839	9	598	organonitrogen compound biosynthetic	BP	1	PRR16,XYLT1,GPAM,MOXD1,ACACB,PPARGC1A,CSGALNACT2,CTIF,SAMD4B	up_AFEM_EC
GO:1901990	0.955	0.1	5	94	regulation of mitotic cell cycle phase transition	BP	1	CDC7,NACC2,CDKN1A,APP,FAM107A	up_ACOR_VSMC
GO:0060047	0.955	0.14	2	57	heart contraction	BP	1	SREBF1,CAV1	down_ACOR_VSMC
GO:0016032	0.955	0.138	2	94	viral process	BP	1	TRIM8,MAVS	down_VCAV_EC
GO:0002460	0.955	0.188	1	61	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	BP	1	LOXL3	down_VCAV_EC
GO:0007219	0.955	0.189	1	59	Notch signaling pathway	BP	1	NOTCH2	down_VCAV_EC
GO:0010212	0.955	0.19	1	60	response to ionizing radiation	BP	1	NABP2	down_VCAV_EC
GO:0031032	0.955	0.19	1	61	actomyosin structure organization	BP	1	ENSCAFG00000014978	down_VCAV_EC
GO:2001252	0.955	0.187	1	61	positive regulation of chromosome organization	BP	1	NABP2	down_VCAV_EC
GO:0034502	0.955	0.191	1	30	protein localization to chromosome	BP	1	ATRX	up_ACOR_VSMC
GO:0044774	0.955	0.193	1	30	mitotic DNA integrity checkpoint	BP	1	CDKN1A	up_ACOR_VSMC
GO:1903725	0.955	0.192	1	30	regulation of phospholipid metabolic process	BP	1	HTR2B	up_ACOR_VSMC
GO:0009889	0.955	0.197	1	1190	regulation of biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0072521	0.955118987	0.1381	2	185	purine-containing compound metabolic	BP	1	GUCY1B1,ALDOC	up_ACOR_EC
GO:0048193	0.955366691	0.18649	1	116	Golgi vesicle transport	BP	1	PREB	up_ACOR_EC
GO:0051726	0.955569761	0.0932	6	393	regulation of cell cycle	BP	1	BRSK1,SOX9,PAK3,FIGNL1,CHMP4B,CCNYL1	up_ACOR_EC
GO:0032386	0.956	0.0865	8	137	regulation of intracellular transport	BP	1	CDH1,RAB11B,ICE1,PIK3R1,GAS1,KCNB1,MAVS,BAG4	up_VSAP_EC
GO:0072657	0.956	0.0882	7	144	protein localization to membrane	BP	1	ACSL3,CAV1,MMP14,TRAM1,EMP2,SAMM50,EZR	down_ACOR_VSMC
GO:0022613	0.956	0.0929	6	208	ribonucleoprotein complex biogenesis	BP	1	RPS10,EIF3K,RPL27,MRPS11,RPS27,RPLP0	down_VCAV_EC
GO:0016053	0.956	0.098	5	97	organic acid biosynthetic process	BP	1	EDN1,ALDOC,DDIT4,PARK7,ELOVL7	up_ACOR_VSMC
GO:0046394	0.956	0.098	5	97	carboxylic acid biosynthetic process	BP	1	EDN1,ALDOC,DDIT4,PARK7,ELOVL7	up_ACOR_VSMC
GO:0080134	0.956	0.0972	5	386	regulation of response to stress	BP	1	LEP,CYLD,AXIN2,NAPEPLD,KANK1	up_AFEM_EC
GO:0007059	0.956	0.104	4	127	chromosome segregation	BP	1	NAA10,CTNNB1,KPNB1,PDS5B	down_VSAP_EC
GO:0090150	0.956	0.118	3	64	establishment of protein localization to membrane	BP	1	RILPL2,RAB11B,KCNB1	up_VSAP_EC
GO:0035265	0.956	0.137	2	54	organ growth	BP	1	POC1A,GLI1	down_ACOR_VSMC
GO:0006650	0.956	0.138	2	78	glycerophospholipid metabolic process	BP	1	NR1H4,SH3GLB1	down_VSAP_EC
GO:0034968	0.956	0.187	1	34	histone lysine methylation	BP	1	EZH2	down_ACOR_VSMC
GO:1901362	0.956	0.197	1	1293	organic cyclic compound biosynthetic process	BP	1	GABPA	down_AFEM_EC

GO:0007062	0.956	0.189	1	29	sister chromatid cohesion	BP	1	ATRX	up_ACOR_VSMC
GO:0006875	0.956	0.183	1	129	cellular metal ion homeostasis	BP	1	DMPK	up_AFEM_EC
GO:0006289	0.956	0.188	1	35	nucleotide-excision repair	BP	1	CUL4A	up_VCAV_EC
GO:0030307	0.956	0.189	1	31	positive regulation of cell growth	BP	1	KDM2B	up_VSAP_EC
GO:0009059	0.957	0.0534	133	1563	macromolecule biosynthetic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,ARHGEF5,OSR2,INSIG2,ZNF367,PPARGC1B,MRPL37,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,GALNT15,WARS2,VDR,SAV1,KLF15,C1QTNF2,ANXA4,ZNF688,ZBTB16,RARG,CBX7,STAT5A,STAT6,GATAD1,PLPP3,ENSCAFG00000000071,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,DDR2,ICE1,ZFP36L1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,FKRP,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,TRERF1,GALNT11,E2F4,NPAS2,ZDHHC8,FARS2,LCAT,LIMD1,UBA52,RPUSD4,RPL15,CDK9,NR2F6,PRMT2,KDM2B,EIF3G,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,COA1,PPP3CB,NCK1,ZNF444,MRPL4,MAVS,CHST7,HMOX1,ZNF662,LARS2,CITED2,B3GALT4,CXXC1,LBH,KEAP1,ZNF772,SOAT1	up_VSAP_EC
GO:0046907	0.957	0.0615	35	536	intracellular transport	BP	1	SREBF1,DDX39A,NEDD4,ZW10,TIMM44,POLA2,HSPA9,RAN,HM13,INSIG1,RANBP1,AAAS,PLK3,ENSCAFG00000011598,PREB,TRAM1,IPO4,YWHAB,NUP62,EMP2,NUP188,TOMM34,SAMM50,TRAK1,DMAP1,DDX39B,SNX15,RAB35,EZR,RBM14,CORO1A,CYC1,TRAPPC6A,PMPCA,NUS1	down_ACOR_VSMC
GO:0071495	0.957	0.0656	23	365	cellular response to endogenous stimulus	BP	1	SREBF1,TFPI,SMC1A,NEDD4,SLC29A1,CAV1,RAD51,TIMELESS,THRAP3,EZH2,GREM1,ADIPOR2,CDK4,SMARCC1,PRCP,NCL,PDXP,IQGAP1,FGF5,EZR,CORO1A,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0033365	0.957	0.0685	19	276	protein localization to organelle	BP	1	PEX7,CDH1,PEX2,VPS36,GLIS2,MORC3,MFN2,PIK3R1,CIZ1,FBXO4,NUP98,FBXO7,LONP2,SNUPN,TAF8,PEX6,MAVS,BAG4,NCOA4	up_VSAP_EC
GO:0044238	0.957	0.0982	8	3383	primary metabolic process	BP	1	NR1H4,STK32B,NR4A2,CCL24,PTGER2,FLRT3,ARHGEF2,NEO1	up_VPUL_EC
GO:0055074	0.957	0.0976	5	95	calcium ion homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:0051604	0.957	0.104	4	102	protein maturation	BP	1	KLKB1,TSPAN15,CASP8,TSPAN14	up_VCAV_EC
GO:0032886	0.957	0.105	4	81	regulation of microtubule-based process	BP	1	FAM107A,CEP85,ABL1,FBXW5	up_VSAP_EC
GO:0009306	0.957	0.114	3	127	protein secretion	BP	1	GPAM,PARK7,MAVS	down_VCAV_EC
GO:0006402	0.957	0.136	2	77	mRNA catabolic process	BP	1	SMG7,CNOT7	down_VSAP_EC
GO:0008033	0.957	0.136	2	52	tRNA processing	BP	1	TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0035150	0.957	0.184	1	36	regulation of tube size	BP	1	CAV1	down_ACOR_VSMC
GO:0050880	0.957	0.184	1	36	regulation of blood vessel size	BP	1	CAV1	down_ACOR_VSMC
GO:1903364	0.957	0.183	1	61	positive regulation of cellular protein catabolic	BP	1	LRP1	down_VCAV_EC
GO:0030183	0.957	0.187	1	30	B cell differentiation	BP	1	PLCG2	up_ACOR_VSMC
GO:0043280	0.957	0.187	1	33	positive regulation of cysteine-type endopeptidase activity	BP	1	DAPK1	up_ACOR_VSMC
GO:1901576	0.957	0.203	1	1877	organic substance biosynthetic process	BP	1	GATA5	up_VCAV_VSMC
GO:0033036	0.957	0.187	1	852	macromolecule localization	BP	1	NR1H4	up_VPUL_EC

GO:0044237	0.958	0.05	315	3491	cellular metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,NAPEPLD,HOXA9,CDON,NECAB3,WNT11,HNF4A,ACSM3,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,RNPEP,TBC1D10C,ACAA1,MRPL37,CEP85,FOXRED2,ALDH3B1,ACACB,TPCN2,EEF2K,IL6R,IRX5,RETREG1,SLIT2,GDA,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,HDAC7,EMP2,DLL1,DLST,SESN1,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,GLUL,CTSS,GALNT15,DTX2,TENT5C,ADHFE1,ENSCAFG00000013986,PDGFD,CERS4,WARS2,VDR,DHRS4,NAA60,SAV1,KDELC2,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,ABHD15,ZNF688,ZBTB16,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,TRMT2A,VPS36,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,RECK,GATAD1,CISH,KLHL24,HSD17B8,PLPP3,ENSCAFG00000000071,SLC25A12,EXOSC7,CAMKK2,FAAH,TNKS1BP1,KLHDC8B,PYM1,AMBRA1,F2RL1,RBL2,LMF1,PHKA2,RAB11B,NFE2L2,GLIS2,DFFB,PPIP5K1,MORC3,DDR2,PDK2,MFN2,ICE1,ZFP36L1,TRAF7,HSF4,FXN,GALK1,RETSAT,PIK3R1,RBCK1,KBTBD12,ENTPD3,GAS1,BATF2,PLA2G6,NEIL2,MYC,PIK3	up_VSAP_EC
GO:0048585	0.958	0.0614	31	475	negative regulation of response to stimulus	BP	1	HMGCR,TFPI,SLC25A5,PPP1R15B,PARPBP,PRELID1,INSIG1,CAV1,NF2,MMP14,EZH2,STMN1,GREM1,ARG2,RNF152,NOC2L,YWHAB,NUP62,CACTIN,HMGB2,GSTO1,DDX39B,EZR,BEND6,PHACTR4,TXNDC12,CTH,NCOA5,ARHGEF2,GLI1,AMER1	down_ACOR_VSMC
GO:0046034	0.958	0.113	3	88	ATP metabolic process	BP	1	ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0003015	0.958	0.132	2	58	heart process	BP	1	SREBF1,CAV1	down_ACOR_VSMC
GO:0015849	0.958	0.132	2	56	organic acid transport	BP	1	ACSL3,PPARD	down_ACOR_VSMC
GO:0046942	0.958	0.132	2	56	carboxylic acid transport	BP	1	ACSL3,PPARD	down_ACOR_VSMC
GO:0071356	0.958	0.134	2	57	cellular response to tumor necrosis factor	BP	1	CACTIN,ARHGEF2	down_ACOR_VSMC
GO:0002761	0.958	0.18	1	36	regulation of myeloid leukocyte differentiation	BP	1	HOXA7	down_ACOR_VSMC
GO:0006354	0.958	0.184	1	30	DNA-templated transcription, elongation	BP	1	ELL2	up_ACOR_VSMC
GO:0006637	0.958	0.181	1	32	acyl-CoA metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0035383	0.958	0.181	1	32	thioester metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0070585	0.958	0.182	1	34	protein localization to mitochondrion	BP	1	MARCH5	up_ACOR_VSMC
GO:0043039	0.958	0.181	1	33	tRNA aminoacylation	BP	1	TARSL2	up_VCAV_EC
GO:0006464	0.958	0.187	1	1162	cellular protein modification process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0036211	0.958	0.187	1	1162	protein modification process	BP	1	ANKRD6	up_VPOR_VSMC
GO:0051641	0.958	0.184	1	858	cellular localization	BP	1	NR1H4	up_VPUL_EC
GO:0008277	0.958	0.184	1	31	regulation of G protein-coupled receptor signaling	BP	1	UBQLN2	up_VSAP_EC
GO:0051726	0.959	0.0604	29	393	regulation of cell cycle	BP	1	LEP,MAP3K8,CDC7,SKP2,NACC2,BMP4,FGFR2,TP53BP1,ATRX,LATS2,CITED2,TP53INP1,PKP4,CCNG2,PTPN3,CDKN2B,CDKN1A,JMY,CRLF3,PRKCE,CCNT1,FZD3,CCPG1,APP,PIK3C3,EDN1,HPGD,FAM107A,RPRD1B	up_ACOR_VSMC
GO:0006974	0.959	0.0701	14	333	cellular response to DNA damage stimulus	BP	1	PLK3,SGK1,CBX5,PTPN11,SESN2,UBA6,DDX39B,LYN,PDS5B,BACH1,GTF2H1,RBBP8,RAD23A,CDKN1A	down_VSAP_EC
GO:0061024	0.959	0.0704	14	215	membrane organization	BP	1	TBC1D10C,TBC1D2B,EMP2,RILPL2,F2RL1,MFN2,LRP4,AZIN2,ZNF205,XKR8,STX4,VPS11,ARHGAP12,FLOT1	up_VSAP_EC
GO:2000146	0.959	0.0994	4	92	negative regulation of cell motility	BP	1	HMGB1,HOXA7,RAP2C,ENSCAFG00000010224	down_ACOR_VSMC
GO:1903076	0.959	0.179	1	32	regulation of protein localization to plasma	BP	1	AR	up_ACOR_VSMC
GO:2001021	0.959	0.178	1	30	negative regulation of response to DNA damage	BP	1	TP53BP1	up_ACOR_VSMC

GO:0006139	0.959	0.197	1	1909	nucleobase-containing compound metabolic	BP	1	GATA5	up_VCAV_VSMC
GO:0007292	0.959	0.18	1	32	female gamete generation	BP	1	HPGD	up_VSAP_EC
GO:0019933	0.959	0.18	1	32	cAMP-mediated signaling	BP	1	ADGRD1	up_VSAP_EC
GO:0050728	0.959	0.18	1	31	negative regulation of inflammatory response	BP	1	NLRX1	up_VSAP_EC
GO:0033554	0.959	0.178	1	708	cellular response to stress	BP	1	CAV1	up_VSAP_VSMC
GO:0009059	0.96	0.0517	80	1563	macromolecule biosynthetic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,AARS,ENSCAFG00000032470,PUM3,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,CHSY1,HIF1A,FOXP4,MRPL1,IWS1,GALNT1,ZPR1,PTPN2,MORF4L2,YARS,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,APOE,WWC3,PPP1R3C,PLOD3,KLF5,STRAP,DDIT3,BACH1,STT3A,EIF5,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,EIF2S1,PRMT1,NR4A2,EXT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,RPN1,KDM3A	down_VSAP_EC
GO:0009719	0.96	0.061	25	395	response to endogenous stimulus	BP	1	SREBF1,TFPI,SREBF2,SMC1A,NEDD4,SLC29A1,CAV1,RAD51,TIMELESS,THRAP3,EZH2,GREM1,ADIPOR2,CDK4,SMARCC1,PRCP,NCL,PDXP,IQGAP1,HMGB2,FGF5,EZR,CORO1A,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0010564	0.96	0.0681	14	217	regulation of cell cycle process	BP	1	FAM107A,AXIN2,CEP85,CRADD,ZFP36L1,CDC25B,FBXW5,FBXO7,CDK9,ZFP36L2,TTL,TPRA1,CDC26,LSM10	up_VSAP_EC
GO:0030003	0.96	0.0794	8	157	cellular cation homeostasis	BP	1	HMGB1,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0055114	0.96	0.0814	7	157	oxidation-reduction process	BP	1	PCDH12,ADGRF5,MTOR,APOD,SLC25A25,PPP1CB,HIF1A	up_VCAV_EC
GO:0006417	0.96	0.0854	6	109	regulation of translation	BP	1	FAM129A,DAPK1,RBM4B,APP,CTIF,NGRN	up_ACOR_VSMC
GO:0008152	0.96	0.104	6	3714	metabolic process	BP	1	HOXA3,BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0007017	0.96	0.107	3	273	microtubule-based process	BP	1	CYLD,DNAL1,KIF1A	up_AFEM_EC
GO:0007033	0.96	0.128	2	82	vacuole organization	BP	1	HOOK3,SH3GLB1	down_VSAP_EC
GO:0099003	0.96	0.129	2	50	vesicle-mediated transport in synapse	BP	1	STX4,PPP3CB	up_VSAP_EC
GO:0042476	0.96	0.174	1	36	odontogenesis	BP	1	NF2	down_ACOR_VSMC
GO:0007266	0.96	0.173	1	64	Rho protein signal transduction	BP	1	ARHGEF25	down_VCAV_EC
GO:0042113	0.96	0.171	1	64	B cell activation	BP	1	ZFP36L1	down_VCAV_EC
GO:0030326	0.96	0.175	1	51	embryonic limb morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0035113	0.96	0.175	1	51	embryonic appendage morphogenesis	BP	1	CTNNB1	down_VSAP_EC
GO:0090257	0.96	0.174	1	52	regulation of muscle system process	BP	1	CALM1	down_VSAP_EC
GO:0006476	0.96	0.175	1	31	protein deacetylation	BP	1	PRKAA2	up_ACOR_VSMC
GO:0007498	0.96	0.176	1	38	mesoderm development	BP	1	NUP133	up_VCAV_EC
GO:1902600	0.96	0.177	1	31	proton transmembrane transport	BP	1	ENSCAFG00000013366	up_VSAP_EC
GO:1903706	0.960941217	0.16861	1	119	regulation of hemopoiesis	BP	1	CLSTN1	up_ACOR_EC
GO:0043549	0.961	0.0664	14	244	regulation of kinase activity	BP	1	IRAK1,HMGCR,SLC29A1,CAV1,NF2,CDKN2C,EZH2,MAP3K20,CKS2,RAP2C,NUP62,EMP2,CLSPN,CCNB3	down_ACOR_VSMC
GO:0009607	0.961	0.0686	13	232	response to biotic stimulus	BP	1	HMGB1,IRAK1,HNRNPUL1,SMC1A,MTDH,PPP1R15B,CAV1,STMN1,CDK4,ARG2,CACTIN,HMGB2,EXOSC5	down_ACOR_VSMC
GO:0033993	0.961	0.0727	10	186	response to lipid	BP	1	IRAK1,TFPI,NEDD4,MTDH,INSIG1,CAV1,THRAP3,CDK4,CACTIN,HMGB2	down_ACOR_VSMC
GO:0031399	0.961	0.0766	8	559	regulation of protein modification process	BP	1	LEP,GREM1,CYLD,LRRC15,DCUN1D3,AXIN2,CCL5,ADAM17	up_AFEM_EC
GO:0006605	0.961	0.0897	5	99	protein targeting	BP	1	TCAF1,SCARB2,SYNJ2BP,LAMP2,INPP5K	up_ACOR_VSMC

GO:0010948	0.961	0.0881	5	96	negative regulation of cell cycle process	BP	1	NACC2,BMP4,ATRX,CDKN1A,FAM107A	up_ACOR_VSMC
GO:0060070	0.961	0.0887	5	105	canonical Wnt signaling pathway	BP	1	FERMT1,RAPGEF1,GATA3,BMP2,MCC	up_VCAV_EC
GO:0072503	0.961	0.0885	5	97	cellular divalent inorganic cation homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:0023061	0.961	0.0952	4	95	signal release	BP	1	SREBF1,BIRC5,FAM129B,ENSCAFG00000005299	down_ACOR_VSMC
GO:0043434	0.961	0.0966	4	80	response to peptide hormone	BP	1	ACTN2,LEP,SESN3,INPP5K	up_ACOR_VSMC
GO:0042391	0.961	0.0969	4	81	regulation of membrane potential	BP	1	TPCN2,KCNE3,KCNB1,FXYD1	up_VSAP_EC
GO:1903522	0.961	0.125	2	58	regulation of blood circulation	BP	1	SREBF1,CAV1	down_ACOR_VSMC
GO:0007179	0.961	0.125	2	57	transforming growth factor beta receptor	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:0007224	0.961	0.125	2	50	smoothened signaling pathway	BP	1	BMP4,FGFR2	up_ACOR_VSMC
GO:0001894	0.961	0.126	2	49	tissue homeostasis	BP	1	CLN8,NOD2	up_ACOR_VSMC
GO:1903828	0.961	0.17	1	38	negative regulation of cellular protein	BP	1	INSIG1	down_ACOR_VSMC
GO:0016482	0.961	0.169	1	63	cytosolic transport	BP	1	RAB7B	down_VCAV_EC
GO:0048015	0.961	0.17	1	48	phosphatidylinositol-mediated signaling	BP	1	PIK3C2A	down_VSAP_EC
GO:0048017	0.961	0.17	1	48	inositol lipid-mediated signaling	BP	1	PIK3C2A	down_VSAP_EC
GO:0016441	0.961	0.173	1	30	posttranscriptional gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:0035194	0.961	0.173	1	30	posttranscriptional gene silencing by RNA	BP	1	BMP4	up_ACOR_VSMC
GO:1905477	0.961	0.173	1	32	positive regulation of protein localization to	BP	1	TCAF1	up_ACOR_VSMC
GO:0001701	0.961	0.168	1	134	in utero embryonic development	BP	1	TMEM100	up_AFEM_EC
GO:0016043	0.961	0.189	1	1973	cellular component organization	BP	1	EYA1	up_AFEM_VSMC
GO:0034654	0.961	0.178	1	1236	nucleobase-containing compound biosynthetic	BP	1	HOXA9	up_AORT_EC
GO:0008203	0.961	0.171	1	37	cholesterol metabolic process	BP	1	ABCA1	up_VCAV_EC
GO:0006464	0.961	0.179	1	1162	cellular protein modification process	BP	1	EYA1	up_VFEM_VSMC
GO:0036211	0.961	0.179	1	1162	protein modification process	BP	1	EYA1	up_VFEM_VSMC
GO:0038127	0.961	0.173	1	32	ERBB signaling pathway	BP	1	ABL1	up_VSAP_EC
GO:0010467	0.962	0.0479	129	1787	gene expression	BP	1	EDNRB,HCLS1,IL7R,KIT,PRKCH,FLI1,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,TSPAN8,RELN,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,WWP1,TLR4,NLRC5,QKI,TSPAN15,GATA3,EDN1,HOXB8,RAB27A,TCF4,SMAD1,FOXN2,MEOX1,ENSCAFG00000017103,IRF8,SOX18,PELI1,PPP3CA,YES1,CASP8,TARSL2,MTOR,TENT2,ELF4,TSPAN14,BMP2,CDYL,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,ENC1,CCAR1,MAPK13,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,PRKD2,THOC1,SMARCA4,TLR3,NCK1,TRMT9B,DPH5,TIMELESS,LDB2,CD200,JAG1,NSD1,MRRF,TOP1,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,ENSCAFG00000002897,HMGB1,AHR,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,ZNF317,USP13,ITGA6,SKIL,GPBP1,WTAP,MTA2,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,ENSCAFG00000002015,RBBP6,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGEF2,CDON,ELK3,PHF3,ZNF609	up_VCAV_EC
GO:0045595	0.962	0.0562	30	469	regulation of cell differentiation	BP	1	HMGB1,SLC29A1,SRRT,FBXO5,HSPA9,PRELID1,INSIG1,PRMT1,CAV1,NF2,MMP14,EZH2,GREM1,HMGB3,HOXA7,PDCD2,PPARD,RAC1,EMP2,HMGB2,TOX,RBM14,BEND6,ASPM,CTH,ARHGEF2,TWIST2,HOXA9,GLI1,SIX4	down_ACOR_VSMC
GO:0043066	0.962	0.063	17	253	negative regulation of apoptotic process	BP	1	WNT11,ACKR3,PTGFR,LIMS2,ABL1,DLL1,OSR1,RARG,AMBRA1,PIK3R1,MYC,KDM2B,RAF1,QARS,ARHGAP10,HMOX1,CITED2	up_VSAP_EC

GO:0055086	0.962	0.0638	15	237	nucleobase-containing small molecule metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENPP4,PTGDR,FUT8,ENSCAFG00000018611,ALDOC,ENTPD3,DDIT4,EXTL2,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0006281	0.962	0.0672	12	208	DNA repair	BP	1	PSME4,FIGNL1,MTOR,TIMELESS,ASF1A,HMGB1,BLM,SMC5,RAD21,RAD17,CUL4A,GINS4	up_VCAV_EC
GO:0016573	0.962	0.123	2	50	histone acetylation	BP	1	PHF20,MAP3K7	up_ACOR_VSMC
GO:0046879	0.962	0.165	1	63	hormone secretion	BP	1	PARK7	down_VCAV_EC
GO:0006352	0.962	0.166	1	56	DNA-templated transcription, initiation	BP	1	CTNNB1	down_VSAP_EC
GO:0043038	0.962	0.168	1	34	amino acid activation	BP	1	TARSL2	up_VCAV_EC
GO:0006725	0.962	0.184	1	1956	cellular aromatic compound metabolic	BP	1	GATA5	up_VCAV_VSMC
GO:0043933	0.962	0.169	1	698	protein-containing complex subunit	BP	1	CAV1	up_VSAP_VSMC
GO:0030097	0.962161782	0.10249	3	244	hemopoiesis	BP	1	FZD5,PTGER4,CLSTN1	up_ACOR_EC
GO:0019219	0.963	0.0494	58	1151	regulation of nucleobase-containing compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,NR1H4,PLK3,ETV6,MEIS2,CBX5,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,IWS1,ZPR1,PTPN2,MORF4L2,YES1,NEO1,PEG3,SMG7,MTDH,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,ENSCAFG00000002015,TFRC,WWC3,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,GLO1,INHBA,LRRFIP2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,KDM3A	down_VSAP_EC
GO:0006396	0.963	0.0622	15	368	RNA processing	BP	1	CELF1,AARS,MRPL1,IWS1,ZPR1,SNRPB2,PRPF3,DDX39B,PDCD11,STRAP,REST,ENSCAFG00000015065,BCAS2,RTCB,SNRPA1	down_VSAP_EC
GO:0030162	0.963	0.0646	13	202	regulation of proteolysis	BP	1	CST3,CRADD,ABTB1,MAP3K5,CCBE1,RECK,GAS1,MYC,RNF166,OSBPL7,TIMP2,UBQLN2,HTRA2	up_VSAP_EC
GO:0055082	0.963	0.0698	10	189	cellular chemical homeostasis	BP	1	HMGB1,BIRC5,CAV1,SLC30A1,TFRC,GSTO1,ENSCAFG00000005299,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0051052	0.963	0.0713	9	145	regulation of DNA metabolic process	BP	1	CDC7,TP53BP1,ATRX,PPARGC1A,ZNF365,ANKRD1,CDKN1A,PARP9,HMBOX1	up_ACOR_VSMC
GO:0034248	0.963	0.0768	7	125	regulation of cellular amide metabolic process	BP	1	FAM129A,DAPK1,RBM4B,ORMDL3,APP,CTIF,NGRN	up_ACOR_VSMC
GO:0070085	0.963	0.0858	5	95	glycosylation	BP	1	GALNT15,LMF1,FKRP,GALNT11,B3GALT4	up_VSAP_EC
GO:0033365	0.963	0.1	3	276	protein localization to organelle	BP	1	LEP,CRY2,RAB7A	up_AFEM_EC
GO:0044085	0.963	0.124	2	1076	cellular component biogenesis	BP	1	EMP1,CAV1	up_VSAP_VSMC
GO:0007368	0.963	0.163	1	37	determination of left/right symmetry	BP	1	RTTN	down_ACOR_VSMC
GO:0018022	0.963	0.165	1	36	peptidyl-lysine methylation	BP	1	EZH2	down_ACOR_VSMC
GO:0032543	0.963	0.166	1	34	mitochondrial translation	BP	1	NGRN	up_ACOR_VSMC
GO:0051028	0.963	0.167	1	33	mRNA transport	BP	1	ZFP36L1	up_VSAP_EC
GO:0120036	0.964	0.0554	23	373	plasma membrane bounded cell projection organization	BP	1	FSCN1,ANLN,NEDD4,SLC29A1,B3GNT2,CFAP298,PRMT1,CAV1,LIMA1,STMN1,POC1A,RAC1,EMP2,IQGAP1,CDC42EP4,RAB35,EZR,CORO1A,ENSCAFG00000010224,RTTN,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0051050	0.964	0.0635	13	235	positive regulation of transport	BP	1	ACSL3,HMGB1,NEDD4,SDC1,RAN,PRELID1,CAV1,GREM1,PLK3,HIST1H1A,GSTO1,DMAP1,EZR	down_ACOR_VSMC
GO:0007005	0.964	0.0678	10	175	mitochondrion organization	BP	1	RHOT1,MX1,PPARGC1A,MARCH5,GABARAPL1,BNIP3,CLN8,TTC19,NAIF1,PARK7	up_ACOR_VSMC
GO:0065003	0.964	0.0696	9	616	protein-containing complex assembly	BP	1	KCNC4,CRYAB,KCND1,PLAGL2,CYLD,DNAL1,ACACB,CDC42EP5,KANK1	up_AFEM_EC
GO:0044238	0.964	0.0803	9	3383	primary metabolic process	BP	1	NR1H4,MAPK10,PLCL1,PCSK1N,GALNT17,ZDHHC16,NPNT,NTRK2,HOXA1	up_APUL_EC
GO:0015031	0.964	0.0736	7	510	protein transport	BP	1	LEP,CRY2,VPS26C,GPAM,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0001654	0.964	0.0837	5	110	eye development	BP	1	NF2,SMG9,PHACTR4,JMJD6,HMGN1	down_ACOR_VSMC
GO:0010720	0.964	0.0829	5	110	positive regulation of cell development	BP	1	SRRT,RAC1,BEND6,ASPM,ARHGEF2	down_ACOR_VSMC

GO:0048880	0.964	0.0837	5	110	sensory system development	BP	1	NF2,SMG9,PHACTR4,JMJD6,HMGN1	down_ACOR_VSMC
GO:0150063	0.964	0.0837	5	110	visual system development	BP	1	NF2,SMG9,PHACTR4,JMJD6,HMGN1	down_ACOR_VSMC
GO:0046578	0.964	0.09	4	77	regulation of Ras protein signal transduction	BP	1	ABCA1,ARHGEF26,F2RL1,NRP1	up_ACOR_VSMC
GO:0032868	0.964	0.101	3	66	response to insulin	BP	1	LEP,SESN3,INPP5K	up_ACOR_VSMC
GO:0032874	0.964	0.117	2	57	positive regulation of stress-activated MAPK	BP	1	HMGB1,MAP3K20	down_ACOR_VSMC
GO:0031330	0.964	0.115	2	85	negative regulation of cellular catabolic process	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0009914	0.964	0.158	1	64	hormone transport	BP	1	PARK7	down_VCAV_EC
GO:0006906	0.964	0.159	1	55	vesicle fusion	BP	1	USO1	down_VSAP_EC
GO:0006418	0.964	0.162	1	31	tRNA aminoacylation for protein translation	BP	1	TARSL2	up_ACOR_VSMC
GO:0030316	0.964	0.164	1	31	osteoclast differentiation	BP	1	RASSF2	up_ACOR_VSMC
GO:0033047	0.964	0.161	1	33	regulation of mitotic sister chromatid segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0010468	0.964	0.167	1	1270	regulation of gene expression	BP	1	HOXA9	up_AORT_EC
GO:0018130	0.964	0.168	1	1261	heterocycle biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0019438	0.964	0.169	1	1258	aromatic compound biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0033047	0.964	0.162	1	33	regulation of mitotic sister chromatid segregation	BP	1	CDC26	up_VSAP_EC
GO:0007612	0.964	0.161	1	33	learning	BP	1	CTNS	up_VSAP_EC
GO:0051261	0.964	0.163	1	33	protein depolymerization	BP	1	F2RL1	up_VSAP_EC
GO:1905952	0.964	0.163	1	33	regulation of lipid localization	BP	1	ACACB	up_VSAP_EC
GO:0006873	0.965	0.0692	8	160	cellular ion homeostasis	BP	1	HMGB1,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0006979	0.965	0.0763	6	130	response to oxidative stress	BP	1	PPP1R15B,EZH2,PLK3,DHCR24,SIGMAR1,MELK	down_ACOR_VSMC
GO:0033044	0.965	0.087	4	127	regulation of chromosome organization	BP	1	IWS1,NAA10,CTNNB1,KDM3A	down_VSAP_EC
GO:0019538	0.965	0.0917	4	1713	protein metabolic process	BP	1	GALNT17,PRR16,TLR2,CAV1	up_VSAP_VSMC
GO:1903532	0.965	0.0973	3	78	positive regulation of secretion by cell	BP	1	HMGB1,SDC1,EZR	down_ACOR_VSMC
GO:0045732	0.965	0.0975	3	78	positive regulation of protein catabolic process	BP	1	PLK2,TNFAIP3,TIPARP	up_VCAV_EC
GO:0051648	0.965	0.0973	3	69	vesicle localization	BP	1	RAB11B,STX4,CEP19	up_VSAP_EC
GO:0050708	0.965	0.114	2	101	regulation of protein secretion	BP	1	GPAM,MAVS	down_VCAV_EC
GO:0006364	0.965	0.114	2	87	rRNA processing	BP	1	MRPL1,PDCD11	down_VSAP_EC
GO:0018393	0.965	0.115	2	51	internal peptidyl-lysine acetylation	BP	1	PHF20,MAP3K7	up_ACOR_VSMC
GO:0006261	0.965	0.154	1	68	DNA-dependent DNA replication	BP	1	FBH1	down_VCAV_EC
GO:0007254	0.965	0.154	1	67	JNK cascade	BP	1	SASH1	down_VCAV_EC
GO:0051650	0.965	0.156	1	65	establishment of vesicle localization	BP	1	TMEM230	down_VCAV_EC
GO:1902652	0.965	0.157	1	38	secondary alcohol metabolic process	BP	1	ABCA1	up_VCAV_EC
GO:0022402	0.965	0.156	1	407	cell cycle process	BP	1	MZT1	up_VPOR_EC
GO:0043412	0.965	0.164	1	1225	macromolecule modification	BP	1	ANKRD6	up_VPOR_VSMC
GO:0016070	0.965	0.167	1	1479	RNA metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0051592	0.965	0.16	1	33	response to calcium ion	BP	1	SLC25A12	up_VSAP_EC
GO:1903321	0.965	0.159	1	33	negative regulation of protein modification by small protein conjugation	BP	1	ABL1	up_VSAP_EC
GO:2001243	0.965	0.16	1	33	negative regulation of intrinsic apoptotic	BP	1	ACKR3	up_VSAP_EC

GO:0009059	0.966	0.042	132	1563	macromolecule biosynthetic process	BP	1	TLR1,SMAD6,GALNT3,LEP,GALNT10,LBH,ST3GAL5,GATA5,GATA4,CDC7,PCGF5,MEIS2,B3GALNT2,NACC2,MLLT3,ITM2C,BMP4,LCAT,ZNF331,TBX18,B3GNT7,FGFR2,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PIGN,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,PIGG,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,MAGT1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,STT3B,PFDN5,ORMDL3,SMARCD3,TBX20,FUT11,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,PIK3C3,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,EOGT,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,RPAIN,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,ZDHHC21,LMF1	up_ACOR_VSMC
GO:0045184	0.966	0.0499	34	532	establishment of protein localization	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,HINFP,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,RAN,HM13,BIRC5,INSIG1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA,CCT4	down_ACOR_VSMC
GO:0040007	0.966	0.0568	16	276	growth	BP	1	SLC29A1,GINS4,MMP14,CDKN2C,EZH2,CDK4,TKT,POC1A,PPARD,IQGAP1,EZR,SGPL1,BAP1,ASPM,GLI1,SIX4	down_ACOR_VSMC
GO:0055080	0.966	0.066	9	176	cation homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0010256	0.966	0.0741	6	129	endomembrane system organization	BP	1	ZW10,CTDNEP1,CAV1,PLK3,REEP4,PRMT5	down_ACOR_VSMC
GO:0002790	0.966	0.0948	3	133	peptide secretion	BP	1	GPAM,PARK7,MAVS	down_VCAV_EC
GO:0043583	0.966	0.112	2	59	ear development	BP	1	INSIG1,SIX4	down_ACOR_VSMC
GO:0001558	0.966	0.111	2	101	regulation of cell growth	BP	1	IGFBP6,TRPV2	down_VCAV_EC
GO:0051054	0.966	0.111	2	81	positive regulation of DNA metabolic process	BP	1	CTNNB1,TFRC	down_VSAP_EC
GO:0043523	0.966	0.112	2	52	regulation of neuron apoptotic process	BP	1	AMBRA1,KDM2B	up_VSAP_EC
GO:0006473	0.966	0.151	1	66	protein acetylation	BP	1	PARK7	down_VCAV_EC
GO:0090174	0.966	0.153	1	56	organelle membrane fusion	BP	1	USO1	down_VSAP_EC
GO:0006400	0.966	0.155	1	33	tRNA modification	BP	1	RPUSD4	up_VSAP_EC
GO:0016070	0.966588538	0.05068	30	1479	RNA metabolic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,SOX9,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:1901576	0.967	0.0498	35	1877	organic substance biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,XYLT1,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,SDR42E1,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A,CSGALNACT2,CTIF,SAMD4B,AGPAT2	up_AFEM_EC
GO:0016192	0.967	0.0479	33	452	vesicle-mediated transport	BP	1	DNM1,ACKR3,TBC1D10C,TBC1D2B,ABL1,EMP2,DLL1,EPN2,VPS36,AP5B1,F2RL1,LMF1,RAB11B,GAS1,ERGIC1,MON1B,SCFD2,CCDC93,DOP1B,DENND5A,AP5Z1,MYO1B,ZFYVE21,CYBA,XKR8,STX4,VPS11,ARHGAP12,UBQLN2,FLOT1,PPP3CB,CEP19,RAB11FIP2	up_VSAP_EC
GO:0006886	0.967	0.0518	23	332	intracellular protein transport	BP	1	PEX7,TBC1D10C,TBC1D2B,CDH1,PEX2,RILPL2,VPS36,TOM1,MFN2,ICE1,PIK3R1,NUP98,HPS4,FBXO7,KCNB1,LONP2,SNUPN,STX4,VPS11,PEX6,MAVS,BAG4,NCOA4	up_VSAP_EC
GO:0019693	0.967	0.0627	10	172	ribose phosphate metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC

GO:0034976	0.967	0.0722	6	112	response to endoplasmic reticulum stress	BP	1	FOXRED2,MAP3K5,PIK3R1,UBQLN2,FLOT1,NCK1	up_VSAP_EC
GO:0071375	0.967	0.0934	3	68	cellular response to peptide hormone stimulus	BP	1	ACTN2,SESN3,INPP5K	up_ACOR_VSMC
GO:0070304	0.967	0.111	2	58	positive regulation of stress-activated protein kinase signaling cascade	BP	1	HMGB1,MAP3K20	down_ACOR_VSMC
GO:0016072	0.967	0.107	2	102	rRNA metabolic process	BP	1	RPL27,MRPS11	down_VCAV_EC
GO:1903320	0.967	0.109	2	102	regulation of protein modification by small protein conjugation or	BP	1	PARK7,SASH1	down_VCAV_EC
GO:0045017	0.967	0.109	2	52	glycerolipid biosynthetic process	BP	1	PLA2G6,LCAT	up_VSAP_EC
GO:0009636	0.967	0.149	1	66	response to toxic substance	BP	1	PARK7	down_VCAV_EC
GO:0060047	0.967	0.149	1	57	heart contraction	BP	1	CALM1	down_VSAP_EC
GO:0071840	0.967	0.166	1	2059	cellular component organization or biogenesis	BP	1	EYA1	up_AFEM_VSMC
GO:0006996	0.967	0.156	1	1301	organelle organization	BP	1	TAOK1	up_AORT_EC
GO:1901362	0.967	0.156	1	1293	organic cyclic compound biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0043484	0.967	0.15	1	43	regulation of RNA splicing	BP	1	WTAP	up_VCAV_EC
GO:0044271	0.967	0.161	1	1501	cellular nitrogen compound biosynthetic	BP	1	GATA5	up_VPUL_VSMC
GO:0002694	0.967857084	0.14522	1	126	regulation of leukocyte activation	BP	1	NOD2	up_ACOR_EC
GO:0019538	0.968	0.0399	146	1713	protein metabolic process	BP	1	FZD1,PRR16,CDON,NECAB3,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,RNPEP,TBC1D10C,MRPL37,CEP85,FOXRED2,EEF2K,IL6R,SLIT2,CST3,CRADD,ABTB1,FGF7,ABL1,KLHL36,KLKB1,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,CTSS,GALNT15,DTX2,PDGFD,WARS2,NAA60,DDB2,KLF15,C1QTNF2,HPSE,CNPPD1,CCBE1,VPS36,RECK,CISH,KLHL24,PLPP3,CAMKK2,APOL5,TNKS1BP1,KLHDC8B,PYM1,F2RL1,LMF1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,PIK3R1,RBCK1,KBTBD12,GAS1,MYC,RNF24,FKRP,FBXW4,DLD,SULF2,CAPN5,EEF2,RTN4RL1,SASH1,FBXO4,RMND5A,LARP6,MYD88,RPL13,LRP4,PASK,ANKHD1,TSPAN5,AZIN2,GALNT11,STK16,NCEH1,PHF1,CFD,FBXW5,FBXO7,MOCOS,ZDHHC8,ASB8,UBA7,EHHADH,FARS2,LCAT,UBA52,RNF166,RPUSD4,LONP2,RPL15,CDK9,KDM2B,FBLN1,RNF216,EIF3G,OSBPL7,SAMD4B,ZFP36L2,WDR82,RAF1,EIF3K,EIF3L,DR1,TTL,TIMP2,QARS,EIF3D,ACVRL1,KDM3B,UBQLN2,CTSF,CDC26,HTRA2,FLOT1,TNRC6C,COA1,PPP3CB,NCK1,MRPL4,MAVS,CHST7,ULK1,LARS2,ZER1,MAP2K2,TGFBR2,B3GALT4,BAG4,KEAP1,SOAT1,LATS2	up_VSAP_EC
GO:0070925	0.968	0.052	20	293	organelle assembly	BP	1	ACTN2,FEZ1,PRKAA2,EVI5L,TP53INP1,ATXN2,NEBL,IFT43,GABARAPL1,PSEN1,PIK3C3,EDN1,ASAP1,ATG16L2,DISC1,KIF9,ATXN10,FEZ2,ENSCAFG00000013536,MYOZ2	up_ACOR_VSMC
GO:0031329	0.968	0.0572	13	241	regulation of cellular catabolic process	BP	1	PLK2,TNFAIP3,RALB,SPTLC2,MTOR,TENT2,DEPP1,SH3GLB1,CNOT7,SMG7,HMGB1,USP13,HIF1A	up_VCAV_EC
GO:1902532	0.968	0.0588	11	204	negative regulation of intracellular signal	BP	1	HMGCR,CAV1,NF2,STMN1,RNF152,NOC2L,NUP62,GSTO1,EZR,TXNDC12,ARHGEF2	down_ACOR_VSMC
GO:0050769	0.968	0.0819	4	95	positive regulation of neurogenesis	BP	1	SRRT,BEND6,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0045666	0.968	0.0914	3	68	positive regulation of neuron differentiation	BP	1	BMP4,NRP1,PSEN1	up_ACOR_VSMC
GO:0006611	0.968	0.107	2	51	protein export from nucleus	BP	1	PARK7,PTPN14	up_ACOR_VSMC
GO:0035107	0.968	0.105	2	60	appendage morphogenesis	BP	1	CHD7,ATRX	up_VCAV_EC
GO:0035108	0.968	0.105	2	60	limb morphogenesis	BP	1	CHD7,ATRX	up_VCAV_EC
GO:0001843	0.968	0.148	1	38	neural tube closure	BP	1	PHACTR4	down_ACOR_VSMC
GO:0000422	0.968	0.147	1	34	autophagy of mitochondrion	BP	1	GABARAPL1	up_ACOR_VSMC
GO:0061726	0.968	0.147	1	34	mitochondrion disassembly	BP	1	GABARAPL1	up_ACOR_VSMC

GO:0090263	0.968	0.15	1	33	positive regulation of canonical Wnt signaling	BP	1	FGFR2	up_ACOR_VSMC
GO:0050778	0.968	0.146	1	141	positive regulation of immune response	BP	1	CYLD	up_AFEM_EC
GO:0008104	0.968	0.149	1	763	protein localization	BP	1	SIX1	up_VFEM_EC
GO:0043412	0.968	0.154	1	1225	macromolecule modification	BP	1	EYA1	up_VFEM_VSMC
GO:0043244	0.968	0.15	1	34	regulation of protein complex disassembly	BP	1	F2RL1	up_VSAP_EC
GO:0071887	0.968	0.149	1	34	leukocyte apoptotic process	BP	1	CD274	up_VSAP_EC
GO:0007059	0.968315608	0.14361	1	127	chromosome segregation	BP	1	CHMP4B	up_ACOR_EC
GO:0043170	0.969	0.0382	222	2980	macromolecule metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,IL7R,ST8SIA6,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PRKCH,CALCRL,FLI1,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,TSPAN8,RELN,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,LYVE1,TSPAN15,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,CTTNBP2NL,FOXN2,MEOX1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,YES1,ENSCAFG00000010893,ODC1,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,TENT2,SAMD8,ELF4,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,MAPK13,ITPKB,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,PAK2,GALNT18,PRKD2,THOC1,SWAP70,CHST1,SMARCA4,TLR3,MFNG,APOD,NCK1,ESCO1,TRMT9B,DPH5,VHL,TIMELESS,OTUD4,LDB2,CD200,WSB1,PARP4,FES,JAG1,NSD1,MRRF,PTGS2,MMD,TOP1,ETAA1,RAPGEF2,TCERG1,PLCG2,CTDSPL2,CREB1,BCL10,SENP6,BASP1,PAN3,USP28,T	up_VCAV_EC
GO:0048513	0.969	0.0413	63	906	animal organ development	BP	1	HMGB1,FLNB,ANLN,EIF4A3,SLC29A1,HOXA3,SF1,FBXO5,HSPA9,NAB2,PRELID1,INSIG1,PRMT1,CAV1,XYLT1,TIMELESS,NF2,MMP14,EZH2,STMN1,GREM1,CDK4,SMARCC1,HMGB3,HOXA7,SMG9,ARG2,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,POC1A,WDR62,E2F8,B4GALT1,TFRC,ADAMTS6,PPARD,FOSL1,PLK4,IQGAP1,HMGB2,ARCN1,HOXB5,TOX,HOXC4,SGPL1,NOLC1,PHACTR4,SLC20A1,ASPM,TBX15,ENSCAFG00000010224,HOXA9,SERPINH1,GLI1,JMJD6,MSC,RTCB,HMGN1,SIX4,AMER1	down_ACOR_VSMC
GO:0009056	0.969	0.0436	49	755	catabolic process	BP	1	PLK2,LYZ,CDA,TNFAIP3,CTSC,TIPARP,WWP1,LYVE1,USP33,RALB,PIPOX,PSME4,PELI1,ODC1,SPTLC2,CASP8,MTOR,TENT2,CNOT6,DEPP1,ENC1,GALE,SH3GLB1,ENSCAFG00000024323,PLCG2,PAN3,USP28,CNOT7,SMG7,LIPA,HMGB1,PMAIP1,RIPK1,USP13,USP38,IMPA1,USP37,BLVRA,C7H18orf25,CUL4A,UBE2D1,HIF1A,RBBP6,DCP2,TNFAIP1,PSMB9,PSMD12,TET2,ITCH	up_VCAV_EC
GO:0030030	0.969	0.0487	23	377	cell projection organization	BP	1	FSCN1,ANLN,NEDD4,SLC29A1,B3GNT2,CFAP298,PRMT1,CAV1,LIMA1,STMN1,POC1A,RAC1,EMP2,IQGAP1,CDC42EP4,RAB35,EZR,CORO1A,ENSCAFG00000010224,RTTN,CEP83,TTLL1,KIF24	down_ACOR_VSMC
GO:0016567	0.969	0.0558	12	232	protein ubiquitination	BP	1	TNFAIP3,PELI1,ASB9,ENC1,UHRF2,VHL,WSB1,BCL10,C7H18orf25,CUL4A,UBE2D1,IVNS1ABP	up_VCAV_EC
GO:0006163	0.969	0.0584	10	174	purine nucleotide metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0034613	0.969	0.0622	8	576	cellular protein localization	BP	1	LEP,CRY2,VPS26C,CYLD,LRRC15,REEP2,RAB7A,AXIN2	up_AFEM_EC
GO:0051052	0.969	0.0627	8	145	regulation of DNA metabolic process	BP	1	AXIN2,STAT6,MYC,CIZ1,FBXO4,NPAS2,CDK9,ACVRL1	up_VSAP_EC
GO:0033674	0.969	0.0649	7	144	positive regulation of kinase activity	BP	1	IRAK1,SLC29A1,EZH2,MAP3K20,CKS2,EMP2,CLSPN	down_ACOR_VSMC
GO:0043010	0.969	0.0797	4	96	camera-type eye development	BP	1	NF2,PHACTR4,JMJD6,HMGN1	down_ACOR_VSMC

GO:1903530	0.969	0.0776	4	165	regulation of secretion by cell	BP	1	GPAM,SDC4,MAVS,RAC2	down_VCAV_EC
GO:0065007	0.969	0.095	4	3499	biological regulation	BP	1	CST3,HDAC7,CITED2,RAB11B	down_VPOR_EC
GO:0032872	0.969	0.0884	3	77	regulation of stress-activated MAPK cascade	BP	1	HMGB1,MAP3K20,EZR	down_ACOR_VSMC
GO:0002791	0.969	0.104	2	104	regulation of peptide secretion	BP	1	GPAM,MAVS	down_VCAV_EC
GO:0000723	0.969	0.104	2	54	telomere maintenance	BP	1	MYC,FBXO4	up_VSAP_EC
GO:0008033	0.969	0.106	2	52	tRNA processing	BP	1	FARS2,RPUSD4	up_VSAP_EC
GO:0032200	0.969	0.104	2	54	telomere organization	BP	1	MYC,FBXO4	up_VSAP_EC
GO:0006937	0.969	0.146	1	40	regulation of muscle contraction	BP	1	CAV1	down_ACOR_VSMC
GO:0002250	0.969	0.143	1	68	adaptive immune response	BP	1	LOXL3	down_VCAV_EC
GO:0045666	0.969	0.143	1	68	positive regulation of neuron differentiation	BP	1	TRPV2	down_VCAV_EC
GO:0003015	0.969	0.142	1	58	heart process	BP	1	CALM1	down_VSAP_EC
GO:0006875	0.969131566	0.14074	1	129	cellular metal ion homeostasis	BP	1	PTH1R	up_ACOR_EC
GO:0034645	0.97	0.0379	130	1546	cellular macromolecule biosynthetic process	BP	1	SMAD6,GALNT3,LEP,GALNT10,LBH,ST3GAL5,GATA5,GATA4,CDC7,PCGF5,MEIS2,B3GALNT2,NACC2,MLLT3,ITM2C,BMP4,LCAT,ZNF331,TBX18,B3GNT7,FGFR2,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PIGN,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,PIGG,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,MAGT1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,STT3B,PFDN5,SMARCD3,TBX20,FUT11,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,PIK3C3,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,EOGT,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,RPAIN,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,ZDHHC21,LMF1	up_ACOR_VSMC
GO:0006996	0.97	0.0412	52	1301	organelle organization	BP	1	SLC35F6,KIRREL1,DCN,SDC4,ATP8B2,COA1,TLN2,NABP2,RPS10,CLIP3,NAGLU,RHOD,ENSCAFG00000014978,GABARAP,AKT2,TTC8,CHCHD10,SYDE1,HR,SCP2,PRMT6,CABIN1,WIPF1,POLDIP2,THY1,WDR45,PEX5,ARHGAP10,ATP6V0C,MYO1B,PARK7,MAST2,CLEC16A,RETREG1,IFT57,MAVS,MRPS11,EMC6,CDH2,MPV17,RPS27,ENSCAFG00000017708,MGARP,ACTR3B,MTFR1L,RAB31,SHC1,PLEKHH2,EVI5L,LONP2,RAC2,BRSK1	down_VCAV_EC
GO:0033043	0.97	0.0447	32	446	regulation of organelle organization	BP	1	WNT11,FAM107A,ARHGEF5,AXIN2,TBC1D10C,CEP85,DDHD1,SLIT2,TBC1D2B,ABL1,CDC42EP5,FUZ,CDC42EP2,F2RL1,MFN2,PIK3R1,MYC,FBXO4,PHF1,FBXW5,FBXO7,CDK9,PIP4K2B,ZNF205,VPS11,UBQLN2,CDC26,HTRA2,NCK1,MAVS,NPRL3,BAG4	up_VSAP_EC
GO:0048646	0.97	0.0485	21	349	anatomical structure formation involved in morphogenesis	BP	1	ELK3,MTDH,HOXA3,CAV1,NF2,ANPEP,MMP14,GREM1,ADIPOR2,HOXA7,E2F8,B4GALT1,PRCP,NCL,EMP2,NOLC1,PHACTR4,ITGA2,JMJD6,NUS1,SIX4	down_ACOR_VSMC
GO:1901137	0.97	0.0511	15	232	carbohydrate derivative biosynthetic process	BP	1	NECAB3,ACACB,GALNT15,LMF1,PDK2,GALK1,FKRP,GALNT11,ACSS2,DCAKD,ENSCAFG00000013366,CHST7,B3GALT4,DDIT4,SOAT1	up_VSAP_EC
GO:0010608	0.97	0.0585	9	154	posttranscriptional regulation of gene	BP	1	NACC2,BMP4,FAM129A,DAPK1,RBM4B,PARP9,APP,CTIF,NGRN	up_ACOR_VSMC
GO:0015833	0.97	0.0641	7	521	peptide transport	BP	1	LEP,CRY2,VPS26C,GPAM,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0045786	0.97	0.0705	5	195	negative regulation of cell cycle	BP	1	NOTCH2,KANK2,NABP2,ZFP36L1,BRSK1	down_VCAV_EC

GO:0044238	0.97	0.0852	5	3383	primary metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0006399	0.97	0.0765	4	87	tRNA metabolic process	BP	1	TARSL2,GTF3C1,TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0043170	0.97	0.0893	4	2980	macromolecule metabolic process	BP	1	HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0044782	0.97	0.0765	4	96	cilium organization	BP	1	NECTIN2,EXOC5,IQUB,SPATA6	up_VCAV_EC
GO:0042391	0.97	0.0863	3	81	regulation of membrane potential	BP	1	NEDD4,PRELID1,CAV1	down_ACOR_VSMC
GO:0015672	0.97	0.0859	3	89	monovalent inorganic cation transport	BP	1	KCNJ3,KCNJ2,SPTBN4	up_VCAV_EC
GO:0016043	0.97	0.111	2	1973	cellular component organization	BP	1	SGCD,TAOK1	up_AORT_EC
GO:0045333	0.97	0.1	2	74	cellular respiration	BP	1	SLC25A25,HIF1A	up_VCAV_EC
GO:0007050	0.97	0.102	2	53	cell cycle arrest	BP	1	CRADD,CDK9	up_VSAP_EC
GO:1901991	0.97	0.139	1	56	negative regulation of mitotic cell cycle phase	BP	1	CDKN1A	down_VSAP_EC
GO:0043039	0.97	0.141	1	33	tRNA aminoacylation	BP	1	TARSL2	up_ACOR_VSMC
GO:0006413	0.97	0.142	1	42	translational initiation	BP	1	NCK1	up_VCAV_EC
GO:0006289	0.97	0.141	1	35	nucleotide-excision repair	BP	1	NEIL2	up_VSAP_EC
GO:0030490	0.97	0.143	1	35	maturation of SSU-rRNA	BP	1	RCL1	up_VSAP_EC
GO:0051298	0.97	0.142	1	35	centrosome duplication	BP	1	FBXW5	up_VSAP_EC
GO:0044237	0.971	0.0375	159	3491	cellular metabolic process	BP	1	CST3,GPAM,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,MAOA,NAB2,NDN,PRNP,LUM,UBA52,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,CHID1,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,SAMD4B,EEF2K,TFE3,ACAA1,ME3,NR3C1,H6PD,HR,RPL23,RPL13,CLSTN1,PLCL1,DDOST,CSPG4,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,THNSL2,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,ASPN,POLDIP2,PIGS,HS3ST3B1,LRPAP1,EIF3K,THY1,NECAB3,RNF216,TEAD1,SUOX,CYP1B1,ADK,WDR45,AHCYL1,MRPL37,PEX5,CC2D1A,B4GALT1,RETSAT,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,ABHD15,CLEC16A,RETREG1,RNPEP,RPL27,COPS7A,CYBA,RBM38,ARL2BP,AMPD2,IFT57,MAVS,MRPS11,EMC6,CDH2,ENSCAFG00000002977,LOXL3,ORMDL3,GSDME,HPDL,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,ACSS2,TSC22D3,MTFR1L,MAPRE3,GLIS2,CDKL2,RAB31,HM13,PRKCSH,DDR2,SHC1,RDH10,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,LONP2,NAPEPLD,GLS2,FOXO3,SO	down_VCAV_EC
GO:0006464	0.971	0.0369	95	1162	cellular protein modification process	BP	1	FZD1,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,KLHL36,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,GALNT15,DTX2,PDGFD,NAA60,DDB2,KLF15,C1QTNF2,CNPPD1,CISH,KLHL24,PLPP3,CAMKK2,TNKS1BP1,KLHDC8B,F2RL1,LMF1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,PIK3R1,RBCK1,KBTBD12,MYC,RNF24,FKRP,DLD,RTN4RL1,SASH1,FBXO4,RMND5A,MYD88,LRP4,PASK,GALNT11,STK16,NCEH1,PHF1,FBXW5,FBXO7,ZDHHC8,ASB8,UBA7,EHHADH,RNF166,CDK9,KDM2B,FBLN1,RNF216,ZFP36L2,WDR82,RAF1,DR1,TTL,QARS,ACVRL1,KDM3B,CDC26,FLOT1,PPP3CB,NCK1,MAVS,ULK1,ZER1,MAP2K2,TGFBR2,B3GALT4,BAG4,KEAP1,LATS2	up_VSAP_EC

GO:0036211	0.971	0.0369	95	1162	protein modification process	BP	1	FZD1,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,KLHL36,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,GALNT15,DTX2,PDGFD,NAA60,DDB2,KLF15,C1QTNF2,CNPPD1,CISH,KLHL24,PLPP3,CAMKK2,TNKS1BP1,KLHDC8B,F2RL1,LMF1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,PIK3R1,RBCK1,KBTBD12,MYC,RNF24,FKRP,DLD,RTN4RL1,SASH1,FBXO4,RMND5A,MYD88,LRP4,PASK,GALNT11,STK16,NCEH1,PHF1,FBXW5,FBXO7,ZDHHC8,ASB8,UBA7,EHHADH,RNF166,CDK9,KDM2B,FBLN1,RNF216,ZFP36L2,WDR82,RAF1,DR1,TTL,QARS,ACVRL1,KDM3B,CDC26,FLOT1,PPP3CB,NCK1,MAVS,ULK1,ZER1,MAP2K2,TGFBR2,B3GALT4,BAG4,KEAP1,LATS2	up_VSAP_EC
GO:1901362	0.971	0.0401	52	1293	organic cyclic compound biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,ADCY6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HSD3B7,HR,SCP2,CLSTN1,CYB5R3,VDR,PRMT6,UROS,ENTPD3,ATP5MC1,CXXC5,TEAD1,ADK,CC2D1A,GLI3,PARK7,MYDGF,AMPD2,MAVS,LOXL3,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0015031	0.971	0.0428	32	510	protein transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,RAN,HM13,BIRC5,INSIG1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA	down_ACOR_VSMC
GO:0009628	0.971	0.0561	9	302	response to abiotic stimulus	BP	1	VASN,NABP2,TRPV2,AKT2,TMEM161A,SCARA5,ZFP36L1,TSC22D3,BRSK1	down_VCAV_EC
GO:0070727	0.971	0.0598	8	579	cellular macromolecule localization	BP	1	LEP,CRY2,VPS26C,CYLD,LRRC15,REEP2,RAB7A,AXIN2	up_AFEM_EC
GO:0051271	0.971	0.0744	4	98	negative regulation of cellular component	BP	1	HMGB1,HOXA7,RAP2C,ENSCAFG00000010224	down_ACOR_VSMC
GO:0070302	0.971	0.0836	3	78	regulation of stress-activated protein kinase	BP	1	HMGB1,MAP3K20,EZR	down_ACOR_VSMC
GO:0030036	0.971	0.0963	2	223	actin cytoskeleton organization	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0006475	0.971	0.0992	2	54	internal protein amino acid acetylation	BP	1	EHHADH,DR1	up_VSAP_EC
GO:0002274	0.971	0.137	1	40	myeloid leukocyte activation	BP	1	JMJD6	down_ACOR_VSMC
GO:0060606	0.971	0.138	1	39	tube closure	BP	1	PHACTR4	down_ACOR_VSMC
GO:0043414	0.971	0.134	1	70	macromolecule methylation	BP	1	PRMT6	down_VCAV_EC
GO:0014902	0.971	0.139	1	34	myotube differentiation	BP	1	DMPK	up_ACOR_VSMC
GO:0031047	0.971	0.136	1	33	gene silencing by RNA	BP	1	BMP4	up_ACOR_VSMC
GO:0033108	0.971	0.136	1	39	mitochondrial respiratory chain complex assembly	BP	1	TTC19	up_ACOR_VSMC
GO:0051641	0.971	0.14	1	858	cellular localization	BP	1	NR1H4	up_APUL_EC
GO:0071704	0.971	0.179	1	3535	organic substance metabolic process	BP	1	HOXA3	up_APUL_VSMC
GO:0001843	0.971	0.137	1	38	neural tube closure	BP	1	BCL10	up_VCAV_EC
GO:0032268	0.971	0.139	1	778	regulation of cellular protein metabolic process	BP	1	MAP2K6	up_VFEM_EC
GO:0034645	0.971	0.148	1	1546	cellular macromolecule biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0006612	0.971	0.136	1	35	protein targeting to membrane	BP	1	KCNB1	up_VSAP_EC

GO:0006950	0.972	0.0369	89	1102	response to stress	BP	1	FZD1,NAPEPLD,HNF4A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ACKR2,INSIG2,PPARGC1B,FOXRED2,CRADD,ABL1,KLKB1,SESN1,OSR1,MAP3K5,CDC42EP5,IL17RC,PDGFD,TRAFD1,DDB2,KLF15,HPSE,CDC42EP2,MGST1,TNKS1BP1,AMBRA1,F2RL1,NFE2L2,PDK2,MFN2,ZFP36L1,FXN,PIK3R1,BATF2,PLA2G6,NEIL2,MYC,SCARA5,TBXA2R,SULF2,SLC12A6,HIC1,RTN4RL1,SASH1,FBXO4,CREBRF,MYD88,NDUFS2,ATRIP,HPS4,PHF1,CFD,NPAS2,FBXO7,LIMD1,NLRX1,TKFC,CDK9,CD83,FBLN1,RNF216,AP5Z1,ZFP36L2,YPEL3,MAPKBP1,ZNF580,CYBA,STX4,ZBTB4,PQBP1,QARS,ACVRL1,IDH1,UBQLN2,UNC93B1,HTRA2,ASS1,FLOT1,NCK1,MAVS,HMOX1,MAP2K2,NPRL3,SAA1,JCHAIN,DDIT4	up_VSAP_EC
GO:0044249	0.972	0.0423	34	1851	cellular biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,XYLT1,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A,CSGALNACT2,CTIF,SAMD4B,AGPAT2	up_AFEM_EC
GO:0098771	0.972	0.0552	9	180	inorganic ion homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0071705	0.972	0.0568	8	582	nitrogen compound transport	BP	1	LEP,CRY2,VPS26C,GPAM,SLC6A6,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0009314	0.972	0.0573	8	143	response to radiation	BP	1	CHRM1,DDB2,TNKS1BP1,PIK3R1,MYC,CTNS,FBXO4,NR2F6	up_VSAP_EC
GO:0042886	0.972	0.0592	7	527	amide transport	BP	1	LEP,CRY2,VPS26C,GPAM,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0034599	0.972	0.0799	3	81	cellular response to oxidative stress	BP	1	EZH2,SIGMAR1,MELK	down_ACOR_VSMC
GO:0016054	0.972	0.0966	2	61	organic acid catabolic process	BP	1	PPARD,ACADL	down_ACOR_VSMC
GO:0046395	0.972	0.0966	2	61	carboxylic acid catabolic process	BP	1	PPARD,ACADL	down_ACOR_VSMC
GO:0034612	0.972	0.0945	2	63	response to tumor necrosis factor	BP	1	CACTIN,ARHGEF2	down_ACOR_VSMC
GO:0045766	0.972	0.0963	2	63	positive regulation of angiogenesis	BP	1	MTDH,GREM1	down_ACOR_VSMC
GO:0006475	0.972	0.0949	2	54	internal protein amino acid acetylation	BP	1	PHF20,MAP3K7	up_ACOR_VSMC
GO:0007034	0.972	0.0945	2	55	vacuolar transport	BP	1	VPS36,NCOA4	up_VSAP_EC
GO:0002700	0.972	0.131	1	40	regulation of production of molecular mediator of immune response	BP	1	TFRC	down_ACOR_VSMC
GO:0006323	0.972	0.133	1	58	DNA packaging	BP	1	BRD2	down_VSAP_EC
GO:1903522	0.972	0.133	1	58	regulation of blood circulation	BP	1	CALM1	down_VSAP_EC
GO:0009059	0.972	0.143	1	1563	macromolecule biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0031109	0.972	0.132	1	36	microtubule polymerization or	BP	1	ABL1	up_VSAP_EC
GO:0030099	0.972515498	0.12861	1	133	myeloid cell differentiation	BP	1	CLSTN1	up_ACOR_EC

GO:1901576	0.973	0.0333	159	1877	organic substance biosynthetic process	BP	1	TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,GALNT10,LBH,ST3GAL5,GATA5,GATA4,CDC7,PCGF5,HTR2B,MEIS2,B3GALNT2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,LCAT,ZNF331,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,FAXDC2,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,UGCG,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,PPIP5K1,ZNF174,PLAC8B,PIGG,ANKRD1,F2RL1,FAM129A,GGPS1,DAPK1,PKNOX2,RBM4B,HKR1,MAGT1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,STT3B,PFDN5,SCP2,ORMDL3,SMARCD3,SMPD1,TBX20,FUT11,MOXD1,CCDC3,CCNT1,CRLS1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,PIK3C3,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,EOGT,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,PTS,RPAIN,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029	up_ACOR_VSMC
GO:0043632	0.973	0.0453	17	262	modification-dependent macromolecule catabolic process	BP	1	FOXRED2,ABTB1,VPS36,EXOSC7,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,FBXO7,UBA7,RNF166,RNF216,UBQLN2,CDC26,KEAP1	up_VSAP_EC
GO:0006518	0.973	0.0784	3	290	peptide metabolic process	BP	1	PRR16,CTIF,SAMD4B	up_AFEM_EC
GO:0071824	0.973	0.0924	2	92	protein-DNA complex subunit organization	BP	1	SMARCA4,BRD2	down_VSAP_EC
GO:0006470	0.973	0.0944	2	54	protein dephosphorylation	BP	1	NCEH1,NCK1	up_VSAP_EC
GO:0018394	0.973	0.0924	2	55	peptidyl-lysine acetylation	BP	1	KLF15,DR1	up_VSAP_EC
GO:0045995	0.973	0.13	1	40	regulation of embryonic development	BP	1	SIX4	down_ACOR_VSMC
GO:0032259	0.973	0.129	1	71	methylation	BP	1	PRMT6	down_VCAV_EC
GO:0006289	0.973	0.13	1	35	nucleotide-excision repair	BP	1	FAN1	up_ACOR_VSMC
GO:0043038	0.973	0.129	1	34	amino acid activation	BP	1	TARSL2	up_ACOR_VSMC
GO:0060606	0.973	0.129	1	39	tube closure	BP	1	BCL10	up_VCAV_EC
GO:0044267	0.973	0.139	1	1583	cellular protein metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0008637	0.973	0.13	1	35	apoptotic mitochondrial changes	BP	1	ZNF205	up_VSAP_EC
GO:0048534	0.973754601	0.07539	3	262	hematopoietic or lymphoid organ	BP	1	FZD5,PTGER4,CLSTN1	up_ACOR_EC
GO:1901698	0.974	0.0451	15	266	response to nitrogen compound	BP	1	SREBF1,SREBF2,HM13,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,UBE2J2,PDXP,EZR,PSMC1,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:1902533	0.974	0.0461	15	271	positive regulation of intracellular signal transduction	BP	1	HMGB1,IRAK1,NEDD4,SLC29A1,MTDH,CAV1,EZH2,GREM1,MAP3K20,DHX33,PPARD,NUP62,GSTO1,MIOS,CTH	down_ACOR_VSMC
GO:0009894	0.974	0.0451	15	277	regulation of catabolic process	BP	1	PLK2,TNFAIP3,TIPARP,RALB,ODC1,SPTLC2,MTOR,TENT2,DEPP1,SH3GLB1,CNOT7,SMG7,HMGB1,USP13,HIF1A	up_VCAV_EC
GO:0043604	0.974	0.0456	14	288	amide biosynthetic process	BP	1	QKI,SPTLC2,ARG2,TARSL2,MTOR,SAMD8,ENC1,SECISBP2L,ELOVL7,NCK1,DPH5,MRRF,CNOT7,GCH1	up_VCAV_EC
GO:0045184	0.974	0.0552	7	532	establishment of protein localization	BP	1	LEP,CRY2,VPS26C,GPAM,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0072507	0.974	0.0625	5	103	divalent inorganic cation homeostasis	BP	1	C5AR2,SLC8B1,ABL1,F2RL1,CYBA	up_VSAP_EC
GO:1901564	0.974	0.0678	5	2053	organonitrogen compound metabolic	BP	1	GATM,GALNT17,PRR16,TLR2,CAV1	up_VSAP_VSMC
GO:0051783	0.974	0.0756	3	72	regulation of nuclear division	BP	1	BMP4,ATRX,EDN1	up_ACOR_VSMC
GO:0090304	0.974	0.0797	3	1694	nucleic acid metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0051783	0.974	0.0767	3	72	regulation of nuclear division	BP	1	CEP85,FBXW5,CDC26	up_VSAP_EC
GO:0031929	0.974	0.0896	2	62	TOR signaling	BP	1	RNF152,MIOS	down_ACOR_VSMC

GO:0046328	0.974	0.0907	2	61	regulation of JNK cascade	BP	1	HMGB1,MAP3K20	down_ACOR_VSMC
GO:0031098	0.974	0.0893	2	109	stress-activated protein kinase signaling cascade	BP	1	ZFP36L1,SASH1	down_VCAV_EC
GO:0060560	0.974	0.0904	2	58	developmental growth involved in	BP	1	IFRD1,RAB11A	up_VCAV_EC
GO:0035051	0.974	0.124	1	41	cardiocyte differentiation	BP	1	GREM1	down_ACOR_VSMC
GO:0002443	0.974	0.125	1	71	leukocyte mediated immunity	BP	1	RAC2	down_VCAV_EC
GO:0001656	0.974	0.127	1	35	metanephros development	BP	1	BMP4	up_ACOR_VSMC
GO:0006941	0.974	0.126	1	36	striated muscle contraction	BP	1	KCNE3	up_VSAP_EC
GO:0006091	0.97429075	0.12205	1	139	generation of precursor metabolites and energy	BP	1	ALDOC	up_ACOR_EC
GO:0034655	0.974358839	0.12183	1	135	nucleobase-containing compound catabolic	BP	1	ALDOC	up_ACOR_EC
GO:0008152	0.975	0.0318	202	3714	metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,P4HB,SULF1,CELF1,ASNS,SERPINH1,CARS,PLOD2,MYH9,NR1H4,PLK3,HSPA5,SERPINE1,SOCS5,ETV6,HM13,ENSCAFG00000009211,MEIS2,SGK1,ERO1A,PRKACB,HSP90B1,ENPP1,ERRFI1,ENSCAFG00000005575,P4HA1,JCAD,SNX25,CBX5,SARS,PGK1,WSB1,BCAR3,NUAK1,PTPN11,AARS,TPI1,ENSCAFG00000032470,ENSCAFG00000028814,TRIB3,PGAM1,ENSCAFG00000007260,TMED2,PUM3,UGCG,PM20D2,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,PRCP,SMARCA4,ANKRA2,SESN2,TGFBR1,PTGS2,PPIB,CEMIP2,CHSY1,MSN,SEL1L,ENSCAFG00000008716,HIF1A,NDUFA4L2,DYNLL1,FOXP4,SLC45A3,USP12,MRPL1,IWS1,NMNAT2,DNAJC10,ACTG2,TNIK,GALNT1,NAA10,NXN,UBA6,ZPR1,PTPN2,ALDH18A1,ENTPD4,UCHL5,MORF4L2,SPOPL,MOGS,YARS,SNRPB2,TARS,YES1,NEO1,PLCL1,PEG3,SMG7,TTLL7,MTDH,NARS,PRPF3,DDX39B,ADAM17,ACTA2,BRD2,EIF4EBP1,CNOT7,MAGED1,DNAJB9,ALDOC,CTNNB1,PAPSS1,CRYAB,SND1,ENSCAFG00000002015,TFRC,CDK8,APOE,WWC3,PPP1R3C,PLOD3,PDCD11,USP48,KLF5,UBA5,LYN,BNIP3,STRAP,DDIT3,PDS5B,FAM162A,BACH1,ASPH,CCNYL1,STT3A,EIF5,MMD,CBLC,ATF3,GSK3B,VLDLR,CDC37,AK5,GT	down_VSAP_EC
GO:0044267	0.975	0.0318	133	1583	cellular protein metabolic process	BP	1	FZD1,PRR16,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,MRPL37,CEP85,FOXRED2,EEF2K,IL6R,SLIT2,CST3,CRADD,ABTB1,FGF7,ABL1,KLHL36,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,CTSS,GALNT15,DTX2,PDGFD,WARS2,NAA60,DDB2,KLF15,C1QTNF2,CNPPD1,CCBE1,VPS36,RECK,CISH,KLHL24,PLPP3,CAMKK2,TNKS1BP1,KLHDC8B,PYM1,F2RL1,LMF1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,PIK3R1,RBCK1,KBTBD12,GAS1,MYC,RNF24,FKRP,FBXW4,DLD,EEF2,RTN4RL1,SASH1,FBXO4,RMND5A,LARP6,MYD88,RPL13,LRP4,PASK,ANKHD1,GALNT11,STK16,NCEH1,PHF1,FBXW5,FBXO7,MOCOS,ZDHHC8,ASB8,UBA7,EHHADH,FARS2,UBA52,RNF166,RPUSD4,LONP2,RPL15,CDK9,KDM2B,FBLN1,RNF216,EIF3G,OSBPL7,SAMD4B,ZFP36L2,WDR82,RAF1,EIF3K,EIF3L,DR1,TTL,TIMP2,QARS,EIF3D,ACVRL1,KDM3B,UBQLN2,CTSF,CDC26,HTRA2,FLOT1,TNRC6C,COA1,PPP3CB,NCK1,MRPL4,MAVS,ULK1,LARS2,ZER1,MAP2K2,TGFBR2,B3GALT4,BAG4,KEAP1,LATS2	up_VSAP_EC
GO:0006355	0.975	0.0368	37	974	regulation of transcription, DNA-templated	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC

GO:0009058	0.975	0.0374	35	1910	biosynthetic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,XYLT1,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,CAMK2A,GREM2,CYLD,SDR42E1,MYBL1,NR3C1,MOXD1,EAF1,YEATS2,ACACB,PPARGC1A,CSGALNACT2,CTIF,SAMD4B,AGPAT2	up_AFEM_EC
GO:0032446	0.975	0.0451	13	255	protein modification by small protein conjugation	BP	1	TNFAIP3,PELI1,ASB9,HMG20A,ENC1,UHRF2,VHL,WSB1,BCL10,C7H18orf25,CUL4A,UBE2D1,IVNS1ABP	up_VCAV_EC
GO:0051640	0.975	0.0479	10	174	organelle localization	BP	1	RAB11B,MFN2,NUP98,SCFD2,BORCS6,STX4,TTL,VPS11,CEP19,CLUH	up_VSAP_EC
GO:0007005	0.975	0.0532	7	175	mitochondrion organization	BP	1	MX2,NECTIN2,CAV2,SH3GLB1,PMAIP1,HIF1A,ATP2A1	up_VCAV_EC
GO:0071704	0.975	0.081	4	3535	organic substance metabolic process	BP	1	HOXA3,GATA5,PHEX,SLIT2	up_VPUL_VSMC
GO:0043170	0.975	0.0858	3	2980	macromolecule metabolic process	BP	1	HOXA3,GATA5,SLIT2	up_VPUL_VSMC
GO:0060249	0.975	0.0858	2	110	anatomical structure homeostasis	BP	1	NABP2,NCDN	down_VCAV_EC
GO:0050792	0.975	0.0886	2	55	regulation of viral process	BP	1	PC,MAVS	up_VSAP_EC
GO:0007188	0.975	0.121	1	41	adenylate cyclase-modulating G protein-coupled receptor signaling	BP	1	PRMT5	down_ACOR_VSMC
GO:0070507	0.975	0.119	1	73	regulation of microtubule cytoskeleton organization	BP	1	CLIP3	down_VCAV_EC
GO:0006275	0.975	0.121	1	38	regulation of DNA replication	BP	1	CIZ1	up_VSAP_EC
GO:0043933	0.976	0.0334	53	698	protein-containing complex subunit organization	BP	1	FAM107A,ARHGEF5,LIPC,ACACB,SLIT2,NDUFS7,ABL1,CDC42EP5,NAA60,SMARCD2,C1QTNF2,CLDN1,CDC42EP2,PSMD9,HSD17B8,PYM1,F2RL1,DDR2,ICE1,DMAC2,SCARA5,SBF2,CLYBL,LOX,NDUFAF3,NDUFB10,NUP98,KCNB1,LCAT,PCBD1,LIMD1,EIF3G,RAF1,CYBA,CENPP,EIF3K,STX4,EIF3L,SMIM20,VPS11,KCNC4,EIF3D,HTRA2,FLOT1,COA1,NCK1,ULK1,HMOX1,BAG4,JCHAIN,DPT,DDIT4,SOAT1	up_VSAP_EC
GO:1903506	0.976	0.0349	37	977	regulation of nucleic acid-templated transcription	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0009057	0.976	0.0356	34	473	macromolecule catabolic process	BP	1	AXIN2,FOXRED2,ABTB1,CTSS,TENT5C,HPSE,VPS36,EXOSC7,PYM1,DFFB,ZFP36L1,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,AZIN2,FBXW5,SMG9,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,SAMD4B,ZFP36L2,TIMP2,UBQLN2,CTSF,CDC26,HTRA2,TNRC6C,KEAP1	up_VSAP_EC
GO:0016050	0.976	0.0556	6	119	vesicle organization	BP	1	PLEKHF1,TBC1D10C,TBC1D2B,HPS4,STX4,VPS11	up_VSAP_EC
GO:0006644	0.976	0.0589	5	118	phospholipid metabolic process	BP	1	ACSL3,MVD,VAC14,FDFT1,NUS1	down_ACOR_VSMC
GO:0009615	0.976	0.0712	3	83	response to virus	BP	1	HNRNPUL1,STMN1,EXOSC5	down_ACOR_VSMC
GO:0071840	0.976	0.0911	2	2059	cellular component organization or biogenesis	BP	1	SGCD,TAOK1	up_AORT_EC
GO:0007098	0.976	0.0858	2	56	centrosome cycle	BP	1	CEP85,FBXW5	up_VSAP_EC
GO:0014020	0.976	0.119	1	41	primary neural tube formation	BP	1	PHACTR4	down_ACOR_VSMC
GO:0060041	0.976	0.116	1	41	retina development in camera-type eye	BP	1	JMJD6	down_ACOR_VSMC
GO:0000724	0.976	0.117	1	57	double-strand break repair via homologous	BP	1	RBBP8	down_VSAP_EC
GO:0007093	0.976	0.118	1	59	mitotic cell cycle checkpoint	BP	1	CDKN1A	down_VSAP_EC
GO:0006119	0.976	0.12	1	40	oxidative phosphorylation	BP	1	PARK7	up_ACOR_VSMC
GO:0001570	0.976	0.117	1	37	vasculogenesis	BP	1	CITED2	up_ACOR_VSMC
GO:0017148	0.976	0.118	1	36	negative regulation of translation	BP	1	DAPK1	up_ACOR_VSMC
GO:0034968	0.976	0.118	1	34	histone lysine methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0042274	0.976	0.116	1	47	ribosomal small subunit biogenesis	BP	1	RIOK3	up_VCAV_EC

GO:2001141	0.977	0.0336	37	979	regulation of RNA biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0044237	0.977	0.0681	5	3491	cellular metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6,CYP26B1	up_VPOR_VSMC
GO:0043161	0.977	0.0611	4	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	RNF216,PARK7,CLEC16A,SEC61B	down_VCAV_EC
GO:0006401	0.977	0.0604	4	88	RNA catabolic process	BP	1	PNRC1,DCP1B,CNOT4,CTIF	up_ACOR_VSMC
GO:0006996	0.977	0.0724	3	1301	organelle organization	BP	1	SPG11,RPSA,STX4	down_ACOR_EC
GO:0031330	0.977	0.0691	3	85	negative regulation of cellular catabolic process	BP	1	SLC29A1,THRAP3,SMARCC1	down_ACOR_VSMC
GO:0045444	0.977	0.0672	3	84	fat cell differentiation	BP	1	SREBF1,INSIG1,PPARD	down_ACOR_VSMC
GO:0006644	0.977	0.0685	3	118	phospholipid metabolic process	BP	1	NR1H4,LYN,SH3GLB1	down_VSAP_EC
GO:0044260	0.977	0.0771	3	2593	cellular macromolecule metabolic process	BP	1	HOXA9,ERC1,TAOK1	up_AORT_EC
GO:0009205	0.977	0.0674	3	98	purine ribonucleoside triphosphate metabolic	BP	1	ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:2001235	0.977	0.0798	2	69	positive regulation of apoptotic signaling	BP	1	CAV1,CASP2	down_ACOR_VSMC
GO:0048738	0.977	0.0823	2	64	cardiac muscle tissue development	BP	1	GREM1,GLI1	down_ACOR_VSMC
GO:0009451	0.977	0.0805	2	59	RNA modification	BP	1	TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0009411	0.977	0.083	2	56	response to UV	BP	1	DDB2,PIK3R1	up_VSAP_EC
GO:0000725	0.977	0.112	1	58	recombinational repair	BP	1	RBBP8	down_VSAP_EC
GO:0030902	0.977	0.114	1	41	hindbrain development	BP	1	PROX1	up_VCAV_EC
GO:0019935	0.977	0.113	1	38	cyclic-nucleotide-mediated signaling	BP	1	ADGRD1	up_VSAP_EC
GO:0007167	0.978	0.0383	15	274	enzyme linked receptor protein signaling pathway	BP	1	SREBF1,SLC29A1,CAV1,STMN1,GREM1,CDK4,SMARCC1,RAC1,NUP62,IQGAP1,FGF5,RBM14,SGPL1,NCOA5,NUS1	down_ACOR_VSMC
GO:0033554	0.978	0.0438	10	708	cellular response to stress	BP	1	LEP,ANGPT4,NFE2L1,CLEC16A,CYLD,AXIN2,PPARGC1A,CDC42EP5,TNC,SOD1	up_AFEM_EC
GO:0098609	0.978	0.0449	9	181	cell-cell adhesion	BP	1	HMGB1,CAV1,NF2,ARG2,TFRC,ITGB3,FAM49B,EZR,CORO1A	down_ACOR_VSMC
GO:0044057	0.978	0.0782	2	110	regulation of system process	BP	1	IRX5,THRB	down_VCAV_EC
GO:0009895	0.978	0.0783	2	94	negative regulation of catabolic process	BP	1	UCHL5,USP14	down_VSAP_EC
GO:0045861	0.978	0.0792	2	71	negative regulation of proteolysis	BP	1	PAK2,PTGS2	up_VCAV_EC
GO:0060840	0.978	0.111	1	42	artery development	BP	1	ADAMTS6	down_ACOR_VSMC
GO:0008152	0.978	0.149	1	3714	metabolic process	BP	1	HOXA3	up_APUL_VSMC
GO:0051246	0.978	0.113	1	832	regulation of protein metabolic process	BP	1	MAP2K6	up_VFEM_EC
GO:0051304	0.978	0.112	1	38	chromosome separation	BP	1	CDC26	up_VSAP_EC
GO:1902904	0.978	0.112	1	38	negative regulation of supramolecular fiber	BP	1	SLIT2	up_VSAP_EC

GO:0016043	0.979	0.0265	169	1973	cellular component organization	BP	1	SYNPO2L,SH3TC2,PDLIM3,FGF13,RHOT1,FMOD,EPB41L4A,DNAJC6,SMAD6,ARHGAP28,ACTN2,PLCG2,DCBLD2,SNAP91,MID1,CDC7,PCGF5,EPYC,USP6NL,MBP,ZRANB1,PRDX4,RECK,SHROOM3,FEZ1,NACC2,PRKAA2,ITM2C,FERMT1,BMP4,SYT16,LCAT,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,FGFR2,PCBD1,TP53BP1,MX1,MFAP4,ABCA1,GJA1,ATRX,TRPS1,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,TP53INP1,ATXN2,RERG,SPINT1,GLRB,PKP4,ZNF365,AR,CTSS,STX11,LMO4,TMEM108,CLCN3,ARHGEF26,NEBL,IFT43,ZMYM2,LIMS2,F2RL1,STN1,MARCH5,ERO1B,GABARAPL1,BNIP3,EGLN1,CACNB3,SLC12A7,CDKN1A,JMY,CRLF3,TSPYL5,CLSTN1,LRRC8C,NRP1,GPM6A,LRPAP1,ULK2,DMPK,NPNT,UNC5B,SCP2,SMARCD3,EVL,SPINT2,SLITRK5,TBX20,P4HA1,DES,PRKCE,MARF1,FZD3,MYO1B,TTC17,RND1,DAG1,APP,ECM2,PSEN1,SGSM2,SYNJ2BP,CHD7,SHPRH,PIK3C3,LAMP2,JUP,DMXL1,SIPA1L1,DDR2,CLN8,PERP,DUSP22,SSH3,EDN1,PHF20,NID1,GTF2A1L,AKTIP,KCNC4,LRRC4,ASAP1,FAM107A,ATG16L2,DMC1,DDIT4,SERPINB5,JAM3,B2M,DISC1,KIF9,SCAMP5,TNFRSF11B,TTC19,TACC1,IGFBP7,SBF2,GAA,ATXN10,FEZ2,SUN1,MAP3K7,INPP5K,FAF2,RAB5C,PFKL,AZIN2,WASL,ATP2C1,N	up_ACOR_VSMC
GO:1901564	0.979	0.0259	150	2053	organonitrogen compound metabolic process	BP	1	ACSL3,PRPSAP1,HMGB1,SREBF1,ACLY,POLE3,USP1,IRAK1,ILF3,ENSCAFG00000016095,USP4,BCAT1,EIF4A3,HMGCR,NNT,HNRNPD,VARS,UBE2S,NEDD4,THOP1,U2AF2,PSMD3,PSMD7,SLC29A1,METAP2,PPM1G,RRBP1,PPP1R15B,MPDU1,SLC35C2,MRPS18B,RAN,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,BIRC5,PRMT1,CAV1,CDK1,RAD51,CASP2,FANCI,XYLT1,TRUB2,NF2,PFAS,AURKB,MMP14,TK1,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,SMARCC1,PLK3,DHX33,ARG2,UHRF1,CKS2,PDCD2,RNF152,DHCR24,BRCA1,MVD,FASTKD3,NOC2L,EIF5A,B4GALT1,PRCP,ELOVL1,FARSA,RAP2C,UBE2J2,YWHAB,CYCS,NCL,RAC1,NUP62,UGDH,MRPL37,EMP2,DTL,PDXP,HASPIN,AADAT,CACTIN,GSTO1,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,ELOVL6,RBM14,RAD23A,SGPL1,CYC1,NOLC1,CDC20,TTK,BAP1,RARS,ATP5F1A,PUM3,MAST2,MELK,DCK,ENSCAFG00000006478,PRPS1,ENSCAFG00000013366,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,ENSCAFG00000005637,PDHA1,TADA2A,PMPCA,SERPINH1,TINF2,JMJD6,GGH,MRPL18,NUDT1,DELE1,PGD,CCNB3,UBE2C,NUS1,UBA2,MTBP,CTPS1,NECAB3,TTLL1,EIF3M,AMER1,ATP5F1D,DCUN1D5,NUDT3,PPI	down_ACOR_VSMC
GO:0051252	0.979	0.0304	40	1051	regulation of RNA metabolic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RBM38,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0051603	0.979	0.0345	20	305	proteolysis involved in cellular protein catabolic process	BP	1	FOXRED2,ABTB1,CTSS,VPS36,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,UBQLN2,CTSF,CDC26,KEAP1	up_VSAP_EC
GO:0006325	0.979	0.0388	14	234	chromatin organization	BP	1	NAA60,SMARCD2,DDB2,GATAD1,MYC,H2AFJ,PHF1,CDK9,KDM2B,WDR82,CENPP,DR1,SMARCA2,KDM3B	up_VSAP_EC
GO:0030162	0.979	0.0435	9	202	regulation of proteolysis	BP	1	TNIP1,CASP8,PAK2,OTUD4,PTGS2,BCL10,HMGB1,PMAIP1,PSMB9	up_VCAV_EC
GO:0002697	0.979	0.062	3	85	regulation of immune effector process	BP	1	HMGB1,TFRC,FAM49B	down_ACOR_VSMC
GO:0042254	0.979	0.0637	3	128	ribosome biogenesis	BP	1	MRPL1,PDCD11,RSL24D1	down_VSAP_EC
GO:0045165	0.979	0.0743	2	65	cell fate commitment	BP	1	HOXC10,ARHGEF2	down_ACOR_VSMC
GO:0032869	0.979	0.0758	2	57	cellular response to insulin stimulus	BP	1	SESN3,INPP5K	up_ACOR_VSMC
GO:0048706	0.979	0.0754	2	59	embryonic skeletal system development	BP	1	BMP4,FGFR2	up_ACOR_VSMC

GO:0030258	0.979	0.0745	2	71	lipid modification	BP	1	APOD,IMPA1	up_VCAV_EC
GO:0006810	0.979	0.0775	2	1244	transport	BP	1	TRIM9,CA9	up_VFEM_EC
GO:0031023	0.979	0.0753	2	58	microtubule organizing center organization	BP	1	CEP85,FBXW5	up_VSAP_EC
GO:0007187	0.979	0.105	1	43	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second	BP	1	PRMT5	down_ACOR_VSMC
GO:0019722	0.979	0.107	1	45	calcium-mediated signaling	BP	1	GSTO1	down_ACOR_VSMC
GO:0097164	0.979	0.106	1	44	ammonium ion metabolic process	BP	1	ACSL3	down_ACOR_VSMC
GO:0032872	0.979	0.105	1	77	regulation of stress-activated MAPK cascade	BP	1	SASH1	down_VCAV_EC
GO:0033045	0.979	0.106	1	38	regulation of sister chromatid segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0033036	0.979	0.108	1	852	macromolecule localization	BP	1	SIX1	up_VFEM_EC
GO:0006405	0.979	0.108	1	39	RNA export from nucleus	BP	1	NUP98	up_VSAP_EC
GO:0006497	0.979	0.106	1	38	protein lipidation	BP	1	ZDHHC8	up_VSAP_EC
GO:0048489	0.979	0.108	1	38	synaptic vesicle transport	BP	1	STX4	up_VSAP_EC
GO:0048813	0.979	0.105	1	39	dendrite morphogenesis	BP	1	PQBP1	up_VSAP_EC
GO:0097480	0.979	0.108	1	38	establishment of synaptic vesicle localization	BP	1	STX4	up_VSAP_EC
GO:0043604	0.979751339	0.06047	3	288	amide biosynthetic process	BP	1	KLHL25,PRKCD,PM20D1	up_ACOR_EC
GO:0050793	0.98	0.0279	48	731	regulation of developmental process	BP	1	HMGB1,FMNL3,HMGA1,SLC29A1,MTDH,SRRT,FBXO5,HSPA9,NAB2,PRELID1,INSIG1,PRMT1,CAV1,NF2,MMP14,EZH2,GREM1,CDK4,HMGB3,HOXA7,ARG2,PDCD2,HOXB7,B4GALT1,TFRC,PPARD,RAC1,EMP2,RSL1D1,HMGB2,CDC42EP4,EZR,TOX,RBM14,CORO1A,SGPL1,BEND6,CDC20,ASPM,CTH,ARHGEF2,TWIST2,HOXA9,GLI1,HMGN1,SIX4,TPBG,ANXA7	down_ACOR_VSMC
GO:0015833	0.98	0.0305	32	521	peptide transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,RAN,HM13,BIRC5,INSIG1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA	down_ACOR_VSMC
GO:0030163	0.98	0.0328	21	365	protein catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,EZR,UBE2K,RAD23A,CDC20,BAP1,PSMC1,UBE2C,AMER1	down_ACOR_VSMC
GO:0009199	0.98	0.0598	3	100	ribonucleoside triphosphate metabolic	BP	1	ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0022412	0.98	0.0618	3	76	cellular process involved in reproduction in multicellular organism	BP	1	SLIT2,ZNF449,ZBTB16	up_VSAP_EC
GO:0045862	0.98	0.0712	2	112	positive regulation of proteolysis	BP	1	IFT57,PACSIN3	down_VCAV_EC
GO:0030029	0.98	0.0727	2	239	actin filament-based process	BP	1	CDC42EP5,KANK1	up_AFEM_EC
GO:0007369	0.98	0.0723	2	63	gastrulation	BP	1	AMOT,HHEX	up_VCAV_EC
GO:0007163	0.98	0.0713	2	60	establishment or maintenance of cell	BP	1	WNT11,RAB11FIP2	up_VSAP_EC
GO:1902275	0.98	0.073	2	60	regulation of chromatin organization	BP	1	PHF1,CDK9	up_VSAP_EC
GO:0070302	0.98	0.1	1	78	regulation of stress-activated protein kinase	BP	1	SASH1	down_VCAV_EC
GO:0007088	0.98	0.0997	1	64	regulation of mitotic nuclear division	BP	1	NAA10	down_VSAP_EC
GO:0018022	0.98	0.102	1	36	peptidyl-lysine methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0008033	0.98	0.101	1	52	tRNA processing	BP	1	TRMT9B	up_VCAV_EC
GO:0051641	0.98	0.105	1	858	cellular localization	BP	1	SIX1	up_VFEM_EC
GO:0090304	0.98	0.109	1	1694	nucleic acid metabolic process	BP	1	GATA5	up_VPUL_VSMC

GO:0043624	0.98	0.101	1	39	cellular protein complex disassembly	BP	1	F2RL1	up_VSAP_EC
GO:1902749	0.98	0.101	1	39	regulation of cell cycle G2/M phase transition	BP	1	CDC25B	up_VSAP_EC
GO:0006518	0.980412641	0.05878	3	290	peptide metabolic process	BP	1	PCSK1N,ENSCAFG00000028814,KLHL25	up_ACOR_EC
GO:0033554	0.981	0.0265	53	708	cellular response to stress	BP	1	FZD1,ACKR3,MAP3K14,ARHGEF5,AXIN2,INSIG2,PPARGC1B,FOXRED2,CRADD,ABL1,SESN1,OSR1,MAP3K5,CDC42EP5,DDB2,MGST1,TNKS1BP1,AMBRA1,F2RL1,NFE2L2,PDK2,MFN2,ZFP36L1,FXN,PIK3R1,NEIL2,MYC,SCARA5,SLC12A6,HIC1,RTN4RL1,SASH1,FBXO4,MYD88,ATRIP,PHF1,NPAS2,FBXO7,CDK9,AP5Z1,YPEL3,ZNF580,ZBTB4,QARS,UBQLN2,HTRA2,ASS1,FLOT1,NCK1,HMOX1,MAP2K2,NPRL3,DDIT4	up_VSAP_EC
GO:1901987	0.981	0.0481	5	107	regulation of cell cycle phase transition	BP	1	CDC7,NACC2,CDKN1A,APP,FAM107A	up_ACOR_VSMC
GO:0000280	0.981	0.0516	4	145	nuclear division	BP	1	MZT1,NAA10,KPNB1,PDS5B	down_VSAP_EC
GO:0050890	0.981	0.0693	2	67	cognition	BP	1	HMGCR,AAAS	down_ACOR_VSMC
GO:0017157	0.981	0.0705	2	58	regulation of exocytosis	BP	1	F2RL1,STX4	up_VSAP_EC
GO:0046488	0.981	0.1	1	44	phosphatidylinositol metabolic process	BP	1	VAC14	down_ACOR_VSMC
GO:0090068	0.981	0.0953	1	78	positive regulation of cell cycle process	BP	1	LSM10	down_VCAV_EC
GO:1901988	0.981	0.0984	1	63	negative regulation of cell cycle phase transition	BP	1	CDKN1A	down_VSAP_EC
GO:2001252	0.981	0.0977	1	61	positive regulation of chromosome organization	BP	1	CTNNB1	down_VSAP_EC
GO:0016525	0.981	0.0997	1	38	negative regulation of angiogenesis	BP	1	SYNJ2BP	up_ACOR_VSMC
GO:0034614	0.981	0.0972	1	39	cellular response to reactive oxygen species	BP	1	PARK7	up_ACOR_VSMC
GO:2000181	0.981	0.0997	1	38	negative regulation of blood vessel	BP	1	SYNJ2BP	up_ACOR_VSMC
GO:0016070	0.981	0.104	1	1479	RNA metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0036503	0.981	0.0973	1	47	ERAD pathway	BP	1	USP13	up_VCAV_EC
GO:0019538	0.981	0.107	1	1713	protein metabolic process	BP	1	SLIT2	up_VPUL_VSMC
GO:0006885	0.981	0.0993	1	39	regulation of pH	BP	1	PDK2	up_VSAP_EC
GO:1990823	0.981	0.0973	1	39	response to leukemia inhibitory factor	BP	1	RARG	up_VSAP_EC
GO:1990830	0.981	0.0973	1	39	cellular response to leukemia inhibitory factor	BP	1	RARG	up_VSAP_EC
GO:0006974	0.981212704	0.05065	4	333	cellular response to DNA damage stimulus	BP	1	BRSK1,FIGNL1,CLU,PRKCD	up_ACOR_EC
GO:0046700	0.9815278	0.09404	1	147	heterocycle catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0002520	0.981687835	0.05552	3	279	immune system development	BP	1	FZD5,PTGER4,CLSTN1	up_ACOR_EC
GO:0008380	0.981778388	0.09301	1	149	RNA splicing	BP	1	RBM38	up_ACOR_EC

GO:0044249	0.982	0.0226	155	1851	cellular biosynthetic process	BP	1	TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,GALNT10,LBH,ST3GAL5,GATA5,GATA4,CDC7,PCGF5,HTR2B,MEIS2,B3GALNT2,MAT2B,NACC2,MLLT3,ITM2C,BMP4,LCAT,ZNF331,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,UGCG,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,PIGG,ANKRD1,F2RL1,FAM129A,GGPS1,DAPK1,PKNOX2,RBM4B,HKR1,MAGT1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,STT3B,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,FUT11,MOXD1,CCNT1,CRLS1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,PIK3C3,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,EOGT,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,PTS,RPAIN,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL	up_ACOR_VSMC
GO:0019438	0.982	0.0256	49	1258	aromatic compound biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,ADCY6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,UROS,ENTPD3,ATP5MC1,CXXC5,TEAD1,ADK,CC2D1A,GLI3,PARK7,MYDGF,AMPD2,MAVS,LOXL3,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0034654	0.982	0.0258	48	1236	nucleobase-containing compound biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,ADCY6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,ENTPD3,ATP5MC1,CXXC5,TEAD1,ADK,CC2D1A,GLI3,PARK7,MYDGF,AMPD2,MAVS,LOXL3,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0044248	0.982	0.0264	43	691	cellular catabolic process	BP	1	PLK2,LYZ,CDA,TNFAIP3,CTSC,WWP1,USP33,RALB,PIPOX,PSME4,PELI1,SPTLC2,CASP8,MTOR,TENT2,CNOT6,DEPP1,ENC1,SH3GLB1,ENSCAFG00000024323,PLCG2,PAN3,USP28,CNOT7,SMG7,HMGB1,PMAIP1,RIPK1,USP13,USP38,USP37,BLVRA,C7H18orf25,CUL4A,UBE2D1,HIF1A,RBBP6,DCP2,TNFAIP1,PSMB9,PSMD12,TET2,ITCH	up_VCAV_EC
GO:0048584	0.982	0.0266	37	592	positive regulation of response to stimulus	BP	1	HMGB1,IRAK1,HMGA1,NEDD4,MNDA,SLC29A1,MTDH,CTDNEP1,SLC35C2,CAV1,CASP2,TIMELESS,EZH2,GREM1,MAP3K20,PCNA,DHX33,ARG2,TFRC,PPARD,FAM49B,RAC1,NUP62,EMP2,CACTIN,HMGB2,GSTO1,EZR,RBM14,MIOS,POLR3F,ASPM,PRMT5,CTH,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0043603	0.982	0.0291	24	372	cellular amide metabolic process	BP	1	EIF4A2,TARSL2,UGCG,NIT2,FAM129A,ERO1B,DAPK1,RBM4B,ENSCAFG00000028814,ORMDL3,SMPD1,SCG5,APP,PSEN1,PCSK6,LAMP2,CLN8,NEU3,UBA52,CTIF,ERAP1,PARK7,ELOVL7,NGRN	up_ACOR_VSMC
GO:0019941	0.982	0.0319	16	258	modification-dependent protein catabolic process	BP	1	FOXRED2,ABTB1,VPS36,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,FBXO7,UBA7,RNF166,RNF216,UBQLN2,CDC26,KEAP1	up_VSAP_EC
GO:0009057	0.982	0.0324	15	473	macromolecule catabolic process	BP	1	LRP1,CHID1,TIMP2,PSMF1,SAMD4B,RNF216,PARK7,ZFP36L1,CLEC16A,SEC61B,HM13,PYM1,FBH1,LONP2,PACSIN3	down_VCAV_EC
GO:0051960	0.982	0.0348	11	216	regulation of nervous system development	BP	1	SRRT,NF2,EZH2,HMGB2,BEND6,CDC20,ASPM,ARHGEF2,GLI1,SIX4,TPBG	down_ACOR_VSMC
GO:0032101	0.982	0.0393	8	173	regulation of response to external stimulus	BP	1	HMGB1,TFPI,CAV1,ARG2,PPARD,RAC1,CACTIN,BAP1	down_ACOR_VSMC
GO:0051046	0.982	0.0385	8	174	regulation of secretion	BP	1	ACSL3,HMGB1,SREBF1,SDC1,BIRC5,ARG2,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:0007423	0.982	0.041	7	155	sensory organ development	BP	1	INSIG1,NF2,SMG9,PHACTR4,JMJD6,HMGN1,SIX4	down_ACOR_VSMC
GO:0006914	0.982	0.0422	6	141	autophagy	BP	1	HMGB1,SREBF1,MTDH,PLK3,RNF152,ANXA7	down_ACOR_VSMC

GO:0061919	0.982	0.0422	6	141	process utilizing autophagic mechanism	BP	1	HMGB1,SREBF1,MTDH,PLK3,RNF152,ANXA7	down_ACOR_VSMC
GO:0006913	0.982	0.0418	6	124	nucleocytoplasmic transport	BP	1	CDH1,ANKRD54,PIK3R1,NUP98,SNUPN,MAVS	up_VSAP_EC
GO:0051169	0.982	0.0418	6	124	nuclear transport	BP	1	CDH1,ANKRD54,PIK3R1,NUP98,SNUPN,MAVS	up_VSAP_EC
GO:0034470	0.982	0.0498	4	154	ncRNA processing	BP	1	AARS,MRPL1,PDCD11,RTCB	down_VSAP_EC
GO:0009144	0.982	0.054	3	103	purine nucleoside triphosphate metabolic	BP	1	ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0061025	0.982	0.0666	2	69	membrane fusion	BP	1	STXBP6,CORO1A	down_ACOR_VSMC
GO:0032103	0.982	0.0675	2	69	positive regulation of response to external	BP	1	HMGB1,RAC1	down_ACOR_VSMC
GO:0045666	0.982	0.065	2	68	positive regulation of neuron differentiation	BP	1	BEND6,ARHGEF2	down_ACOR_VSMC
GO:0007093	0.982	0.0681	2	59	mitotic cell cycle checkpoint	BP	1	CDKN2B,CDKN1A	up_ACOR_VSMC
GO:0051168	0.982	0.0662	2	57	nuclear export	BP	1	PARK7,PTPN14	up_ACOR_VSMC
GO:0033554	0.982	0.0674	2	708	cellular response to stress	BP	1	CXHXorf57,ARHGEF2	up_VPOR_EC
GO:0008643	0.982	0.0944	1	45	carbohydrate transport	BP	1	EZR	down_ACOR_VSMC
GO:0001841	0.982	0.0959	1	44	neural tube formation	BP	1	PHACTR4	down_ACOR_VSMC
GO:0031503	0.982	0.0919	1	79	protein-containing complex localization	BP	1	IFT57	down_VCAV_EC
GO:0006888	0.982	0.092	1	49	ER to Golgi vesicle-mediated transport	BP	1	ZW10	up_VCAV_EC
GO:0030010	0.982	0.0938	1	41	establishment of cell polarity	BP	1	RAB11FIP2	up_VSAP_EC
GO:0099173	0.982	0.0938	1	40	postsynapse organization	BP	1	LRP4	up_VSAP_EC
GO:0019439	0.982975725	0.08811	1	150	aromatic compound catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0009058	0.983	0.0215	160	1910	biosynthetic process	BP	1	TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,GALNT10,LBH,ST3GAL5,GATA5,GATA4,CDC7,PCGF5,HTR2B,MEIS2,B3GALNT2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,LCAT,ZNF331,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,FAXDC2,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,UGCG,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,PPIP5K1,ZNF174,PLAC8B,PIGG,ANKRD1,F2RL1,FAM129A,GGPS1,DAPK1,PKNOX2,RBM4B,HKR1,MAGT1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,STT3B,PFDN5,SCP2,ORMDL3,SMARCD3,SMPD1,TBX20,FUT11,MOXD1,CCDC3,CCNT1,CRLS1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,POMK,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,PIK3C3,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,EOGT,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,PTS,RPAIN,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029	up_ACOR_VSMC
GO:0018130	0.983	0.0242	49	1261	heterocycle biosynthetic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,ADCY6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,UROS,ENTPD3,ATP5MC1,CXXC5,TEAD1,ADK,CC2D1A,GLI3,PARK7,MYDGF,AMPD2,MAVS,LOXL3,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0016310	0.983	0.0254	41	641	phosphorylation	BP	1	HMGB1,IRAK1,MCM7,ILF3,HMGCR,SLC29A1,PPP1R15B,BIRC5,CAV1,CDK1,RAD51,NF2,AURKB,CDKN2C,EZH2,GREM1,MAP3K20,NEK2,CDK4,DHX33,CKS2,RAP2C,CYCS,RAC1,NUP62,EMP2,HASPIN,CACTIN,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,CYC1,TTK,MAST2,MELK,ARHGEF2,TADA2A,CCNB3,PIK3CD	down_ACOR_VSMC

GO:0042886	0.983	0.0258	32	527	amide transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,RAN,HM13,BIRC5,INSIG1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA	down_ACOR_VSMC
GO:0010564	0.983	0.0322	13	217	regulation of cell cycle process	BP	1	CDC7,NACC2,BMP4,ATRX,PKP4,CDKN1A,CRLF3,PRKCE,APP,PIK3C3,EDN1,FAM107A,RPRD1B	up_ACOR_VSMC
GO:0007420	0.983	0.0374	8	169	brain development	BP	1	NF2,EZH2,SMG9,WDR62,ARCN1,ASPM,ENSCAFG00000010224,GLI1	down_ACOR_VSMC
GO:0016049	0.983	0.0439	5	124	cell growth	BP	1	SLC29A1,MMP14,CDKN2C,IQGAP1,BAP1	down_ACOR_VSMC
GO:0007178	0.983	0.0457	4	107	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	1	SLC29A1,CAV1,GREM1,RBM14	down_ACOR_VSMC
GO:0090068	0.983	0.0527	3	78	positive regulation of cell cycle process	BP	1	CRADD,CDC25B,LSM10	up_VSAP_EC
GO:0007254	0.983	0.0618	2	67	JNK cascade	BP	1	HMGB1,MAP3K20	down_ACOR_VSMC
GO:0007265	0.983	0.061	2	121	Ras protein signal transduction	BP	1	NOTCH2,ARHGEF25	down_VCAV_EC
GO:0006310	0.983	0.0641	2	93	DNA recombination	BP	1	TFRC,RBBP8	down_VSAP_EC
GO:0051234	0.983	0.0671	2	1283	establishment of localization	BP	1	TRIM9,CA9	up_VFEM_EC
GO:0032434	0.983	0.0641	2	59	regulation of proteasomal ubiquitin-dependent protein catabolic process	BP	1	RNF166,UBQLN2	up_VSAP_EC
GO:0007411	0.983	0.0878	1	45	axon guidance	BP	1	B3GNT2	down_ACOR_VSMC
GO:0097485	0.983	0.0878	1	45	neuron projection guidance	BP	1	B3GNT2	down_ACOR_VSMC
GO:0071103	0.983	0.0904	1	80	DNA conformation change	BP	1	CABIN1	down_VCAV_EC
GO:0006643	0.983	0.0894	1	68	membrane lipid metabolic process	BP	1	UGCG	down_VSAP_EC
GO:0044271	0.983	0.0942	1	1501	cellular nitrogen compound biosynthetic	BP	1	HOXA9	up_AORT_EC
GO:0007041	0.983	0.0907	1	41	lysosomal transport	BP	1	NCOA4	up_VSAP_EC
GO:0034641	0.984	0.0207	155	2171	cellular nitrogen compound metabolic process	BP	1	EDNRB,HCLS1,NPR1,KIT,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,TNIP1,PDGFB,TMEM173,RELN,CD34,MOV10,IWS1,MEF2C,ATF3,CHD7,DLL4,WWP1,TLR4,NOS3,NLRC5,QKI,GATA3,EDN1,HOXB8,TCF4,SMAD1,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,PSME4,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,ADSS,YES1,GUCY1A1,ODC1,SPTLC2,ARG2,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,BMP2,HMG20A,HHEX,CREM,TUT7,SCAF11,CNOT6,RSC1A1,ENC1,CCAR1,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,ARID4B,HMBOX1,BAZ1A,PRKD2,THOC1,SWAP70,SMARCA4,ELOVL7,TLR3,ENSCAFG00000024323,NCK1,ESCO1,TRMT9B,DPH5,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,JAG1,NSD1,GUCY1B1,MRRF,TOP1,ETAA1,TCERG1,CTDSPL2,CREB1,BCL10,BASP1,PAN3,PRPF39,CNOT7,SMG7,GCH1,ENSCAFG00000002897,DCK,ASF1A,HMGB1,AHR,NOS2,BDP1,U2SURP,ZNF789,BLM,NUP133,NR4A2,RIPK1,SMC5,ZNF317,USP13,ITGA6,RAD21,RAD17,SKIL,GPBP1,USP37,BLVRA,WTAP,MTA2,CUL4A,NR1D2,KDM5A,HIF1A,KDM3A,ZNF146,ATRX,NR4A1,HIST2H2AC,HP1BP3,ARID5A,TOPBP1,ENSCAFG00000002015,RBBP6,ZC3H13,ZNF354A,DCP2,IVNS1ABP,ZEB1,TET2,ARHGE	up_VCAV_EC
GO:0065003	0.984	0.0228	45	616	protein-containing complex assembly	BP	1	FAM107A,ARHGEF5,ACACB,SLIT2,NDUFS7,ABL1,CDC42EP5,NAA60,C1QTNF2,CLDN1,CDC42EP2,PSMD9,HSD17B8,ICE1,DMAC2,SCARA5,SBF2,CLYBL,NDUFAF3,NDUFB10,NUP98,KCNB1,LCAT,PCBD1,LIMD1,EIF3G,RAF1,CYBA,CENPP,EIF3K,STX4,EIF3L,SMIM20,VPS11,KCNC4,EIF3D,HTRA2,FLOT1,COA1,NCK1,ULK1,HMOX1,BAG4,JCHAIN,SOAT1	up_VSAP_EC
GO:0072359	0.984	0.0271	21	368	circulatory system development	BP	1	ELK3,MTDH,HOXA3,CAV1,ANPEP,GREM1,ADIPOR2,HOXA7,SMG9,E2F8,B4GALT1,PRCP,ADAMTS6,NCL,EMP2,FOSL1,SGPL1,CTH,GLI1,JMJD6,NUS1	down_ACOR_VSMC

GO:1901700	0.984	0.0272	21	364	response to oxygen-containing compound	BP	1	SREBF1,IRAK1,MTDH,PPP1R15B,BIRC5,INSIG1,CAV1,RAD51,TIMELESS,EZH2,CDK4,SMARCC1,PLK3,PDXP,CACTIN,HMGB2,ENSCAFG00000005299,EZR,SIGMAR1,NCOA5,ARHGEF2	down_ACOR_VSMC
GO:0006935	0.984	0.0373	6	143	chemotaxis	BP	1	HMGB1,B3GNT2,RAC1,HMGB2,CORO1A,PIK3CD	down_ACOR_VSMC
GO:0042330	0.984	0.0373	6	143	taxis	BP	1	HMGB1,B3GNT2,RAC1,HMGB2,CORO1A,PIK3CD	down_ACOR_VSMC
GO:0018205	0.984	0.0381	6	122	peptidyl-lysine modification	BP	1	LIPT2,PRKAA2,ATRX,PHF20,MAP3K7,PARK7	up_ACOR_VSMC
GO:0007265	0.984	0.0378	6	121	Ras protein signal transduction	BP	1	ABCA1,ARHGEF26,F2RL1,CDKN1A,NRP1,SYNJ2BP	up_ACOR_VSMC
GO:0033044	0.984	0.0376	6	127	regulation of chromosome organization	BP	1	AXIN2,MYC,FBXO4,PHF1,CDK9,CDC26	up_VSAP_EC
GO:0060271	0.984	0.0493	3	89	cilium assembly	BP	1	EXOC5,IQUB,SPATA6	up_VCAV_EC
GO:0045732	0.984	0.0491	3	78	positive regulation of protein catabolic process	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:0010948	0.984	0.0605	2	96	negative regulation of cell cycle process	BP	1	NAA10,CDKN1A	down_VSAP_EC
GO:0006006	0.984	0.0613	2	61	glucose metabolic process	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:0034641	0.984	0.0671	2	2171	cellular nitrogen compound metabolic	BP	1	HOXA9,LNPEP	up_AORT_EC
GO:0009612	0.984	0.0834	1	47	response to mechanical stimulus	BP	1	CASP2	down_ACOR_VSMC
GO:0042445	0.984	0.0872	1	46	hormone metabolic process	BP	1	SGPL1	down_ACOR_VSMC
GO:0030509	0.984	0.0858	1	47	BMP signaling pathway	BP	1	GREM1	down_ACOR_VSMC
GO:0032886	0.984	0.0855	1	81	regulation of microtubule-based process	BP	1	CLIP3	down_VCAV_EC
GO:0030856	0.984	0.0869	1	41	regulation of epithelial cell differentiation	BP	1	BMP4	up_ACOR_VSMC
GO:0097479	0.984	0.0856	1	41	synaptic vesicle localization	BP	1	STX4	up_VSAP_EC
GO:0055114	0.984232624	0.08283	1	157	oxidation-reduction process	BP	1	FMO3	up_ACOR_EC
GO:1901361	0.984759176	0.08063	1	154	organic cyclic compound catabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0006464	0.985	0.0197	80	1162	cellular protein modification process	BP	1	HMGB1,SREBF1,POLE3,USP1,IRAK1,ILF3,USP4,HMGCR,UBE2S,U2AF2,SLC29A1,METAP2,PPM1G,PPP1R15B,MPDU1,SLC35C2,B3GNT2,UBE2T,BIRC5,PRMT1,CAV1,CDK1,RAD51,FANCI,NF2,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,DHX33,UHRF1,CKS2,RNF152,BRCA1,NOC2L,B4GALT1,RAP2C,UBE2J2,YWHAB,RAC1,NUP62,EMP2,DTL,HASPIN,CACTIN,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,RBM14,CDC20,TTK,BAP1,PUM3,MAST2,MELK,PRMT5,CTH,ARHGEF2,TADA2A,TINF2,JMJD6,CCNB3,UBE2C,NUS1,UBA2,MTBP,TTLL1,AMER1,DCUN1D5,PPIB,PIK3CD	down_ACOR_VSMC
GO:0036211	0.985	0.0197	80	1162	protein modification process	BP	1	HMGB1,SREBF1,POLE3,USP1,IRAK1,ILF3,USP4,HMGCR,UBE2S,U2AF2,SLC29A1,METAP2,PPM1G,PPP1R15B,MPDU1,SLC35C2,B3GNT2,UBE2T,BIRC5,PRMT1,CAV1,CDK1,RAD51,FANCI,NF2,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,DHX33,UHRF1,CKS2,RNF152,BRCA1,NOC2L,B4GALT1,RAP2C,UBE2J2,YWHAB,RAC1,NUP62,EMP2,DTL,HASPIN,CACTIN,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,RBM14,CDC20,TTK,BAP1,PUM3,MAST2,MELK,PRMT5,CTH,ARHGEF2,TADA2A,TINF2,JMJD6,CCNB3,UBE2C,NUS1,UBA2,MTBP,TTLL1,AMER1,DCUN1D5,PPIB,PIK3CD	down_ACOR_VSMC
GO:0006351	0.985	0.0225	40	1069	transcription, DNA-templated	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC

GO:0044267	0.985	0.0248	27	1583	cellular protein metabolic process	BP	1	LEP,PRR16,USP54,GAS1,CRYAB,CTSS,F3,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CLEC16A,CYLD,LRRC15,RECK,DCUN1D3,RAB7A,AXIN2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,RNF181	up_AFEM_EC
GO:0010562	0.985	0.0261	17	312	positive regulation of phosphorus metabolic process	BP	1	ACSL3,HMGB1,IRAK1,SLC29A1,CAV1,CDK1,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,EMP2,CLSPN,ARHGEF2	down_ACOR_VSMC
GO:0045937	0.985	0.0261	17	312	positive regulation of phosphate metabolic process	BP	1	ACSL3,HMGB1,IRAK1,SLC29A1,CAV1,CDK1,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,EMP2,CLSPN,ARHGEF2	down_ACOR_VSMC
GO:0046903	0.985	0.029	13	255	secretion	BP	1	ACSL3,HMGB1,SREBF1,STXBP6,SDC1,BIRC5,CAV1,FAM129B,ARG2,PREB,ENSCAFG00000005299,EZR,CORO1A	down_ACOR_VSMC
GO:0048285	0.985	0.032	9	166	organelle fission	BP	1	BMP4,MX1,ATRX,MARCH5,BNIP3,MARF1,EDN1,DMC1,SUN1	up_ACOR_VSMC
GO:0044281	0.985	0.0327	8	622	small molecule metabolic process	BP	1	LEP,XYLT1,GPAM,ATP6V1B2,MOXD1,ACACB,NAPEPLD,PPARGC1A	up_AFEM_EC
GO:0016569	0.985	0.0333	7	144	covalent chromatin modification	BP	1	DDB2,PHF1,CDK9,KDM2B,WDR82,DR1,KDM3B	up_VSAP_EC
GO:0016570	0.985	0.0351	7	143	histone modification	BP	1	DDB2,PHF1,CDK9,KDM2B,WDR82,DR1,KDM3B	up_VSAP_EC
GO:0022618	0.985	0.0387	5	111	ribonucleoprotein complex assembly	BP	1	LIMD1,EIF3G,EIF3K,EIF3L,EIF3D	up_VSAP_EC
GO:0006807	0.985	0.0495	4	3221	nitrogen compound metabolic process	BP	1	HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0003012	0.985	0.0464	3	90	muscle system process	BP	1	CAV1,EZH2,ARG2	down_ACOR_VSMC
GO:0061136	0.985	0.0472	3	78	regulation of proteasomal protein catabolic process	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:0071103	0.985	0.0482	3	80	DNA conformation change	BP	1	NAA60,GATAD1,CENPP	up_VSAP_EC
GO:0016051	0.985	0.056	2	63	carbohydrate biosynthetic process	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:0019827	0.985	0.0573	2	59	stem cell population maintenance	BP	1	LBH,MED14	up_ACOR_VSMC
GO:0016485	0.985	0.0572	2	73	protein processing	BP	1	KLKB1,CASP8	up_VCAV_EC
GO:0050821	0.985	0.0829	1	48	protein stabilization	BP	1	CCT4	down_ACOR_VSMC
GO:0072331	0.985	0.0798	1	49	signal transduction by p53 class mediator	BP	1	CASP2	down_ACOR_VSMC
GO:0034645	0.985	0.0858	1	1546	cellular macromolecule biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0031123	0.985	0.0795	1	48	RNA 3'-end processing	BP	1	TUT7	up_VCAV_EC
GO:0090305	0.985	0.0791	1	49	nucleic acid phosphodiester bond	BP	1	MOV10	up_VCAV_EC
GO:0010608	0.985222116	0.07866	1	154	posttranscriptional regulation of gene	BP	1	KLHL25	up_ACOR_EC
GO:0006897	0.985588768	0.07707	1	158	endocytosis	BP	1	CALY	up_ACOR_EC
GO:0022607	0.986	0.0192	75	969	cellular component assembly	BP	1	FZD1,WNT11,FAM107A,ARHGEF5,WASF3,AMIGO1,LRRN3,ACACB,SLIT2,NDUFS7,ABL1,HDAC7,EMP2,CDC42EP5,FUZ,NAA60,C1QTNF2,RILPL2,CLDN1,CDC42EP2,PSMD9,GATAD1,HSD17B8,AMBRA1,F2RL1,MFN2,ICE1,FXN,PIK3R1,DMAC2,SCARA5,FGD4,SBF2,CLYBL,LOX,NDUFAF3,LRP4,NDUFB10,NUP98,HPS4,E2F4,KIF27,TMEM17,KCNB1,LCAT,PCBD1,LIMD1,PIP4K2B,EIF3G,MYO1B,RAF1,CYBA,CENPP,EIF3K,STX4,EIF3L,SMIM20,VPS11,KCNC4,EIF3D,ACVRL1,TTC8,UBQLN2,EMP3,HTRA2,FLOT1,COA1,NCK1,ULK1,CEP19,HMOX1,NPRL3,BAG4,JCHAIN,SOAT1	up_VSAP_EC
GO:0016070	0.986	0.0196	73	1479	RNA metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,CBX5,SARS,AARS,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,ZPR1,PTPN2,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,SND1,ENSCAFG00000002015,WWC3,PDCD11,KLF5,STRAP,DDIT3,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,ARF4,YWHAH,RTCB,SNRPA1,KDM3A	down_VSAP_EC

GO:0032774	0.986	0.0209	40	1073	RNA biosynthetic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0097659	0.986	0.0213	40	1072	nucleic acid-templated transcription	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,MYDGF,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,CRCP,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0016043	0.986	0.0218	35	1973	cellular component organization	BP	1	KCNC4,PRR16,RAB20,DLL1,CRYAB,KCND1,CTSS,PLXNA4,MLLT11,NEFH,MFAP4,PLAGL2,GREM1,CAMK2A,CLEC16A,CYLD,DNAL1,POSTN,CHCHD10,RECK,DCUN1D3,REEP2,BVES,RAB7A,AXIN2,ACACB,PPARGC1A,SPATA6,CDC42EP5,FAP,DMPK,ADAM17,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0090304	0.986	0.0221	29	1694	nucleic acid metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,MLLT11,LMCD1,THRB,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0044257	0.986	0.0235	21	327	cellular protein catabolic process	BP	1	FOXRED2,ABTB1,CTSS,VPS36,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,UBQLN2,CTSF,CDC26,HTRA2,KEAP1	up_VSAP_EC
GO:0000278	0.986	0.0289	9	331	mitotic cell cycle	BP	1	SNX18,KANK2,NABP2,POLDIP2,ZFP36L1,LSM10,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0006954	0.986	0.0341	6	147	inflammatory response	BP	1	HMGB1,B4GALT1,PRCP,HMGB2,BAP1,PIK3CD	down_ACOR_VSMC
GO:0006260	0.986	0.0405	4	98	DNA replication	BP	1	CIZ1,NUP98,CDK9,NFIB	up_VSAP_EC
GO:0016043	0.986	0.0437	4	1973	cellular component organization	BP	1	PRR16,EMP1,CAV1,SHOX2	up_VSAP_VSMC
GO:0051403	0.986	0.0441	3	89	stress-activated MAPK cascade	BP	1	HMGB1,MAP3K20,EZR	down_ACOR_VSMC
GO:0007018	0.986	0.0458	3	82	microtubule-based movement	BP	1	KIF21B,KIF3C,HIF1A	up_VCAV_EC
GO:0002573	0.986	0.0533	2	71	myeloid leukocyte differentiation	BP	1	HOXA7,TFRC	down_ACOR_VSMC
GO:0000077	0.986	0.0551	2	60	DNA damage checkpoint	BP	1	TP53BP1,CDKN1A	up_ACOR_VSMC
GO:0098727	0.986	0.0529	2	60	maintenance of cell number	BP	1	LBH,MED14	up_ACOR_VSMC
GO:2001252	0.986	0.0534	2	61	positive regulation of chromosome organization	BP	1	ATRX,HMBOX1	up_ACOR_VSMC
GO:1903047	0.986	0.0527	2	257	mitotic cell cycle process	BP	1	CAMK2A,DCUN1D3	up_AFEM_EC
GO:0044260	0.986	0.0604	2	2593	cellular macromolecule metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0010970	0.986	0.0786	1	48	transport along microtubule	BP	1	TRAK1	down_ACOR_VSMC
GO:0030308	0.986	0.0745	1	49	negative regulation of cell growth	BP	1	CDKN2C	down_ACOR_VSMC
GO:0099111	0.986	0.0786	1	48	microtubule-based transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0065004	0.986	0.0749	1	81	protein-DNA complex assembly	BP	1	CABIN1	down_VCAV_EC
GO:0001505	0.986	0.0767	1	69	regulation of neurotransmitter levels	BP	1	GSK3B	down_VSAP_EC
GO:0061025	0.986	0.0781	1	69	membrane fusion	BP	1	USO1	down_VSAP_EC
GO:0016571	0.986	0.0783	1	39	histone methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0033865	0.986	0.0764	1	43	nucleoside bisphosphate metabolic process	BP	1	ELOVL7	up_ACOR_VSMC
GO:0033875	0.986	0.0764	1	43	ribonucleoside bisphosphate metabolic	BP	1	ELOVL7	up_ACOR_VSMC
GO:0034032	0.986	0.0764	1	43	purine nucleoside bisphosphate metabolic	BP	1	ELOVL7	up_ACOR_VSMC
GO:0009059	0.986	0.0822	1	1563	macromolecule biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0006997	0.986	0.0773	1	42	nucleus organization	BP	1	NUP98	up_VSAP_EC
GO:0055067	0.986	0.0779	1	42	monovalent inorganic cation homeostasis	BP	1	PDK2	up_VSAP_EC

GO:0043170	0.987	0.0176	130	2980	macromolecule metabolic process	BP	1	PCOLCE,CST3,ADAMTS2,NOTCH2,PDGFRB,KIRREL1,SMAD9,LRP1,DCN,CFD,NAB2,NDN,PRNP,LUM,UBA52,FBN1,GLIPR2,BGN,LARP6,KANK2,COA1,BMPR1A,KRTCAP2,VKORC1,NABP2,LMO4,RECK,CLIP3,NUMBL,CHID1,ENSCAFG00000014978,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,PSMF1,LCAT,RHBDL1,SAMD4B,EEF2K,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,PCSK7,PLCL1,DDOST,CSPG4,VDR,PRMT6,TMEM161A,CXXC5,GFPT2,ASPN,PIGS,HS3ST3B1,LRPAP1,EIF3K,THY1,NECAB3,RNF216,TEAD1,WDR45,MRPL37,CC2D1A,B4GALT1,GLI3,PARK7,RPL27A,EEF2,MAST2,ZFP36L1,MYDGF,SASH1,SEC11C,CLEC16A,RNPEP,RPL27,COPS7A,RBM38,ARL2BP,IFT57,MAVS,MRPS11,CDH2,LOXL3,ORMDL3,GSDME,CAMK2D,RPS27,FUT8,ENSCAFG00000017708,SPRED1,RAB7B,A2M,SEC61B,IRX5,TSC22D3,MAPRE3,GLIS2,CDKL2,RAB31,HM13,PRKCSH,DDR2,SHC1,CRTAP,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,RPN2,KLHL29,ATOX1,LONP2,FOXO3,SOAT1,THRB,PACSIN3,ZBTB16,EIF4EBP1,RGMA,BRSK1,CDK14	down_VCAV_EC
GO:0001932	0.987	0.0217	24	416	regulation of protein phosphorylation	BP	1	HMGB1,IRAK1,HMGCR,SLC29A1,PPP1R15B,CAV1,RAD51,NF2,CDKN2C,EZH2,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,NUP62,EMP2,CACTIN,EZR,CLSPN,ARHGEF2,TADA2A,CCNB3	down_ACOR_VSMC
GO:0018193	0.987	0.0213	24	368	peptidyl-amino acid modification	BP	1	ENPP2,IL6R,FGF7,ABL1,OSR1,PDGFD,NAA60,KLF15,PLPP3,CAMKK2,TNKS1BP1,MORC3,LRP4,GALNT11,PHF1,WDR82,RAF1,DR1,TTL,NCK1,ULK1,TGFBR2,BAG4,LATS2	up_VSAP_EC
GO:0030163	0.987	0.0221	24	365	protein catabolic process	BP	1	FOXRED2,ABTB1,CTSS,HPSE,VPS36,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,AZIN2,FBXW5,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,TIMP2,UBQLN2,CTSF,CDC26,HTRA2,KEAP1	up_VSAP_EC
GO:0022610	0.987	0.0225	18	326	biological adhesion	BP	1	HMGB1,SLC29A1,CAV1,NF2,GREM1,HOXA7,ARG2,B4GALT1,TFRC,PPARD,ITGB3,FAM49B,RAC1,EMP2,EZR,CORO1A,RADIL,ITGA2	down_ACOR_VSMC
GO:0007346	0.987	0.0251	12	210	regulation of mitotic cell cycle	BP	1	MAP3K8,CDC7,NACC2,BMP4,ATRX,PTPN3,CDKN2B,CDKN1A,FZD3,APP,EDN1,FAM107A	up_ACOR_VSMC
GO:0071702	0.987	0.0287	9	687	organic substance transport	BP	1	LEP,CRY2,VPS26C,GPAM,SLC17A5,SLC6A6,REEP2,RAB7A,CCL5	up_AFEM_EC
GO:0010256	0.987	0.0321	6	129	endomembrane system organization	BP	1	PLEKHF1,RAB30,ATP8B2,XKR8,VPS11,FLOT1	up_VSAP_EC
GO:0008152	0.987	0.0412	5	3714	metabolic process	BP	1	HOXC10,HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0006807	0.987	0.0458	4	3221	nitrogen compound metabolic process	BP	1	BARX1,NKX2-5,BAMBI,ANKRD6	up_VPOR_VSMC
GO:0009895	0.987	0.0408	3	94	negative regulation of catabolic process	BP	1	SLC29A1,THRAP3,SMARCC1	down_ACOR_VSMC
GO:0090287	0.987	0.0428	3	91	regulation of cellular response to growth factor	BP	1	SLC29A1,CAV1,GREM1	down_ACOR_VSMC
GO:0071560	0.987	0.0498	2	72	cellular response to transforming growth	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:0033044	0.987	0.0486	2	127	regulation of chromosome organization	BP	1	NABP2,PRMT6	down_VCAV_EC
GO:0031570	0.987	0.0511	2	61	DNA integrity checkpoint	BP	1	TP53BP1,CDKN1A	up_ACOR_VSMC
GO:0034764	0.987	0.0703	1	50	positive regulation of transmembrane transport	BP	1	GSTO1	down_ACOR_VSMC
GO:0003279	0.987	0.0731	1	48	cardiac septum development	BP	1	ADAMTS6	down_ACOR_VSMC
GO:0044249	0.987	0.08	1	1851	cellular biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0090304	0.987763969	0.01955	33	1694	nucleic acid metabolic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC

GO:0019219	0.988	0.0175	43	1151	regulation of nucleobase-containing compound metabolic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,TMEM161A,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RBM38,MAVS,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,FBH1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0070727	0.988	0.0176	41	579	cellular macromolecule localization	BP	1	PEX7,WNT11,AXIN2,PLEKHF1,TBC1D10C,TBC1D2B,CDH1,FGF7,PEX2,EMP2,RILPL2,VPS36,TOM1,RAB11B,GLIS2,MORC3,MFN2,ICE1,ZFP36L1,PIK3R1,CRACR2B,CIZ1,FBXO4,LRP4,NUP98,TSPAN5,HPS4,FRMD6,FBXO7,KCNB1,LONP2,SNUPN,TAF8,STX4,VPS11,FLOT1,PEX6,MAVS,BAG4,NCOA4,LATS2	up_VSAP_EC
GO:0006518	0.988	0.0222	17	290	peptide metabolic process	BP	1	EIF4A2,TARSL2,FAM129A,ERO1B,DAPK1,RBM4B,ENSCAFG00000028814,SCG5,APP,PSEN1,PCSK6,LAMP2,UBA52,CTIF,ERAP1,PARK7,NGRN	up_ACOR_VSMC
GO:0006511	0.988	0.0228	15	253	ubiquitin-dependent protein catabolic process	BP	1	FOXRED2,ABTB1,VPS36,RBCK1,RNF24,FBXW4,FBXO4,RMND5A,FBXW5,FBXO7,RNF166,RNF216,UBQLN2,CDC26,KEAP1	up_VSAP_EC
GO:0001934	0.988	0.022	14	274	positive regulation of protein phosphorylation	BP	1	HMGB1,IRAK1,SLC29A1,CAV1,EZH2,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,EMP2,CLSPN,ARHGEF2	down_ACOR_VSMC
GO:0051093	0.988	0.0224	14	273	negative regulation of developmental process	BP	1	HMGB1,HSPA9,INSIG1,PRMT1,CAV1,EZH2,GREM1,HMGB3,HOXA7,PPARD,ASPM,TWIST2,HOXA9,SIX4	down_ACOR_VSMC
GO:0043408	0.988	0.0251	10	211	regulation of MAPK cascade	BP	1	HMGB1,IRAK1,HMGCR,CAV1,NF2,EZH2,MAP3K20,DHX33,NUP62,EZR	down_ACOR_VSMC
GO:1903530	0.988	0.0279	7	165	regulation of secretion by cell	BP	1	HMGB1,SREBF1,SDC1,BIRC5,ARG2,ENSCAFG00000005299,EZR	down_ACOR_VSMC
GO:1901342	0.988	0.0344	4	114	regulation of vasculature development	BP	1	MTDH,GREM1,EMP2,CTH	down_ACOR_VSMC
GO:0071103	0.988	0.0397	3	80	DNA conformation change	BP	1	ATRX,TSPYL5,SHPRH	up_ACOR_VSMC
GO:0007224	0.988	0.0671	1	50	smoothened signaling pathway	BP	1	GLI1	down_ACOR_VSMC
GO:0045055	0.988	0.0658	1	52	regulated exocytosis	BP	1	CORO1A	down_ACOR_VSMC
GO:0071772	0.988	0.0692	1	50	response to BMP	BP	1	GREM1	down_ACOR_VSMC
GO:0071773	0.988	0.0692	1	50	cellular response to BMP stimulus	BP	1	GREM1	down_ACOR_VSMC
GO:0051783	0.988	0.0656	1	72	regulation of nuclear division	BP	1	NAA10	down_VSAP_EC
GO:0030326	0.988	0.0682	1	51	embryonic limb morphogenesis	BP	1	CHD7	up_VCAV_EC
GO:0035113	0.988	0.0682	1	51	embryonic appendage morphogenesis	BP	1	CHD7	up_VCAV_EC
GO:0044267	0.988	0.0743	1	1583	cellular protein metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:1901576	0.988	0.0758	1	1877	organic substance biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0001764	0.988	0.0662	1	45	neuron migration	BP	1	PEX7	up_VSAP_EC
GO:0051053	0.988	0.0666	1	45	negative regulation of DNA metabolic process	BP	1	ACVRL1	up_VSAP_EC
GO:0051494	0.988	0.0698	1	44	negative regulation of cytoskeleton organization	BP	1	SLIT2	up_VSAP_EC
GO:0071705	0.989	0.0166	35	582	nitrogen compound transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,SLC35C2,RAN,HM13,BIRC5,INSIG1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA,MRPL18,SLC25A19	down_ACOR_VSMC
GO:0042327	0.989	0.0211	15	289	positive regulation of phosphorylation	BP	1	HMGB1,IRAK1,SLC29A1,CAV1,CDK1,EZH2,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,EMP2,CLSPN,ARHGEF2	down_ACOR_VSMC
GO:0022607	0.989	0.0212	14	969	cellular component assembly	BP	1	KCNC4,RAB20,CRYAB,KCND1,MFAP4,PLAGL2,GREM1,CYLD,DNAL1,RAB7A,ACACB,SPATA6,CDC42EP5,KANK1	up_AFEM_EC
GO:0032940	0.989	0.0229	11	231	secretion by cell	BP	1	HMGB1,SREBF1,STXBP6,SDC1,BIRC5,FAM129B,ARG2,PREB,ENSCAFG00000005299,EZR,CORO1A	down_ACOR_VSMC
GO:0043207	0.989	0.0222	10	216	response to external biotic stimulus	BP	1	IRAK1,HNRNPUL1,MTDH,CAV1,STMN1,CDK4,ARG2,CACTIN,HMGB2,EXOSC5	down_ACOR_VSMC
GO:0051707	0.989	0.0222	10	216	response to other organism	BP	1	IRAK1,HNRNPUL1,MTDH,CAV1,STMN1,CDK4,ARG2,CACTIN,HMGB2,EXOSC5	down_ACOR_VSMC

GO:0050801	0.989	0.0232	9	200	ion homeostasis	BP	1	HMGB1,HOXA3,CAV1,SLC30A1,TFRC,GSTO1,CORO1A,THADA,ANXA7	down_ACOR_VSMC
GO:0006397	0.989	0.0259	7	168	mRNA processing	BP	1	IWS1,QKI,SCAF11,PAN3,PRPF39,WTAP,RBBP6	up_VCAV_EC
GO:0005996	0.989	0.0351	3	85	monosaccharide metabolic process	BP	1	LEP,PRKCE,INPP5K	up_ACOR_VSMC
GO:0006139	0.989	0.0393	3	1909	nucleobase-containing compound metabolic	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0009141	0.989	0.0359	3	110	nucleoside triphosphate metabolic process	BP	1	ENSCAFG00000024323,SLC25A25,HIF1A	up_VCAV_EC
GO:0019318	0.989	0.0443	2	75	hexose metabolic process	BP	1	B4GALT1,GALE	down_ACOR_VSMC
GO:0006936	0.989	0.0451	2	74	muscle contraction	BP	1	CAV1,ARG2	down_ACOR_VSMC
GO:0019058	0.989	0.0438	2	64	viral life cycle	BP	1	PC,MAVS	up_VSAP_EC
GO:0016043	0.989	0.0672	1	1973	cellular component organization	BP	1	HDAC7	down_VPOR_EC
GO:0006261	0.989	0.0603	1	68	DNA-dependent DNA replication	BP	1	ZPR1	down_VSAP_EC
GO:0090288	0.989	0.0633	1	44	negative regulation of cellular response to growth factor stimulus	BP	1	SMAD6	up_ACOR_VSMC
GO:0140053	0.989	0.0615	1	47	mitochondrial gene expression	BP	1	NGRN	up_ACOR_VSMC
GO:0006139	0.989	0.0698	1	1909	nucleobase-containing compound metabolic	BP	1	GATA5	up_VPUL_VSMC
GO:0009058	0.989	0.0706	1	1910	biosynthetic process	BP	1	GATA5	up_VPUL_VSMC
GO:0055002	0.989	0.0632	1	45	striated muscle cell development	BP	1	SHOX2	up_VSAP_EC
GO:0044271	0.99	0.0128	121	1501	cellular nitrogen compound biosynthetic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,NACC2,MLLT3,BMP4,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,UGCG,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,CLSTN1,NPNT,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,MOXD1,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,LHX9,WFS1,AZIN2,PTS,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,NGRN,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0009987	0.99	0.0153	108	5086	cellular process	BP	1	TBX15,HOXA9,CMKLR1,MT2A,IRX3,IRX5,HOXC10,HOXA10,LEP,KCNC4,LBH,PRR16,USP54,CRY2,ENSCAFG00000009113,RAB20,XYLT1,GAS1,ANGPT4,HOXA7,CD40,DLL1,CRYAB,CPNE7,KCND1,CTSS,F3,VXN,PLXNA4,BPI,GPAM,FIBIN,MLLT11,NEFH,ENSCAFG00000018194,GPR1,LMCD1,CHRM2,TWIST2,MAB21L1,THRB,LGI4,MYO1D,MFAP4,ATP6V1B2,HCK,TMEM100,SLC6A6,PLAGL2,GREM1,KLHDC8B,HTR1D,NFE2L1,OVOL1,FAM53B,TPST2,AVPR1A,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,DNAL1,RASGEF1B,POSTN,CHCHD10,LRRC15,FAM13A,MYBL1,RECK,NR3C1,PTHLH,TBXA2R,EVI2B,KIF1A,MOXD1,DCUN1D3,UNC45B,REEP2,EAF1,BVES,LGR6,RAB7A,AXIN2,YEATS2,ATP6V0B,ALDH3B1,ACACB,NAPEPLD,PPARGC1A,SPATA6,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,LRRN2,AGPAT2,GCNT4,FOSL2,KANK1,TNC,RNF181,ANXA11,SOD1	up_AFEM_EC

GO:0048731	0.99	0.0139	86	1247	system development	BP	1	ELK3,HMGB1,FLNB,USP1,ANLN,ACSL4,EIF4A3,NEDD4,SLC29A1,MTDH,HOXA3,SF1,SRRT,FBXO5,HSPA9,NAB2,B3GNT2,PRELID1,INSIG1,PRMT1,CAV1,XYLT1,TIMELESS,NF2,ANPEP,MMP14,EZH2,STMN1,GREM1,ADIPOR2,CDK4,SMARCC1,HMGB3,HOXA7,SMG9,ARG2,PDCD2,HOXC10,HOXB7,GMNN,DHCR24,POC1A,WDR62,E2F8,B4GALT1,NAV2,PRCP,TFRC,ADAMTS6,PPARD,NCL,RAC1,EMP2,FOSL1,PLK4,IQGAP1,HOXC6,HMGB2,ARCN1,RAB35,HOXB5,TOX,HOXC4,SGPL1,NOLC1,BEND6,PHACTR4,CDC20,SLC20A1,ASPM,PRPS1,TBX15,ENSCAFG00000010224,CTH,ARHGEF2,HOXA9,SERPINH1,GLI1,JMJD6,MSC,RTCB,NUS1,HMGN1,SIX4,TPBG,AMER1	down_ACOR_VSMC
GO:0010468	0.99	0.015	48	1270	regulation of gene expression	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,SAMD4B,TFE3,NR3C1,HR,CLSTN1,PRMT6,CXXC5,EIF3K,TEAD1,CC2D1A,GLI3,PARK7,EEF2,ZFP36L1,MYDGF,RBM38,MAVS,LOXL3,FUT8,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,GREM1,FOXO3,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0006725	0.99	0.0161	34	1956	cellular aromatic compound metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,MOXD1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B,GCNT4	up_AFEM_EC
GO:0006508	0.99	0.0156	33	483	proteolysis	BP	1	RNPEP,FOXRED2,CST3,CRADD,ABTB1,KLKB1,MAP3K5,CTSS,CCBE1,VPS36,RECK,RBCK1,GAS1,MYC,RNF24,FKRP,FBXW4,CAPN5,FBXO4,RMND5A,FBXW5,FBXO7,UBA7,RNF166,LONP2,RNF216,OSBPL7,TIMP2,UBQLN2,CTSF,CDC26,HTRA2,KEAP1	up_VSAP_EC
GO:0019538	0.99	0.0172	29	1713	protein metabolic process	BP	1	LEP,PRR16,USP54,XYLT1,GAS1,CRYAB,CTSS,F3,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CLEC16A,CYLD,LRRC15,RECK,DCUN1D3,RAB7A,AXIN2,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,RNF181	up_AFEM_EC
GO:0007010	0.99	0.0168	29	441	cytoskeleton organization	BP	1	WNT11,FAM107A,ARHGEF5,WASF3,PPARGC1B,CEP85,SLIT2,FGF7,ABL1,EMP2,CDC42EP5,CORO2B,CDC42EP2,KLHL24,F2RL1,PIK3R1,DPYSL2,FRMD6,WIPF1,FBXW5,LIMD1,MYO1B,RAF1,TTL,ARHGAP12,ARHGAP10,NCK1,CEP19,BAG4	up_VSAP_EC
GO:0051241	0.99	0.0173	18	336	negative regulation of multicellular organismal process	BP	1	HMGB1,TFPI,SLC29A1,HSPA9,PRMT1,GREM1,HMGB3,HOXA7,ARG2,ANXA5,HOXC10,RAC1,CACTIN,EZR,ASPM,TWIST2,HOXA9,SIX4	down_ACOR_VSMC
GO:0030163	0.99	0.0209	10	365	protein catabolic process	BP	1	LRP1,TIMP2,PSMF1,RNF216,PARK7,CLEC16A,SEC61B,HM13,LONP2,PACSIN3	down_VCAV_EC
GO:0008104	0.99	0.0212	10	763	protein localization	BP	1	LEP,CRY2,VPS26C,GPAM,CYLD,LRRC15,REEP2,RAB7A,AXIN2,CCL5	up_AFEM_EC
GO:0048193	0.99	0.0272	5	116	Golgi vesicle transport	BP	1	SEC24B,KLHL20,MYO1B,SGSM2,LMF1	up_ACOR_VSMC
GO:0071826	0.99	0.0267	5	117	ribonucleoprotein complex subunit	BP	1	LIMD1,EIF3G,EIF3K,EIF3L,EIF3D	up_VSAP_EC
GO:0071840	0.99	0.0314	4	2059	cellular component organization or biogenesis	BP	1	PRR16,EMP1,CAV1,SHOX2	up_VSAP_VSMC
GO:0050808	0.99	0.0347	3	93	synapse organization	BP	1	CDC20,SIX4,TPBG	down_ACOR_VSMC
GO:0071559	0.99	0.0408	2	75	response to transforming growth factor beta	BP	1	SLC29A1,CAV1	down_ACOR_VSMC
GO:0051656	0.99	0.04	2	129	establishment of organelle localization	BP	1	TMEM230,RAC2	down_VCAV_EC
GO:0032102	0.99	0.0391	2	67	negative regulation of response to external	BP	1	LEP,NRP1	up_ACOR_VSMC
GO:0006261	0.99	0.04	2	68	DNA-dependent DNA replication	BP	1	CIZ1,CDK9	up_VSAP_EC
GO:0002440	0.99	0.0586	1	51	production of molecular mediator of immune	BP	1	TFRC	down_ACOR_VSMC
GO:0090257	0.99	0.0604	1	52	regulation of muscle system process	BP	1	CAV1	down_ACOR_VSMC
GO:0071229	0.99	0.057	1	51	cellular response to acid chemical	BP	1	CDK4	down_ACOR_VSMC
GO:0006839	0.99	0.0563	1	86	mitochondrial transport	BP	1	SLC35F6	down_VCAV_EC

GO:0007600	0.99	0.0589	1	73	sensory perception	BP	1	RPGR	down_VSAP_EC
GO:0090304	0.99	0.0631	1	1694	nucleic acid metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0044267	0.99	0.0604	1	1583	cellular protein metabolic process	BP	1	EYA1	up_VFEM_VSMC
GO:0006725	0.99	0.0631	1	1956	cellular aromatic compound metabolic	BP	1	GATA5	up_VPUL_VSMC
GO:0046483	0.99	0.0642	1	1948	heterocycle metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:0051701	0.99	0.0602	1	45	interaction with host	BP	1	PC	up_VSAP_EC
GO:0044267	0.991	0.0121	110	1583	cellular protein metabolic process	BP	1	HMGB1,SREBF1,POLE3,USP1,IRAK1,ILF3,USP4,EIF4A3,HMGCR,HNRNPD,VARS,UBE2S,NEDD4,U2AF2,PSMD3,PSMD7,SLC29A1,METAP2,PPM1G,RRBP1,PPP1R15B,MPDU1,SLC35C2,MRPS18B,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,BIRC5,PRMT1,CAV1,CDK1,RAD51,FANCI,TRUB2,NF2,AURKB,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,SMARCC1,PLK3,DHX33,UHRF1,CKS2,PDCD2,RNF152,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,B4GALT1,FARSA,RAP2C,UBE2J2,YWHAB,CYCS,NCL,RAC1,NUP62,MRPL37,EMP2,DTL,HASPIN,CACTIN,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,RBM14,RAD23A,NOLC1,CDC20,TTK,BAP1,RARS,PUM3,MAST2,MELK,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,TADA2A,PMPCA,TINF2,JMJD6,MRPL18,CCNB3,UBE2C,NUS1,UBA2,MTBP,TTLL1,EIF3M,AMER1,DCUN1D5,PPIB,PIK3CD	down_ACOR_VSMC
GO:0051641	0.991	0.0131	64	858	cellular localization	BP	1	PEX7,WNT11,AXIN2,SLC8B1,PLEKHF1,TBC1D10C,TBC1D2B,CDH1,SLC6A4,FGF7,ABL1,PEX2,EMP2,RILPL2,ANKRD54,VPS36,AP5B1,TOM1,LMF1,RAB11B,GLIS2,MORC3,MFN2,ICE1,ZFP36L1,PIK3R1,CRACR2B,GAS1,CIZ1,FBXO4,ERGIC1,LRP4,NUP98,SCFD2,TSPAN5,HPS4,FRMD6,FBXO7,KCNB1,LONP2,BORCS6,SNUPN,DOP1B,DENND5A,AP5Z1,FTL,RAF1,TAF8,ZFYVE21,CYBA,STX4,TTL,VPS11,KCNC4,FLOT1,PPP3CB,PEX6,MAVS,CEP19,BAG4,NCOA4,CLUH,RAB11FIP2,LATS2	up_VSAP_EC
GO:0034613	0.991	0.0131	40	576	cellular protein localization	BP	1	PEX7,WNT11,AXIN2,PLEKHF1,TBC1D10C,TBC1D2B,CDH1,FGF7,PEX2,EMP2,RILPL2,VPS36,TOM1,RAB11B,GLIS2,MORC3,MFN2,ICE1,PIK3R1,CRACR2B,CIZ1,FBXO4,LRP4,NUP98,TSPAN5,HPS4,FRMD6,FBXO7,KCNB1,LONP2,SNUPN,TAF8,STX4,VPS11,FLOT1,PEX6,MAVS,BAG4,NCOA4,LATS2	up_VSAP_EC
GO:1901564	0.991	0.0143	36	2053	organonitrogen compound metabolic process	BP	1	LEP,PRR16,USP54,XYLT1,GAS1,CRYAB,CTSS,F3,GPAM,ATP6V1B2,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CLEC16A,CYLD,LRRC15,RECK,MOXD1,DCUN1D3,RAB7A,AXIN2,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,GCNT4,RNF181	up_AFEM_EC
GO:1901360	0.991	0.014	35	2016	organic cyclic compound metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,SDR42E1,MYBL1,NR3C1,MOXD1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B,GCNT4	up_AFEM_EC
GO:0019220	0.991	0.0143	31	525	regulation of phosphate metabolic process	BP	1	ACSL3,HMGB1,IRAK1,MCM7,HMGCR,SLC29A1,PPP1R15B,CAV1,CDK1,RAD51,NF2,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,RAP2C,YWHAB,RAC1,NUP62,EMP2,IQGAP1,CACTIN,EZR,CLSPN,ARHGEF2,KNL1,TADA2A,CCNB3	down_ACOR_VSMC
GO:0051174	0.991	0.0143	31	525	regulation of phosphorus metabolic process	BP	1	ACSL3,HMGB1,IRAK1,MCM7,HMGCR,SLC29A1,PPP1R15B,CAV1,CDK1,RAD51,NF2,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,DHX33,CKS2,RAP2C,YWHAB,RAC1,NUP62,EMP2,IQGAP1,CACTIN,EZR,CLSPN,ARHGEF2,KNL1,TADA2A,CCNB3	down_ACOR_VSMC

GO:1901565	0.991	0.0158	25	442	organonitrogen compound catabolic process	BP	1	USP1,USP4,UBE2S,NEDD4,PSMD3,PSMD7,SLC29A1,HM13,PSMD13,SMARCC1,PLK3,UBE2J2,DTL,PDXP,EZR,UBE2K,RAD23A,SGPL1,CDC20,BAP1,PSMC1,NUDT1,UBE2C,AMER1,NUDT3	down_ACOR_VSMC
GO:0065003	0.991	0.0166	20	616	protein-containing complex assembly	BP	1	KIRREL1,PRNP,COA1,LMO4,RPS10,COL6A1,CLIP3,ENSCAFG00000014978,LCAT,CLSTN1,CABIN1,EIF3K,B4GALT1,SCARA5,CYBA,MRPS11,RPS27,NCLN,ACTR3B,SOAT1	down_VCAV_EC
GO:0044265	0.991	0.018	12	423	cellular macromolecule catabolic process	BP	1	LRP1,PSMF1,SAMD4B,RNF216,PARK7,ZFP36L1,CLEC16A,SEC61B,HM13,PYM1,FBH1,LONP2	down_VCAV_EC
GO:0006753	0.991	0.0192	11	211	nucleoside phosphate metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,ENTPD3,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0044238	0.991	0.0327	4	3383	primary metabolic process	BP	1	HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0006887	0.991	0.0309	3	99	exocytosis	BP	1	STXBP6,SDC1,CORO1A	down_ACOR_VSMC
GO:0006259	0.991	0.0286	3	354	DNA metabolic process	BP	1	GREM1,AXIN2,PPARGC1A	up_AFEM_EC
GO:0006725	0.991	0.0334	3	1956	cellular aromatic compound metabolic	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0046483	0.991	0.0343	3	1948	heterocycle metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:0016072	0.991	0.0293	3	102	rRNA metabolic process	BP	1	MTOR,RIOK3,SMARCA4	up_VCAV_EC
GO:0065004	0.991	0.0528	1	81	protein-DNA complex assembly	BP	1	BRD2	down_VSAP_EC
GO:0050684	0.991	0.0518	1	46	regulation of mRNA processing	BP	1	CCNT1	up_ACOR_VSMC
GO:0016043	0.991	0.0607	1	1973	cellular component organization	BP	1	SLIT2	up_VPUL_VSMC
GO:0042274	0.991	0.0522	1	47	ribosomal small subunit biogenesis	BP	1	RCL1	up_VSAP_EC
GO:0055001	0.991	0.0537	1	47	muscle cell development	BP	1	SHOX2	up_VSAP_EC
GO:0043412	0.992	0.0102	96	1225	macromolecule modification	BP	1	FZD1,CDON,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,ENPP2,TBC1D10C,CEP85,EEF2K,IL6R,SLIT2,FGF7,ABL1,KLHL36,EMP2,DLST,OSR1,MAP3K5,CDC42EP5,GALNT15,DTX2,PDGFD,NAA60,DDB2,KLF15,C1QTNF2,CNPPD1,CISH,KLHL24,PLPP3,CAMKK2,TNKS1BP1,KLHDC8B,F2RL1,LMF1,PHKA2,MORC3,DDR2,ZFP36L1,TRAF7,FXN,PIK3R1,RBCK1,KBTBD12,MYC,RNF24,FKRP,DLD,RTN4RL1,SASH1,FBXO4,RMND5A,MYD88,LRP4,PASK,GALNT11,STK16,NCEH1,PHF1,FBXW5,FBXO7,ZDHHC8,ASB8,UBA7,EHHADH,RNF166,RPUSD4,CDK9,KDM2B,FBLN1,RNF216,ZFP36L2,WDR82,RAF1,DR1,TTL,QARS,ACVRL1,KDM3B,CDC26,FLOT1,PPP3CB,NCK1,MAVS,ULK1,ZER1,MAP2K2,TGFBR2,B3GALT4,BAG4,KEAP1,LATS2	up_VSAP_EC
GO:0006139	0.992	0.0122	37	1909	nucleobase-containing compound metabolic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,AK7,RBM38,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0010467	0.992	0.0131	34	1787	gene expression	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,SOX9,PKNOX2,PCSK1N,ENSCAFG00000004331,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,KLHL25,ZMYND8,PIAS1,MAVS,FOXC2,LRP4,CLSTN1,RBM38,CLU,SFMBT2,ZNF229,TP53INP2,GMEB2,RIOX2,EFEMP1,TLE2	up_ACOR_EC
GO:0009967	0.992	0.0131	24	435	positive regulation of signal transduction	BP	1	HMGB1,IRAK1,NEDD4,SLC29A1,MTDH,CTDNEP1,SLC35C2,CAV1,CASP2,EZH2,GREM1,MAP3K20,DHX33,PPARD,NUP62,EMP2,GSTO1,MIOS,ASPM,PRMT5,CTH,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0033554	0.992	0.0131	23	708	cellular response to stress	BP	1	VASN,BMPR1A,NABP2,ENSCAFG00000014978,GABARAP,PDIA4,PRMT6,TMEM161A,THY1,PARK7,SCARA5,ZFP36L1,SASH1,CLEC16A,MPV17,FUT8,SPRED1,SEC61B,HM13,FBH1,FOXO3,RGMA,BRSK1	down_VCAV_EC
GO:0051129	0.992	0.0169	12	221	negative regulation of cellular component	BP	1	FAM107A,SLIT2,RTN4RL1,LRP4,PHF1,FBLN1,RAF1,ACVRL1,UBQLN2,HTRA2,ULK1,BAG4	up_VSAP_EC

GO:0071363	0.992	0.0187	8	188	cellular response to growth factor stimulus	BP	1	SLC29A1,CAV1,GREM1,NCL,IQGAP1,FGF5,CORO1A,NUS1	down_ACOR_VSMC
GO:0016567	0.992	0.0213	5	232	protein ubiquitination	BP	1	RNF216,PARK7,SASH1,FBH1,KLHL29	down_VCAV_EC
GO:0006260	0.992	0.0248	4	98	DNA replication	BP	1	CDC7,ATRX,ZNF365,RPAIN	up_ACOR_VSMC
GO:0034622	0.992	0.024	4	421	cellular protein-containing complex assembly	BP	1	CRYAB,DNAL1,CDC42EP5,KANK1	up_AFEM_EC
GO:0001558	0.992	0.0262	3	101	regulation of cell growth	BP	1	MMP14,CDKN2C,BAP1	down_ACOR_VSMC
GO:0098542	0.992	0.0262	3	100	defense response to other organism	BP	1	ARG2,HMGB2,EXOSC5	down_ACOR_VSMC
GO:0006650	0.992	0.033	2	78	glycerophospholipid metabolic process	BP	1	ACSL3,VAC14	down_ACOR_VSMC
GO:0016042	0.992	0.0333	2	80	lipid catabolic process	BP	1	PLCG2,LIPA	up_VCAV_EC
GO:0043414	0.992	0.0325	2	70	macromolecule methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:2000058	0.992	0.033	2	68	regulation of ubiquitin-dependent protein catabolic process	BP	1	RNF166,UBQLN2	up_VSAP_EC
GO:0010001	0.992	0.0467	1	54	glial cell differentiation	BP	1	NAB2	down_ACOR_VSMC
GO:0006260	0.992	0.0468	1	98	DNA replication	BP	1	FBH1	down_VCAV_EC
GO:0071824	0.992	0.0489	1	92	protein-DNA complex subunit organization	BP	1	CABIN1	down_VCAV_EC
GO:0071840	0.992	0.0553	1	2059	cellular component organization or biogenesis	BP	1	HDAC7	down_VPOR_EC
GO:0006479	0.992	0.05	1	45	protein methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0008213	0.992	0.05	1	45	protein alkylation	BP	1	ATRX	up_ACOR_VSMC
GO:0051983	0.992	0.0478	1	47	regulation of chromosome segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0019538	0.992	0.053	1	1713	protein metabolic process	BP	1	ANKRD6	up_VPOR_VSMC
GO:1901360	0.992	0.0552	1	2016	organic cyclic compound metabolic process	BP	1	GATA5	up_VPUL_VSMC
GO:1901564	0.992	0.052	1	2053	organonitrogen compound metabolic	BP	1	SLIT2	up_VPUL_VSMC
GO:2001251	0.992	0.0499	1	49	negative regulation of chromosome organization	BP	1	PHF1	up_VSAP_EC
GO:0006807	0.993	0.0088	232	3221	nitrogen compound metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,NPR1,ST8SIA6,KIT,PRCP,PPP2R5A,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,RELN,CD34,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NOS3,NLRC5,QKI,LYVE1,TSPAN15,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,TCF4,SMAD1,CTTNBP2NL,SNCAIP,FOXN2,MEOX1,PIPOX,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,SERINC5,ADSS,YES1,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,PAK2,GALNT18,PRKD2,THOC1,SWAP70,CHST1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,ESCO1,TRMT9B,DPH5,VHL,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,WSB1,PARP4,FES,JAG1,NSD1,GUCY1B1,MRRF,PTGS2,MMD,TOP1,ET	up_VCAV_EC
GO:0051239	0.993	0.0101	55	859	regulation of multicellular organismal process	BP	1	HMGB1,SREBF1,IRAK1,TFPI,SLC29A1,MTDH,SRRT,FBXO5,HSPA9,PRELID1,PRMT1,CAV1,NF2,MMP14,EZH2,GREM1,ADIPOR2,CDK4,HMGB3,DHX33,HOXA7,ARG2,ANXA5,PDCD2,HOXC10,HOXB7,B4GALT1,PRCP,TFRC,PPARD,FAM49B,RAC1,EMP2,IQGAP1,CACTIN,HMGB2,EZR,TOX,ELOVL6,SGPL1,BEND6,POLR3F,CDC20,BAP1,ASPM,MAST2,CTH,ARHGEF2,TWIST2,HOXA9,GLI1,NUS1,AMOTL1,SIX4,TPBG	down_ACOR_VSMC

GO:0051649	0.993	0.0105	44	630	establishment of localization in cell	BP	1	PEX7,SLC8B1,TBC1D10C,TBC1D2B,CDH1,SLC6A4,ABL1,PEX2,EMP2,RILPL2,ANKRD54,VPS36,AP5B1,TOM1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,GAS1,ERGIC1,NUP98,HPS4,FBXO7,KCNB1,LONP2,SNUPN,DOP1B,DENND5A,AP5Z1,RAF1,ZFYVE21,CYBA,STX4,TTL,VPS11,KCNC4,PPP3CB,PEX6,MAVS,CEP19,BAG4,NCOA4,RAB11FIP2	up_VSAP_EC
GO:0034641	0.993	0.0119	43	2171	cellular nitrogen compound metabolic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,PCSK1N,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,ENSCAFG00000028814,SMAD6,KLHL25,ZMYND8,NIT2,GUCY1B1,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,AK7,RBM38,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,AZIN2,PRKCD,PM20D1,EFEMP1,TLE2	up_ACOR_EC
GO:0007166	0.993	0.0108	42	686	cell surface receptor signaling pathway	BP	1	SREBF1,IRAK1,MNDA,SLC29A1,MTDH,HEY1,SDC1,CTDNEP1,SLC35C2,CAV1,CASP2,MMP14,STMN1,GREM1,ADIPOR2,CDK4,SMARCC1,ITGB3,ARHGDIA,RAC1,NUP62,EMP2,IQGAP1,CACTIN,HMGB2,FGF5,EZR,RBM14,CORO1A,SGPL1,BEND6,PHACTR4,ASPM,ITGA2,NCOA5,ARHGEF2,GLI1,JMJD6,DELE1,NUS1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0006725	0.993	0.0116	38	1956	cellular aromatic compound metabolic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,AK7,RBM38,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0006974	0.993	0.0126	21	333	cellular response to DNA damage stimulus	BP	1	CDC7,NACC2,TP53BP1,ATRX,ZBTB40,ZNF365,ZBTB4,POLK,ANKRD1,CDKN1A,CHD2,MARF1,PARP9,PSEN1,SHPRH,DMC1,DDIT4,RPAIN,WDR48,PARK7,FAN1	up_ACOR_VSMC
GO:0007155	0.993	0.0138	17	324	cell adhesion	BP	1	HMGB1,CAV1,NF2,GREM1,HOXA7,ARG2,B4GALT1,TFRC,PPARD,ITGB3,FAM49B,RAC1,EMP2,EZR,CORO1A,RADIL,ITGA2	down_ACOR_VSMC
GO:0010564	0.993	0.0176	6	217	regulation of cell cycle process	BP	1	PLK3,NAA10,CTNNB1,SND1,CALM1,CDKN1A	down_VSAP_EC
GO:0016192	0.993	0.0189	5	452	vesicle-mediated transport	BP	1	CALY,ACTN2,PREB,VPS16,ABCB9	up_ACOR_EC
GO:0008380	0.993	0.0186	5	149	RNA splicing	BP	1	QKI,SCAF11,PRPF39,WTAP,IVNS1ABP	up_VCAV_EC
GO:0006281	0.993	0.0219	4	208	DNA repair	BP	1	NABP2,TMEM161A,PARK7,FBH1	down_VCAV_EC
GO:0051640	0.993	0.023	3	174	organelle localization	BP	1	TMEM230,CDH2,RAC2	down_VCAV_EC
GO:1901360	0.993	0.027	3	2016	organic cyclic compound metabolic process	BP	1	NR1H4,NPNT,HOXA1	up_APUL_EC
GO:1903050	0.993	0.0233	3	88	regulation of proteolysis involved in cellular protein catabolic process	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:1903047	0.993	0.03	2	257	mitotic cell cycle process	BP	1	BRSK1,CHMP4B	up_ACOR_EC
GO:0031330	0.993	0.0291	2	85	negative regulation of cellular catabolic process	BP	1	MTOR,TENT2	up_VCAV_EC
GO:0032259	0.993	0.0301	2	71	methylation	BP	1	PHF1,WDR82	up_VSAP_EC
GO:0017157	0.993	0.042	1	58	regulation of exocytosis	BP	1	SDC1	down_ACOR_VSMC
GO:0030705	0.993	0.0418	1	56	cytoskeleton-dependent intracellular transport	BP	1	TRAK1	down_ACOR_VSMC
GO:0045665	0.993	0.0458	1	55	negative regulation of neuron differentiation	BP	1	ASPM	down_ACOR_VSMC
GO:0070374	0.993	0.0409	1	57	positive regulation of ERK1 and ERK2 cascade	BP	1	HMGB1	down_ACOR_VSMC
GO:0023061	0.993	0.0433	1	95	signal release	BP	1	PARK7	down_VCAV_EC
GO:0090068	0.993	0.0443	1	78	positive regulation of cell cycle process	BP	1	CDKN1A	down_VSAP_EC
GO:0005975	0.993	0.0422	1	183	carbohydrate metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0010467	0.993	0.0468	1	1787	gene expression	BP	1	HOXA9	up_AORT_EC
GO:0044242	0.993	0.0455	1	57	cellular lipid catabolic process	BP	1	PLCG2	up_VCAV_EC
GO:0071840	0.993	0.0502	1	2059	cellular component organization or biogenesis	BP	1	SLIT2	up_VPUL_VSMC

GO:0001894	0.993	0.045	1	49	tissue homeostasis	BP	1	PPARGC1B	up_VSAP_EC
GO:0016573	0.993	0.0414	1	50	histone acetylation	BP	1	DR1	up_VSAP_EC
GO:0010467	0.994	0.00743	145	1787	gene expression	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,AXIN2,OSR2,INSIG2,PTGFR,ZNF367,PPARGC1B,MRPL37,ACACB,IRX5,ZHX3,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,ZNF250,HDAC7,KLKB1,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,WARS2,VDR,NAA60,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,CCBE1,TRMT2A,CBX7,STAT5A,STAT6,GATAD1,PLPP3,EXOSC7,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,DDR2,ICE1,ZFP36L1,HSF4,PIK3R1,RBCK1,GAS1,BATF2,MYC,SSBP2,IRX3,ZEB1,FKRP,SHOX2,H2AFJ,ZC3H10,TLE2,YBX3,EEF2,FBXO4,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,NUP98,ANKHD1,TSPAN5,TRERF1,E2F4,NPAS2,PRKAB1,SMG9,RCL1,FARS2,LIMD1,UBA52,RPUSD4,LONP2,RPL15,PC,CDK9,NR2F6,PRMT2,KDM2B,EIF3G,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,MAPKBP1,TAF8,NFIB,ZNF580,ABHD14B,ZBTB25,ZNF205,NCOA2,EIF3K,EIF3L,PQBP1,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,ZNF517,TNRC6C,COA1,PPP3CB,NCK1,ZNF444,MRPL4,MAVS,INTS12,HMOX1,ZNF662,LARS2,TGFBR2,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0022607	0.994	0.0104	34	969	cellular component assembly	BP	1	KIRREL1,PRNP,SDC4,COA1,LOX,LMO4,RPS10,COL6A1,CLIP3,RHOD,ENSCAFG00000014978,GABARAP,TTC8,LCAT,CLSTN1,CABIN1,EIF3K,THY1,WDR45,MYO1B,B4GALT1,SCARA5,CYBA,IFT57,MRPS11,EMC6,CDH2,RPS27,NCLN,ACTR3B,GREM1,EVI5L,RAC2,SOAT1	down_VCAV_EC
GO:0006139	0.994	0.01	32	1909	nucleobase-containing compound metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0042325	0.994	0.0108	26	463	regulation of phosphorylation	BP	1	HMGB1,IRAK1,MCM7,HMGCR,SLC29A1,PPP1R15B,CAV1,CDK1,RAD51,NF2,CDKN2C,EZH2,GREM1,MAP3K20,DHX33,CKS2,RAP2C,RAC1,NUP62,EMP2,CACTIN,EZR,CLSPN,ARHGEF2,TADA2A,CCNB3	down_ACOR_VSMC
GO:0007417	0.994	0.0138	11	235	central nervous system development	BP	1	SLC29A1,NF2,EZH2,SMG9,HOXC10,WDR62,NAV2,ARCN1,ASPM,ENSCAFG00000010224,GLI1	down_ACOR_VSMC
GO:0033036	0.994	0.0131	11	852	macromolecule localization	BP	1	LEP,CRY2,VPS26C,GPAM,CYLD,LRRC15,REEP2,RAB7A,AXIN2,ACACB,CCL5	up_AFEM_EC
GO:0070848	0.994	0.0145	8	193	response to growth factor	BP	1	SLC29A1,CAV1,GREM1,NCL,IQGAP1,FGF5,CORO1A,NUS1	down_ACOR_VSMC
GO:0044257	0.994	0.0141	8	327	cellular protein catabolic process	BP	1	LRP1,PSMF1,RNF216,PARK7,CLEC16A,SEC61B,HM13,LONP2	down_VCAV_EC
GO:0007049	0.994	0.0142	7	560	cell cycle	BP	1	BRSK1,SOX9,PAK3,FIGNL1,CHMP4B,PRKCD,CCNYL1	up_ACOR_EC
GO:0031344	0.994	0.0149	6	161	regulation of cell projection organization	BP	1	FSCN1,ANLN,CAV1,RAC1,CDC42EP4,EZR	down_ACOR_VSMC
GO:0120035	0.994	0.0157	6	160	regulation of plasma membrane bounded cell projection organization	BP	1	FSCN1,ANLN,CAV1,RAC1,CDC42EP4,EZR	down_ACOR_VSMC
GO:0043161	0.994	0.0146	6	171	proteasome-mediated ubiquitin-dependent protein catabolic process	BP	1	WWP1,PELI1,C7H18orf25,CUL4A,TNFAIP1,PSMD12	up_VCAV_EC
GO:0007010	0.994	0.0182	4	441	cytoskeleton organization	BP	1	CYLD,DNAL1,CDC42EP5,KANK1	up_AFEM_EC
GO:0044237	0.994	0.0242	4	3491	cellular metabolic process	BP	1	HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0045765	0.994	0.0208	3	105	regulation of angiogenesis	BP	1	MTDH,GREM1,EMP2	down_ACOR_VSMC
GO:0000278	0.994	0.0206	3	331	mitotic cell cycle	BP	1	BRSK1,PAK3,CHMP4B	up_ACOR_EC
GO:0044237	0.994	0.0281	3	3491	cellular metabolic process	BP	1	GATA5,PHEX,SLIT2	up_VPUL_VSMC
GO:0000075	0.994	0.0206	3	91	cell cycle checkpoint	BP	1	CRADD,FBXO4,ATRIP	up_VSAP_EC
GO:0016569	0.994	0.0257	2	144	covalent chromatin modification	BP	1	HR,PRMT6	down_VCAV_EC

GO:0016570	0.994	0.0266	2	143	histone modification	BP	1	HR,PRMT6	down_VCAV_EC
GO:0006399	0.994	0.0273	2	87	tRNA metabolic process	BP	1	TARSL2,TRMT9B	up_VCAV_EC
GO:0051607	0.994	0.0372	1	58	defense response to virus	BP	1	EXOSC5	down_ACOR_VSMC
GO:0071103	0.994	0.0401	1	80	DNA conformation change	BP	1	BRD2	down_VSAP_EC
GO:0007030	0.994	0.04	1	49	Golgi organization	BP	1	USP6NL	up_ACOR_VSMC
GO:0006281	0.994	0.0398	1	208	DNA repair	BP	1	AXIN2	up_AFEM_EC
GO:0016054	0.994	0.0361	1	61	organic acid catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0046395	0.994	0.0361	1	61	carboxylic acid catabolic process	BP	1	PIPOX	up_VCAV_EC
GO:0019538	0.994	0.0427	1	1713	protein metabolic process	BP	1	EYA1	up_VFEM_VSMC
GO:0018393	0.994	0.0379	1	51	internal peptidyl-lysine acetylation	BP	1	DR1	up_VSAP_EC
GO:0071704	0.995	0.00631	255	3535	organic substance metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,IL7R,NPR1,ADGRF5,ST8SIA6,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PANK3,PRKCH,CALCRL,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,TSPAN8,RELN,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,LYVE1,TSPAN15,GK5,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,CTTNBP2NL,SNCAIP,FOXN2,MEOX1,PIPOX,PTGS1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,SERINC5,ADSS,YES1,FAM3C,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PGM2,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,GDPD5,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,GALE,PAK2,GALNT18,PRKD2,THOC1,SH3GLB1,SWAP70,CHST1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,ESCO1,TRMT9B,DPH5,	up_VCAV_EC
GO:0071702	0.995	0.00777	41	687	organic substance transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,SREBF2,NEDD4,RRBP1,TIMM44,POLA2,HSPA9,SLC35C2,RAN,PRELID1,HM13,BIRC5,INSIG1,LIMA1,PLK3,ARG2,ENSCAFG00000011598,PREB,TFRC,PPARD,TRAM1,IPO4,YWHAB,NUP62,NUP188,TOMM34,SAMM50,DMAP1,ARCN1,DDX39B,SNX15,ENSCAFG00000005299,EZR,PMPCA,MRPL18,LIPC,NUS1,SLC25A19	down_ACOR_VSMC
GO:0046483	0.995	0.0079	37	1948	heterocycle metabolic process	BP	1	NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,AK7,RBM38,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0071840	0.995	0.00902	35	2059	cellular component organization or biogenesis	BP	1	KCNC4,PRR16,RAB20,DLL1,CRYAB,KCND1,CTSS,PLXNA4,MLLT11,NEFH,MFAP4,PLAGL2,GREM1,CAMK2A,CLEC16A,CYLD,DNAL1,POSTN,CHCHD10,RECK,DCUN1D3,REEP2,BVES,RAB7A,AXIN2,ACACB,PPARGC1A,SPATA6,CDC42EP5,FAP,DMPK,ADAM17,LRRN2,KANK1,TNC	up_AFEM_EC
GO:0048468	0.995	0.00774	32	553	cell development	BP	1	FLNB,NEDD4,SLC29A1,TRIP13,SRRT,SDC1,FBXO5,B3GNT2,PRMT1,CASP2,NF2,EZH2,STMN1,POC1A,B4GALT1,RAP2C,RAC1,IQGAP1,HMGB2,RAB35,EZR,NOLC1,BEND6,PHACTR4,ASPM,ENSCAFG00000010224,RADIL,ARHGEF2,SERPINH1,JMJD6,SIX4,TTLL1	down_ACOR_VSMC
GO:0022008	0.995	0.00956	22	406	neurogenesis	BP	1	ACSL4,NEDD4,SLC29A1,SRRT,NAB2,B3GNT2,PRMT1,NF2,EZH2,STMN1,HOXC10,WDR62,NAV2,RAC1,IQGAP1,HMGB2,RAB35,BEND6,ASPM,ENSCAFG00000010224,ARHGEF2,SIX4	down_ACOR_VSMC

GO:0051276	0.995	0.0103	14	398	chromosome organization	BP	1	NR1H4,SMARCA4,IWS1,NAA10,MORF4L2,SMG7,BRD2,CTNNB1,KPNB1,PDS5B,REST,ZMYND8,PRMT1,KDM3A	down_VSAP_EC
GO:0006281	0.995	0.0108	11	208	DNA repair	BP	1	CDC7,TP53BP1,ZNF365,POLK,MARF1,PARP9,DMC1,RPAIN,WDR48,PARK7,FAN1	up_ACOR_VSMC
GO:0009117	0.995	0.0109	10	208	nucleotide metabolic process	BP	1	PPARGC1A,PDE5A,ADCY6,ENSCAFG00000018611,ALDOC,DDIT4,NT5C2,NMNAT1,PARK7,ELOVL7	up_ACOR_VSMC
GO:0048729	0.995	0.0126	9	209	tissue morphogenesis	BP	1	TIMELESS,NF2,MMP14,GREM1,HOXB7,B4GALT1,PHACTR4,ITGA2,SIX4	down_ACOR_VSMC
GO:0002009	0.995	0.0127	7	177	morphogenesis of an epithelium	BP	1	TIMELESS,MMP14,GREM1,HOXB7,B4GALT1,PHACTR4,SIX4	down_ACOR_VSMC
GO:0051603	0.995	0.0121	7	305	proteolysis involved in cellular protein catabolic	BP	1	PSMF1,RNF216,PARK7,CLEC16A,SEC61B,HM13,LONP2	down_VCAV_EC
GO:0048858	0.995	0.0127	6	159	cell projection morphogenesis	BP	1	SLC29A1,B3GNT2,CFAP298,STMN1,IQGAP1,ENSCAFG00000010224	down_ACOR_VSMC
GO:0043410	0.995	0.0135	5	144	positive regulation of MAPK cascade	BP	1	HMGB1,IRAK1,EZH2,MAP3K20,DHX33	down_ACOR_VSMC
GO:0010564	0.995	0.0146	4	217	regulation of cell cycle process	BP	1	KANK2,ZFP36L1,LSM10,BRSK1	down_VCAV_EC
GO:0071704	0.995	0.0215	4	3535	organic substance metabolic process	BP	1	HOXA9,LNPEP,ERC1,TAOK1	up_AORT_EC
GO:0000075	0.995	0.0183	3	91	cell cycle checkpoint	BP	1	TP53BP1,CDKN2B,CDKN1A	up_ACOR_VSMC
GO:0071824	0.995	0.0195	3	92	protein-DNA complex subunit organization	BP	1	NAA60,SMARCD2,CENPP	up_VSAP_EC
GO:0070372	0.995	0.022	2	85	regulation of ERK1 and ERK2 cascade	BP	1	HMGB1,EZR	down_ACOR_VSMC
GO:0019318	0.995	0.0223	2	75	hexose metabolic process	BP	1	LEP,INPP5K	up_ACOR_VSMC
GO:0021915	0.995	0.0333	1	58	neural tube development	BP	1	PHACTR4	down_ACOR_VSMC
GO:0016358	0.995	0.0348	1	58	dendrite development	BP	1	ENSCAFG00000010224	down_ACOR_VSMC
GO:0017144	0.995	0.0328	1	199	drug metabolic process	BP	1	ALDOC	up_ACOR_EC
GO:0045786	0.995	0.0317	1	195	negative regulation of cell cycle	BP	1	BRSK1	up_ACOR_EC
GO:2001251	0.995	0.0351	1	49	negative regulation of chromosome organization	BP	1	ATRX	up_ACOR_VSMC
GO:0006139	0.995	0.0352	1	1909	nucleobase-containing compound metabolic	BP	1	HOXA9	up_AORT_EC
GO:0044249	0.995	0.0386	1	1851	cellular biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:1901576	0.995	0.0357	1	1877	organic substance biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:1903364	0.995	0.0309	1	61	positive regulation of cellular protein catabolic	BP	1	TNFAIP3	up_VCAV_EC
GO:0034641	0.995	0.039	1	2171	cellular nitrogen compound metabolic	BP	1	GATA5	up_VPUL_VSMC
GO:0044238	0.996	0.00467	242	3383	primary metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,NPR1,ADGRF5,ST8SIA6,KIT,PRCP,PPP2R5A,PANK3,PRKCH,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,RELN,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NLRC5,QKI,TSPAN15,GK5,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,TCF4,SMAD1,CTTNBP2NL,FOXN2,MEOX1,PIPOX,PTGS1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,SERINC5,ADSS,YES1,FAM3C,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PGM2,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,GDPD5,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,GALE,PAK2,GALNT18,PRKD2,THOC1,SH3GLB1,SWAP70,CHST1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,ESCO1,TRMT9B,DPH5,VHL,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,WSB1,PARP4,FES,JAG1	up_VCAV_EC

GO:0009987	0.996	0.006	234	5086	cellular process	BP	1	PCOLCE,CST3,ADAMTS2,GPAM,NOTCH2,HSPB6,PDGFRB,SLC35F6,KIRREL1,SNX18,FBLN2,SMAD9,ITGB5,LRP1,DCN,MAOA,NAB2,NDN,ANGPT1,PRNP,LUM,MT2A,SDC4,UBA52,VASN,ATP8B2,FBN1,ADCY6,GLIPR2,BGN,LARP6,KANK2,SH3BP1,COA1,BMPR1A,LOX,TLN2,KRTCAP2,VKORC1,NABP2,LMO4,EVC,RECK,IGFBP6,RPS10,TRPV2,ANPEP,COL6A1,CLIP3,NUMBL,FKBP10,CHID1,ARHGEF25,NAGLU,RHOD,OSMR,ENSCAFG00000014978,GABARAP,AKT1S1,CHRDL1,SSBP2,TIMP2,TBX15,AKT2,DOCK10,PSMF1,TTC8,LCAT,SAMD4B,EEF2K,TFE3,ACAA1,CHCHD10,ME3,ENSCAFG00000018277,NR3C1,H6PD,SYDE1,HSD3B7,HR,SCP2,PDIA4,RPL23,SLC39A6,LAMA3,RPL13,CLSTN1,PLCL1,DDOST,CACNB3,CSPG4,VDR,PRMT6,ENSCAFG00000013404,CABIN1,UROS,PRELP,NT5C2,EPHX1,ANXA11,ENTPD3,WIPF1,THNSL2,PGLS,TMEM161A,ATP5MC1,RASSF8,CXXC5,GFPT2,UQCR10,SEMA3C,ASPN,POLDIP2,CRISPLD2,PIGS,HS3ST3B1,LRPAP1,GNAZ,EIF3K,THY1,FKBP5,NECAB3,RNF216,TEAD1,SUOX,CYP1B1,ADK,WDR45,AHCYL1,MRPL37,PEX5,ARHGAP10,TLX2,FKBP11,CC2D1A,ATP6V0C,MYO1B,B4GALT1,RETSAT,GLI3,PARK7,RPL27A,ZMAT3,ADAMTSL4,EEF2,MAST2,SCARA5,ZFP36L1,MY	down_VCAV_EC
GO:0071840	0.996	0.00541	170	2059	cellular component organization or biogenesis	BP	1	SYNPO2L,SH3TC2,PDLIM3,FGF13,RHOT1,FMOD,EPB41L4A,DNAJC6,SMAD6,ARHGAP28,ACTN2,PLCG2,DCBLD2,SNAP91,MID1,CDC7,PCGF5,EPYC,USP6NL,MBP,ZRANB1,PRDX4,RECK,SHROOM3,FEZ1,NACC2,PRKAA2,ITM2C,FERMT1,BMP4,SYT16,LCAT,EVI5L,CRIM1,LNPK,SYNPO2,TUBB4A,FGFR2,PCBD1,TP53BP1,MX1,MFAP4,ABCA1,GJA1,ATRX,TRPS1,SEC24B,XIRP1,WASF3,PPARGC1A,LATS2,TP53INP1,ATXN2,RERG,SPINT1,GLRB,PKP4,ZNF365,AR,CTSS,STX11,LMO4,TMEM108,CLCN3,ARHGEF26,NEBL,IFT43,ZMYM2,LIMS2,F2RL1,STN1,MARCH5,ERO1B,GABARAPL1,BNIP3,EGLN1,CACNB3,SLC12A7,CDKN1A,JMY,CRLF3,TSPYL5,CLSTN1,LRRC8C,NRP1,GPM6A,LRPAP1,ULK2,DMPK,NPNT,UNC5B,SCP2,ORMDL3,SMARCD3,EVL,SPINT2,SLITRK5,TBX20,P4HA1,DES,PRKCE,MARF1,FZD3,MYO1B,TTC17,RND1,DAG1,APP,ECM2,PSEN1,SGSM2,SYNJ2BP,CHD7,SHPRH,PIK3C3,LAMP2,JUP,DMXL1,SIPA1L1,DDR2,CLN8,PERP,DUSP22,SSH3,EDN1,PHF20,NID1,GTF2A1L,AKTIP,KCNC4,LRRC4,ASAP1,FAM107A,ATG16L2,DMC1,DDIT4,SERPINB5,JAM3,B2M,DISC1,KIF9,SCAMP5,TNFRSF11B,TTC19,TACC1,IGFBP7,SBF2,GAA,ATXN10,FEZ2,SUN1,MAP3K7,INPP5K,FAF2,RAB5C,PFKL,AZIN2,WASL,A	up_ACOR_VSMC
GO:1901360	0.996	0.00477	164	2016	organic cyclic compound metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ACSM3,ARHGEF5,AXIN2,LIPC,OSR2,INSIG2,ZNF367,PPARGC1B,ACAA1,ACACB,IRX5,GDA,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,SULT1A1,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,ENSCAFG00000013986,HSD17B14,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,HSD3B7,ZNF688,ZBTB16,COQ9,ALDH6A1,RARG,TRMT2A,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,GATAD1,HSD17B8,PLPP3,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,LMF1,NFE2L2,GLIS2,DFFB,DDR2,PDK2,ICE1,ZFP36L1,HSF4,FXN,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,CTNS,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,ENSCAFG00000016140,CLYBL,LARP6,MYD88,NDUFS2,IKZF2,TFE3,LRP4,NUP98,NT5C2,TRERF1,E2F4,NPAS2,SMG9,RCL1,MOCOS,FARS2,LCAT,PCBD1,LIMD1,RPUSD4,ACSS2,CDK9,DHRS9,NR2F6,PRMT2,KDM2B,MVK,LIPE,PNPO,AP5Z1,DCAKD,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,CYB5R3,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,NDUFV1,MAVS,INT	up_VSAP_EC

GO:0070887	0.996	0.00595	47	775	cellular response to chemical stimulus	BP	1	HMGB1,SREBF1,FLNB,IRAK1,MCM7,TFPI,NEDD4,SLC29A1,MTDH,SLC25A5,B3GNT2,BIRC5,INSIG1,CAV1,RAD51,TIMELESS,THRAP3,EZH2,GREM1,ADIPOR2,CDK4,SMARCC1,PLK3,PRCP,TFRC,PPARD,NCL,RAC1,PDXP,IQGAP1,SUV39H1,CACTIN,HMGB2,GSTO1,CDC42EP4,FGF5,ENSCAFG00000005299,EZR,CORO1A,SIGMAR1,MELK,CTH,NCOA5,ARHGEF2,MSC,NUS1,PIK3CD	down_ACOR_VSMC
GO:0071310	0.996	0.00619	37	634	cellular response to organic substance	BP	1	SREBF1,FLNB,IRAK1,TFPI,NEDD4,SLC29A1,MTDH,SLC25A5,B3GNT2,BIRC5,INSIG1,CAV1,RAD51,TIMELESS,THRAP3,EZH2,GREM1,ADIPOR2,CDK4,SMARCC1,PRCP,TFRC,NCL,PDXP,IQGAP1,CACTIN,HMGB2,CDC42EP4,FGF5,ENSCAFG00000005299,EZR,CORO1A,CTH,NCOA5,ARHGEF2,MSC,NUS1	down_ACOR_VSMC
GO:0046483	0.996	0.00648	32	1948	heterocycle metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,EAF1,AXIN2,YEATS2,ACACB,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:0048699	0.996	0.007	19	371	generation of neurons	BP	1	ACSL4,NEDD4,SLC29A1,SRRT,B3GNT2,PRMT1,NF2,EZH2,STMN1,HOXC10,RAC1,IQGAP1,HMGB2,RAB35,BEND6,ASPM,ENSCAFG00000010224,ARHGEF2,SIX4	down_ACOR_VSMC
GO:0000278	0.996	0.00735	19	331	mitotic cell cycle	BP	1	FAM107A,MAP3K14,CEP85,CRADD,ABL1,ZFP36L1,GAS1,POLDIP2,E2F4,FBXW5,FBXO7,TTC28,ZFP36L2,TTL,TPRA1,CDC26,LSM10,MAP2K2,LATS2	up_VSAP_EC
GO:0006974	0.996	0.00766	19	333	cellular response to DNA damage stimulus	BP	1	ACKR3,AXIN2,CRADD,ABL1,DDB2,TNKS1BP1,PIK3R1,NEIL2,MYC,HIC1,FBXO4,ATRIP,PHF1,NPAS2,CDK9,AP5Z1,ZBTB4,HTRA2,DDIT4	up_VSAP_EC
GO:1903047	0.996	0.00853	14	257	mitotic cell cycle process	BP	1	CDC7,SKP2,NACC2,BMP4,ATRX,LATS2,CDKN2B,CDKN1A,CRLF3,APP,MITD1,EDN1,FAM107A,KLF11	up_ACOR_VSMC
GO:0034622	0.996	0.00782	11	421	cellular protein-containing complex assembly	BP	1	KIRREL1,COA1,RPS10,CLIP3,ENSCAFG00000014978,CABIN1,EIF3K,CYBA,MRPS11,RPS27,ACTR3B	down_VCAV_EC
GO:0000226	0.996	0.00978	10	197	microtubule cytoskeleton organization	BP	1	FGF13,MID1,PRKAA2,TUBB4A,ATRX,DAG1,FAM107A,DISC1,TACC1,SUN1	up_ACOR_VSMC
GO:0006412	0.996	0.00899	9	245	translation	BP	1	QKI,TARSL2,MTOR,ENC1,SECISBP2L,NCK1,DPH5,MRRF,CNOT7	up_VCAV_EC
GO:0005975	0.996	0.0107	7	183	carbohydrate metabolic process	BP	1	MPDU1,B3GNT2,B4GALT1,GSTO1,GALE,PGD,GK5	down_ACOR_VSMC
GO:0002252	0.996	0.0101	6	166	immune effector process	BP	1	HMGB1,TFRC,FAM49B,EMP2,CORO1A,EXOSC5	down_ACOR_VSMC
GO:0050877	0.996	0.0116	6	164	nervous system process	BP	1	HMGCR,B3GNT2,AAAS,HOXC10,NAV2,NOB1	down_ACOR_VSMC
GO:0007610	0.996	0.0116	5	146	behavior	BP	1	HMGCR,AAAS,NAV2,ARCN1,ANXA7	down_ACOR_VSMC
GO:0006511	0.996	0.0111	5	253	ubiquitin-dependent protein catabolic process	BP	1	PSMF1,RNF216,PARK7,CLEC16A,SEC61B	down_VCAV_EC
GO:0022402	0.996	0.0136	4	407	cell cycle process	BP	1	BRSK1,SOX9,FIGNL1,CHMP4B	up_ACOR_EC
GO:0044057	0.996	0.0141	3	110	regulation of system process	BP	1	SREBF1,CAV1,EMP2	down_ACOR_VSMC
GO:0051052	0.996	0.014	3	145	regulation of DNA metabolic process	BP	1	CTNNB1,TFRC,CDKN1A	down_VSAP_EC
GO:0040029	0.996	0.0164	2	74	regulation of gene expression, epigenetic	BP	1	PCGF5,BMP4	up_ACOR_VSMC
GO:0009895	0.996	0.0164	2	94	negative regulation of catabolic process	BP	1	MTOR,TENT2	up_VCAV_EC
GO:0043547	0.996	0.0282	1	61	positive regulation of GTPase activity	BP	1	EZH2	down_ACOR_VSMC
GO:0031056	0.996	0.0301	1	50	regulation of histone modification	BP	1	ATRX	up_ACOR_VSMC
GO:0006725	0.996	0.0308	1	1956	cellular aromatic compound metabolic	BP	1	HOXA9	up_AORT_EC
GO:0009058	0.996	0.0326	1	1910	biosynthetic process	BP	1	HOXA9	up_AORT_EC
GO:0046483	0.996	0.0315	1	1948	heterocycle metabolic process	BP	1	HOXA9	up_AORT_EC
GO:0000724	0.996	0.0265	1	57	double-strand break repair via homologous	BP	1	AP5Z1	up_VSAP_EC
GO:0007611	0.996	0.0285	1	54	learning or memory	BP	1	CTNS	up_VSAP_EC

GO:0019538	0.997	0.00467	117	1713	protein metabolic process	BP	1	HMGB1,SREBF1,POLE3,USP1,IRAK1,ILF3,USP4,EIF4A3,HMGCR,HNRNPD,VARS,UBE2S,NEDD4,U2AF2,PSMD3,PSMD7,SLC29A1,METAP2,PPM1G,RRBP1,PPP1R15B,MPDU1,SLC35C2,MRPS18B,B3GNT2,PRELID1,HM13,UBE2T,PSMD13,BIRC5,PRMT1,CAV1,CDK1,RAD51,CASP2,FANCI,XYLT1,TRUB2,NF2,AURKB,MMP14,CDKN2C,EZH2,PPP2R5D,GREM1,MAP3K20,NEK2,FBL,CDK4,SMARCC1,PLK3,DHX33,UHRF1,CKS2,PDCD2,RNF152,DHCR24,BRCA1,FASTKD3,NOC2L,EIF5A,B4GALT1,PRCP,FARSA,RAP2C,UBE2J2,YWHAB,CYCS,NCL,RAC1,NUP62,MRPL37,EMP2,DTL,HASPIN,CACTIN,DMAP1,CDK2,CCNA2,ENSCAFG00000005299,EZR,CLSPN,UBE2K,RBM14,RAD23A,NOLC1,CDC20,TTK,BAP1,RARS,PUM3,MAST2,MELK,PRMT5,PSMC1,CTH,AIFM1,ARHGEF2,TADA2A,PMPCA,SERPINH1,TINF2,JMJD6,MRPL18,DELE1,CCNB3,UBE2C,NUS1,UBA2,MTBP,NECAB3,TTLL1,EIF3M,AMER1,DCUN1D5,PPIB,PIK3CD	down_ACOR_VSMC
GO:0016070	0.997	0.00416	115	1479	RNA metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,WARS2,VDR,SAV1,KLF15,ANXA4,ZNF688,ZBTB16,RARG,TRMT2A,CBX7,STAT5A,STAT6,GATAD1,PLPP3,EXOSC7,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DDR2,ICE1,ZFP36L1,HSF4,PIK3R1,RBCK1,BATF2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,YBX3,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,TRERF1,E2F4,NPAS2,SMG9,RCL1,FARS2,LIMD1,RPUSD4,CDK9,NR2F6,PRMT2,KDM2B,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,MAVS,INTS12,HMOX1,ZNF662,LARS2,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0051234	0.997	0.00486	84	1283	establishment of localization	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,STXBP6,NNT,SREBF2,HINFP,NEDD4,ZW10,CENPA,HOXA3,RRBP1,SLC25A5,TIMM44,POLA2,SDC1,ARFGAP1,HSPA9,SLC35C2,SLC25A15,RAN,PRELID1,HM13,BIRC5,INSIG1,CAV1,RANBP1,LIMA1,FAM129B,AAAS,SLC30A1,GREM1,CLIC1,PLK3,ARG2,KIF22,NKAIN1,CDCA8,SLC17A9,ENSCAFG00000011598,PREB,TFRC,PPARD,TRAM1,NDC80,IPO4,YWHAB,HIST1H1A,NUP62,EMP2,NUP188,TOMM34,SAMM50,GSTO1,TRAK1,DMAP1,ARCN1,CDK2,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,NIPA2,RBM14,CORO1A,CYC1,SLC20A1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A16,TRAPPC6A,PMPCA,JMJD6,MRPL18,LIPC,NUS1,CCT4,CEP83,ZWINT,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0048583	0.997	0.00388	70	1095	regulation of response to stimulus	BP	1	HMGB1,USP1,IRAK1,HMGA1,HMGCR,TFPI,NEDD4,WDR76,MNDA,SLC29A1,MTDH,SLC25A5,PPP1R15B,PARPBP,CTDNEP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,RAD51,CASP2,TIMELESS,NF2,PSD4,MMP14,EZH2,STMN1,GREM1,MAP3K20,CDK4,RNASEH2B,PCNA,DHX33,ARG2,RNF152,NOC2L,PRCP,TFRC,PPARD,YWHAB,FAM49B,RAC1,NUP62,EMP2,RSL1D1,CACTIN,HMGB2,GSTO1,DDX39B,ENSCAFG00000005299,EZR,RBM14,MIOS,BEND6,POLR3F,PHACTR4,BAP1,ASPM,TXNDC12,PRMT5,CTH,NCOA5,ARHGEF2,GLI1,CDC42SE1,DEPDC1B,AMER1,NET1	down_ACOR_VSMC

GO:0043170	0.997	0.00429	54	2980	macromolecule metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,MLLT11,LMCD1,THRB,HCK,TMEM100,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ACACB,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,TNC,RNF181	up_AFEM_EC
GO:1901360	0.997	0.00578	38	2016	organic cyclic compound metabolic process	BP	1	CDH3,NR1H4,GATA4,TRPS1,TBX18,PKIB,SOX9,NMNAT2,PKNOX2,FZD5,HSF4,DUSP26,RASL11A,NOD2,IL33,RGMA,LHX9,SMAD6,ZMYND8,GUCY1B1,PIAS1,MAVS,FOXC2,FIGNL1,LRP4,CLSTN1,AK7,RBM38,CLU,SFMBT2,ALDOC,ZNF229,TP53INP2,GMEB2,RIOX2,PRKCD,EFEMP1,TLE2	up_ACOR_EC
GO:0044085	0.997	0.00465	37	1076	cellular component biogenesis	BP	1	KIRREL1,PRNP,SDC4,COA1,LOX,LMO4,RPS10,COL6A1,CLIP3,RHOD,ENSCAFG00000014978,GABARAP,TTC8,LCAT,CLSTN1,CABIN1,EIF3K,THY1,WDR45,MYO1B,B4GALT1,SCARA5,RPL27,CYBA,IFT57,MRPS11,EMC6,CDH2,ORMDL3,RPS27,NCLN,ACTR3B,GREM1,RPLP0,EVI5L,RAC2,SOAT1	down_VCAV_EC
GO:0010647	0.997	0.00539	24	460	positive regulation of cell communication	BP	1	HMGB1,IRAK1,NEDD4,SLC29A1,MTDH,CTDNEP1,SLC35C2,CAV1,CASP2,EZH2,GREM1,MAP3K20,DHX33,PPARD,NUP62,EMP2,GSTO1,MIOS,ASPM,PRMT5,CTH,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0023056	0.997	0.00498	24	462	positive regulation of signaling	BP	1	HMGB1,IRAK1,NEDD4,SLC29A1,MTDH,CTDNEP1,SLC35C2,CAV1,CASP2,EZH2,GREM1,MAP3K20,DHX33,PPARD,NUP62,EMP2,GSTO1,MIOS,ASPM,PRMT5,CTH,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0003008	0.997	0.00547	16	336	system process	BP	1	SREBF1,HMGCR,B3GNT2,CAV1,LIMA1,FAM129B,AAAS,EZH2,ARG2,HOXC10,TRPV4,NAV2,PRCP,EMP2,EZR,NOB1	down_ACOR_VSMC
GO:0006464	0.997	0.00667	16	1162	cellular protein modification process	BP	1	LEP,USP54,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CYLD,LRRC15,DCUN1D3,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,RNF181	up_AFEM_EC
GO:0036211	0.997	0.00667	16	1162	protein modification process	BP	1	LEP,USP54,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CYLD,LRRC15,DCUN1D3,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,RNF181	up_AFEM_EC
GO:0000165	0.997	0.00778	10	236	MAPK cascade	BP	1	HMGB1,IRAK1,HMGCR,CAV1,NF2,EZH2,MAP3K20,DHX33,NUP62,EZR	down_ACOR_VSMC
GO:0022402	0.997	0.00732	10	407	cell cycle process	BP	1	NOTCH2,SNX18,KANK2,NABP2,ANXA11,ZFP36L1,LSM10,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0043043	0.997	0.00802	9	247	peptide biosynthetic process	BP	1	QKI,TARSL2,MTOR,ENC1,SECISBP2L,NCK1,DPH5,MRRF,CNOT7	up_VCAV_EC
GO:0050767	0.997	0.00847	7	184	regulation of neurogenesis	BP	1	SRRT,NF2,EZH2,HMGB2,BEND6,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0032990	0.997	0.00847	6	167	cell part morphogenesis	BP	1	SLC29A1,B3GNT2,CFAP298,STMN1,IQGAP1,ENSCAFG00000010224	down_ACOR_VSMC
GO:0000280	0.997	0.00907	6	145	nuclear division	BP	1	BMP4,ATRX,MARF1,EDN1,DMC1,SUN1	up_ACOR_VSMC
GO:0019941	0.997	0.00928	5	258	modification-dependent protein catabolic process	BP	1	PSMF1,RNF216,PARK7,CLEC16A,SEC61B	down_VCAV_EC
GO:0032446	0.997	0.0095	5	255	protein modification by small protein conjugation	BP	1	RNF216,PARK7,SASH1,FBH1,KLHL29	down_VCAV_EC
GO:0043632	0.997	0.00805	5	262	modification-dependent macromolecule catabolic	BP	1	PSMF1,RNF216,PARK7,CLEC16A,SEC61B	down_VCAV_EC
GO:0006281	0.997	0.00851	5	208	DNA repair	BP	1	PDS5B,BACH1,GTF2H1,RBBP8,RAD23A	down_VSAP_EC
GO:0042176	0.997	0.00908	4	140	regulation of protein catabolic process	BP	1	PLK2,TNFAIP3,TIPARP,ODC1	up_VCAV_EC
GO:0007409	0.997	0.0123	3	109	axonogenesis	BP	1	SLC29A1,B3GNT2,STMN1	down_ACOR_VSMC
GO:0031098	0.997	0.0123	3	109	stress-activated protein kinase signaling cascade	BP	1	HMGB1,MAP3K20,EZR	down_ACOR_VSMC
GO:0000226	0.997	0.0111	3	197	microtubule cytoskeleton organization	BP	1	CLIP3,GABARAP,BRSK1	down_VCAV_EC
GO:0006259	0.997	0.012	3	354	DNA metabolic process	BP	1	PKIB,FIGNL1,PRKCD	up_ACOR_EC
GO:0000375	0.997	0.0115	3	120	RNA splicing, via transesterification	BP	1	SCAF11,PRPF39,WTAP	up_VCAV_EC
GO:0000377	0.997	0.0124	3	119	RNA splicing, via transesterification reactions with bulged	BP	1	SCAF11,PRPF39,WTAP	up_VCAV_EC
GO:0000398	0.997	0.0124	3	119	mRNA splicing, via spliceosome	BP	1	SCAF11,PRPF39,WTAP	up_VCAV_EC

GO:0098813	0.997	0.0107	3	102	nuclear chromosome segregation	BP	1	AXIN2,TTL,CDC26	up_VSAP_EC
GO:1903362	0.997	0.01	3	100	regulation of cellular protein catabolic process	BP	1	RNF166,OSBPL7,UBQLN2	up_VSAP_EC
GO:0070371	0.997	0.0145	2	91	ERK1 and ERK2 cascade	BP	1	HMGB1,EZR	down_ACOR_VSMC
GO:0034470	0.997	0.0138	2	154	ncRNA processing	BP	1	RPL27,MRPS11	down_VCAV_EC
GO:0001101	0.997	0.0196	1	65	response to acid chemical	BP	1	CDK4	down_ACOR_VSMC
GO:0050768	0.997	0.0194	1	66	negative regulation of neurogenesis	BP	1	ASPM	down_ACOR_VSMC
GO:0051650	0.997	0.0241	1	65	establishment of vesicle localization	BP	1	PREB	down_ACOR_VSMC
GO:1901990	0.997	0.0197	1	94	regulation of mitotic cell cycle phase transition	BP	1	CDKN1A	down_VSAP_EC
GO:2001020	0.997	0.0236	1	88	regulation of response to DNA damage stimulus	BP	1	DDX39B	down_VSAP_EC
GO:0006281	0.997	0.0219	1	208	DNA repair	BP	1	FIGNL1	up_ACOR_EC
GO:1901360	0.997	0.0261	1	2016	organic cyclic compound metabolic process	BP	1	HOXA9	up_AORT_EC
GO:1901564	0.997	0.022	1	2053	organonitrogen compound metabolic	BP	1	ANKRD6	up_VPOR_VSMC
GO:0000725	0.997	0.0243	1	58	recombinational repair	BP	1	AP5Z1	up_VSAP_EC
GO:0051168	0.997	0.0239	1	57	nuclear export	BP	1	NUP98	up_VSAP_EC
GO:0016358	0.997	0.0213	1	58	dendrite development	BP	1	PQBP1	up_VSAP_EC
GO:0009987	0.998	0.00307	457	5086	cellular process	BP	1	GPR1,TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,PEX7,NAPEPLD,TWIST2,HOXA9,ADGRD1,SEZ6L,ENSCAFG00000009113,CDON,NECAB3,WNT11,HNF4A,ACSM3,FAM107A,CD274,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,LIPC,WASF3,OSR2,AMIGO1,INSIG2,ENPP2,LRRN3,PTGFR,SLC8B1,RADIL,ZNF367,PPARGC1B,PLEKHF1,SH2D4A,RNPEP,TBC1D10C,MAB21L1,ACAA1,MRPL37,CEP85,GJB5,LIMS2,FOXRED2,ARHGEF6,ALDH3B1,ACACB,TPCN2,EEF2K,DDHD1,IL6R,IRX5,RETREG1,SLIT2,GDA,CST3,CRADD,CRIP2,LRRC28,ZHX3,TBC1D2B,NDUFS7,ABTB1,HOXD3,CDH1,SLC6A4,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,EBF2,BTG1,HDAC7,EMP2,KCNE3,CHRM1,DLL1,EPN2,DLST,SESN1,OSR1,MAP3K5,ZNF449,CDC42EP5,INPP5E,IL17RC,GLUL,CTSS,GALNT15,DTX2,TENT5C,FUZ,CORO2B,ADHFE1,ADAMTSL4,ENSCAFG00000013986,PDGFD,CERS4,WARS2,VDR,DHRS4,NAA60,SAV1,RHPN1,SMARCD2,KDELC2,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,PLXNA4,RASGRP2,ARL4A,RILPL2,ANKRD54,CLDN1,CDC42EP2,ABHD15,HSD3B7,ZNF688,ZBTB16,TOX,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,MGST1,TRMT2A,PTGES2,VPS36,NDUFS1,PSMD9,CBX7,STAT5A,STAT6,E	up_VSAP_EC

GO:0043170	0.998	0.00241	251	2980	macromolecule metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,MEIS2,INTS9,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,CPXM1,LCAT,ZNF331,TBX18,B3GNT7,FGFR2,TP53BP1,CCDC126,ABCA1,EIF4A2,GJA1,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,PIGS,ISG15,ZNRF3,ZNF782,ZNF365,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,TMX3,CDKN2B,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,STN1,FAM129A,CAMK2D,MARCH5,PSEN2,ERO1B,DAPK1,APOL6,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,JMY,C1S,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,OS9,STT3B,PFDN5,ORMDL3,SMARCD3,SMPD1,TBX20,FUT11,C7,UBE2H,SH3RF1,PYGM,RNF24,P4HA1,PRKCE,CCNT1,MARF1,FRS2,RNF19A,CCPG1,LYPLAL1,SCG5,ENSCAFG00000030568,ZNF175,DAG1,ZNF79,FUT8,POMK,PARP9,CHD6,APP,PSEN1,TGFBR	up_ACOR_VSMC
GO:0044260	0.998	0.00237	215	2593	cellular macromolecule metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,TBC1D10C,MRPL37,CEP85,FOXRED2,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,FGF7,ABL1,PEX2,KLHL36,ZNF250,HDAC7,EMP2,DLL1,DLST,OSR1,MAP3K5,ZNF449,CDC42EP5,CTSS,GALNT15,DTX2,TENT5C,PDGFD,WARS2,VDR,NAA60,SAV1,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,VPS36,CBX7,STAT5A,STAT6,RECK,GATAD1,CISH,KLHL24,PLPP3,EXOSC7,CAMKK2,TNKS1BP1,KLHDC8B,PYM1,F2RL1,RBL2,LMF1,PHKA2,RAB11B,NFE2L2,GLIS2,DFFB,MORC3,DDR2,ICE1,ZFP36L1,TRAF7,HSF4,FXN,PIK3R1,RBCK1,KBTBD12,GAS1,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,RNF24,FKRP,FBXW4,DLD,SULF2,SHOX2,H2AFJ,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,RMND5A,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,TRERF1,GALNT11,STK16,NCEH1,PHF1,E2F4,NPAS2,FBXW5,SMG9,FBXO7,MOCOS,ZDHHC8,ASB8,UBA7,EHHADH,FARS2,LCAT,LIMD1,UBA52,RNF166,RPUSD4,LONP2,RPL15,CDK9,NR2F6,PRMT2,KDM2B,FBLN1,RNF	up_VSAP_EC
GO:0016043	0.998	0.00252	157	1973	cellular component organization	BP	1	FZD1,PRR16,PEX7,SEZ6L,WNT11,HNF4A,FAM107A,ARHGEF5,AXIN2,LIPC,WASF3,AMIGO1,ENPP2,LRRN3,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,CEP85,LIMS2,ACACB,TPCN2,DDHD1,RETREG1,SLIT2,TBC1D2B,NDUFS7,CDH1,FGF7,ABL1,PEX2,HDAC7,EMP2,DLL1,CDC42EP5,CTSS,FUZ,CORO2B,ADAMTSL4,NAA60,SMARCD2,DDB2,C1QTNF2,PLXNA4,RILPL2,CLDN1,CDC42EP2,PSMD9,RECK,GATAD1,KLHL24,HSD17B8,PYM1,AMBRA1,F2RL1,DFFB,DDR2,MFN2,ICE1,FXN,PIK3R1,DMAC2,MYC,SCARA5,SULF2,SHOX2,H2AFJ,FGD4,RTN4RL1,FBXO4,SBF2,POLDIP2,CLYBL,LOX,NDUFAF3,LRP4,NDUFB10,DPYSL2,AJM1,NUP98,GDPD5,ECM2,AZIN2,HPS4,FRMD6,PHF1,WIPF1,E2F4,FBXW5,KIF27,FBXO7,TMEM17,KCNB1,WISP2,LCAT,PCBD1,LIMD1,LONP2,RAB30,CDK9,KDM2B,FBLN1,PIP4K2B,ATP8B2,EIF3G,MYO1B,IGFBP6,WDR82,MTFR1L,RAF1,NFIB,CYBA,ZNF205,XKR8,CENPP,EIF3K,CDNF,STX4,EIF3L,PQBP1,SMIM20,DR1,TTL,VPS11,KCNC4,SMARCA2,EIF3D,ARHGAP12,ACVRL1,KDM3B,TTC8,UBQLN2,EMP3,ARHGAP10,CDC26,HTRA2,FLOT1,COA1,PPP3CB,PEX6,NCK1,MAVS,ULK1,CEP19,HMOX1,MAP2K2,NPRL3,OGN,BAG4,JCHAIN,DEDD2,DPT,FUNDC2,CLUH,DDIT4,SOAT1,LATS2	up_VSAP_EC

GO:0044085	0.998	0.00319	79	1076	cellular component biogenesis	BP	1	FZD1,WNT11,FAM107A,ARHGEF5,WASF3,AMIGO1,LRRN3,ACACB,SLIT2,NDUFS7,ABL1,HDAC7,EMP2,CDC42EP5,FUZ,NAA60,C1QTNF2,RILPL2,CLDN1,CDC42EP2,PSMD9,GATAD1,HSD17B8,ENSCAFG00000000071,EXOSC7,AMBRA1,F2RL1,MFN2,ICE1,FXN,PIK3R1,DMAC2,SCARA5,FGD4,SBF2,CLYBL,LOX,NDUFAF3,LRP4,NDUFB10,NUP98,HPS4,E2F4,RCL1,KIF27,TMEM17,KCNB1,LCAT,PCBD1,LIMD1,PIP4K2B,EIF3G,MRPL10,MYO1B,RAF1,CYBA,CENPP,EIF3K,STX4,EIF3L,SMIM20,VPS11,KCNC4,EIF3D,ACVRL1,TTC8,UBQLN2,EMP3,HTRA2,FLOT1,COA1,NCK1,ULK1,CEP19,HMOX1,NPRL3,BAG4,JCHAIN,SOAT1	up_VSAP_EC
GO:0022607	0.998	0.0023	69	969	cellular component assembly	BP	1	SYNPO2L,FGF13,SMAD6,ARHGAP28,ACTN2,SNAP91,FEZ1,NACC2,PRKAA2,LCAT,EVI5L,SYNPO2,TUBB4A,PCBD1,TP53BP1,MX1,MFAP4,ABCA1,ATRX,TRPS1,SEC24B,WASF3,TP53INP1,ATXN2,PKP4,LMO4,ARHGEF26,NEBL,IFT43,F2RL1,GABARAPL1,JMY,TSPYL5,CLSTN1,LRRC8C,NRP1,EVL,SLITRK5,TBX20,PRKCE,MYO1B,TTC17,DAG1,APP,PSEN1,SHPRH,PIK3C3,JUP,DMXL1,DUSP22,SSH3,EDN1,KCNC4,ASAP1,FAM107A,ATG16L2,DMC1,DISC1,KIF9,TTC19,SBF2,ATXN10,FEZ2,INPP5K,PFKL,WASL,ENSCAFG00000013536,CRKL,MYOZ2	up_ACOR_VSMC
GO:0010467	0.998	0.00342	68	1787	gene expression	BP	1	ADAMTS2,NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,UBA52,FBN1,LARP6,KANK2,COA1,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,RHBDL1,SAMD4B,TFE3,NR3C1,HR,RPL23,RPL13,CLSTN1,PCSK7,VDR,PRMT6,CXXC5,EIF3K,TEAD1,MRPL37,CC2D1A,GLI3,PARK7,RPL27A,EEF2,ZFP36L1,MYDGF,SEC11C,RPL27,RBM38,MAVS,MRPS11,LOXL3,RPS27,FUT8,RAB7B,A2M,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PCSK6,ENSCAFG00000015122,PYM1,CRCP,GREM1,ATOX1,LONP2,FOXO3,THRB,ZBTB16,EIF4EBP1,RGMA	down_VCAV_EC
GO:0046907	0.998	0.00373	34	536	intracellular transport	BP	1	PEX7,TBC1D10C,TBC1D2B,CDH1,PEX2,EMP2,RILPL2,ANKRD54,VPS36,AP5B1,TOM1,LMF1,RAB11B,MFN2,ICE1,PIK3R1,GAS1,ERGIC1,NUP98,HPS4,FBXO7,KCNB1,LONP2,SNUPN,DOP1B,DENND5A,AP5Z1,ZFYVE21,STX4,VPS11,PEX6,MAVS,BAG4,NCOA4	up_VSAP_EC
GO:0007399	0.998	0.00297	31	564	nervous system development	BP	1	ACSL4,NEDD4,SLC29A1,HOXA3,SRRT,NAB2,B3GNT2,PRMT1,NF2,EZH2,STMN1,SMG9,HOXC10,WDR62,NAV2,PPARD,RAC1,IQGAP1,HMGB2,ARCN1,RAB35,BEND6,PHACTR4,CDC20,ASPM,PRPS1,ENSCAFG00000010224,ARHGEF2,GLI1,SIX4,TPBG	down_ACOR_VSMC
GO:2000026	0.998	0.00423	31	560	regulation of multicellular organismal development	BP	1	HMGB1,MTDH,SRRT,FBXO5,HSPA9,PRELID1,PRMT1,CAV1,NF2,MMP14,EZH2,GREM1,HMGB3,HOXA7,PDCD2,HOXB7,B4GALT1,TFRC,PPARD,EMP2,HMGB2,TOX,BEND6,CDC20,ASPM,CTH,ARHGEF2,HOXA9,GLI1,SIX4,TPBG	down_ACOR_VSMC
GO:0034622	0.998	0.00358	25	421	cellular protein-containing complex assembly	BP	1	FAM107A,SLIT2,NDUFS7,ABL1,CDC42EP5,NAA60,CDC42EP2,PSMD9,DMAC2,NDUFAF3,NDUFB10,NUP98,LIMD1,EIF3G,CYBA,CENPP,EIF3K,STX4,EIF3L,SMIM20,VPS11,EIF3D,COA1,NCK1,BAG4	up_VSAP_EC
GO:0022402	0.998	0.00281	24	407	cell cycle process	BP	1	CDC7,SKP2,NACC2,BMP4,ATRX,LATS2,TP53INP1,PKP4,CDKN2B,CDKN1A,JMY,CRLF3,PRKCE,MARF1,APP,PIK3C3,MITD1,EDN1,FAM107A,DMC1,KLF11,RPRD1B,SUN1,WASL	up_ACOR_VSMC
GO:0043603	0.998	0.00327	15	372	cellular amide metabolic process	BP	1	QKI,PIPOX,SPTLC2,ARG2,TARSL2,MTOR,SAMD8,ENC1,SECISBP2L,ELOVL7,NCK1,DPH5,MRRF,CNOT7,GCH1	up_VCAV_EC
GO:0070925	0.998	0.00343	15	293	organelle assembly	BP	1	ARHGEF5,FUZ,RILPL2,AMBRA1,MFN2,HPS4,E2F4,KIF27,TMEM17,LIMD1,PIP4K2B,TTC8,UBQLN2,CEP19,NPRL3	up_VSAP_EC
GO:0044085	0.998	0.00522	14	1076	cellular component biogenesis	BP	1	KCNC4,RAB20,CRYAB,KCND1,MFAP4,PLAGL2,GREM1,CYLD,DNAL1,RAB7A,ACACB,SPATA6,CDC42EP5,KANK1	up_AFEM_EC
GO:0016071	0.998	0.00396	12	248	mRNA metabolic process	BP	1	AXIN2,TENT5C,EXOSC7,PYM1,ZFP36L1,NUP98,SMG9,CDK9,SAMD4B,ZFP36L2,PQBP1,TNRC6C	up_VSAP_EC

GO:0006259	0.998	0.00481	11	354	DNA metabolic process	BP	1	SESN2,ZPR1,SMG7,CTNNB1,TFRC,PDS5B,BACH1,GTF2H1,RBBP8,RAD23A,CDKN1A	down_VSAP_EC
GO:0023014	0.998	0.00415	10	248	signal transduction by protein phosphorylation	BP	1	HMGB1,IRAK1,HMGCR,CAV1,NF2,EZH2,MAP3K20,DHX33,NUP62,EZR	down_ACOR_VSMC
GO:0051726	0.998	0.00469	9	393	regulation of cell cycle	BP	1	NOTCH2,KANK2,NABP2,POLDIP2,ZFP36L1,LSM10,MAPRE3,EIF4EBP1,BRSK1	down_VCAV_EC
GO:0060284	0.998	0.00453	8	212	regulation of cell development	BP	1	SRRT,NF2,EZH2,RAC1,HMGB2,BEND6,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0006974	0.998	0.0058	7	333	cellular response to DNA damage stimulus	BP	1	NABP2,TMEM161A,PARK7,SPRED1,FBH1,FOXO3,BRSK1	down_VCAV_EC
GO:0022613	0.998	0.00569	7	208	ribonucleoprotein complex biogenesis	BP	1	SCAF11,CNOT6,RIOK3,PAN3,PRPF39,CNOT7,LSM14A	up_VCAV_EC
GO:0048812	0.998	0.0076	5	151	neuron projection morphogenesis	BP	1	SLC29A1,B3GNT2,STMN1,IQGAP1,ENSCAFG00000010224	down_ACOR_VSMC
GO:0120039	0.998	0.00496	5	158	plasma membrane bounded cell projection	BP	1	SLC29A1,B3GNT2,STMN1,IQGAP1,ENSCAFG00000010224	down_ACOR_VSMC
GO:0007017	0.998	0.00649	5	273	microtubule-based process	BP	1	CLIP3,GABARAP,IFT57,MGARP,BRSK1	down_VCAV_EC
GO:0042176	0.998	0.0053	5	140	regulation of protein catabolic process	BP	1	AZIN2,RNF166,OSBPL7,TIMP2,UBQLN2	up_VSAP_EC
GO:0007059	0.998	0.00556	4	127	chromosome segregation	BP	1	AXIN2,NAA60,TTL,CDC26	up_VSAP_EC
GO:0018205	0.998	0.00736	4	122	peptidyl-lysine modification	BP	1	KLF15,PHF1,WDR82,DR1	up_VSAP_EC
GO:0061564	0.998	0.00641	3	119	axon development	BP	1	SLC29A1,B3GNT2,STMN1	down_ACOR_VSMC
GO:0098813	0.998	0.00695	3	102	nuclear chromosome segregation	BP	1	ATRX,DMC1,SUN1	up_ACOR_VSMC
GO:0048285	0.998	0.00944	2	166	organelle fission	BP	1	DCN,MTFR1L	down_VCAV_EC
GO:0006807	0.998	0.0135	2	3221	nitrogen compound metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0006364	0.998	0.0079	2	87	rRNA processing	BP	1	EXOSC7,RCL1	up_VSAP_EC
GO:0000819	0.998	0.00891	2	87	sister chromatid segregation	BP	1	AXIN2,CDC26	up_VSAP_EC
GO:0065004	0.998	0.012	2	81	protein-DNA complex assembly	BP	1	NAA60,CENPP	up_VSAP_EC
GO:0001505	0.998	0.0173	1	69	regulation of neurotransmitter levels	BP	1	CAV1	down_ACOR_VSMC
GO:0010769	0.998	0.0154	1	69	regulation of cell morphogenesis involved	BP	1	RAC1	down_ACOR_VSMC
GO:0030258	0.998	0.0144	1	71	lipid modification	BP	1	PPARD	down_ACOR_VSMC
GO:0051648	0.998	0.0176	1	69	vesicle localization	BP	1	PREB	down_ACOR_VSMC
GO:0003205	0.998	0.0174	1	67	cardiac chamber development	BP	1	ADAMTS6	down_ACOR_VSMC
GO:0045926	0.998	0.0136	1	72	negative regulation of growth	BP	1	CDKN2C	down_ACOR_VSMC
GO:0006302	0.998	0.0121	1	97	double-strand break repair	BP	1	RBBP8	down_VSAP_EC
GO:0006412	0.998	0.0128	1	245	translation	BP	1	KLHL25	up_ACOR_EC
GO:0043043	0.998	0.0122	1	247	peptide biosynthetic process	BP	1	KLHL25	up_ACOR_EC
GO:0016458	0.998	0.0153	1	59	gene silencing	BP	1	BMP4	up_ACOR_VSMC
GO:0009451	0.998	0.017	1	59	RNA modification	BP	1	RPUSD4	up_VSAP_EC
GO:0007093	0.998	0.0183	1	59	mitotic cell cycle checkpoint	BP	1	CRADD	up_VSAP_EC
GO:0007281	0.998	0.0177	1	60	germ cell development	BP	1	ZBTB16	up_VSAP_EC
GO:0044839	0.998	0.0156	1	61	cell cycle G2/M phase transition	BP	1	CDC25B	up_VSAP_EC
GO:0006996	0.998	0.0154	1	1301	organelle organization	BP	1	CAV1	up_VSAP_VSMC

GO:0008152	0.999	0.00067	314	3714	metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MEIS2,INTS9,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,FEZ1,ENSCAFG00000002977,SKP2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,CPXM1,LCAT,ZNF331,AHCYL1,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,FAXDC2,CCDC126,MFAP4,ABCA1,EIF4A2,GJA1,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,LPL,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,MAOA,PIGS,ISG15,UGCG,ACSL6,ZNRF3,ZNF782,ZNF365,PLPP2,AR,ZNF484,SASH1,CTSS,FRRS1,LMO4,GTF3C1,PTPN3,ZNF572,PFKM,FGF18,FMO4,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,PPIP5K1,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,ACAD11,STN1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,ERO1B,GGPS1,GABARAPL1,DAPK1,APOL6,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,LIPE,JMY,C1S,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,CYP2J2,OS9,ENSCAFG00000028814,ATP	up_ACOR_VSMC
GO:0044237	0.999	0.00091	294	3491	cellular metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MEIS2,INTS9,MBP,ZRANB1,PRDX4,RECK,LIPT2,B3GALNT2,FEZ1,ENSCAFG00000002977,SKP2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,PNRC1,LCAT,ZNF331,AHCYL1,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,MAOA,PIGS,ISG15,UGCG,ZNRF3,ZNF782,ZNF365,PLPP2,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,PFKM,FGF18,FMO4,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,PPIP5K1,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,ACAD11,STN1,FAM129A,CAMK2D,MARCH5,ENPP4,ERO1B,GGPS1,GABARAPL1,DAPK1,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,CYP2J2,OS9,ENSCAFG00000028814,STT3B,PFDN5,ORMDL3,SMARCD3,SMPD1,PTGDR,TBX20,FUT11,UBE2H,MOXD1,SH3RF1,P	up_ACOR_VSMC
GO:0006807	0.999	0.00119	272	3221	nitrogen compound metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,NAPEPLD,HOXA9,CDON,NECAB3,WNT11,HNF4A,ACSM3,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,ZNF367,PPARGC1B,RNPEP,TBC1D10C,MRPL37,CEP85,FOXRED2,ACACB,EEF2K,IL6R,IRX5,SLIT2,GDA,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,KLHL36,SULT1A1,ZNF250,GOT1,HDAC7,KLKB1,EMP2,DLL1,DLST,OSR1,MAP3K5,ZNF449,CDC42EP5,GLUL,CTSS,GALNT15,DTX2,TENT5C,ADHFE1,ENSCAFG00000013986,PDGFD,CERS4,WARS2,VDR,NAA60,SAV1,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,ZNF688,ZBTB16,CNPPD1,COQ9,ALDH6A1,RARG,CCBE1,TRMT2A,VPS36,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,RECK,GATAD1,CISH,KLHL24,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,APOL5,TNKS1BP1,KLHDC8B,PYM1,F2RL1,RBL2,LMF1,PHKA2,NFE2L2,GLIS2,DFFB,MORC3,DDR2,PDK2,ICE1,ZFP36L1,TRAF7,HSF4,FXN,GALK1,PIK3R1,RBCK1,KBTBD12,ENTPD3,GAS1,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,RNF24,SUOX,FKRP,FBXW4,CTNS,DLD,HACD4,SULF2,SHOX2,CAPN5,ABAT,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,BCKDHB,FBXO4,RMND5A,	up_VSAP_EC

GO:0044237	0.999	0.00198	247	3491	cellular metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,NPR1,ADGRF5,ST8SIA6,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PANK3,PRKCH,CALCRL,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,RELN,CD34,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,ATF3,CHD7,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NOS3,NLRC5,QKI,GK5,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,CTTNBP2NL,SNCAIP,FOXN2,MEOX1,PIPOX,PTGS1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,SERINC5,ADSS,YES1,FAM3C,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,ASB9,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,DEPP1,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,PAK2,GALNT18,PRKD2,THOC1,SH3GLB1,SWAP70,CHST1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,ESCO1,TRMT9B,DPH5,VHL,TIMELESS,OTUD4,LDB2,CD200,SLC25A25,WSB1,PAR	up_VCAV_EC
GO:0071840	0.999	0.00078	161	2059	cellular component organization or biogenesis	BP	1	FZD1,PRR16,PEX7,SEZ6L,WNT11,HNF4A,FAM107A,ARHGEF5,AXIN2,LIPC,WASF3,AMIGO1,ENPP2,LRRN3,RADIL,PPARGC1B,PLEKHF1,TBC1D10C,CEP85,LIMS2,ACACB,TPCN2,DDHD1,RETREG1,SLIT2,TBC1D2B,NDUFS7,CDH1,FGF7,ABL1,PEX2,HDAC7,EMP2,DLL1,CDC42EP5,CTSS,FUZ,CORO2B,ADAMTSL4,NAA60,SMARCD2,DDB2,C1QTNF2,PLXNA4,RILPL2,CLDN1,CDC42EP2,PSMD9,RECK,GATAD1,KLHL24,HSD17B8,ENSCAFG00000000071,EXOSC7,PYM1,AMBRA1,F2RL1,DFFB,DDR2,MFN2,ICE1,FXN,PIK3R1,DMAC2,MYC,SCARA5,SULF2,SHOX2,H2AFJ,FGD4,RTN4RL1,FBXO4,SBF2,POLDIP2,CLYBL,LOX,NDUFAF3,LRP4,NDUFB10,DPYSL2,AJM1,NUP98,GDPD5,ECM2,AZIN2,HPS4,FRMD6,PHF1,WIPF1,E2F4,FBXW5,RCL1,KIF27,FBXO7,TMEM17,KCNB1,WISP2,LCAT,PCBD1,LIMD1,LONP2,RAB30,CDK9,KDM2B,FBLN1,PIP4K2B,ATP8B2,EIF3G,MRPL10,MYO1B,IGFBP6,WDR82,MTFR1L,RAF1,NFIB,CYBA,ZNF205,XKR8,CENPP,EIF3K,CDNF,STX4,EIF3L,PQBP1,SMIM20,DR1,TTL,VPS11,KCNC4,SMARCA2,EIF3D,ARHGAP12,ACVRL1,KDM3B,TTC8,UBQLN2,EMP3,ARHGAP10,CDC26,HTRA2,FLOT1,COA1,PPP3CB,PEX6,NCK1,MAVS,ULK1,CEP19,HMOX1,MAP2K2,NPRL3,OGN,BAG4,JCHAIN,DEDD2,D	up_VSAP_EC
GO:0046483	0.999	0.00086	152	1948	heterocycle metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ACSM3,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,GDA,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,ENSCAFG00000013986,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,ZNF688,ZBTB16,COQ9,ALDH6A1,RARG,TRMT2A,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,GATAD1,PLPP3,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DFFB,DDR2,PDK2,ICE1,ZFP36L1,HSF4,FXN,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,CTNS,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,ENSCAFG00000016140,CLYBL,LARP6,MYD88,NDUFS2,IKZF2,TFE3,LRP4,NUP98,NT5C2,TRERF1,E2F4,NPAS2,SMG9,RCL1,MOCOS,FARS2,PCBD1,LIMD1,RPUSD4,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,MVK,PNPO,AP5Z1,DCAKD,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,NDUFV1,MAVS,INTS12,HMOX1,ZNF662,LARS2,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772,IDO2	up_VSAP_EC

GO:0007165	0.999	0.00141	98	1496	signal transduction	BP	1	HMGB1,SREBF1,IRAK1,RACGAP1,HMGCR,NEDD4,MNDA,SLC29A1,MTDH,HEY1,RRBP1,SLC25A5,PPP1R15B,SDC1,CTDNEP1,RANGAP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,THRAP3,ENSCAFG00000008236,NF2,PSD4,MMP14,EZH2,STMN1,DEPDC1,PPP2R5D,GREM1,MAP3K20,ADIPOR2,CDK4,SMARCC1,DHX33,RNF152,NOC2L,PRCP,NRAS,PPARD,ITGB3,RAP2C,ARHGDIA,YWHAB,RAC1,NUP62,EMP2,DTL,GNB2,IQGAP1,HASPIN,IQGAP2,CACTIN,HMGB2,GSTO1,CDC42EP4,CDK2,FGF5,CCNA2,SNX15,ENSCAFG00000005299,EZR,RBM14,MIOS,CORO1A,SGPL1,BEND6,PHACTR4,ASPM,MAST2,MELK,PRKD3,ENSCAFG00000010224,TXNDC12,RADIL,REM1,PRMT5,ITGA2,PDE8A,CTH,NCOA5,AIFM1,ARHGEF2,GLI1,JMJD6,CDC42SE1,CDC5L,RGS9,DELE1,NUS1,AMOTL1,DEPDC1B,AMER1,NET1,PIK3CD	down_ACOR_VSMC
GO:0046483	0.999	0.00085	90	1948	heterocycle metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,PGAM1,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,SND1,ENSCAFG00000002015,TFRC,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,RTCB,SNRPA1,KDM3A,CMPK1	down_VSAP_EC
GO:0006139	0.999	0.00086	88	1909	nucleobase-containing compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,PGAM1,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,SND1,ENSCAFG00000002015,TFRC,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,RTCB,SNRPA1,KDM3A,CMPK1	down_VSAP_EC
GO:0034641	0.999	0.00168	84	2171	cellular nitrogen compound metabolic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,NDN,PRNP,LUM,UBA52,FBN1,ADCY6,LARP6,KANK2,COA1,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,H6PD,HR,RPL23,RPL13,CLSTN1,VDR,PRMT6,UROS,NT5C2,ENTPD3,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,EIF3K,TEAD1,ADK,MRPL37,CC2D1A,GLI3,PARK7,RPL27A,EEF2,ZFP36L1,MYDGF,SEC11C,RNPEP,RPL27,RBM38,AMPD2,MAVS,MRPS11,LOXL3,ORMDL3,RPS27,FUT8,ENSCAFG00000017708,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PCSK6,ENSCAFG00000015122,PYM1,CRCP,FBH1,GREM1,NAPEPLD,FOXO3,THRB,ZBTB16,EIF4EBP1,RGMA,ACAT1	down_VCAV_EC

GO:0006810	0.999	0.00157	78	1244	transport	BP	1	ACSL3,HMGB1,SREBF1,DDX39A,STXBP6,NNT,SREBF2,NEDD4,ZW10,HOXA3,RRBP1,SLC25A5,TIMM44,POLA2,SDC1,ARFGAP1,HSPA9,SLC35C2,SLC25A15,RAN,PRELID1,HM13,BIRC5,INSIG1,CAV1,RANBP1,LIMA1,FAM129B,AAAS,SLC30A1,GREM1,CLIC1,PLK3,ARG2,NKAIN1,SLC17A9,ENSCAFG00000011598,PREB,TFRC,PPARD,TRAM1,IPO4,YWHAB,HIST1H1A,NUP62,EMP2,NUP188,TOMM34,SAMM50,GSTO1,TRAK1,DMAP1,ARCN1,CDK2,DDX39B,SNX15,RAB35,ENSCAFG00000005299,EZR,NIPA2,RBM14,CORO1A,CYC1,SLC20A1,ATP5F1A,ENSCAFG00000013366,REM1,SLC25A16,TRAPPC6A,PMPCA,JMJD6,MRPL18,LIPC,NUS1,CCT4,CEP83,SLC25A19,ATP5F1D	down_ACOR_VSMC
GO:0090304	0.999	0.0014	78	1694	nucleic acid metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,CBX5,SARS,AARS,ILK,FHL2,BHLHE40,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,ZPR1,PTPN2,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,CTNNB1,SND1,ENSCAFG00000002015,TFRC,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,ATF3,VLDLR,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,RTCB,SNRPA1,KDM3A	down_VSAP_EC
GO:1901360	0.999	0.00133	76	2016	organic cyclic compound metabolic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,MAOA,NAB2,NDN,PRNP,LUM,FBN1,ADCY6,LARP6,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,LCAT,SAMD4B,TFE3,ACAA1,NR3C1,H6PD,HSD3B7,HR,SCP2,CLSTN1,CYB5R3,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,TEAD1,CYP1B1,ADK,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,AMPD2,MAVS,MRPS11,LOXL3,HPDL,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,SOAT1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0042221	0.999	0.00085	60	1012	response to chemical	BP	1	HMGB1,SREBF1,FLNB,IRAK1,MCM7,TFPI,SREBF2,NEDD4,SLC29A1,MTDH,SLC25A5,PPP1R15B,RAD54L,TENT4A,B3GNT2,HM13,BIRC5,INSIG1,CAV1,RFC3,RAD51,TIMELESS,THRAP3,EZH2,SLC30A1,GREM1,ADIPOR2,CDK4,SMARCC1,PLK3,ANXA5,PRCP,TFRC,PPARD,UBE2J2,NCL,RAC1,PDXP,IQGAP1,SUV39H1,CACTIN,HMGB2,GSTO1,CDC42EP4,CDK2,FGF5,ENSCAFG00000005299,EZR,RBM14,CORO1A,SIGMAR1,BAP1,MELK,PSMC1,CTH,NCOA5,ARHGEF2,MSC,NUS1,PIK3CD	down_ACOR_VSMC
GO:0006807	0.999	0.00116	57	3221	nitrogen compound metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,HCK,TMEM100,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,MOXD1,DCUN1D3,EAF1,RAB7A,AXIN2,YEATS2,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,GCNT4,RNF181	up_AFEM_EC
GO:0009966	0.999	0.00103	50	868	regulation of signal transduction	BP	1	HMGB1,IRAK1,HMGCR,NEDD4,SLC29A1,MTDH,SLC25A5,CTDNEP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,NF2,PSD4,MMP14,EZH2,STMN1,GREM1,MAP3K20,CDK4,DHX33,RNF152,NOC2L,PRCP,PPARD,YWHAB,NUP62,EMP2,CACTIN,HMGB2,GSTO1,ENSCAFG00000005299,EZR,MIOS,BEND6,PHACTR4,ASPM,TXNDC12,PRMT5,CTH,NCOA5,ARHGEF2,GLI1,CDC42SE1,DEPDC1B,AMER1,NET1	down_ACOR_VSMC

GO:0043933	0.999	0.00218	46	698	protein-containing complex subunit organization	BP	1	FGF13,FMOD,DNAJC6,SMAD6,ACTN2,SNAP91,MID1,NACC2,PRKAA2,LCAT,TUBB4A,PCBD1,TP53BP1,MX1,ABCA1,ATRX,TRPS1,SEC24B,ATXN2,LMO4,F2RL1,BNIP3,JMY,TSPYL5,CLSTN1,LRRC8C,SMARCD3,EVL,TBX20,P4HA1,PRKCE,TTC17,SHPRH,LAMP2,DMXL1,DDR2,KCNC4,ASAP1,FAM107A,DMC1,DDIT4,KIF9,TTC19,SBF2,PFKL,WASL	up_ACOR_VSMC
GO:0010033	0.999	0.00164	44	772	response to organic substance	BP	1	SREBF1,FLNB,IRAK1,TFPI,SREBF2,NEDD4,SLC29A1,MTDH,SLC25A5,B3GNT2,HM13,BIRC5,INSIG1,CAV1,RFC3,RAD51,TIMELESS,THRAP3,EZH2,GREM1,ADIPOR2,CDK4,SMARCC1,ANXA5,PRCP,TFRC,UBE2J2,NCL,PDXP,IQGAP1,CACTIN,HMGB2,CDC42EP4,CDK2,FGF5,ENSCAFG00000005299,EZR,CORO1A,PSMC1,CTH,NCOA5,ARHGEF2,MSC,NUS1	down_ACOR_VSMC
GO:0007049	0.999	0.00239	36	560	cell cycle	BP	1	LEP,MAP3K8,CDC7,SKP2,NACC2,BMP4,FGFR2,TP53BP1,ATRX,LATS2,CITED2,TP53INP1,PKP4,CCNG2,PTPN3,CDKN2B,CDKN1A,JMY,CRLF3,PRKCE,CCNT1,MARF1,FZD3,CCPG1,APP,PIK3C3,SPECC1L,MITD1,EDN1,HPGD,FAM107A,DMC1,KLF11,RPRD1B,SUN1,WASL	up_ACOR_VSMC
GO:0034641	0.999	0.00242	35	2171	cellular nitrogen compound metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,CRY2,HOXA7,DLL1,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,TMEM100,GREM1,NFE2L1,TENT5C,CAMK2A,GREM2,CYLD,MYBL1,NR3C1,MOXD1,EAF1,AXIN2,YEATS2,ACACB,NAPEPLD,PPARGC1A,CTIF,SAMD4B	up_AFEM_EC
GO:1902531	0.999	0.00102	27	536	regulation of intracellular signal transduction	BP	1	HMGB1,IRAK1,HMGCR,NEDD4,SLC29A1,MTDH,ENSCAFG00000030005,CAV1,NF2,PSD4,EZH2,STMN1,GREM1,MAP3K20,DHX33,RNF152,NOC2L,PPARD,NUP62,GSTO1,EZR,MIOS,TXNDC12,CTH,ARHGEF2,CDC42SE1,NET1	down_ACOR_VSMC
GO:0016192	0.999	0.00251	22	452	vesicle-mediated transport	BP	1	ACSL3,HMGB1,STXBP6,NEDD4,ZW10,SDC1,ARFGAP1,INSIG1,CAV1,GREM1,PREB,TFRC,HIST1H1A,EMP2,TRAK1,ARCN1,RAB35,EZR,CORO1A,TRAPPC6A,JMJD6,CEP83	down_ACOR_VSMC
GO:0000278	0.999	0.00138	17	331	mitotic cell cycle	BP	1	MAP3K8,CDC7,SKP2,NACC2,BMP4,ATRX,LATS2,PTPN3,CDKN2B,CDKN1A,CRLF3,FZD3,APP,MITD1,EDN1,FAM107A,KLF11	up_ACOR_VSMC
GO:0043412	0.999	0.00282	16	1225	macromolecule modification	BP	1	LEP,USP54,HCK,GREM1,KLHDC8B,TPST2,CAMK2A,CYLD,LRRC15,DCUN1D3,AXIN2,CCL5,CDC42EP5,DMPK,ADAM17,RNF181	up_AFEM_EC
GO:0022603	0.999	0.00317	13	301	regulation of anatomical structure morphogenesis	BP	1	FMNL3,MTDH,GREM1,HOXB7,B4GALT1,RAC1,EMP2,CDC42EP4,EZR,CORO1A,GLI1,SIX4,ANXA7	down_ACOR_VSMC
GO:0043604	0.999	0.00163	13	288	amide biosynthetic process	BP	1	EIF4A2,TARSL2,UGCG,FAM129A,DAPK1,RBM4B,ORMDL3,SMPD1,APP,UBA52,CTIF,ELOVL7,NGRN	up_ACOR_VSMC
GO:1903047	0.999	0.00261	12	257	mitotic cell cycle process	BP	1	FAM107A,CEP85,CRADD,ZFP36L1,E2F4,FBXW5,FBXO7,ZFP36L2,TPRA1,CDC26,LSM10,LATS2	up_VSAP_EC
GO:0034660	0.999	0.00301	9	211	ncRNA metabolic process	BP	1	WARS2,EXOSC7,ICE1,RCL1,FARS2,RPUSD4,QARS,INTS12,LARS2	up_VSAP_EC
GO:0031175	0.999	0.00226	8	224	neuron projection development	BP	1	NEDD4,SLC29A1,B3GNT2,PRMT1,STMN1,IQGAP1,RAB35,ENSCAFG00000010224	down_ACOR_VSMC
GO:0034660	0.999	0.00269	7	211	ncRNA metabolic process	BP	1	TARSL2,MTOR,TENT2,TUT7,RIOK3,SMARCA4,TRMT9B	up_VCAV_EC
GO:0000904	0.999	0.00365	6	181	cell morphogenesis involved in differentiation	BP	1	FLNB,SLC29A1,B3GNT2,STMN1,RAC1,RADIL	down_ACOR_VSMC
GO:0070647	0.999	0.004	6	311	protein modification by small protein conjugation	BP	1	RNF216,PARK7,SASH1,COPS7A,FBH1,KLHL29	down_VCAV_EC
GO:0016569	0.999	0.00272	5	144	covalent chromatin modification	BP	1	PCGF5,PRKAA2,ATRX,PHF20,MAP3K7	up_ACOR_VSMC
GO:0016570	0.999	0.00296	5	143	histone modification	BP	1	PCGF5,PRKAA2,ATRX,PHF20,MAP3K7	up_ACOR_VSMC
GO:0034470	0.999	0.00213	5	154	ncRNA processing	BP	1	EXOSC7,RCL1,FARS2,RPUSD4,INTS12	up_VSAP_EC
GO:0010639	0.999	0.00474	4	128	negative regulation of organelle organization	BP	1	SLIT2,PHF1,HTRA2,BAG4	up_VSAP_EC
GO:0051656	0.999	0.00418	4	129	establishment of organelle localization	BP	1	RAB11B,STX4,TTL,CEP19	up_VSAP_EC
GO:0006325	0.999	0.00262	3	234	chromatin organization	BP	1	HR,PRMT6,CABIN1	down_VCAV_EC
GO:0140014	0.999	0.00424	3	110	mitotic nuclear division	BP	1	BMP4,ATRX,EDN1	up_ACOR_VSMC
GO:0060249	0.999	0.00536	3	110	anatomical structure homeostasis	BP	1	PPARGC1B,MYC,FBXO4	up_VSAP_EC

GO:0140014	0.999	0.00543	3	110	mitotic nuclear division	BP	1	CEP85,FBXW5,CDC26	up_VSAP_EC
GO:0044238	0.999	0.00862	2	3383	primary metabolic process	BP	1	GATA5,SLIT2	up_VPUL_VSMC
GO:0006302	0.999	0.00436	2	97	double-strand break repair	BP	1	TNKS1BP1,AP5Z1	up_VSAP_EC
GO:0006310	0.999	0.00585	2	93	DNA recombination	BP	1	STAT6,AP5Z1	up_VSAP_EC
GO:0007033	0.999	0.00653	1	82	vacuole organization	BP	1	CORO1A	down_ACOR_VSMC
GO:0010721	0.999	0.0112	1	73	negative regulation of cell development	BP	1	ASPM	down_ACOR_VSMC
GO:0019932	0.999	0.00634	1	82	second-messenger-mediated signaling	BP	1	GSTO1	down_ACOR_VSMC
GO:0051961	0.999	0.0113	1	73	negative regulation of nervous system	BP	1	ASPM	down_ACOR_VSMC
GO:0016197	0.999	0.00955	1	78	endosomal transport	BP	1	RAB35	down_ACOR_VSMC
GO:0050727	0.999	0.0115	1	74	regulation of inflammatory response	BP	1	BAP1	down_ACOR_VSMC
GO:0006260	0.999	0.0109	1	98	DNA replication	BP	1	ZPR1	down_VSAP_EC
GO:1901987	0.999	0.00976	1	107	regulation of cell cycle phase transition	BP	1	CDKN1A	down_VSAP_EC
GO:0007051	0.999	0.00541	1	70	spindle organization	BP	1	ATRX	up_ACOR_VSMC
GO:0032259	0.999	0.00542	1	71	methylation	BP	1	ATRX	up_ACOR_VSMC
GO:0043414	0.999	0.00587	1	70	macromolecule methylation	BP	1	ATRX	up_ACOR_VSMC
GO:1902275	0.999	0.0117	1	60	regulation of chromatin organization	BP	1	ATRX	up_ACOR_VSMC
GO:1903311	0.999	0.00518	1	72	regulation of mRNA metabolic process	BP	1	CCNT1	up_ACOR_VSMC
GO:0006364	0.999	0.00685	1	87	rRNA processing	BP	1	RIOK3	up_VCAV_EC
GO:0000070	0.999	0.00494	1	75	mitotic sister chromatid segregation	BP	1	CDC26	up_VSAP_EC
GO:0071704	1	0.00035	295	3535	organic substance metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MEIS2,INTS9,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,ENSCAFG00000002977,SKP2,MAT2B,NACC2,PRKAA2,MLLT3,ITM2C,FERMT1,BMP4,PNRC1,CPXM1,LCAT,ZNF331,TBX18,B3GNT7,CHPT1,FGFR2,PCBD1,TP53BP1,FAXDC2,CCDC126,ABCA1,EIF4A2,GJA1,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,LPL,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ATXN2,ZNF550,MAOA,PIGS,ISG15,UGCG,ZNRF3,ZNF782,ZNF365,PLPP2,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,PFKM,FGF18,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,PPIP5K1,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,ACAD11,STN1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,ERO1B,GGPS1,DAPK1,APOL6,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,LIPE,JMY,C1S,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,LRPAP1,ULK2,DMPK,NPNT,CYP2J2,OS9,ENSCAFG00000028814,STT3B,PFDN5,SCP2,ORMDL3,SMARCD3,SMPD1,PTGDR,TBX20	up_ACOR_VSMC

GO:0044238	1	0.00021	279	3383	primary metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,PIP5K1B,PLCG2,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MEIS2,INTS9,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,ENSCAFG00000002977,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,PNRC1,CPXM1,LCAT,ZNF331,TBX18,B3GNT7,CHPT1,FGFR2,TP53BP1,FAXDC2,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,LPL,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,PIGS,ISG15,UGCG,ZNRF3,ZNF782,ZNF365,PLPP2,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,PIP5K1,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,ACAD11,STN1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,ERO1B,GGPS1,DAPK1,APOL6,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,LIPE,JMY,C1S,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,ULK2,DMPK,NPNT,CYP2J2,OS9,STT3B,PFDN5,SCP2,ORMDL3,SMARCD3,SMPD1,PTGDR,TBX20,FUT11,C7,UBE2H,SH3RF1,PYGM,RNF24,CCDC3,P4HA1,GLB1L,PRKCE,CCNT1,MA	up_ACOR_VSMC
GO:0006807	1	0.00022	264	3221	nitrogen compound metabolic process	BP	1	FGF13,ADRA1B,TLR1,SMAD6,GALNT3,LEP,PLCL1,GALNT10,LBH,ST3GAL5,MAP3K8,MID1,GATA5,GATA4,CDC7,PCGF5,HTR2B,RASSF2,TPST2,ENOSF1,MEIS2,INTS9,MBP,ZRANB1,FBXL20,PRDX4,RECK,LIPT2,B3GALNT2,ENSCAFG00000002977,SKP2,NACC2,PRKAA2,MLLT3,ITM2C,BMP4,PNRC1,CPXM1,LCAT,ZNF331,TBX18,B3GNT7,FGFR2,PCBD1,TP53BP1,CCDC126,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,SH3RF2,ELL2,PPARGC1A,LATS2,PIGN,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,MAOA,PIGS,ISG15,UGCG,ZNRF3,ZNF782,ZNF365,AR,ZNF484,SASH1,CTSS,LMO4,GTF3C1,PTPN3,ZNF572,FGF18,NDRG2,NIT2,TMX3,CDKN2B,ADCY6,USP53,POLK,GRK7,CST3,ZNF174,PLAC8B,PIGG,KLHL20,ANKRD1,F2RL1,STN1,FAM129A,CAMK2D,MARCH5,PSEN2,ENPP4,ERO1B,DAPK1,APOL6,PKNOX2,CTSB,RBM4B,HKR1,MAGT1,BNIP3,EGLN1,SUMF1,NCEH1,CDKN1A,JMY,C1S,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NRP1,UBR1,PTPN22,ULK2,DMPK,NPNT,OS9,ENSCAFG00000028814,STT3B,PFDN5,ORMDL3,SMARCD3,SMPD1,PTGDR,TBX20,FUT11,C7,UBE2H,MOXD1,SH3RF1,RNF24,P4HA1,PRKCE,CCNT1,MARF1,SARDH,FRS2,RNF19A,CCPG1,LYPLAL1,SCG5,ENSCAFG00	up_ACOR_VSMC
GO:0008152	1	0.00053	260	3714	metabolic process	BP	1	EPHB1,PLK2,EDNRB,TEK,HCLS1,PCDH12,IL7R,NPR1,ADGRF5,ST8SIA6,KIT,SELE,LYZ,PRCP,PPP2R5A,CXCL8,PANK3,PRKCH,CALCRL,FLI1,CDA,TNFAIP3,PPARG,MAP3K11,TNIP1,PDGFB,STK10,SH2D3C,TMEM173,TSPAN8,RELN,CD34,ST6GAL1,CTSC,PDE4D,MOV10,IWS1,MEF2C,FERMT1,ATF3,CHD7,KLKB1,TIPARP,DLL4,RAPGEF1,WWP1,TLR4,NOS3,NLRC5,QKI,LYVE1,TSPAN15,GK5,GATA3,USP33,EDN1,HOXB8,RALB,APLNR,RAB27A,TCF4,SMAD1,CTTNBP2NL,SNCAIP,FOXN2,MEOX1,PIPOX,PTGS1,ENSCAFG00000017103,ZDHHC22,PSME4,NEDD9,IRF8,SOX18,FIGNL1,PELI1,PPP3CA,SERINC5,ADSS,YES1,FAM3C,GUCY1A1,ENSCAFG00000010893,ODC1,SPTLC2,ARG2,CASP8,EPHB4,B3GNT5,TARSL2,MTOR,ACPP,TENT2,SAMD8,ELF4,ASB9,TSPAN14,HHAT,MAP3K3,BMP2,CDYL,HMG20A,HHEX,CHST7,CREM,PGM2,PREX2,TUT7,SLK,BMP2K,SH3BP5,SCAF11,CNOT6,DEPP1,RSC1A1,ST3GAL6,ENC1,CCAR1,ABCA1,PPP1R2,ERC1,AADAT,MAPK13,ITPKB,GDPD5,RIOK3,PROX1,UHRF2,SECISBP2L,MDFI,ENSCAFG00000010596,MADD,ARID4B,HMBOX1,BAZ1A,GALE,PAK2,GALNT18,PRKD2,THOC1,SH3GLB1,SWAP70,CHST1,SMARCA4,ELOVL7,TLR3,MFNG,ENSCAFG00000024323,APOD,NCK1,E	up_VCAV_EC

GO:0043170	1	2.1E-05	236	2980	macromolecule metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,NECAB3,WNT11,FAM107A,ACKR3,MAP3K14,ARHGEF5,AXIN2,C5AR2,OSR2,INSIG2,ENPP2,PTGFR,ZNF367,PPARGC1B,RNPEP,TBC1D10C,MRPL37,CEP85,FOXRED2,ACACB,EEF2K,IL6R,IRX5,SLIT2,CST3,CRADD,ZHX3,ABTB1,HOXD3,CDH1,SLC6A4,FGF7,ABL1,PEX2,KLHL36,ZNF250,HDAC7,KLKB1,EMP2,DLL1,DLST,OSR1,MAP3K5,ZNF449,CDC42EP5,CTSS,GALNT15,DTX2,TENT5C,PDGFD,WARS2,VDR,NAA60,SAV1,DDB2,KLF15,C1QTNF2,ANXA4,HPSE,ZNF688,ZBTB16,CNPPD1,RARG,CCBE1,TRMT2A,VPS36,CBX7,STAT5A,STAT6,RECK,GATAD1,CISH,KLHL24,PLPP3,ENSCAFG00000000071,EXOSC7,CAMKK2,APOL5,TNKS1BP1,KLHDC8B,PYM1,F2RL1,RBL2,LMF1,PHKA2,RAB11B,NFE2L2,GLIS2,DFFB,MORC3,DDR2,ICE1,ZFP36L1,TRAF7,HSF4,FXN,PIK3R1,RBCK1,KBTBD12,GAS1,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,RNF24,FKRP,FBXW4,DLD,SULF2,SHOX2,CAPN5,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,RTN4RL1,SASH1,FBXO4,RMND5A,LARP6,MYD88,IKZF2,TFE3,RPL13,LRP4,PASK,NUP98,ANKHD1,TSPAN5,AZIN2,TRERF1,GALNT11,STK16,NCEH1,PHF1,E2F4,CFD,NPAS2,PRKAB1,FBXW5,SMG9,RCL1,FBXO7,MOCOS,	up_VSAP_EC
GO:0034641	1	0.00054	171	2171	cellular nitrogen compound metabolic process	BP	1	TBX15,HOXA11,FZD1,PRR16,THRB,EMX2,HOXA7,HOXA10,NAPEPLD,HOXA9,CDON,WNT11,ACSM3,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,RNPEP,MRPL37,ACACB,IRX5,GDA,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,ENSCAFG00000013986,CERS4,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,ZNF688,ZBTB16,COQ9,ALDH6A1,RARG,TRMT2A,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,GATAD1,PLPP3,ENSCAFG00000000071,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DFFB,DDR2,PDK2,ICE1,ZFP36L1,HSF4,FXN,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,CTNS,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,EEF2,FBXO4,LARP6,MYD88,NDUFS2,IKZF2,TFE3,RPL13,LRP4,NUP98,ANKHD1,NT5C2,AZIN2,TRERF1,E2F4,NPAS2,SMG9,RCL1,FARS2,PCBD1,LIMD1,UBA52,RPUSD4,RPL15,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,MVK,PNPO,AP5Z1,DCAKD,EIF3G,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,EIF3K,EIF3L,PQBP1,QARS,SMARCA2,EIF3D,ACVRL1,KDM3B,IDH1,ZNF517,ASS1,TNRC6C,COA1,PPP3CB,NCK1,Z	up_VSAP_EC
GO:0006725	1	0.00049	151	1956	cellular aromatic compound metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ACSM3,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,GDA,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,SULT1A1,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,ENSCAFG00000013986,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,ZNF688,ZBTB16,COQ9,ALDH6A1,RARG,TRMT2A,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,GATAD1,PLPP3,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DFFB,DDR2,PDK2,ICE1,ZFP36L1,HSF4,FXN,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,CTNS,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,CLYBL,LARP6,MYD88,NDUFS2,IKZF2,TFE3,LRP4,NUP98,NT5C2,TRERF1,E2F4,NPAS2,SMG9,RCL1,FARS2,PCBD1,LIMD1,RPUSD4,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,MVK,PNPO,AP5Z1,DCAKD,SAMD4B,ZFP36L2,ESRRA,CPOX,ENSCAFG00000013366,YEATS2,RAF1,PNP,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,NDUFV1,MAVS,INTS12,HMOX1,ZNF662,LARS2,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772,IDO2	up_VSAP_EC

GO:0034641	1	1E-07	150	2171	cellular nitrogen compound metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,UGCG,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,NIT2,ADCY6,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,FAM129A,ENPP4,ERO1B,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,ENSCAFG00000028814,PFDN5,ORMDL3,SMARCD3,SMPD1,PTGDR,TBX20,MOXD1,CCNT1,MARF1,CCPG1,SCG5,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,PCSK6,MXI1,CHD7,LAMP2,JUP,TLE4,ZNF432,DDR2,CLN8,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,DMC1,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,NEU3,EXTL2,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,AZIN2,PTS,RPAIN,UBA52,WDR48,CTIF,NT5C2,ZKSCAN1,ZNF529,ERAP1,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,NGR	up_ACOR_VSMC
GO:0006139	1	0.00019	144	1909	nucleobase-containing compound metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ACSM3,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,ACACB,IRX5,GDA,ZHX3,HOXD3,CDH1,NADK,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,ZNF688,ZBTB16,COQ9,ALDH6A1,RARG,TRMT2A,NDUFS1,CBX7,STAT5A,STAT6,ENSCAFG00000004260,GATAD1,PLPP3,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DFFB,DDR2,PDK2,ICE1,ZFP36L1,HSF4,FXN,GALK1,PIK3R1,RBCK1,ENTPD3,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,CTNS,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,LARP6,MYD88,NDUFS2,IKZF2,TFE3,LRP4,NUP98,NT5C2,TRERF1,E2F4,NPAS2,SMG9,RCL1,FARS2,LIMD1,RPUSD4,ACSS2,CDK9,NR2F6,PRMT2,KDM2B,MVK,AP5Z1,DCAKD,SAMD4B,ZFP36L2,ESRRA,ENSCAFG00000013366,YEATS2,RAF1,PNP,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,NDUFV1,MAVS,INTS12,HMOX1,ZNF662,LARS2,CITED2,CXXC1,LBH,KEAP1,DDIT4,ZNF772	up_VSAP_EC
GO:1901360	1	3.5E-07	140	2016	organic cyclic compound metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,LCAT,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,ABCA1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,MAOA,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,ENPP4,PKNOX2,HKR1,EGLN1,CDKN1A,LIPE,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SCP2,SMARCD3,PTGDR,TBX20,MOXD1,CCNT1,MARF1,DKKL1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,CLN8,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,DMC1,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,EXTL2,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,PTS,RPAIN,WDR48,CTIF,NT5C2,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,LMF1,FAN1	up_ACOR_VSMC

GO:0006725	1	1.4E-07	133	1956	cellular aromatic compound metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,MAOA,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,ENPP4,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SMARCD3,PTGDR,TBX20,MOXD1,CCNT1,MARF1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,DMC1,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,EXTL2,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,PTS,RPAIN,WDR48,CTIF,NT5C2,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,FAN1	up_ACOR_VSMC
GO:0046483	1	7E-08	131	1948	heterocycle metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,PCBD1,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,ENPP4,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SMARCD3,PTGDR,TBX20,CCNT1,MARF1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,DMC1,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,EXTL2,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,PTS,RPAIN,WDR48,CTIF,NT5C2,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,FAN1	up_ACOR_VSMC
GO:0010467	1	4.4E-05	130	1787	gene expression	BP	1	SMAD6,PLCG2,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,INTS9,PRDX4,LIPT2,NACC2,PRKAA2,MLLT3,FERMT1,BMP4,PNRC1,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,GJA1,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,FAM129A,PSEN2,ERO1B,DAPK1,PKNOX2,RBM4B,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,PTPN22,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,MARF1,CCPG1,SCG5,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,PARP9,CHD6,APP,PSEN1,TGFBR1,PCSK6,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,PERP,DUSP22,MED23,EDN1,RNF141,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,NCSTN,OSGEPL1,LHX9,WFS1,UBA52,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,NGRN,STC2,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,LMF1,CRKL	up_ACOR_VSMC

GO:0006139	1	1.3E-07	129	1909	nucleobase-containing compound metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,PDE5A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,ADCY6,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,ENPP4,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SMARCD3,PTGDR,TBX20,CCNT1,MARF1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,FUT8,ENSCAFG00000018611,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,ALDOC,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ENTPD3,DMC1,ZNF629,ZFP3,DDIT4,ENSCAFG00000018360,KLF11,EXTL2,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,RPAIN,WDR48,CTIF,NT5C2,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,NMNAT1,PARK7,ELOVL7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,FAN1	up_ACOR_VSMC
GO:0090304	1	6.3E-05	122	1694	nucleic acid metabolic process	BP	1	TBX15,HOXA11,FZD1,THRB,EMX2,HOXA7,HOXA10,HOXA9,CDON,WNT11,ARHGEF5,AXIN2,OSR2,INSIG2,ZNF367,PPARGC1B,IRX5,ZHX3,HOXD3,CDH1,FGF7,ABL1,PEX2,ZNF250,HDAC7,DLL1,OSR1,MAP3K5,ZNF449,TENT5C,WARS2,VDR,SAV1,DDB2,KLF15,ANXA4,ZNF688,ZBTB16,RARG,TRMT2A,CBX7,STAT5A,STAT6,GATAD1,PLPP3,EXOSC7,TNKS1BP1,PYM1,F2RL1,RBL2,NFE2L2,GLIS2,DFFB,DDR2,ICE1,ZFP36L1,HSF4,PIK3R1,RBCK1,BATF2,NEIL2,MYC,SSBP2,IRX3,ZEB1,SHOX2,H2AFJ,ZC3H10,TLE2,CIZ1,YBX3,FBXO4,LARP6,MYD88,IKZF2,TFE3,LRP4,NUP98,TRERF1,E2F4,NPAS2,SMG9,RCL1,FARS2,LIMD1,RPUSD4,CDK9,NR2F6,PRMT2,KDM2B,AP5Z1,SAMD4B,ZFP36L2,ESRRA,YEATS2,RAF1,MAPKBP1,TAF8,NFIB,ABHD14B,ZNF205,NCOA2,PQBP1,QARS,SMARCA2,ACVRL1,KDM3B,ZNF517,TNRC6C,PPP3CB,NCK1,ZNF444,MAVS,INTS12,HMOX1,ZNF662,LARS2,CITED2,CXXC1,LBH,KEAP1,ZNF772	up_VSAP_EC
GO:0090304	1	1.5E-06	116	1694	nucleic acid metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,CDC7,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,ZNF365,AR,ZNF484,LMO4,GTF3C1,ZNF572,POLK,ZNF174,PLAC8B,ANKRD1,F2RL1,STN1,PKNOX2,HKR1,EGLN1,CDKN1A,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,MARF1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,DMC1,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,RPAIN,WDR48,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1,FAN1	up_ACOR_VSMC

GO:0016070	1	9E-05	106	1479	RNA metabolic process	BP	1	SMAD6,LEP,LBH,GATA5,GATA4,PCGF5,MEIS2,INTS9,NACC2,MLLT3,BMP4,PNRC1,ZNF331,TBX18,FGFR2,TP53BP1,EIF4A2,ELF1,ATRX,MED14,TARSL2,TRPS1,TLR3,ELL2,PPARGC1A,ZNF821,CITED2,TP53INP1,ZNF550,ZNF782,AR,ZNF484,LMO4,GTF3C1,ZNF572,ZNF174,PLAC8B,ANKRD1,F2RL1,PKNOX2,HKR1,EGLN1,JMY,CRLF3,ENSCAFG00000006238,DCP1B,CLSTN1,NPNT,PFDN5,SMARCD3,TBX20,CCNT1,CCPG1,ENSCAFG00000030568,ZNF175,ZNF79,PARP9,CHD6,APP,PSEN1,TGFBR1,MXI1,CHD7,JUP,TLE4,ZNF432,DDR2,NR3C1,WWC2,DUSP22,MED23,EDN1,RNF141,GTF2A1L,TRMT9B,DUSP26,CBX7,NOD2,ARID5B,ZNF629,ZFP3,ENSCAFG00000018360,KLF11,RPRD1B,ZNF461,ZNF252,ENSCAFG00000030317,MAP3K7,INPP5K,CNOT4,OSGEPL1,LHX9,WFS1,CTIF,ZKSCAN1,ZNF529,ENSCAFG00000029553,YEATS2,ID3,PARK7,TEAD1,ZNF454,IL18R1,HMBOX1,SSBP2,RREB1	up_ACOR_VSMC
GO:0007154	1	0.00036	104	1622	cell communication	BP	1	HMGB1,SREBF1,IRAK1,RACGAP1,HMGCR,SREBF2,NEDD4,MNDA,SLC29A1,MTDH,HEY1,RRBP1,SLC25A5,PPP1R15B,SDC1,CTDNEP1,RANGAP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,THRAP3,FAM129B,ENSCAFG00000008236,NF2,PSD4,MMP14,EZH2,STMN1,DEPDC1,PPP2R5D,GREM1,MAP3K20,ADIPOR2,CDK4,SMARCC1,DHX33,RNF152,NOC2L,PRCP,NRAS,PPARD,ITGB3,RAP2C,ARHGDIA,YWHAB,RAC1,NUP62,EMP2,DTL,GNB2,PDXP,FOSL1,IQGAP1,HASPIN,IQGAP2,CACTIN,HMGB2,GSTO1,CDC42EP4,CDK2,FGF5,CCNA2,SNX15,ENSCAFG00000005299,EZR,RBM14,MIOS,CORO1A,SGPL1,BEND6,PHACTR4,CDC20,ASPM,MAST2,MELK,PRKD3,ENSCAFG00000010224,TXNDC12,RADIL,REM1,PRMT5,ITGA2,PDE8A,CTH,NCOA5,AIFM1,ARHGEF2,GLI1,JMJD6,CDC42SE1,CDC5L,RGS9,NUDT1,DELE1,NUS1,AMOTL1,DEPDC1B,AMER1,NET1,PIK3CD	down_ACOR_VSMC
GO:0023052	1	0.00019	101	1602	signaling	BP	1	HMGB1,SREBF1,IRAK1,RACGAP1,HMGCR,NEDD4,MNDA,SLC29A1,MTDH,HEY1,RRBP1,SLC25A5,PPP1R15B,SDC1,CTDNEP1,RANGAP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,THRAP3,FAM129B,ENSCAFG00000008236,NF2,PSD4,MMP14,EZH2,STMN1,DEPDC1,PPP2R5D,GREM1,MAP3K20,ADIPOR2,CDK4,SMARCC1,DHX33,RNF152,NOC2L,PRCP,NRAS,PPARD,ITGB3,RAP2C,ARHGDIA,YWHAB,RAC1,NUP62,EMP2,DTL,GNB2,IQGAP1,HASPIN,IQGAP2,CACTIN,HMGB2,GSTO1,CDC42EP4,CDK2,FGF5,CCNA2,SNX15,ENSCAFG00000005299,EZR,RBM14,MIOS,CORO1A,SGPL1,BEND6,PHACTR4,CDC20,DLGAP5,ASPM,MAST2,MELK,PRKD3,ENSCAFG00000010224,TXNDC12,RADIL,REM1,PRMT5,ITGA2,PDE8A,CTH,NCOA5,AIFM1,ARHGEF2,GLI1,JMJD6,CDC42SE1,CDC5L,RGS9,DELE1,NUS1,AMOTL1,DEPDC1B,AMER1,NET1,PIK3CD	down_ACOR_VSMC
GO:0034641	1	0.00022	98	2171	cellular nitrogen compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,ASNS,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,ENSCAFG00000028814,PGAM1,PUM3,UGCG,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,EIF4EBP1,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,SND1,ENSCAFG00000002015,TFRC,APOE,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,EIF5,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,EIF2S1,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,RSL24D1,ARF4,YWHAH,RTCB,SNRPA1,KDM3A,CMPK1	down_VSAP_EC

GO:1901360	1	0.00027	91	2016	organic cyclic compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,PGAM1,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ALDH18A1,ENTPD4,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,SND1,ENSCAFG00000002015,TFRC,APOE,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,RTCB,SNRPA1,KDM3A,CMPK1	down_VSAP_EC
GO:0006725	1	0.00047	89	1956	cellular aromatic compound metabolic process	BP	1	ARHGEF2,PRICKLE1,VEGFA,SULF1,CELF1,CARS,NR1H4,PLK3,ETV6,MEIS2,ENPP1,CBX5,SARS,PGK1,AARS,TPI1,PGAM1,ILK,FHL2,BHLHE40,ALDH1L2,PPP1R12A,SMARCA4,ANKRA2,SESN2,TGFBR1,HIF1A,FOXP4,MRPL1,IWS1,NMNAT2,ZPR1,PTPN2,ENTPD4,MORF4L2,YARS,SNRPB2,TARS,YES1,NEO1,PEG3,SMG7,MTDH,NARS,PRPF3,DDX39B,BRD2,CNOT7,MAGED1,ALDOC,CTNNB1,PAPSS1,SND1,ENSCAFG00000002015,TFRC,WWC3,PDCD11,KLF5,STRAP,DDIT3,PDS5B,BACH1,ATF3,VLDLR,AK5,GTF2H1,ARMCX3,REST,RBBP8,ZMYND8,PRMT1,NR4A2,GLO1,ENSCAFG00000015065,RAD23A,INHBA,LRRFIP2,BCAS2,NR4A1,ENSCAFG00000018360,HIF1AN,SIX4,CDKN1A,ARF4,YWHAH,RTCB,SNRPA1,KDM3A,CMPK1	down_VSAP_EC
GO:0006996	1	4.3E-05	89	1301	organelle organization	BP	1	SYNPO2L,PDLIM3,FGF13,RHOT1,EPB41L4A,ARHGAP28,ACTN2,MID1,PCGF5,USP6NL,ZRANB1,FEZ1,PRKAA2,BMP4,SYT16,EVI5L,LNPK,SYNPO2,TUBB4A,MX1,ABCA1,ATRX,SEC24B,XIRP1,WASF3,PPARGC1A,TP53INP1,ATXN2,ZNF365,STX11,TMEM108,NEBL,IFT43,ZMYM2,F2RL1,STN1,MARCH5,GABARAPL1,BNIP3,JMY,TSPYL5,NRP1,DMPK,SCP2,SMARCD3,EVL,DES,PRKCE,MARF1,MYO1B,TTC17,RND1,DAG1,PSEN1,SGSM2,CHD7,SHPRH,PIK3C3,SIPA1L1,CLN8,SSH3,EDN1,PHF20,AKTIP,LRRC4,ASAP1,FAM107A,ATG16L2,DMC1,JAM3,DISC1,KIF9,TTC19,TACC1,GAA,ATXN10,FEZ2,SUN1,MAP3K7,INPP5K,FAF2,WASL,ATP2C1,NAIF1,ACP2,PARK7,ENSCAFG00000013536,HMBOX1,MYOZ2	up_ACOR_VSMC
GO:0006996	1	6.2E-05	88	1301	organelle organization	BP	1	PEX7,WNT11,FAM107A,ARHGEF5,AXIN2,WASF3,PPARGC1B,PLEKHF1,TBC1D10C,CEP85,TPCN2,DDHD1,RETREG1,SLIT2,TBC1D2B,NDUFS7,FGF7,ABL1,PEX2,EMP2,CDC42EP5,FUZ,CORO2B,NAA60,SMARCD2,DDB2,RILPL2,CDC42EP2,GATAD1,KLHL24,AMBRA1,F2RL1,MFN2,FXN,PIK3R1,DMAC2,MYC,H2AFJ,FBXO4,POLDIP2,NDUFAF3,NDUFB10,DPYSL2,NUP98,HPS4,FRMD6,PHF1,WIPF1,E2F4,FBXW5,KIF27,FBXO7,TMEM17,LIMD1,LONP2,RAB30,CDK9,KDM2B,PIP4K2B,ATP8B2,MYO1B,WDR82,MTFR1L,RAF1,ZNF205,CENPP,STX4,SMIM20,DR1,TTL,VPS11,SMARCA2,ARHGAP12,KDM3B,TTC8,UBQLN2,ARHGAP10,CDC26,HTRA2,COA1,PEX6,NCK1,MAVS,CEP19,NPRL3,BAG4,FUNDC2,CLUH	up_VSAP_EC
GO:0044085	1	7.1E-05	70	1076	cellular component biogenesis	BP	1	SYNPO2L,FGF13,SMAD6,ARHGAP28,ACTN2,SNAP91,FEZ1,NACC2,PRKAA2,LCAT,EVI5L,SYNPO2,TUBB4A,PCBD1,TP53BP1,MX1,MFAP4,ABCA1,ATRX,TRPS1,SEC24B,WASF3,TP53INP1,ATXN2,PKP4,LMO4,ARHGEF26,NEBL,IFT43,F2RL1,GABARAPL1,JMY,TSPYL5,CLSTN1,LRRC8C,NRP1,ORMDL3,EVL,SLITRK5,TBX20,PRKCE,MYO1B,TTC17,DAG1,APP,PSEN1,SHPRH,PIK3C3,JUP,DMXL1,DUSP22,SSH3,EDN1,KCNC4,ASAP1,FAM107A,ATG16L2,DMC1,DISC1,KIF9,TTC19,SBF2,ATXN10,FEZ2,INPP5K,PFKL,WASL,ENSCAFG00000013536,CRKL,MYOZ2	up_ACOR_VSMC

GO:0006725	1	0.00019	69	1956	cellular aromatic compound metabolic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,MAOA,NAB2,NDN,PRNP,LUM,FBN1,ADCY6,LARP6,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,H6PD,HR,CLSTN1,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,TEAD1,ADK,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,AMPD2,MAVS,MRPS11,LOXL3,HPDL,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0046483	1	8.2E-05	67	1948	heterocycle metabolic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,NDN,PRNP,LUM,FBN1,ADCY6,LARP6,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,H6PD,HR,CLSTN1,VDR,PRMT6,UROS,NT5C2,EPHX1,ENTPD3,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,TEAD1,ADK,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,AMPD2,MAVS,MRPS11,LOXL3,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0008152	1	0.0005	67	3714	metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXC10,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,GPAM,MLLT11,LMCD1,THRB,MYO1D,MFAP4,ATP6V1B2,HCK,TMEM100,PLAGL2,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,SDR42E1,LRRC15,MYBL1,RECK,NR3C1,MOXD1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ALDH3B1,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,AGPAT2,GCNT4,TNC,RNF181,SOD1	up_AFEM_EC
GO:0006139	1	7.3E-05	65	1909	nucleobase-containing compound metabolic process	BP	1	GPAM,NOTCH2,SMAD9,DCN,NAB2,NDN,PRNP,LUM,FBN1,ADCY6,LARP6,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,H6PD,HR,CLSTN1,VDR,PRMT6,NT5C2,ENTPD3,PGLS,TMEM161A,ATP5MC1,CXXC5,GFPT2,UQCR10,TEAD1,ADK,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,AMPD2,MAVS,MRPS11,LOXL3,FUT8,RAB7B,IRX5,ACSS2,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,THRB,ZBTB16,RGMA,ACAT1	down_VCAV_EC
GO:0071704	1	0.00057	63	3535	organic substance metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,HCK,TMEM100,PLAGL2,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,SDR42E1,LRRC15,MYBL1,RECK,NR3C1,MOXD1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ALDH3B1,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,AGPAT2,GCNT4,TNC,RNF181	up_AFEM_EC
GO:0044237	1	0.00058	62	3491	cellular metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,GPAM,MLLT11,LMCD1,THRB,MYO1D,ATP6V1B2,HCK,TMEM100,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,LRRC15,MYBL1,RECK,NR3C1,MOXD1,DCUN1D3,EAF1,BVES,RAB7A,AXIN2,YEATS2,ALDH3B1,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,AGPAT2,GCNT4,RNF181,SOD1	up_AFEM_EC

GO:0044238	1	0.00024	58	3383	primary metabolic process	BP	1	TBX15,HOXA9,CMKLR1,IRX3,IRX5,HOXA10,LEP,LBH,PRR16,USP54,CRY2,XYLT1,GAS1,HOXA7,DLL1,CRYAB,CTSS,F3,GPAM,MLLT11,LMCD1,THRB,ATP6V1B2,HCK,TMEM100,PLAGL2,GREM1,KLHDC8B,NFE2L1,TPST2,TENT5C,CAMK2A,GREM2,CLEC16A,CYLD,SDR42E1,LRRC15,MYBL1,RECK,NR3C1,DCUN1D3,EAF1,RAB7A,AXIN2,YEATS2,ACACB,NAPEPLD,PPARGC1A,CSGALNACT2,CCL5,CDC42EP5,CTIF,FAP,DMPK,ADAM17,SAMD4B,AGPAT2,RNF181	up_AFEM_EC
GO:0010646	1	0.00018	52	945	regulation of cell communication	BP	1	HMGB1,SREBF1,IRAK1,HMGCR,NEDD4,SLC29A1,MTDH,SLC25A5,CTDNEP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,NF2,PSD4,MMP14,EZH2,STMN1,GREM1,MAP3K20,CDK4,DHX33,RNF152,NOC2L,PRCP,PPARD,YWHAB,NUP62,EMP2,CACTIN,HMGB2,GSTO1,ENSCAFG00000005299,EZR,MIOS,BEND6,PHACTR4,CDC20,ASPM,TXNDC12,PRMT5,CTH,NCOA5,ARHGEF2,GLI1,CDC42SE1,DEPDC1B,AMER1,NET1	down_ACOR_VSMC
GO:0023051	1	0.00013	52	954	regulation of signaling	BP	1	HMGB1,SREBF1,IRAK1,HMGCR,NEDD4,SLC29A1,MTDH,SLC25A5,CTDNEP1,SLC35C2,PRELID1,BIRC5,INSIG1,ENSCAFG00000030005,CAV1,CASP2,NF2,PSD4,MMP14,EZH2,STMN1,GREM1,MAP3K20,CDK4,DHX33,RNF152,NOC2L,PRCP,PPARD,YWHAB,NUP62,EMP2,CACTIN,HMGB2,GSTO1,ENSCAFG00000005299,EZR,MIOS,BEND6,PHACTR4,CDC20,ASPM,TXNDC12,PRMT5,CTH,NCOA5,ARHGEF2,GLI1,CDC42SE1,DEPDC1B,AMER1,NET1	down_ACOR_VSMC
GO:0090304	1	2.6E-06	50	1694	nucleic acid metabolic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,NABP2,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,TMEM161A,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,MAVS,MRPS11,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,FBH1,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0035556	1	0.00074	48	845	intracellular signal transduction	BP	1	HMGB1,IRAK1,RACGAP1,HMGCR,NEDD4,SLC29A1,MTDH,ENSCAFG00000030005,CAV1,CASP2,NF2,PSD4,EZH2,STMN1,DEPDC1,GREM1,MAP3K20,DHX33,RNF152,NOC2L,PPARD,RAP2C,ARHGDIA,RAC1,NUP62,DTL,HASPIN,GSTO1,CDC42EP4,CDK2,CCNA2,EZR,MIOS,PHACTR4,MAST2,MELK,PRKD3,TXNDC12,CTH,AIFM1,ARHGEF2,CDC42SE1,CDC5L,RGS9,AMOTL1,DEPDC1B,NET1,PIK3CD	down_ACOR_VSMC
GO:0016070	1	0.00011	47	1479	RNA metabolic process	BP	1	NOTCH2,SMAD9,DCN,NAB2,PRNP,LUM,FBN1,LARP6,KANK2,BMPR1A,LMO4,ENSCAFG00000014978,CHRDL1,SSBP2,TBX15,SAMD4B,TFE3,NR3C1,HR,CLSTN1,VDR,PRMT6,CXXC5,TEAD1,CC2D1A,GLI3,PARK7,ZFP36L1,MYDGF,RPL27,RBM38,MAVS,MRPS11,LOXL3,RAB7B,IRX5,TSC22D3,MAPRE3,GLIS2,DDR2,SHC1,PYM1,CRCP,GREM1,THRB,ZBTB16,RGMA	down_VCAV_EC
GO:0065003	1	0.00043	36	616	protein-containing complex assembly	BP	1	FGF13,SMAD6,ACTN2,SNAP91,NACC2,PRKAA2,LCAT,TUBB4A,PCBD1,TP53BP1,MX1,ABCA1,ATRX,TRPS1,SEC24B,ATXN2,LMO4,JMY,TSPYL5,CLSTN1,LRRC8C,EVL,TBX20,PRKCE,TTC17,SHPRH,DMXL1,KCNC4,ASAP1,FAM107A,DMC1,KIF9,TTC19,SBF2,PFKL,WASL	up_ACOR_VSMC
GO:0007049	1	0.00013	30	560	cell cycle	BP	1	FAM107A,MAP3K14,AXIN2,CEP85,CRADD,SLC6A4,ABL1,CNPPD1,RBL2,ZFP36L1,GAS1,CDC25B,FBXO4,POLDIP2,ATRIP,GDPD5,E2F4,FBXW5,FBXO7,CDK9,TTC28,ZFP36L2,HPGD,TTL,TPRA1,CDC26,LSM10,MAP2K2,CITED2,LATS2	up_VSAP_EC
GO:0009605	1	0.00061	26	538	response to external stimulus	BP	1	HMGB1,SREBF1,IRAK1,HNRNPUL1,TFPI,SREBF2,MTDH,B3GNT2,CAV1,CASP2,STMN1,CDK4,ARG2,RNF152,PPARD,RAC1,PDXP,FOSL1,CACTIN,HMGB2,MIOS,CORO1A,BAP1,NUDT1,EXOSC5,PIK3CD	down_ACOR_VSMC
GO:0034622	1	0.00042	21	421	cellular protein-containing complex assembly	BP	1	FGF13,SMAD6,SNAP91,PRKAA2,TUBB4A,MX1,ATRX,SEC24B,ATXN2,JMY,TSPYL5,EVL,TBX20,PRKCE,TTC17,SHPRH,DMXL1,FAM107A,DMC1,TTC19,WASL	up_ACOR_VSMC

GO:0051276	1	0.00013	18	398	chromosome organization	BP	1	AXIN2,NAA60,SMARCD2,DDB2,GATAD1,MYC,H2AFJ,FBXO4,NUP98,PHF1,CDK9,KDM2B,WDR82,CENPP,DR1,SMARCA2,KDM3B,CDC26	up_VSAP_EC
GO:0006259	1	0.00025	17	354	DNA metabolic process	BP	1	CDC7,TP53BP1,ATRX,PPARGC1A,ZNF365,POLK,ANKRD1,STN1,CDKN1A,MARF1,PARP9,DMC1,RPAIN,WDR48,PARK7,HMBOX1,FAN1	up_ACOR_VSMC
GO:0022402	1	1E-05	16	407	cell cycle process	BP	1	FAM107A,AXIN2,CEP85,CRADD,ZFP36L1,CDC25B,E2F4,FBXW5,FBXO7,CDK9,ZFP36L2,TTL,TPRA1,CDC26,LSM10,LATS2	up_VSAP_EC
GO:0006996	1	0.00042	15	1301	organelle organization	BP	1	RAB20,MLLT11,CAMK2A,CLEC16A,CYLD,DNAL1,CHCHD10,REEP2,RAB7A,AXIN2,PPARGC1A,SPATA6,CDC42EP5,DMPK,KANK1	up_AFEM_EC
GO:0006259	1	0.00013	15	354	DNA metabolic process	BP	1	AXIN2,DDB2,STAT6,TNKS1BP1,DFFB,NEIL2,MYC,CIZ1,FBXO4,NUP98,NPAS2,CDK9,AP5Z1,NFIB,ACVRL1	up_VSAP_EC
GO:0051276	1	7.1E-07	14	398	chromosome organization	BP	1	PCGF5,PRKAA2,ATRX,ZNF365,STN1,TSPYL5,SMARCD3,CHD7,SHPRH,PHF20,DMC1,SUN1,MAP3K7,HMBOX1	up_ACOR_VSMC
GO:0006396	1	1.4E-05	14	368	RNA processing	BP	1	TRMT2A,EXOSC7,ZFP36L1,PIK3R1,ZC3H10,LARP6,NUP98,RCL1,FARS2,RPUSD4,CDK9,MAPKBP1,PQBP1,INTS12	up_VSAP_EC
GO:0007267	1	0.00065	13	332	cell-cell signaling	BP	1	SREBF1,SDC1,CTDNEP1,BIRC5,CAV1,FAM129B,GREM1,ENSCAFG00000005299,CDC20,ASPM,GLI1,DEPDC1B,AMER1	down_ACOR_VSMC
GO:0030182	1	0.00074	13	327	neuron differentiation	BP	1	ACSL4,NEDD4,SLC29A1,B3GNT2,PRMT1,STMN1,HOXC10,IQGAP1,RAB35,BEND6,ASPM,ENSCAFG00000010224,ARHGEF2	down_ACOR_VSMC
GO:0006396	1	0.00018	13	368	RNA processing	BP	1	IWS1,QKI,PPP3CA,TUT7,SCAF11,RIOK3,TRMT9B,PAN3,PRPF39,U2SURP,WTAP,RBBP6,IVNS1ABP	up_VCAV_EC
GO:0007049	1	0.00035	12	560	cell cycle	BP	1	NOTCH2,SNX18,KANK2,NABP2,ANXA11,POLDIP2,ZFP36L1,LSM10,MAPRE3,EIF4EBP1,BRSK1,CDK14	down_VCAV_EC
GO:0006325	1	0.00036	9	234	chromatin organization	BP	1	PCGF5,PRKAA2,ATRX,TSPYL5,SMARCD3,CHD7,SHPRH,PHF20,MAP3K7	up_ACOR_VSMC
GO:0006412	1	0.00058	9	245	translation	BP	1	EIF4A2,TARSL2,FAM129A,DAPK1,RBM4B,APP,UBA52,CTIF,NGRN	up_ACOR_VSMC
GO:0043043	1	0.0005	9	247	peptide biosynthetic process	BP	1	EIF4A2,TARSL2,FAM129A,DAPK1,RBM4B,APP,UBA52,CTIF,NGRN	up_ACOR_VSMC
GO:0006518	1	0.00099	9	290	peptide metabolic process	BP	1	QKI,TARSL2,MTOR,ENC1,SECISBP2L,NCK1,DPH5,MRRF,CNOT7	up_VCAV_EC
GO:0048666	1	0.0003	8	258	neuron development	BP	1	NEDD4,SLC29A1,B3GNT2,PRMT1,STMN1,IQGAP1,RAB35,ENSCAFG00000010224	down_ACOR_VSMC
GO:0022613	1	0.00128	8	208	ribonucleoprotein complex biogenesis	BP	1	EXOSC7,RCL1,LIMD1,EIF3G,MRPL10,EIF3K,EIF3L,EIF3D	up_VSAP_EC
GO:0006281	1	0.0006	7	208	DNA repair	BP	1	AXIN2,DDB2,TNKS1BP1,NEIL2,NPAS2,CDK9,AP5Z1	up_VSAP_EC
GO:0007017	1	4.9E-06	7	273	microtubule-based process	BP	1	FAM107A,CEP85,ABL1,FBXW5,KIF27,TTL,CEP19	up_VSAP_EC
GO:0006396	1	2E-10	6	368	RNA processing	BP	1	INTS9,BMP4,CCNT1,APP,TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0016071	1	4.8E-06	6	248	mRNA metabolic process	BP	1	PNRC1,DCP1B,CCNT1,APP,CNOT4,CTIF	up_ACOR_VSMC
GO:0034660	1	9.4E-05	6	211	ncRNA metabolic process	BP	1	INTS9,TARSL2,ELL2,GTF3C1,TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0000226	1	0.00039	6	197	microtubule cytoskeleton organization	BP	1	FAM107A,CEP85,ABL1,FBXW5,TTL,CEP19	up_VSAP_EC
GO:0007507	1	0.00058	5	194	heart development	BP	1	GREM1,SMG9,ADAMTS6,GLI1,JMJD6	down_ACOR_VSMC
GO:0006259	1	0.00033	5	354	DNA metabolic process	BP	1	NABP2,TMEM161A,PARK7,FBH1,GREM1	down_VCAV_EC
GO:0006396	1	0.00014	5	368	RNA processing	BP	1	LARP6,ZFP36L1,RPL27,RBM38,MRPS11	down_VCAV_EC
GO:0048285	1	0.001	5	166	organelle fission	BP	1	CEP85,DDHD1,FBXW5,MTFR1L,CDC26	up_VSAP_EC
GO:0051276	1	1.3E-05	4	398	chromosome organization	BP	1	NABP2,HR,PRMT6,CABIN1	down_VCAV_EC
GO:0006397	1	0.0002	4	168	mRNA processing	BP	1	ZFP36L1,NUP98,CDK9,PQBP1	up_VSAP_EC
GO:0008380	1	0.00081	4	149	RNA splicing	BP	1	PIK3R1,NUP98,MAPKBP1,PQBP1	up_VSAP_EC
GO:0045664	1	0.00126	3	144	regulation of neuron differentiation	BP	1	BEND6,ASPM,ARHGEF2	down_ACOR_VSMC
GO:0048667	1	0.00142	3	140	cell morphogenesis involved in neuron	BP	1	SLC29A1,B3GNT2,STMN1	down_ACOR_VSMC
GO:0016071	1	0.00133	3	248	mRNA metabolic process	BP	1	SAMD4B,ZFP36L1,PYM1	down_VCAV_EC

GO:0007059	1	0.00101	3	127	chromosome segregation	BP	1	ATRX,DMC1,SUN1	up_ACOR_VSMC
GO:0034470	1	0.00017	3	154	ncRNA processing	BP	1	INTS9,TRMT9B,OSGEPL1	up_ACOR_VSMC
GO:0034470	1	0.00139	3	154	ncRNA processing	BP	1	TUT7,RIOK3,TRMT9B	up_VCAV_EC
GO:0000280	1	0.00035	3	145	nuclear division	BP	1	CEP85,FBXW5,CDC26	up_VSAP_EC
GO:0042254	1	0.00113	3	128	ribosome biogenesis	BP	1	EXOSC7,RCL1,MRPL10	up_VSAP_EC
GO:0034660	1	0.00133	2	211	ncRNA metabolic process	BP	1	RPL27,MRPS11	down_VCAV_EC
GO:0006397	1	6E-06	2	168	mRNA processing	BP	1	CCNT1,APP	up_ACOR_VSMC
GO:0022613	1	2.1E-07	2	208	ribonucleoprotein complex biogenesis	BP	1	PRKAA2,ATXN2	up_ACOR_VSMC
GO:0022618	1	0.00117	2	111	ribonucleoprotein complex assembly	BP	1	PRKAA2,ATXN2	up_ACOR_VSMC
GO:0033044	1	0.00017	2	127	regulation of chromosome organization	BP	1	ATRX,HMBOX1	up_ACOR_VSMC
GO:0071826	1	0.00068	2	117	ribonucleoprotein complex subunit	BP	1	PRKAA2,ATXN2	up_ACOR_VSMC
GO:0000375	1	0.00045	2	120	RNA splicing, via transesterification	BP	1	NUP98,PQBP1	up_VSAP_EC
GO:0000377	1	0.00049	2	119	RNA splicing, via transesterification reactions with bulged	BP	1	NUP98,PQBP1	up_VSAP_EC
GO:0000398	1	0.00049	2	119	mRNA splicing, via spliceosome	BP	1	NUP98,PQBP1	up_VSAP_EC
GO:0016072	1	0.00245	2	102	rRNA metabolic process	BP	1	EXOSC7,RCL1	up_VSAP_EC
GO:0007268	1	0.00011	1	130	chemical synaptic transmission	BP	1	CDC20	down_ACOR_VSMC
GO:0050804	1	0.00386	1	87	modulation of chemical synaptic transmission	BP	1	CDC20	down_ACOR_VSMC
GO:0098916	1	0.00011	1	130	anterograde trans-synaptic signaling	BP	1	CDC20	down_ACOR_VSMC
GO:0099177	1	0.00386	1	87	regulation of trans-synaptic signaling	BP	1	CDC20	down_ACOR_VSMC
GO:0099536	1	8.8E-05	1	133	synaptic signaling	BP	1	CDC20	down_ACOR_VSMC
GO:0099537	1	0.0001	1	131	trans-synaptic signaling	BP	1	CDC20	down_ACOR_VSMC
GO:0006397	1	0.00176	1	168	mRNA processing	BP	1	ZFP36L1	down_VCAV_EC
GO:0008380	1	0.00375	1	149	RNA splicing	BP	1	RBM38	down_VCAV_EC
GO:0006396	1	0.00047	1	368	RNA processing	BP	1	RBM38	up_ACOR_EC
GO:0000070	1	0.00412	1	75	mitotic sister chromatid segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0000819	1	0.00122	1	87	sister chromatid segregation	BP	1	ATRX	up_ACOR_VSMC
GO:0016072	1	0.00038	1	102	rRNA metabolic process	BP	1	GTF3C1	up_ACOR_VSMC
GO:0051276	1	0.00062	1	398	chromosome organization	BP	1	AXIN2	up_AFEM_EC
GO:0006974	1	0.00269	1	333	cellular response to DNA damage stimulus	BP	1	AXIN2	up_AFEM_EC
GO:0042254	1	0.00044	1	128	ribosome biogenesis	BP	1	RIOK3	up_VCAV_EC
GO:1903362	1	0.00193	1	100	regulation of cellular protein catabolic process	BP	1	TNFAIP3	up_VCAV_EC
GO:0006457	1	0.00321	1	77	protein folding	BP	1	ZFYVE21	up_VSAP_EC
GO:0007018	1	0.00316	1	82	microtubule-based movement	BP	1	KIF27	up_VSAP_EC